



## wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 09:58 PM UTC

PDB ID : 5LZZ / pdb\_00005lzz  
EMDB ID : EMD-4137  
Title : Structure of the mammalian rescue complex with Pelota and Hbs1l (combined)  
Authors : Shao, S.; Murray, J.; Brown, A.; Taunton, J.; Ramakrishnan, V.; Hegde, R.S.  
Deposited on : 2016-10-02  
Resolution : 3.47 Å(reported)

This is a wwPDB 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:

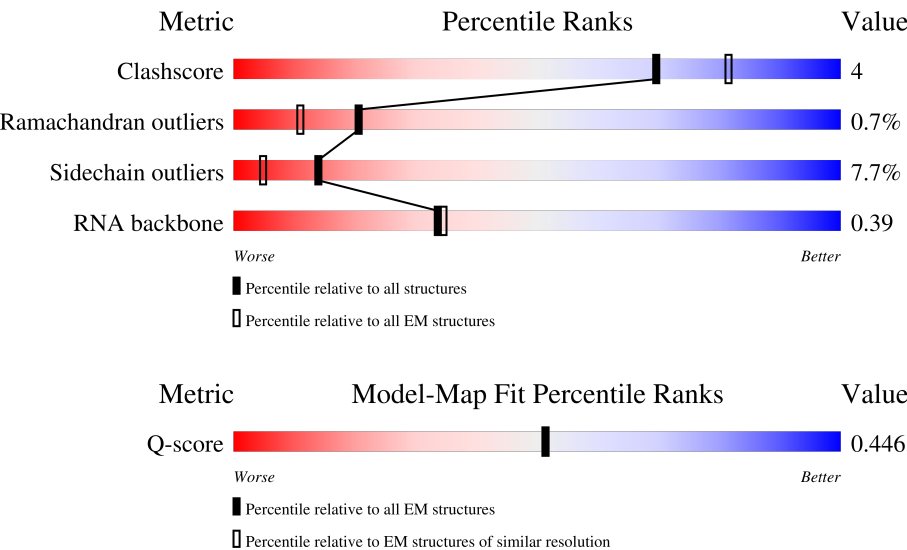
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (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 i

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

The reported resolution of this entry is 3.47 Å.

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



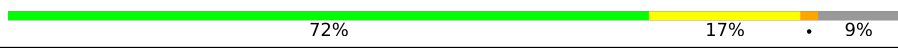
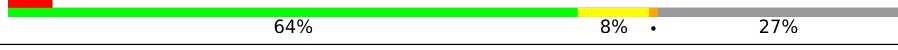
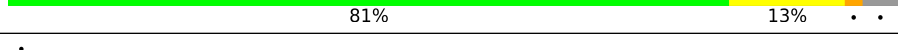
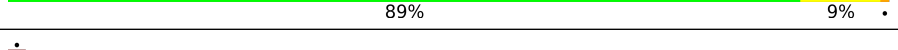
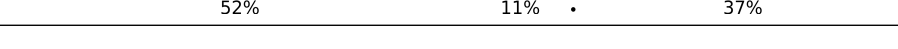
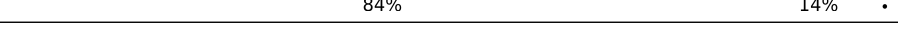
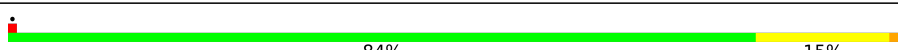
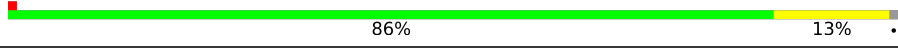
| Metric                | Whole archive<br>(#Entries) | EM structures<br>(#Entries) | Similar EM resolution<br>(#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|-----------------------------|----------------------------------------------------------|
| Clashscore            | 229148                      | 23984                       | -                                                        |
| Ramachandran outliers | 224038                      | 23583                       | -                                                        |
| Sidechain outliers    | 223484                      | 23102                       | -                                                        |
| RNA backbone          | 8273                        | 3508                        | -                                                        |
| Q-score               | -                           | 25397                       | 13733 ( 2.97 - 3.97 )                                    |

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   | A     | 257    | <div><div></div><div>76%19% . .</div></div>   |
| 2   | B     | 403    | <div><div></div><div>78%18% ..</div></div>    |
| 3   | C     | 425    | <div><div></div><div>70%13% . 15%</div></div> |

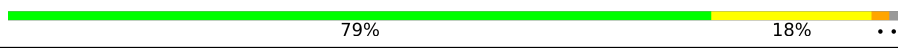
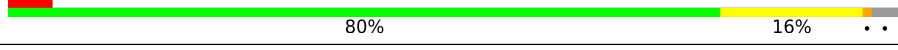
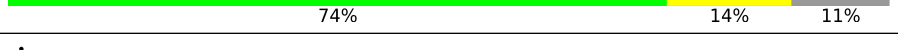
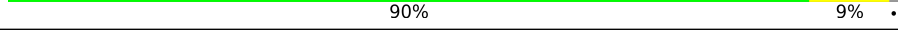
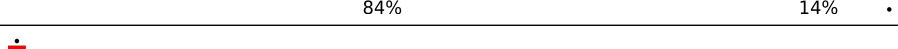
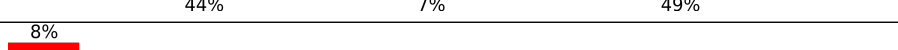
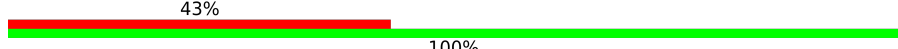
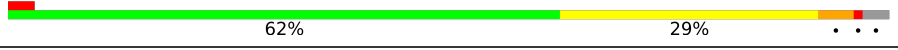
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| Mol | Chain | Length | Quality of chain                                                                     |
|-----|-------|--------|--------------------------------------------------------------------------------------|
| 4   | D     | 297    |    |
| 5   | E     | 291    |    |
| 6   | F     | 247    |    |
| 7   | G     | 319    |    |
| 8   | H     | 192    |    |
| 9   | I     | 214    |    |
| 10  | J     | 178    |    |
| 11  | L     | 211    |    |
| 12  | M     | 218    |    |
| 13  | N     | 204    |    |
| 14  | O     | 203    |    |
| 15  | P     | 184    |  |
| 16  | Q     | 188    |  |
| 17  | R     | 196    |  |
| 18  | S     | 176    |  |
| 19  | T     | 160    |  |
| 20  | U     | 128    |  |
| 21  | V     | 140    |  |
| 22  | W     | 157    |  |
| 23  | X     | 156    |  |
| 24  | Y     | 145    |  |
| 25  | Z     | 136    |  |
| 26  | a     | 148    |  |
| 27  | b     | 245    |  |
| 28  | c     | 115    |  |

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| Mol | Chain | Length | Quality of chain                                                                     |
|-----|-------|--------|--------------------------------------------------------------------------------------|
| 29  | d     | 125    |    |
| 30  | e     | 135    |    |
| 31  | f     | 110    |    |
| 32  | g     | 117    |    |
| 33  | h     | 123    |    |
| 34  | i     | 105    |    |
| 35  | j     | 97     |    |
| 36  | k     | 70     |    |
| 37  | l     | 51     |    |
| 38  | m     | 102    |    |
| 39  | n     | 25     |    |
| 40  | o     | 106    |  |
| 41  | p     | 92     |  |
| 42  | r     | 137    |  |
| 43  | s     | 318    |  |
| 44  | t     | 165    |  |
| 45  | 1     | 7      |  |
| 46  | 2     | 76     |  |
| 47  | 3     | 75     |  |
| 48  | 5     | 3543   |  |
| 49  | 7     | 120    |  |
| 50  | 8     | 156    |  |
| 51  | 9     | 1869   |  |
| 52  | AA    | 295    |  |
| 53  | BB    | 264    |  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 54  | CC    | 293    |                  |
| 55  | DD    | 243    |                  |
| 56  | EE    | 263    |                  |
| 57  | FF    | 204    |                  |
| 58  | GG    | 249    |                  |
| 59  | HH    | 194    |                  |
| 60  | II    | 208    |                  |
| 61  | JJ    | 194    |                  |
| 62  | KK    | 165    |                  |
| 63  | LL    | 158    |                  |
| 64  | MM    | 132    |                  |
| 65  | NN    | 151    |                  |
| 66  | OO    | 168    |                  |
| 67  | PP    | 145    |                  |
| 68  | QQ    | 146    |                  |
| 69  | RR    | 135    |                  |
| 70  | SS    | 152    |                  |
| 71  | TT    | 145    |                  |
| 72  | UU    | 119    |                  |
| 73  | VV    | 83     |                  |
| 74  | WW    | 130    |                  |
| 75  | XX    | 143    |                  |
| 76  | YY    | 130    |                  |
| 77  | ZZ    | 125    |                  |
| 78  | aa    | 115    |                  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 79  | bb    | 84     |                  |
| 80  | cc    | 69     |                  |
| 81  | dd    | 56     |                  |
| 82  | ee    | 133    |                  |
| 83  | ff    | 156    |                  |
| 84  | gg    | 317    |                  |
| 85  | hh    | 8      |                  |
| 86  | ii    | 403    |                  |
| 87  | jj    | 710    |                  |

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 |
|-----|------|-------|-----|-----------|----------|---------|------------------|
| 89  | ZN   | ff    | 200 | -         | -        | X       | -                |

## 2 Entry composition

There are 90 unique types of molecules in this entry. The entry contains 222005 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called uL2.

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

- Molecule 2 is a protein called uL3.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 3 is a protein called uL4.

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

- Molecule 6 is a protein called uL30.

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

There are 4 discrepancies between the modelled and reference sequences:

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 8 is a protein called uL6.

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

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

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

- Molecule 10 is a protein called uL5.

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

- Molecule 11 is a protein called eL13.

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

- Molecule 12 is a protein called eL14.

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

- Molecule 13 is a protein called Ribosomal protein L15.

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

- Molecule 14 is a protein called uL13.

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

- Molecule 15 is a protein called uL22.

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

- Molecule 16 is a protein called eL18.

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

- Molecule 17 is a protein called eL19.

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

- Molecule 18 is a protein called eL20.

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

- Molecule 19 is a protein called eL21.

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

- Molecule 20 is a protein called eL22.

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

- Molecule 21 is a protein called uL14.

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

- Molecule 22 is a protein called eL24.

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

- Molecule 23 is a protein called uL23.

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

- Molecule 24 is a protein called uL24.

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

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

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

- Molecule 26 is a protein called uL15.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 27 is a protein called eL29.

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

- Molecule 28 is a protein called eL30.

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

- Molecule 29 is a protein called eL31.

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

- Molecule 30 is a protein called eL32.

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

- Molecule 31 is a protein called eL33.

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

- Molecule 32 is a protein called eL34.

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

- Molecule 33 is a protein called uL29.

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

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

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

- Molecule 35 is a protein called Ribosomal protein L37.

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

- Molecule 36 is a protein called eL38.

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

- Molecule 37 is a protein called eL39.

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

- Molecule 38 is a protein called eL40.

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

- Molecule 39 is a protein called eL41.

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

- Molecule 40 is a protein called eL42.

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

- Molecule 41 is a protein called eL43.

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

- Molecule 42 is a protein called eL28.

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

- Molecule 43 is a protein called uL10.

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

- Molecule 44 is a protein called uL11.

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

- Molecule 45 is a protein called Nascent chain.

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 52 is a protein called uS2.

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

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

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

- Molecule 54 is a protein called uS5.

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

- Molecule 55 is a protein called uS3.

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

- Molecule 56 is a protein called eS4.

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

- Molecule 57 is a protein called uS7.

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

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

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

- Molecule 59 is a protein called eS7.

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

- Molecule 62 is a protein called eS10.

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

- Molecule 63 is a protein called uS17.

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

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

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

- Molecule 65 is a protein called uS15.

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

- Molecule 66 is a protein called uS11.

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

- Molecule 67 is a protein called uS19.

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

- Molecule 68 is a protein called uS9.

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

- Molecule 69 is a protein called eS17.

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

- Molecule 70 is a protein called uS13.

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

- Molecule 71 is a protein called eS19.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 72 is a protein called uS10.

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

- Molecule 73 is a protein called eS21.

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

- Molecule 74 is a protein called uS8.

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

- Molecule 75 is a protein called uS12.

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

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

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

- Molecule 77 is a protein called eS25.

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

- Molecule 78 is a protein called eS26.

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

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

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

- Molecule 80 is a protein called eS28.

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

- Molecule 81 is a protein called uS14.

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

- Molecule 82 is a protein called eS30.

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

- Molecule 83 is a protein called eS31.

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

- Molecule 84 is a protein called RACK1.

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

- Molecule 85 is a RNA chain called mRNA.

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

- Molecule 86 is a protein called Protein pelota homolog.

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

There are 19 discrepancies between the modelled and reference sequences:

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

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

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

There are 26 discrepancies between the modelled and reference sequences:

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

- Molecule 88 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms           | AltConf |
|-----|-------|----------|-----------------|---------|
| 88  | B     | 1        | Total Mg<br>1 1 | 0       |
| 88  | I     | 1        | Total Mg<br>1 1 | 0       |
| 88  | L     | 1        | Total Mg<br>1 1 | 0       |
| 88  | P     | 1        | Total Mg<br>1 1 | 0       |
| 88  | V     | 1        | Total Mg<br>1 1 | 0       |
| 88  | a     | 1        | Total Mg<br>1 1 | 0       |

*Continued on next page...*

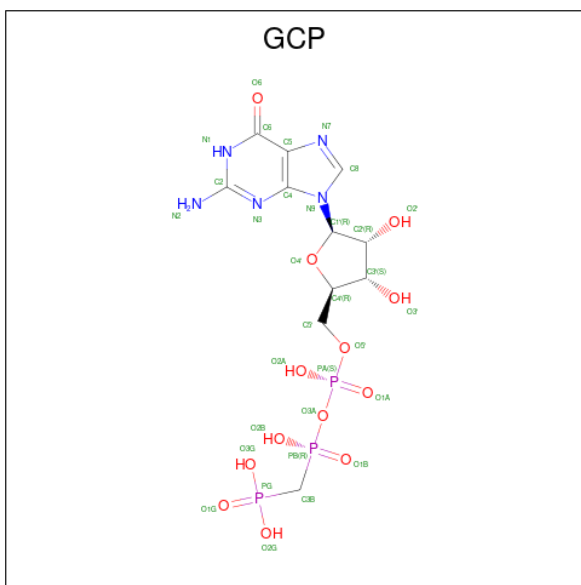
*Continued from previous page...*

| Mol | Chain | Residues | Atoms        |           | AltConf |
|-----|-------|----------|--------------|-----------|---------|
| 88  | e     | 1        | Total<br>1   | Mg<br>1   | 0       |
| 88  | g     | 1        | Total<br>1   | Mg<br>1   | 0       |
| 88  | j     | 1        | Total<br>1   | Mg<br>1   | 0       |
| 88  | 5     | 178      | Total<br>178 | Mg<br>178 | 0       |
| 88  | 7     | 5        | Total<br>5   | Mg<br>5   | 0       |
| 88  | 8     | 5        | Total<br>5   | Mg<br>5   | 0       |
| 88  | 9     | 66       | Total<br>66  | Mg<br>66  | 0       |
| 88  | jj    | 1        | Total<br>1   | Mg<br>1   | 0       |

- Molecule 89 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 90 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: C<sub>11</sub>H<sub>18</sub>N<sub>5</sub>O<sub>13</sub>P<sub>3</sub>).

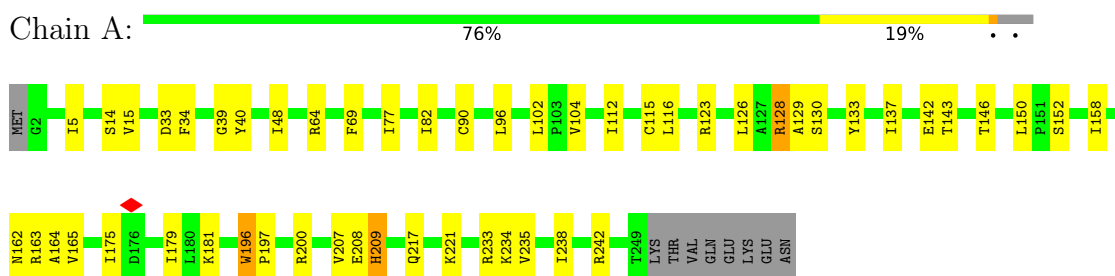


| Mol | Chain | Residues | Atoms |    |   |    |   | AltConf |
|-----|-------|----------|-------|----|---|----|---|---------|
| 90  | jj    | 1        | Total | C  | N | O  | P | 0       |
|     |       |          | 32    | 11 | 5 | 13 | 3 |         |

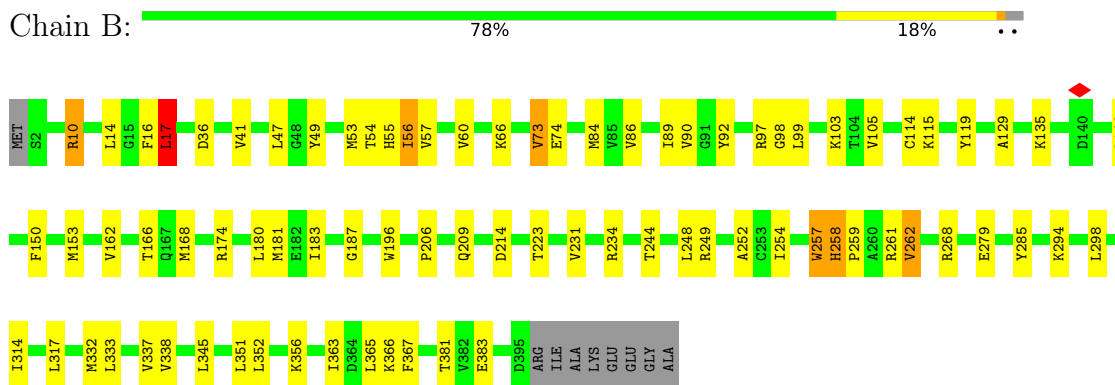
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and 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.

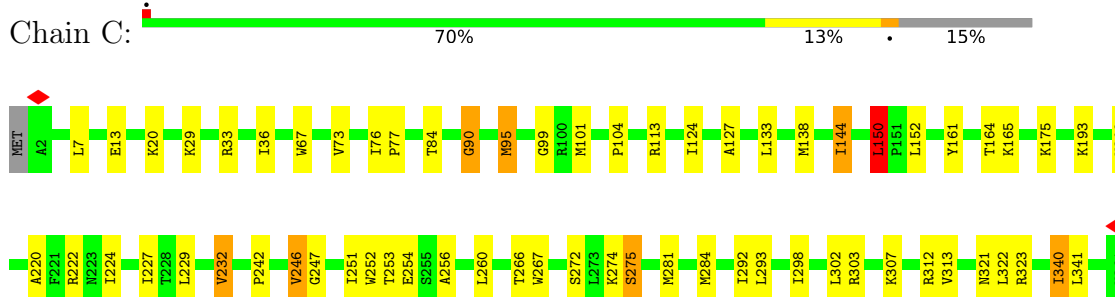
#### • Molecule 1: uL2

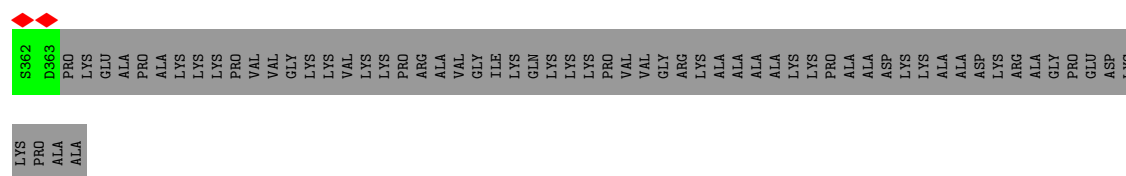


#### • Molecule 2: uL3

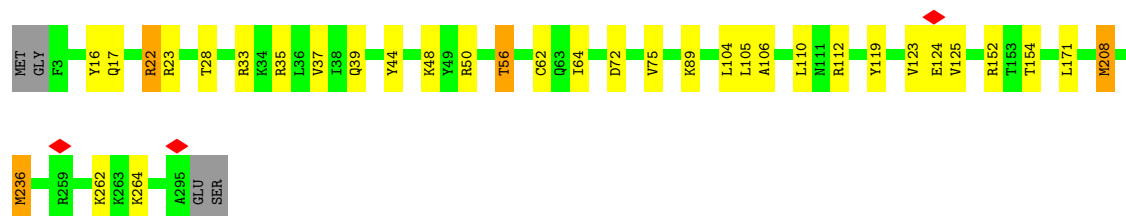
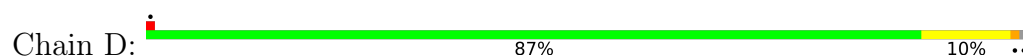


#### • Molecule 3: uL4

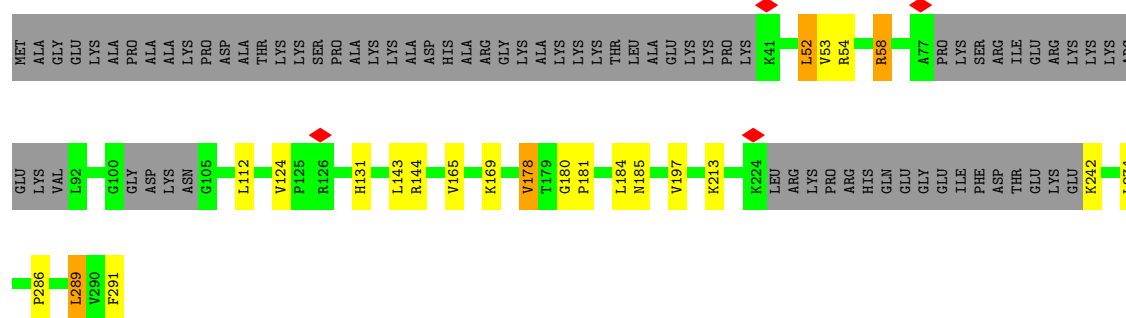




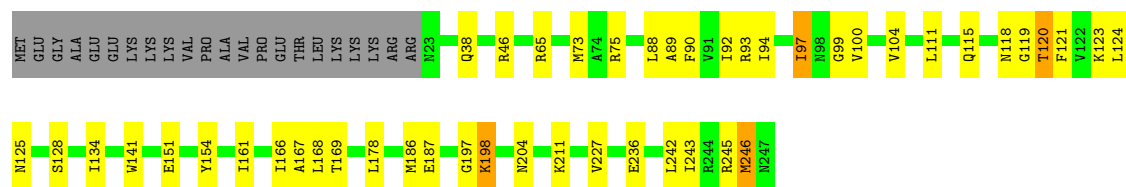
- Molecule 4: 60S ribosomal protein L5



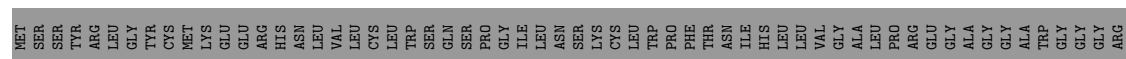
- Molecule 5: 60S ribosomal protein L6

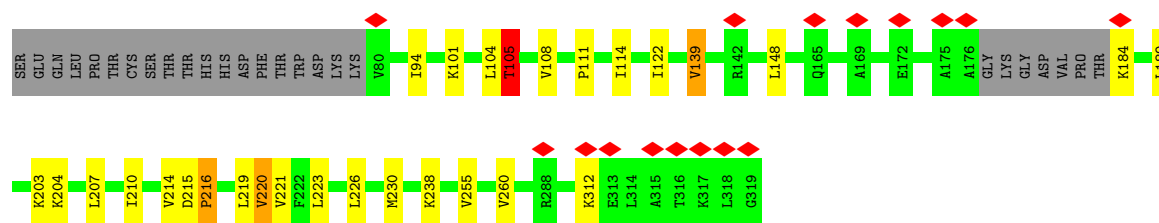


- Molecule 6: uL30

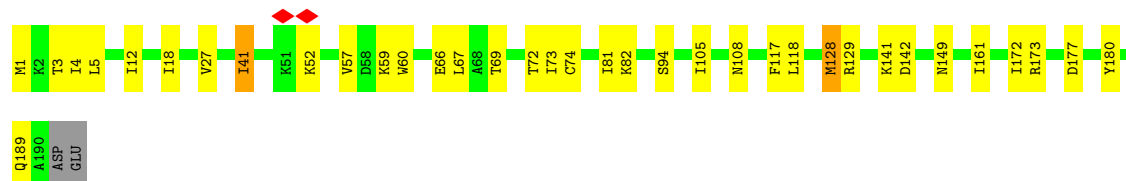
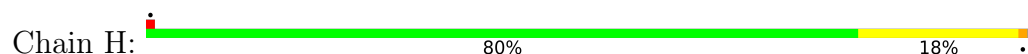


- Molecule 7: 60S ribosomal protein L7a,eL8

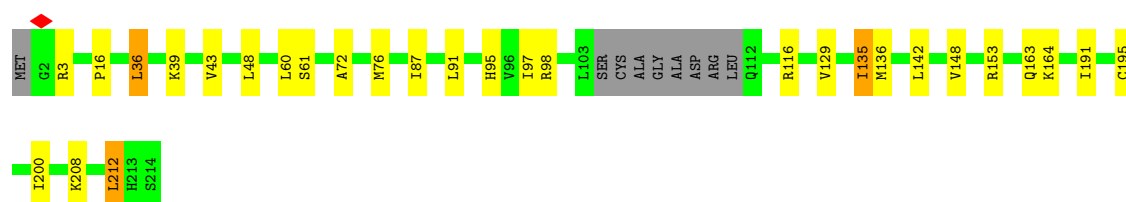
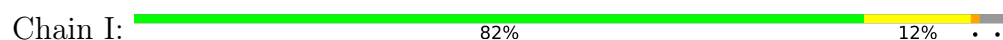




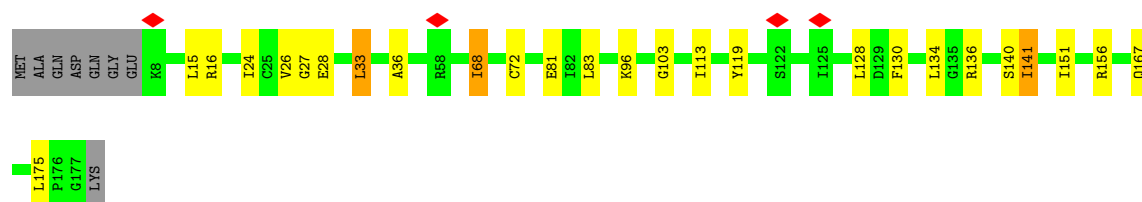
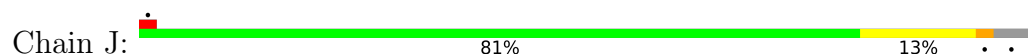
• Molecule 8: uL6



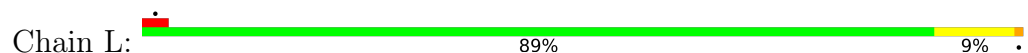
• Molecule 9: Ribosomal protein L10 (Predicted)



• Molecule 10: uL5

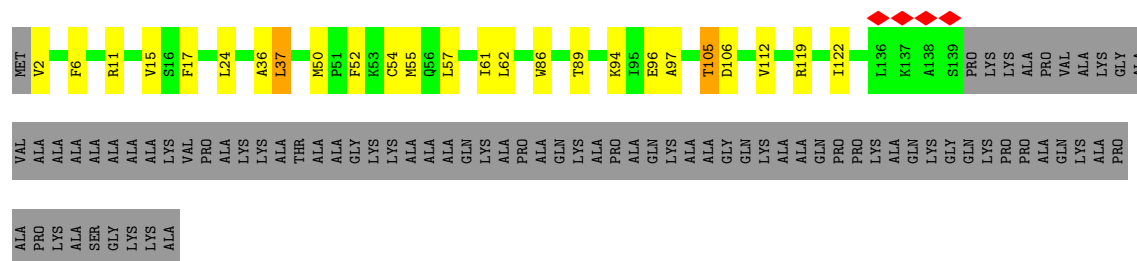


• Molecule 11: eL13



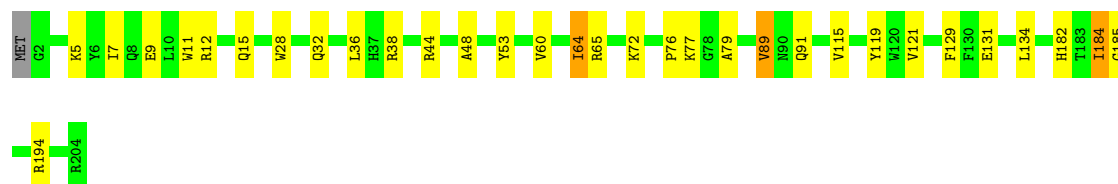
• Molecule 12: eL14





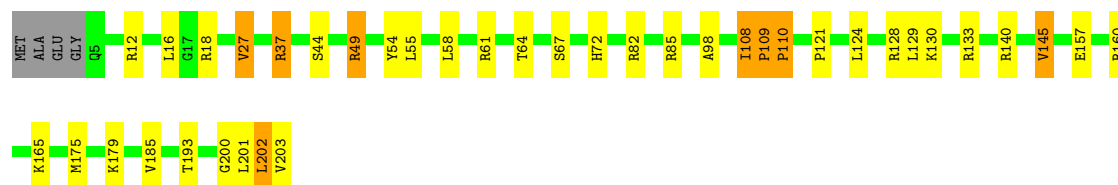
• Molecule 13: Ribosomal protein L15

Chain N: 84% 14% .



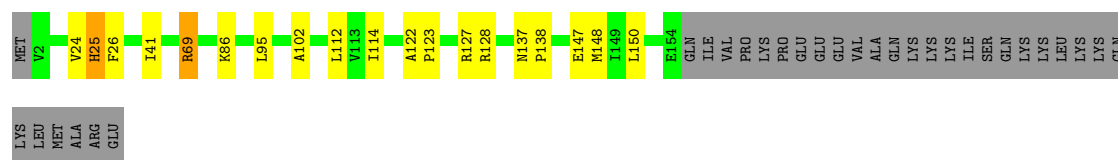
• Molecule 14: uL13

Chain O: 79% 15% . .



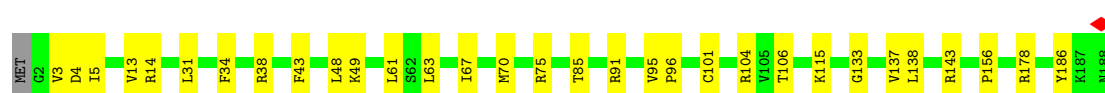
• Molecule 15: uL22

Chain P: 73% 9% . 17%



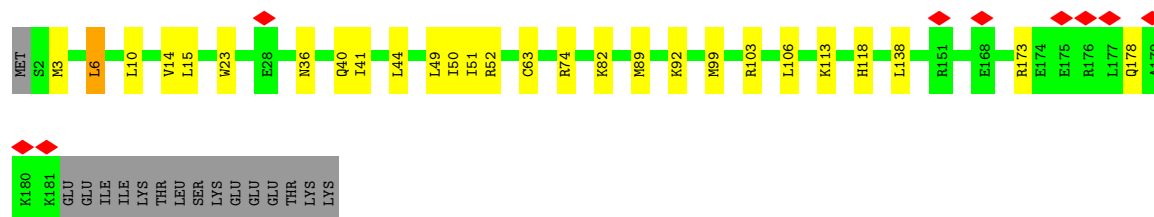
• Molecule 16: eL18

Chain Q: 83% 16% .

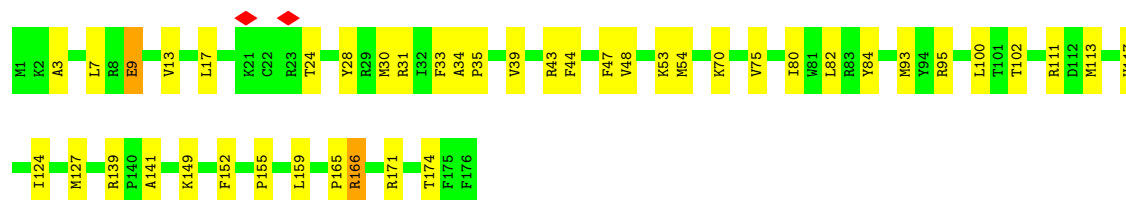
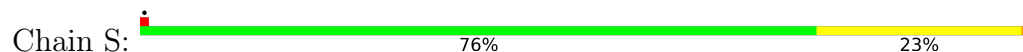


• Molecule 17: eL19

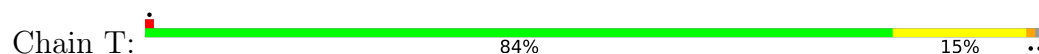
Chain R: 5% 78% 13% . 8%



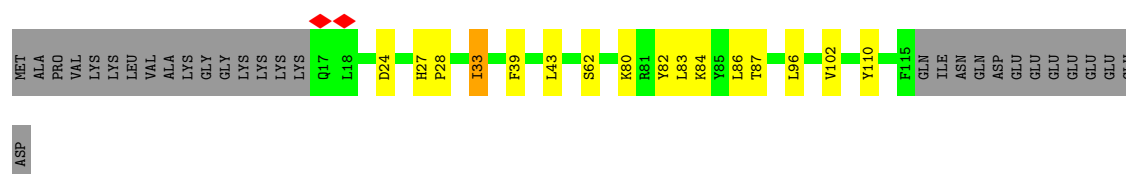
• Molecule 18: eL20



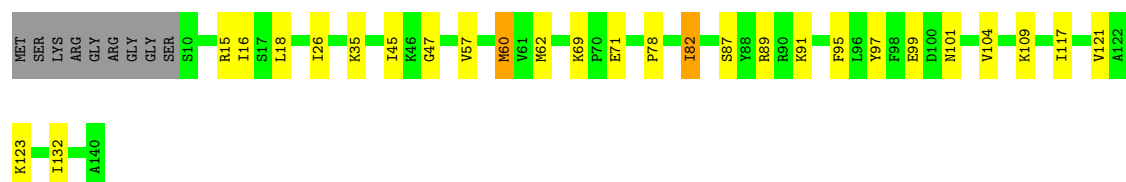
• Molecule 19: eL21



• Molecule 20: eL22



• Molecule 21: uL14



• Molecule 22: eL24



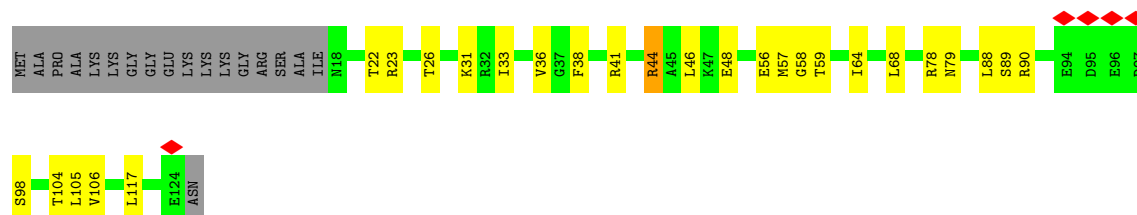


Chain c: 



• Molecule 29: eL31

Chain d: 



• Molecule 30: eL32

Chain e: 



• Molecule 31: eL33

Chain f: 



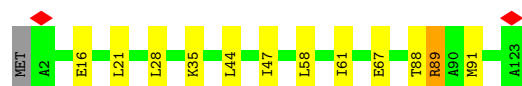
• Molecule 32: eL34

Chain g: 



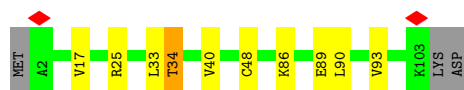
• Molecule 33: uL29

Chain h: 



• Molecule 34: 60S ribosomal protein L36

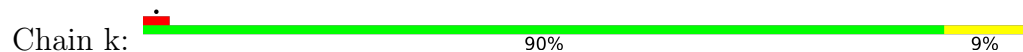
Chain i: 



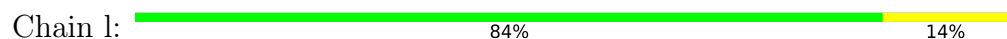
- Molecule 35: Ribosomal protein L37



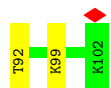
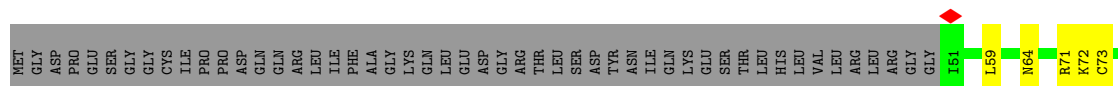
- Molecule 36: eL38



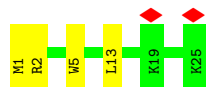
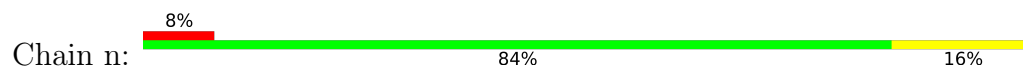
- Molecule 37: eL39



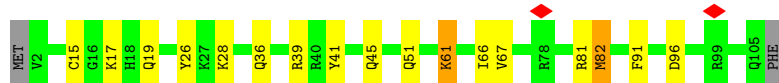
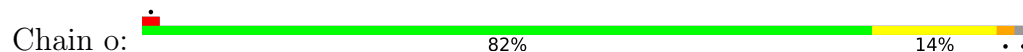
- Molecule 38: eL40



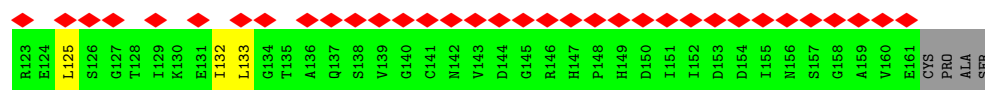
- Molecule 39: eL41



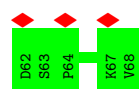
- Molecule 40: eL42



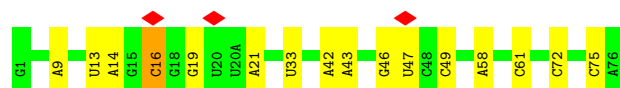
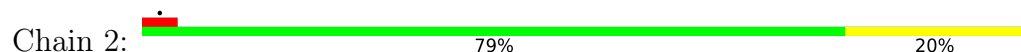
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |      |      |      |      |      |      |      |     |      |      |      |      |      |      |      |      |      |      |      |      |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|
| K61 | L62 | T63 | I64 | Q65 | M66 | R67 | Q68 | A69 | Q70 | I71 | E72 | V73 | V74 |     | A77 | S78 | A79 | L80 | I81 | I82 | K83 | A84 | L85 | K86 | E87 | P88 | P89 | R90 | D91 | R92 | K93 | K94 | Q95 | K96 | N97 | I98 | K99 | H100 | S101 | G102 | M103 | I104 | T105 | F106 | D107 |     | V110 | M111 | I112 | A113 | R114 | Q115 | M116 | R117 | H118 | R119 | S120 | L121 | I122 |
| PR0 | PR0 | LVS | PHE | ASP | PR0 | ASN | E9  | I10 | K11 | V12 | V13 | Y14 | L15 | R16 | C17 | T18 | G19 | G20 | E21 | V22 | G23 | A24 | T25 | S26 | A27 | L28 | A29 | P30 | K31 | I32 | G33 | P34 | L35 | G36 | L37 | S38 | P39 | K40  | K41  | V42  | G43  | D44  | D45  | I46  | K47  | K48 | A49  | T50  | G51  | D52  | W53  | K54  | G55  | L56  | R57  | I58  | T59  | V60  |      |



• Molecule 45: Nascent chain



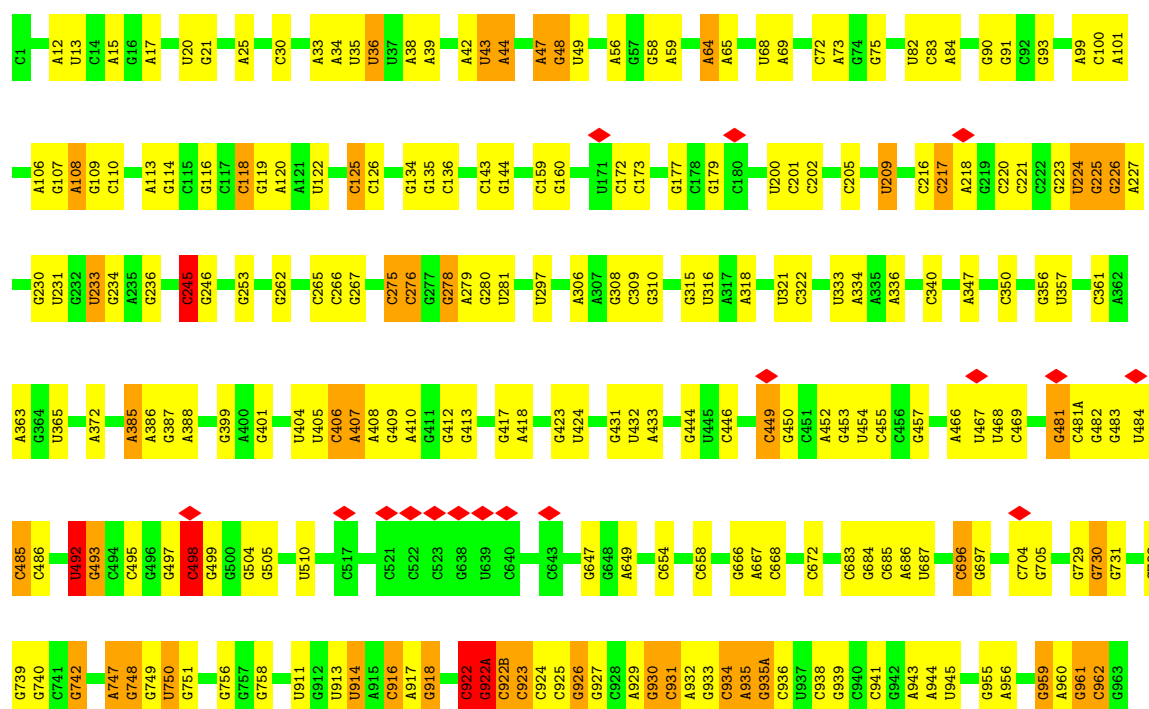
• Molecule 46: P-site tRNA

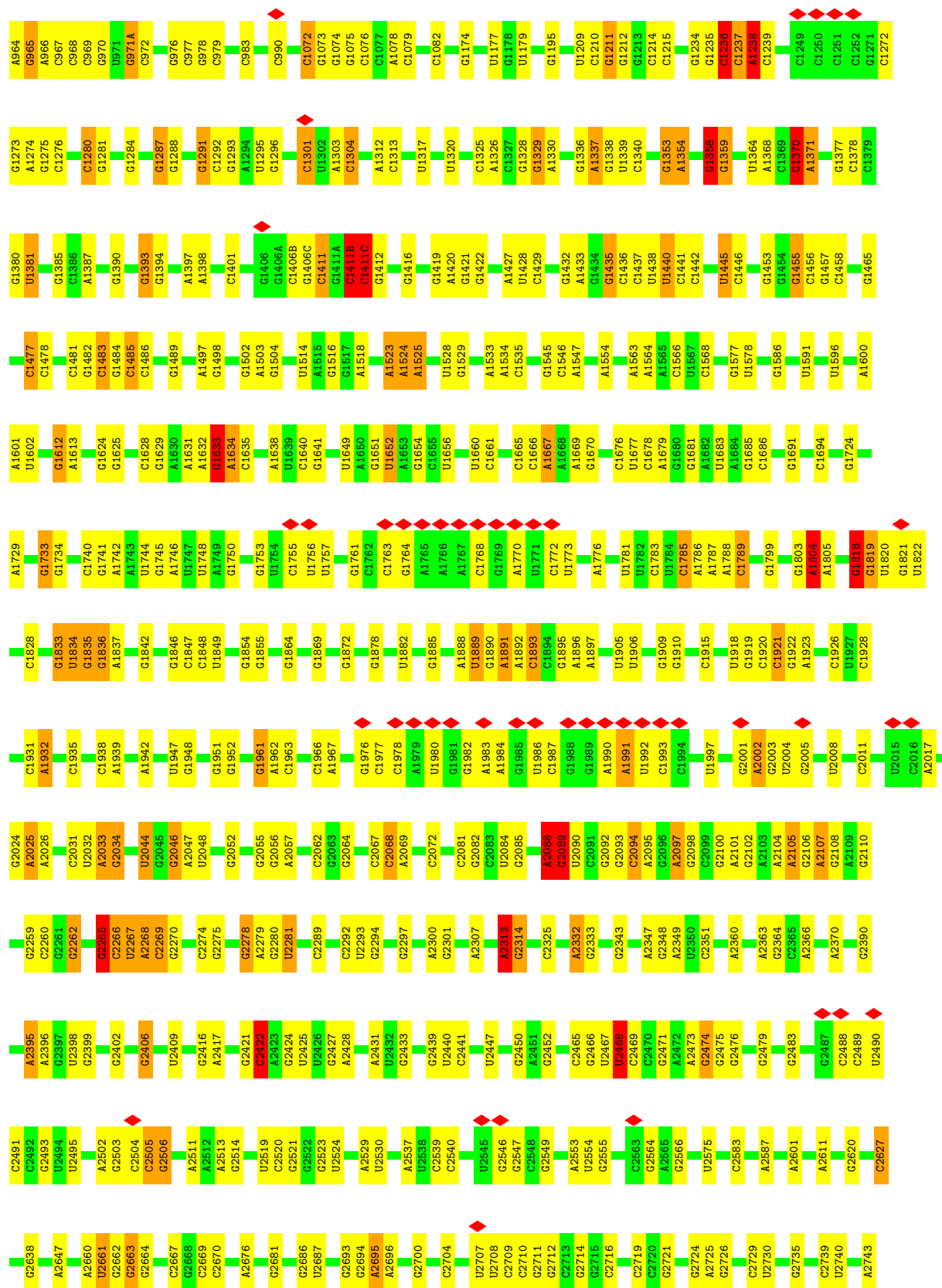


• Molecule 47: E-site tRNA

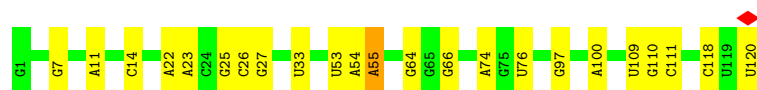


• Molecule 48: 28S ribosomal RNA

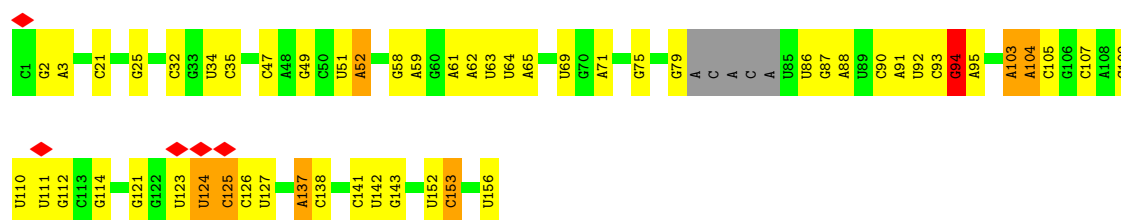




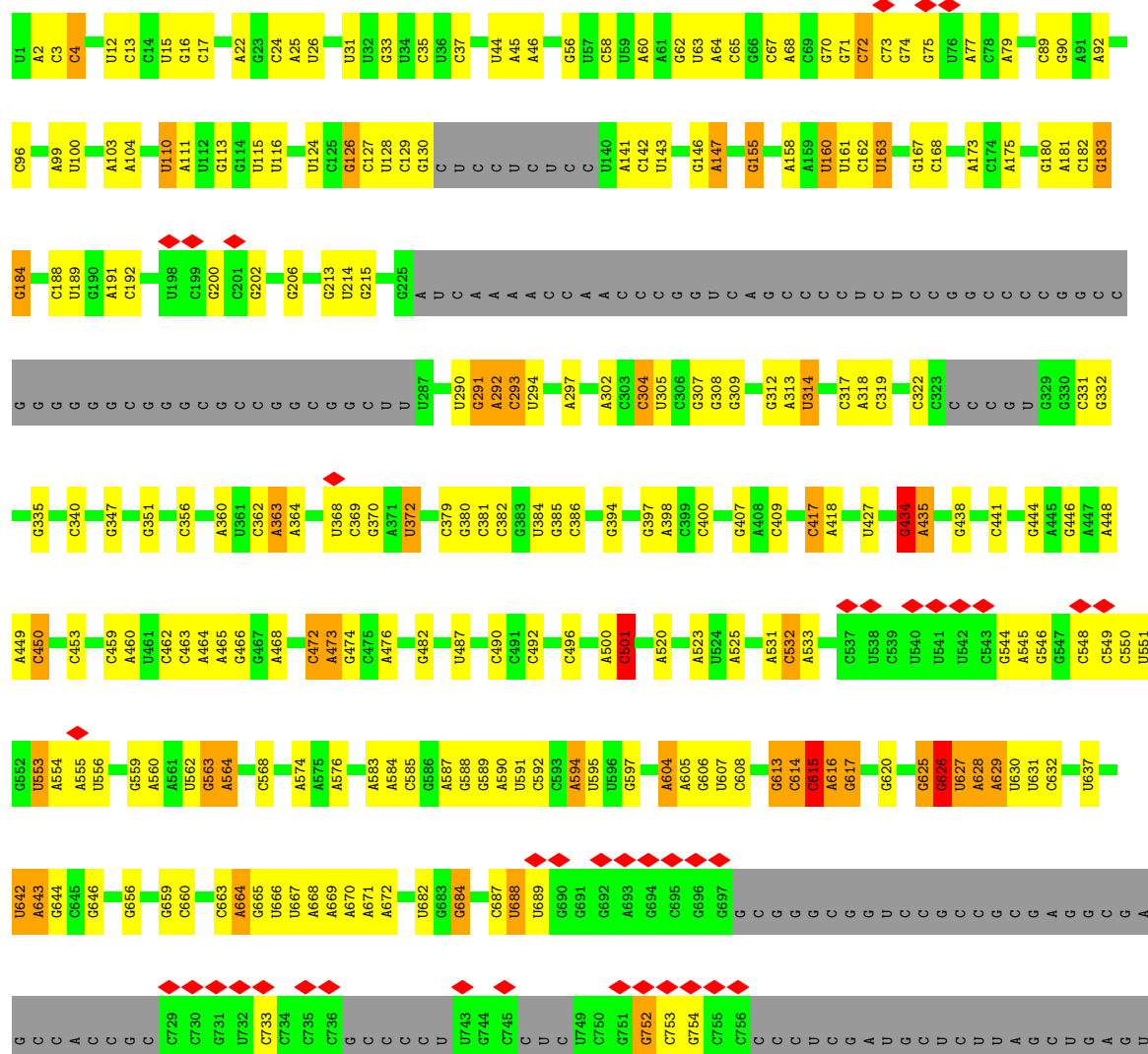


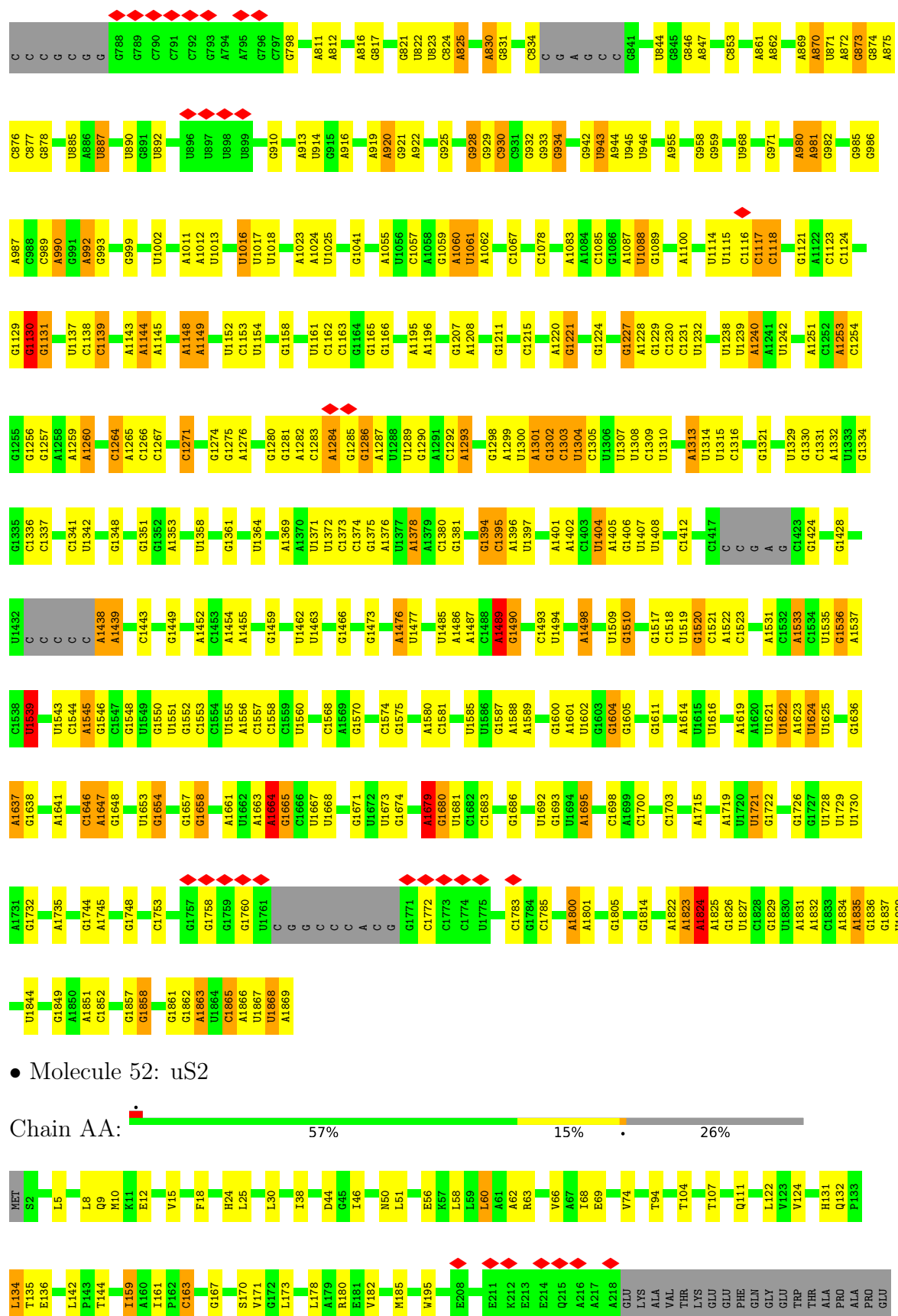


- Molecule 50: 5.8S ribosomal RNA



- Molecule 51: 18S ribosomal RNA







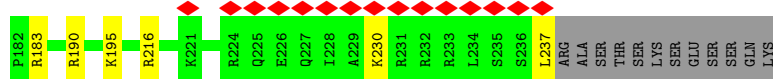
- Molecule 57: uS7

Chain FF:  81% 9% 9%



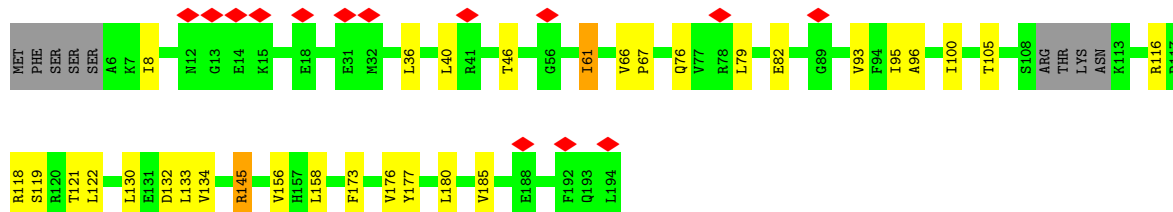
- Molecule 58: 40S ribosomal protein S6

Chain GG:  81% 14% 5%



- Molecule 59: eS7

Chain HH:  79% 15% 5%



- Molecule 60: 40S ribosomal protein S8

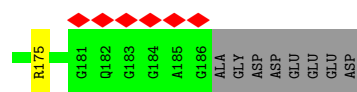
Chain II:  81% 17% 2%



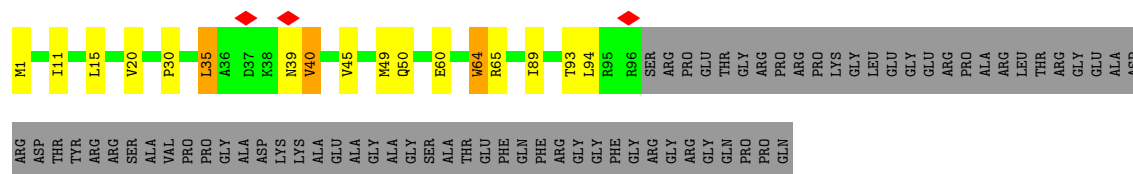
- Molecule 61: Ribosomal protein S9 (Predicted)

Chain JJ:  78% 15% 5%

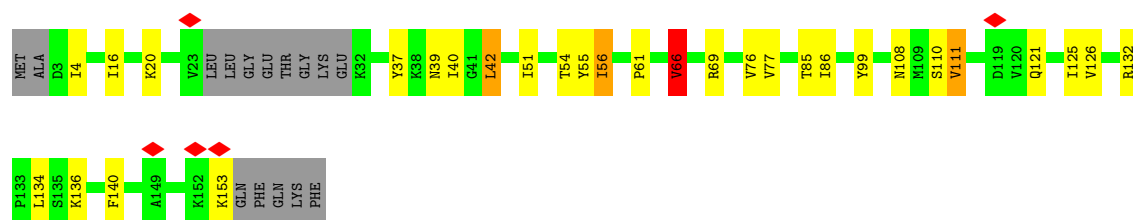




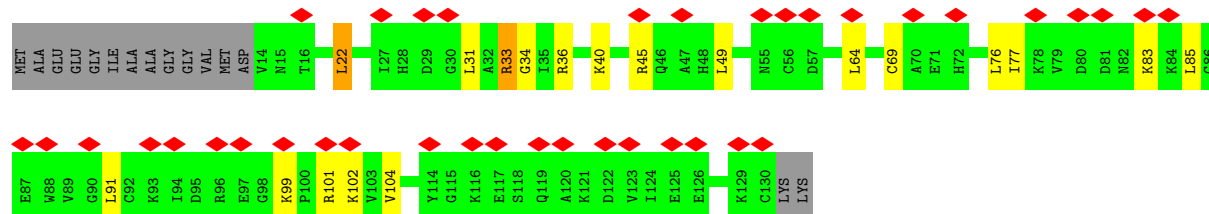
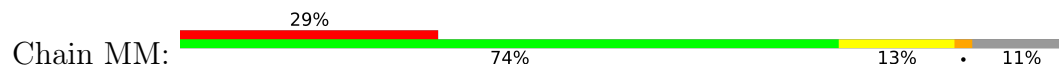
• Molecule 62: eS10



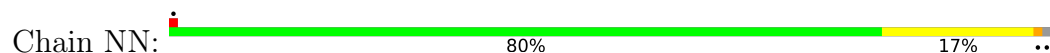
• Molecule 63: uS17



• Molecule 64: 40S ribosomal protein S12



• Molecule 65: uS15

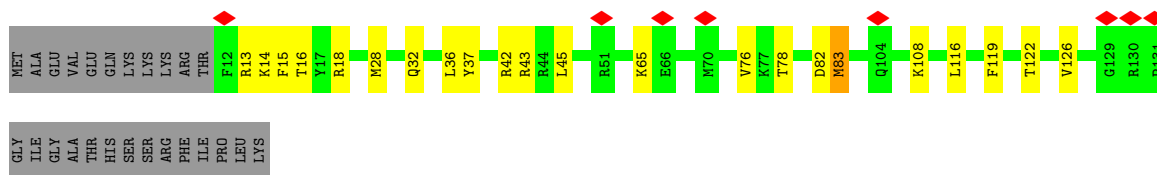


• Molecule 66: uS11

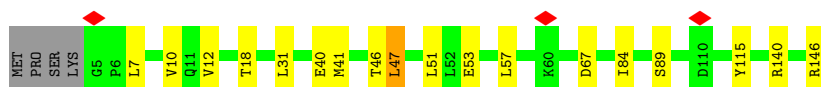
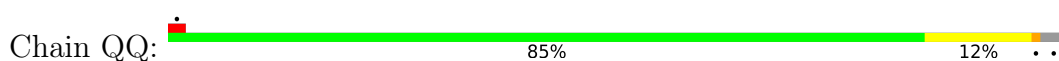




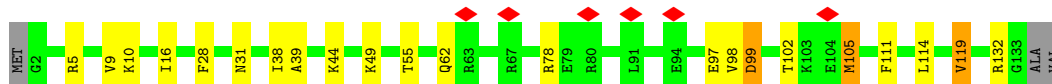
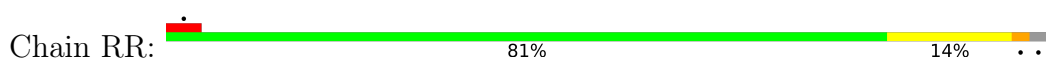
• Molecule 67: uS19



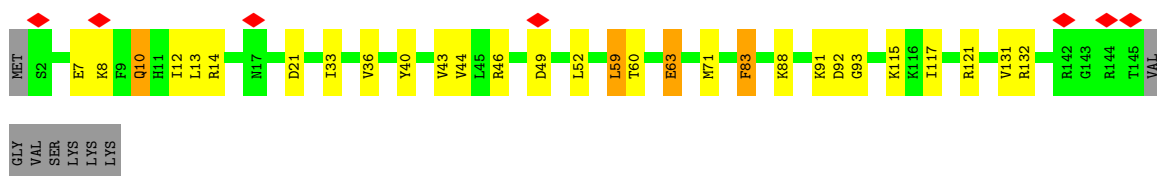
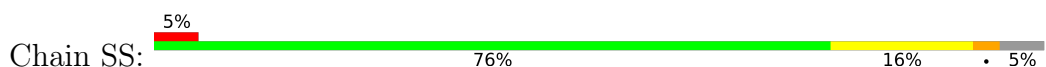
• Molecule 68: uS9



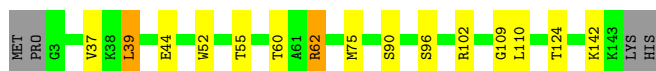
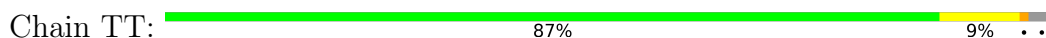
• Molecule 69: eS17



• Molecule 70: uS13

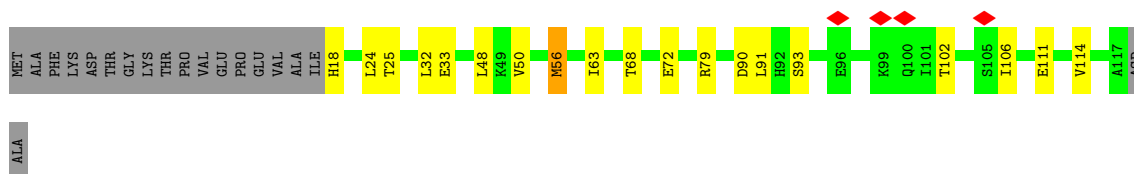


• Molecule 71: eS19



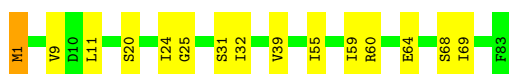
• Molecule 72: uS10





• Molecule 73: eS21

Chain VV: 82% 17%



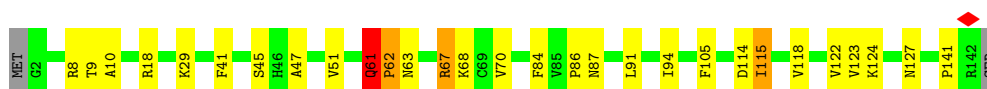
• Molecule 74: uS8

Chain WW: 74% 23%



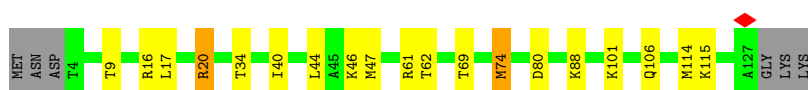
• Molecule 75: uS12

Chain XX: 78% 17%



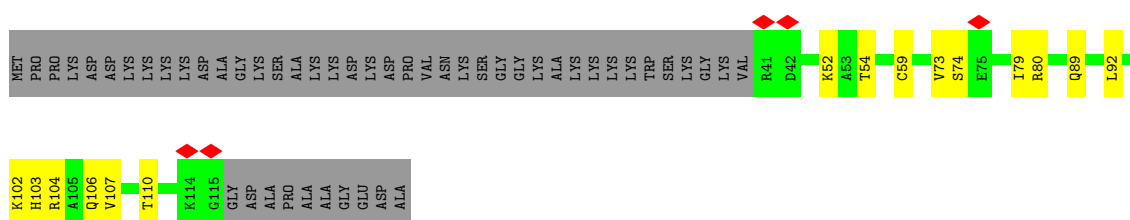
• Molecule 76: 40S ribosomal protein S24

Chain YY: 81% 13% 5%



• Molecule 77: eS25

Chain ZZ: 48% 12% 40%



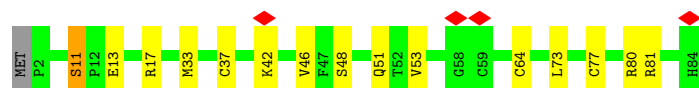
• Molecule 78: eS26

Chain aa: 



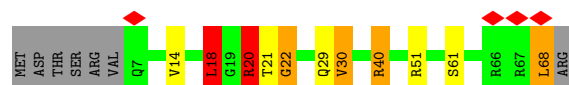
- Molecule 79: 40S ribosomal protein S27

Chain bb: 



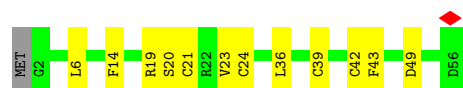
- Molecule 80: eS28

Chain cc: 



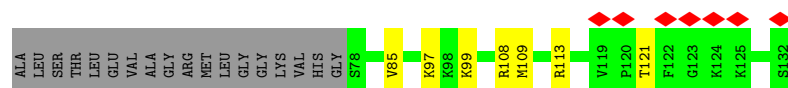
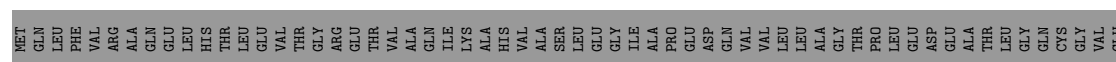
- Molecule 81: uS14

Chain dd: 



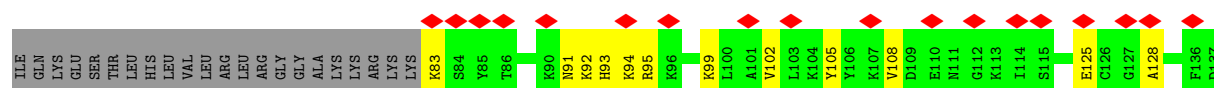
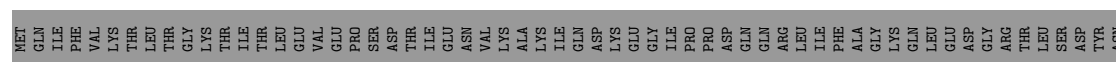
- Molecule 82: eS30

Chain ee: 

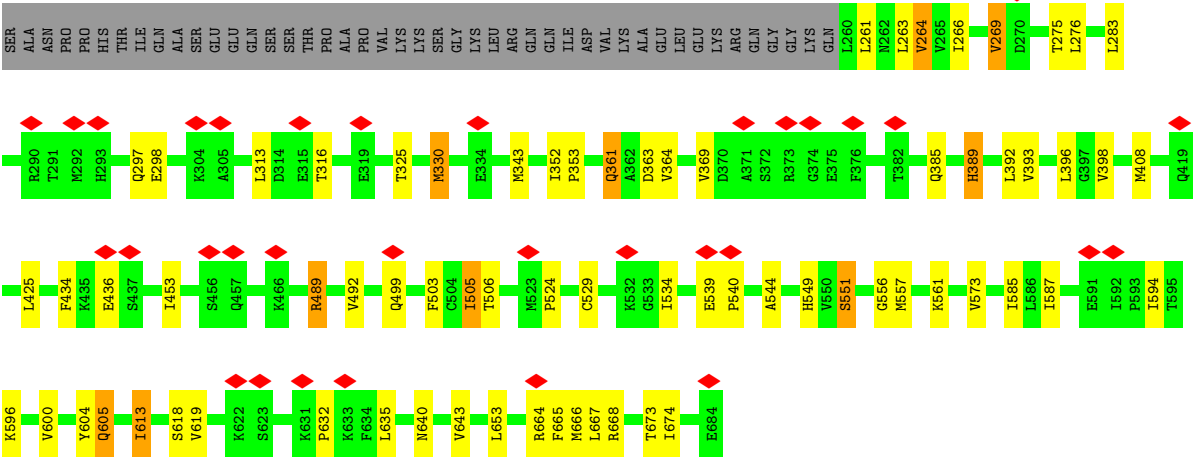


- Molecule 83: eS31

Chain ff: 







## 4 Experimental information

| Property                             | Value                                   | Source    |
|--------------------------------------|-----------------------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE                         | Depositor |
| Imposed symmetry                     | POINT, C1                               | Depositor |
| Number of particles used             | 58773                                   | Depositor |
| Resolution determination method      | FSC 0.143 CUT-OFF                       | Depositor |
| CTF correction method                | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope                           | FEI TITAN KRIOS                         | Depositor |
| Voltage (kV)                         | 300                                     | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 30                                      | Depositor |
| Minimum defocus (nm)                 | Not provided                            |           |
| Maximum defocus (nm)                 | Not provided                            |           |
| Magnification                        | 104478                                  | Depositor |
| Image detector                       | FEI FALCON II (4k x 4k)                 | Depositor |
| Maximum map value                    | 0.747                                   | Depositor |
| Minimum map value                    | -0.536                                  | Depositor |
| Average map value                    | 0.001                                   | Depositor |
| Map value standard deviation         | 0.022                                   | Depositor |
| Recommended contour level            | 0.08                                    | Depositor |
| Map size (Å)                         | 562.8, 562.8, 562.8                     | wwPDB     |
| Map dimensions                       | 420, 420, 420                           | wwPDB     |
| Map angles (°)                       | 90.0, 90.0, 90.0                        | wwPDB     |
| Pixel spacing (Å)                    | 1.3399999, 1.3399999, 1.3399999         | Depositor |

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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   | A     | 0.62         | 0/1936      | 0.91        | 4/2596 (0.2%) |
| 2   | B     | 0.65         | 0/3240      | 0.88        | 2/4339 (0.0%) |
| 3   | C     | 0.63         | 0/2937      | 0.91        | 5/3946 (0.1%) |
| 4   | D     | 0.51         | 0/2437      | 0.85        | 1/3264 (0.0%) |
| 5   | E     | 0.53         | 0/1762      | 0.81        | 0/2362        |
| 6   | F     | 0.72         | 0/1911      | 0.95        | 3/2549 (0.1%) |
| 7   | G     | 0.56         | 0/1910      | 0.87        | 0/2569        |
| 8   | H     | 0.56         | 0/1535      | 0.80        | 0/2063        |
| 9   | I     | 0.56         | 0/1702      | 0.82        | 1/2272 (0.0%) |
| 10  | J     | 0.51         | 0/1385      | 0.83        | 0/1852        |
| 11  | L     | 0.54         | 0/1733      | 0.85        | 0/2316        |
| 12  | M     | 0.57         | 0/1158      | 0.87        | 0/1547        |
| 13  | N     | 0.57         | 0/1746      | 0.88        | 1/2338 (0.0%) |
| 14  | O     | 0.62         | 0/1662      | 0.91        | 5/2222 (0.2%) |
| 15  | P     | 0.66         | 0/1268      | 0.86        | 0/1700        |
| 16  | Q     | 0.61         | 0/1539      | 0.90        | 1/2054 (0.0%) |
| 17  | R     | 0.56         | 0/1524      | 0.87        | 0/2013        |
| 18  | S     | 0.74         | 0/1501      | 0.90        | 2/2012 (0.1%) |
| 19  | T     | 0.54         | 0/1326      | 0.81        | 0/1770        |
| 20  | U     | 0.52         | 0/823       | 0.78        | 0/1104        |
| 21  | V     | 0.60         | 0/993       | 0.86        | 1/1332 (0.1%) |
| 22  | W     | 0.59         | 0/873       | 0.83        | 0/1158        |
| 23  | X     | 0.51         | 0/984       | 0.80        | 0/1323        |
| 24  | Y     | 0.57         | 0/1132      | 0.85        | 0/1504        |
| 25  | Z     | 0.57         | 0/1130      | 0.83        | 1/1507 (0.1%) |
| 26  | a     | 0.59         | 0/1191      | 0.89        | 1/1590 (0.1%) |
| 27  | b     | 0.51         | 0/861       | 0.83        | 0/1138        |
| 28  | c     | 0.54         | 0/771       | 0.79        | 0/1034        |
| 29  | d     | 0.61         | 0/903       | 0.85        | 1/1216 (0.1%) |
| 30  | e     | 0.61         | 0/1071      | 0.85        | 0/1429        |
| 31  | f     | 0.65         | 0/895       | 0.88        | 0/1198        |
| 32  | g     | 0.54         | 0/916       | 0.83        | 1/1220 (0.1%) |

| Mol | Chain | Bond lengths |                | Bond angles |                   |
|-----|-------|--------------|----------------|-------------|-------------------|
|     |       | RMSZ         | # Z  >5        | RMSZ        | # Z  >5           |
| 33  | h     | 0.51         | 0/1021         | 0.84        | 0/1348            |
| 34  | i     | 0.58         | 0/841          | 0.81        | 0/1112            |
| 35  | j     | 0.58         | 0/720          | 0.87        | 0/952             |
| 36  | k     | 0.46         | 0/575          | 0.75        | 0/761             |
| 37  | l     | 0.56         | 0/459          | 0.83        | 0/608             |
| 38  | m     | 0.67         | 0/435          | 0.90        | 0/575             |
| 39  | n     | 0.49         | 0/240          | 0.84        | 0/305             |
| 40  | o     | 0.59         | 0/864          | 0.82        | 0/1140            |
| 41  | p     | 0.63         | 0/718          | 0.88        | 0/953             |
| 42  | r     | 0.66         | 0/1010         | 0.93        | 2/1354 (0.1%)     |
| 43  | s     | 0.55         | 0/1530         | 0.73        | 0/2064            |
| 44  | t     | 0.59         | 0/1174         | 0.82        | 0/1582            |
| 45  | 1     | 0.61         | 0/49           | 0.97        | 0/65              |
| 46  | 2     | 0.37         | 0/1805         | 0.72        | 0/2809            |
| 47  | 3     | 0.37         | 0/1777         | 0.70        | 0/2763            |
| 48  | 5     | 0.43         | 5/84961 (0.0%) | 0.83        | 173/132460 (0.1%) |
| 49  | 7     | 0.42         | 0/2858         | 0.77        | 1/4455 (0.0%)     |
| 50  | 8     | 0.41         | 0/3581         | 0.78        | 4/5577 (0.1%)     |
| 51  | 9     | 0.42         | 0/40523        | 0.82        | 61/63130 (0.1%)   |
| 52  | AA    | 0.57         | 0/1747         | 0.88        | 0/2374            |
| 53  | BB    | 0.47         | 0/1756         | 0.82        | 0/2350            |
| 54  | CC    | 0.55         | 0/1753         | 0.91        | 1/2369 (0.0%)     |
| 55  | DD    | 0.53         | 0/1796         | 0.81        | 0/2417            |
| 56  | EE    | 0.50         | 0/2118         | 0.84        | 1/2849 (0.0%)     |
| 57  | FF    | 0.48         | 0/1492         | 0.87        | 0/2005            |
| 58  | GG    | 0.51         | 0/1946         | 0.83        | 2/2590 (0.1%)     |
| 59  | HH    | 0.51         | 0/1510         | 0.81        | 0/2022            |
| 60  | II    | 0.54         | 0/1715         | 0.83        | 1/2287 (0.0%)     |
| 61  | JJ    | 0.53         | 0/1550         | 0.91        | 2/2069 (0.1%)     |
| 62  | KK    | 0.51         | 0/834          | 0.84        | 0/1125            |
| 63  | LL    | 0.54         | 0/1195         | 0.87        | 1/1597 (0.1%)     |
| 64  | MM    | 0.54         | 0/918          | 0.85        | 0/1233            |
| 65  | NN    | 0.55         | 0/1226         | 0.91        | 0/1649            |
| 66  | OO    | 0.58         | 0/1029         | 0.97        | 1/1380 (0.1%)     |
| 67  | PP    | 0.57         | 0/1017         | 0.88        | 0/1358            |
| 68  | QQ    | 0.49         | 0/1146         | 0.81        | 0/1534            |
| 69  | RR    | 0.50         | 0/1082         | 0.81        | 0/1452            |
| 70  | SS    | 0.52         | 0/1208         | 0.86        | 0/1618            |
| 71  | TT    | 0.49         | 0/1115         | 0.87        | 0/1493            |
| 72  | UU    | 0.50         | 0/805          | 0.87        | 2/1081 (0.2%)     |
| 73  | VV    | 0.56         | 0/643          | 0.91        | 1/860 (0.1%)      |
| 74  | WW    | 0.61         | 0/1051         | 0.90        | 0/1406            |
| 75  | XX    | 0.59         | 0/1116         | 0.89        | 1/1490 (0.1%)     |

| Mol | Chain | Bond lengths |                 | Bond angles |                   |
|-----|-------|--------------|-----------------|-------------|-------------------|
|     |       | RMSZ         | # Z  >5         | RMSZ        | # Z  >5           |
| 76  | YY    | 0.47         | 0/1028          | 0.79        | 0/1366            |
| 77  | ZZ    | 0.49         | 0/604           | 0.87        | 0/810             |
| 78  | aa    | 0.57         | 0/828           | 0.89        | 0/1109            |
| 79  | bb    | 0.50         | 0/665           | 0.81        | 0/891             |
| 80  | cc    | 0.49         | 0/490           | 0.83        | 0/656             |
| 81  | dd    | 0.54         | 0/470           | 0.80        | 0/623             |
| 82  | ee    | 0.50         | 0/447           | 0.81        | 0/587             |
| 83  | ff    | 0.52         | 0/567           | 0.75        | 0/753             |
| 84  | gg    | 0.46         | 0/2493          | 0.72        | 1/3394 (0.0%)     |
| 85  | hh    | 0.39         | 0/188           | 0.83        | 0/290             |
| 86  | ii    | 0.47         | 0/2996          | 0.80        | 2/4050 (0.0%)     |
| 87  | jj    | 0.48         | 0/3352          | 0.79        | 1/4523 (0.0%)     |
| All | All   | 0.49         | 5/237792 (0.0%) | 0.83        | 288/348210 (0.1%) |

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

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

All (5) bond length outliers are listed below:

| Mol | Chain | Res     | Type | Atoms   | Z     | Observed(Å) | Ideal(Å) |
|-----|-------|---------|------|---------|-------|-------------|----------|
| 48  | 5     | 922(A)  | G    | O3'-P   | 9.08  | 1.72        | 1.61     |
| 48  | 5     | 935     | A    | C5-C6   | -7.20 | 1.26        | 1.41     |
| 48  | 5     | 1411(B) | C    | O3'-P   | 7.03  | 1.69        | 1.61     |
| 48  | 5     | 922     | C    | O3'-P   | 5.78  | 1.68        | 1.61     |
| 48  | 5     | 1411(C) | C    | O5'-C5' | 5.50  | 1.50        | 1.42     |

The worst 5 of 288 bond angle outliers are listed below:

| Mol | Chain | Res  | Type | Atoms       | Z      | Observed(°) | Ideal(°) |
|-----|-------|------|------|-------------|--------|-------------|----------|
| 48  | 5     | 922  | C    | C2'-C3'-O3' | 15.80  | 137.40      | 113.70   |
| 48  | 5     | 481  | G    | N1-C2-N2    | -15.79 | 68.83       | 116.20   |
| 51  | 9     | 1835 | A    | C2'-C3'-O3' | 14.23  | 130.85      | 109.50   |
| 48  | 5     | 1411 | C    | C2'-C3'-O3' | -13.13 | 94.00       | 113.70   |
| 48  | 5     | 935  | A    | C5-C6-N6    | -12.99 | 84.72       | 123.70   |

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

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

## 5.2 Too-close contacts [i](#)

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

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1   | A     | 1898  | 0        | 1993     | 28      | 0            |
| 2   | B     | 3172  | 0        | 3310     | 35      | 0            |
| 3   | C     | 2883  | 0        | 3053     | 35      | 0            |
| 4   | D     | 2391  | 0        | 2424     | 17      | 0            |
| 5   | E     | 1729  | 0        | 1887     | 11      | 0            |
| 6   | F     | 1875  | 0        | 1995     | 18      | 0            |
| 7   | G     | 1879  | 0        | 2027     | 15      | 0            |
| 8   | H     | 1516  | 0        | 1597     | 24      | 0            |
| 9   | I     | 1664  | 0        | 1712     | 12      | 0            |
| 10  | J     | 1362  | 0        | 1399     | 10      | 0            |
| 11  | L     | 1702  | 0        | 1820     | 9       | 0            |
| 12  | M     | 1137  | 0        | 1211     | 15      | 0            |
| 13  | N     | 1701  | 0        | 1749     | 17      | 0            |
| 14  | O     | 1630  | 0        | 1778     | 23      | 0            |
| 15  | P     | 1242  | 0        | 1274     | 9       | 0            |
| 16  | Q     | 1515  | 0        | 1634     | 15      | 0            |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 17  | R     | 1508  | 0        | 1664     | 9       | 0            |
| 18  | S     | 1462  | 0        | 1508     | 25      | 0            |
| 19  | T     | 1298  | 0        | 1366     | 12      | 0            |
| 20  | U     | 809   | 0        | 833      | 7       | 0            |
| 21  | V     | 979   | 0        | 1039     | 9       | 0            |
| 22  | W     | 860   | 0        | 903      | 11      | 0            |
| 23  | X     | 967   | 0        | 1040     | 2       | 0            |
| 24  | Y     | 1115  | 0        | 1205     | 7       | 0            |
| 25  | Z     | 1107  | 0        | 1182     | 9       | 0            |
| 26  | a     | 1162  | 0        | 1209     | 18      | 0            |
| 27  | b     | 848   | 0        | 920      | 0       | 0            |
| 28  | c     | 761   | 0        | 794      | 9       | 0            |
| 29  | d     | 888   | 0        | 930      | 15      | 0            |
| 30  | e     | 1053  | 0        | 1147     | 8       | 0            |
| 31  | f     | 876   | 0        | 912      | 8       | 0            |
| 32  | g     | 906   | 0        | 1002     | 7       | 0            |
| 33  | h     | 1013  | 0        | 1147     | 5       | 0            |
| 34  | i     | 830   | 0        | 916      | 5       | 0            |
| 35  | j     | 705   | 0        | 738      | 6       | 0            |
| 36  | k     | 569   | 0        | 637      | 2       | 0            |
| 37  | l     | 447   | 0        | 480      | 5       | 0            |
| 38  | m     | 429   | 0        | 466      | 5       | 0            |
| 39  | n     | 239   | 0        | 289      | 1       | 0            |
| 40  | o     | 851   | 0        | 920      | 10      | 0            |
| 41  | p     | 708   | 0        | 756      | 6       | 0            |
| 42  | r     | 994   | 0        | 1051     | 12      | 0            |
| 43  | s     | 1507  | 0        | 1564     | 0       | 0            |
| 44  | t     | 1160  | 0        | 1218     | 2       | 0            |
| 45  | 1     | 49    | 0        | 51       | 0       | 0            |
| 46  | 2     | 1616  | 0        | 824      | 2       | 0            |
| 47  | 3     | 1593  | 0        | 811      | 5       | 0            |
| 48  | 5     | 75972 | 0        | 38398    | 352     | 0            |
| 49  | 7     | 2558  | 0        | 1296     | 7       | 0            |
| 50  | 8     | 3208  | 0        | 1629     | 15      | 0            |
| 51  | 9     | 36249 | 0        | 18317    | 277     | 0            |
| 52  | AA    | 1710  | 0        | 1708     | 24      | 0            |
| 53  | BB    | 1729  | 0        | 1803     | 20      | 0            |
| 54  | CC    | 1716  | 0        | 1806     | 14      | 0            |
| 55  | DD    | 1768  | 0        | 1866     | 10      | 0            |
| 56  | EE    | 2076  | 0        | 2177     | 14      | 0            |
| 57  | FF    | 1471  | 0        | 1522     | 8       | 0            |
| 58  | GG    | 1923  | 0        | 2089     | 13      | 0            |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 59  | HH    | 1488  | 0        | 1582     | 15      | 0            |
| 60  | II    | 1686  | 0        | 1772     | 14      | 0            |
| 61  | JJ    | 1525  | 0        | 1640     | 10      | 0            |
| 62  | KK    | 810   | 0        | 836      | 11      | 0            |
| 63  | LL    | 1175  | 0        | 1249     | 10      | 0            |
| 64  | MM    | 908   | 0        | 939      | 21      | 0            |
| 65  | NN    | 1202  | 0        | 1289     | 11      | 0            |
| 66  | OO    | 1016  | 0        | 1039     | 15      | 0            |
| 67  | PP    | 997   | 0        | 1045     | 20      | 0            |
| 68  | QQ    | 1128  | 0        | 1195     | 8       | 0            |
| 69  | RR    | 1068  | 0        | 1121     | 9       | 0            |
| 70  | SS    | 1190  | 0        | 1249     | 23      | 0            |
| 71  | TT    | 1097  | 0        | 1132     | 5       | 0            |
| 72  | UU    | 795   | 0        | 862      | 6       | 0            |
| 73  | VV    | 636   | 0        | 637      | 7       | 0            |
| 74  | WW    | 1034  | 0        | 1080     | 15      | 0            |
| 75  | XX    | 1098  | 0        | 1167     | 14      | 0            |
| 76  | YY    | 1011  | 0        | 1083     | 3       | 0            |
| 77  | ZZ    | 598   | 0        | 656      | 4       | 0            |
| 78  | aa    | 814   | 0        | 863      | 10      | 0            |
| 79  | bb    | 651   | 0        | 672      | 5       | 0            |
| 80  | cc    | 488   | 0        | 514      | 17      | 0            |
| 81  | dd    | 459   | 0        | 449      | 9       | 0            |
| 82  | ee    | 443   | 0        | 492      | 0       | 0            |
| 83  | ff    | 555   | 0        | 565      | 65      | 0            |
| 84  | gg    | 2436  | 0        | 2393     | 16      | 0            |
| 85  | hh    | 169   | 0        | 86       | 1       | 0            |
| 86  | ii    | 2947  | 0        | 2957     | 21      | 0            |
| 87  | jj    | 3292  | 0        | 3371     | 33      | 0            |
| 88  | 5     | 178   | 0        | 0        | 0       | 0            |
| 88  | 7     | 5     | 0        | 0        | 0       | 0            |
| 88  | 8     | 5     | 0        | 0        | 0       | 0            |
| 88  | 9     | 66    | 0        | 0        | 0       | 0            |
| 88  | B     | 1     | 0        | 0        | 0       | 0            |
| 88  | I     | 1     | 0        | 0        | 0       | 0            |
| 88  | L     | 1     | 0        | 0        | 0       | 0            |
| 88  | P     | 1     | 0        | 0        | 0       | 0            |
| 88  | V     | 1     | 0        | 0        | 0       | 0            |
| 88  | a     | 1     | 0        | 0        | 0       | 0            |
| 88  | e     | 1     | 0        | 0        | 0       | 0            |
| 88  | g     | 1     | 0        | 0        | 0       | 0            |
| 88  | j     | 1     | 0        | 0        | 0       | 0            |

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| Mol | Chain | Non-H  | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|--------|----------|----------|---------|--------------|
| 88  | jj    | 1      | 0        | 0        | 0       | 0            |
| 89  | aa    | 1      | 0        | 0        | 0       | 0            |
| 89  | dd    | 1      | 0        | 0        | 0       | 0            |
| 89  | ff    | 1      | 0        | 0        | 2       | 0            |
| 89  | g     | 1      | 0        | 0        | 1       | 0            |
| 89  | j     | 1      | 0        | 0        | 0       | 0            |
| 89  | m     | 1      | 0        | 0        | 1       | 0            |
| 89  | o     | 1      | 0        | 0        | 0       | 0            |
| 89  | p     | 1      | 0        | 0        | 0       | 0            |
| 90  | jj    | 32     | 0        | 14       | 1       | 0            |
| All | All   | 222005 | 0        | 166945   | 1371    | 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 4.

The worst 5 of 1371 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) |
|------------------|-------------------|--------------------------|-------------------|
| 86:ii:45:ARG:NH1 | 86:ii:100:HIS:ND1 | 1.65                     | 1.41              |
| 51:9:1304:U:H5'  | 83:ff:93:HIS:N    | 1.13                     | 1.39              |
| 48:5:3914:U:O4   | 48:5:4378:A:N1    | 1.58                     | 1.35              |
| 48:5:922:C:C5'   | 48:5:922(A):G:H3' | 1.59                     | 1.31              |
| 51:9:1304:U:C5'  | 83:ff:93:HIS:N    | 1.94                     | 1.31              |

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

| Mol | Chain | Analysed      | Favoured  | Allowed  | Outliers | Percentiles |    |
|-----|-------|---------------|-----------|----------|----------|-------------|----|
| 1   | A     | 246/257 (96%) | 220 (89%) | 24 (10%) | 2 (1%)   | 16          | 49 |
| 2   | B     | 392/403 (97%) | 355 (91%) | 35 (9%)  | 2 (0%)   | 24          | 58 |

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| Mol | Chain | Analysed      | Favoured  | Allowed  | Outliers | Percentiles |     |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 3   | C     | 360/425 (85%) | 332 (92%) | 23 (6%)  | 5 (1%)   | 9           | 38  |
| 4   | D     | 291/297 (98%) | 278 (96%) | 10 (3%)  | 3 (1%)   | 12          | 44  |
| 5   | E     | 208/291 (72%) | 189 (91%) | 19 (9%)  | 0        | 100         | 100 |
| 6   | F     | 223/247 (90%) | 204 (92%) | 16 (7%)  | 3 (1%)   | 9           | 39  |
| 7   | G     | 229/319 (72%) | 216 (94%) | 11 (5%)  | 2 (1%)   | 14          | 47  |
| 8   | H     | 188/192 (98%) | 172 (92%) | 16 (8%)  | 0        | 100         | 100 |
| 9   | I     | 201/214 (94%) | 177 (88%) | 23 (11%) | 1 (0%)   | 24          | 58  |
| 10  | J     | 168/178 (94%) | 157 (94%) | 9 (5%)   | 2 (1%)   | 10          | 41  |
| 11  | L     | 208/211 (99%) | 193 (93%) | 14 (7%)  | 1 (0%)   | 24          | 58  |
| 12  | M     | 136/218 (62%) | 125 (92%) | 11 (8%)  | 0        | 100         | 100 |
| 13  | N     | 201/204 (98%) | 181 (90%) | 19 (10%) | 1 (0%)   | 24          | 58  |
| 14  | O     | 197/203 (97%) | 183 (93%) | 13 (7%)  | 1 (0%)   | 24          | 58  |
| 15  | P     | 151/184 (82%) | 140 (93%) | 9 (6%)   | 2 (1%)   | 9           | 39  |
| 16  | Q     | 185/188 (98%) | 168 (91%) | 16 (9%)  | 1 (0%)   | 24          | 58  |
| 17  | R     | 178/196 (91%) | 171 (96%) | 6 (3%)   | 1 (1%)   | 21          | 53  |
| 18  | S     | 174/176 (99%) | 159 (91%) | 12 (7%)  | 3 (2%)   | 7           | 34  |
| 19  | T     | 157/160 (98%) | 142 (90%) | 15 (10%) | 0        | 100         | 100 |
| 20  | U     | 97/128 (76%)  | 86 (89%)  | 9 (9%)   | 2 (2%)   | 5           | 31  |
| 21  | V     | 129/140 (92%) | 113 (88%) | 16 (12%) | 0        | 100         | 100 |
| 22  | W     | 102/157 (65%) | 93 (91%)  | 8 (8%)   | 1 (1%)   | 12          | 44  |
| 23  | X     | 116/156 (74%) | 109 (94%) | 6 (5%)   | 1 (1%)   | 14          | 47  |
| 24  | Y     | 132/145 (91%) | 126 (96%) | 5 (4%)   | 1 (1%)   | 16          | 49  |
| 25  | Z     | 133/136 (98%) | 123 (92%) | 8 (6%)   | 2 (2%)   | 8           | 37  |
| 26  | a     | 145/148 (98%) | 135 (93%) | 10 (7%)  | 0        | 100         | 100 |
| 27  | b     | 100/245 (41%) | 93 (93%)  | 6 (6%)   | 1 (1%)   | 12          | 44  |
| 28  | c     | 96/115 (84%)  | 89 (93%)  | 7 (7%)   | 0        | 100         | 100 |
| 29  | d     | 105/125 (84%) | 94 (90%)  | 10 (10%) | 1 (1%)   | 12          | 44  |
| 30  | e     | 126/135 (93%) | 121 (96%) | 5 (4%)   | 0        | 100         | 100 |
| 31  | f     | 107/110 (97%) | 97 (91%)  | 8 (8%)   | 2 (2%)   | 6           | 32  |
| 32  | g     | 112/117 (96%) | 103 (92%) | 8 (7%)   | 1 (1%)   | 14          | 47  |
| 33  | h     | 120/123 (98%) | 116 (97%) | 3 (2%)   | 1 (1%)   | 16          | 49  |

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| Mol | Chain | Analysed      | Favoured  | Allowed  | Outliers | Percentiles |     |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 34  | i     | 100/105 (95%) | 92 (92%)  | 8 (8%)   | 0        | 100         | 100 |
| 35  | j     | 84/97 (87%)   | 74 (88%)  | 9 (11%)  | 1 (1%)   | 10          | 41  |
| 36  | k     | 67/70 (96%)   | 63 (94%)  | 3 (4%)   | 1 (2%)   | 8           | 37  |
| 37  | l     | 48/51 (94%)   | 41 (85%)  | 7 (15%)  | 0        | 100         | 100 |
| 38  | m     | 50/102 (49%)  | 46 (92%)  | 4 (8%)   | 0        | 100         | 100 |
| 39  | n     | 23/25 (92%)   | 22 (96%)  | 1 (4%)   | 0        | 100         | 100 |
| 40  | o     | 102/106 (96%) | 92 (90%)  | 9 (9%)   | 1 (1%)   | 12          | 44  |
| 41  | p     | 89/92 (97%)   | 81 (91%)  | 7 (8%)   | 1 (1%)   | 11          | 42  |
| 42  | r     | 122/137 (89%) | 104 (85%) | 14 (12%) | 4 (3%)   | 3           | 23  |
| 43  | s     | 194/318 (61%) | 174 (90%) | 18 (9%)  | 2 (1%)   | 12          | 44  |
| 44  | t     | 151/165 (92%) | 134 (89%) | 15 (10%) | 2 (1%)   | 9           | 39  |
| 45  | 1     | 5/7 (71%)     | 2 (40%)   | 3 (60%)  | 0        | 100         | 100 |
| 52  | AA    | 215/295 (73%) | 195 (91%) | 19 (9%)  | 1 (0%)   | 24          | 58  |
| 53  | BB    | 211/264 (80%) | 199 (94%) | 12 (6%)  | 0        | 100         | 100 |
| 54  | CC    | 219/293 (75%) | 202 (92%) | 16 (7%)  | 1 (0%)   | 24          | 58  |
| 55  | DD    | 226/243 (93%) | 206 (91%) | 18 (8%)  | 2 (1%)   | 14          | 47  |
| 56  | EE    | 260/263 (99%) | 242 (93%) | 18 (7%)  | 0        | 100         | 100 |
| 57  | FF    | 181/204 (89%) | 168 (93%) | 10 (6%)  | 3 (2%)   | 7           | 34  |
| 58  | GG    | 235/249 (94%) | 217 (92%) | 17 (7%)  | 1 (0%)   | 30          | 62  |
| 59  | HH    | 181/194 (93%) | 168 (93%) | 13 (7%)  | 0        | 100         | 100 |
| 60  | II    | 204/208 (98%) | 191 (94%) | 11 (5%)  | 2 (1%)   | 12          | 44  |
| 61  | JJ    | 183/194 (94%) | 175 (96%) | 8 (4%)   | 0        | 100         | 100 |
| 62  | KK    | 94/165 (57%)  | 85 (90%)  | 6 (6%)   | 3 (3%)   | 3           | 24  |
| 63  | LL    | 139/158 (88%) | 124 (89%) | 14 (10%) | 1 (1%)   | 18          | 51  |
| 64  | MM    | 115/132 (87%) | 99 (86%)  | 16 (14%) | 0        | 100         | 100 |
| 65  | NN    | 147/151 (97%) | 134 (91%) | 13 (9%)  | 0        | 100         | 100 |
| 66  | OO    | 134/168 (80%) | 120 (90%) | 13 (10%) | 1 (1%)   | 18          | 51  |
| 67  | PP    | 118/145 (81%) | 103 (87%) | 14 (12%) | 1 (1%)   | 16          | 49  |
| 68  | QQ    | 140/146 (96%) | 132 (94%) | 8 (6%)   | 0        | 100         | 100 |
| 69  | RR    | 130/135 (96%) | 115 (88%) | 14 (11%) | 1 (1%)   | 16          | 49  |
| 70  | SS    | 142/152 (93%) | 134 (94%) | 8 (6%)   | 0        | 100         | 100 |

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| Mol | Chain | Analysed          | Favoured    | Allowed  | Outliers | Percentiles |     |
|-----|-------|-------------------|-------------|----------|----------|-------------|-----|
| 71  | TT    | 139/145 (96%)     | 131 (94%)   | 7 (5%)   | 1 (1%)   | 18          | 51  |
| 72  | UU    | 98/119 (82%)      | 92 (94%)    | 6 (6%)   | 0        | 100         | 100 |
| 73  | VV    | 81/83 (98%)       | 76 (94%)    | 5 (6%)   | 0        | 100         | 100 |
| 74  | WW    | 127/130 (98%)     | 116 (91%)   | 9 (7%)   | 2 (2%)   | 7           | 36  |
| 75  | XX    | 139/143 (97%)     | 124 (89%)   | 12 (9%)  | 3 (2%)   | 5           | 30  |
| 76  | YY    | 122/130 (94%)     | 116 (95%)   | 6 (5%)   | 0        | 100         | 100 |
| 77  | ZZ    | 73/125 (58%)      | 71 (97%)    | 2 (3%)   | 0        | 100         | 100 |
| 78  | aa    | 99/115 (86%)      | 88 (89%)    | 9 (9%)   | 2 (2%)   | 6           | 32  |
| 79  | bb    | 81/84 (96%)       | 73 (90%)    | 7 (9%)   | 1 (1%)   | 10          | 41  |
| 80  | cc    | 60/69 (87%)       | 55 (92%)    | 3 (5%)   | 2 (3%)   | 3           | 23  |
| 81  | dd    | 53/56 (95%)       | 48 (91%)    | 5 (9%)   | 0        | 100         | 100 |
| 82  | ee    | 53/133 (40%)      | 50 (94%)    | 3 (6%)   | 0        | 100         | 100 |
| 83  | ff    | 66/156 (42%)      | 60 (91%)    | 5 (8%)   | 1 (2%)   | 8           | 37  |
| 84  | gg    | 311/317 (98%)     | 284 (91%)   | 24 (8%)  | 3 (1%)   | 12          | 44  |
| 86  | ii    | 370/403 (92%)     | 343 (93%)   | 26 (7%)  | 1 (0%)   | 36          | 67  |
| 87  | jj    | 423/710 (60%)     | 381 (90%)   | 38 (9%)  | 4 (1%)   | 14          | 47  |
| All | All   | 12317/14495 (85%) | 11302 (92%) | 923 (8%) | 92 (1%)  | 20          | 51  |

5 of 92 Ramachandran outliers are listed below:

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

### 5.3.2 Protein sidechains ⓘ

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

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

| Mol | Chain | Analysed       | Rotameric | Outliers | Percentiles |     |
|-----|-------|----------------|-----------|----------|-------------|-----|
| 1   | A     | 190/199 (96%)  | 177 (93%) | 13 (7%)  | 14          | 41  |
| 2   | B     | 342/348 (98%)  | 310 (91%) | 32 (9%)  | 8           | 31  |
| 3   | C     | 302/347 (87%)  | 282 (93%) | 20 (7%)  | 15          | 42  |
| 4   | D     | 247/250 (99%)  | 235 (95%) | 12 (5%)  | 22          | 49  |
| 5   | E     | 190/251 (76%)  | 178 (94%) | 12 (6%)  | 16          | 43  |
| 6   | F     | 196/215 (91%)  | 177 (90%) | 19 (10%) | 8           | 30  |
| 7   | G     | 200/272 (74%)  | 186 (93%) | 14 (7%)  | 14          | 40  |
| 8   | H     | 169/171 (99%)  | 155 (92%) | 14 (8%)  | 10          | 35  |
| 9   | I     | 175/181 (97%)  | 161 (92%) | 14 (8%)  | 11          | 36  |
| 10  | J     | 143/149 (96%)  | 132 (92%) | 11 (8%)  | 12          | 37  |
| 11  | L     | 175/176 (99%)  | 165 (94%) | 10 (6%)  | 18          | 45  |
| 12  | M     | 117/161 (73%)  | 109 (93%) | 8 (7%)   | 14          | 41  |
| 13  | N     | 171/172 (99%)  | 162 (95%) | 9 (5%)   | 20          | 47  |
| 14  | O     | 171/173 (99%)  | 155 (91%) | 16 (9%)  | 8           | 31  |
| 15  | P     | 134/163 (82%)  | 129 (96%) | 5 (4%)   | 30          | 56  |
| 16  | Q     | 164/165 (99%)  | 151 (92%) | 13 (8%)  | 11          | 36  |
| 17  | R     | 159/175 (91%)  | 143 (90%) | 16 (10%) | 7           | 28  |
| 18  | S     | 157/157 (100%) | 144 (92%) | 13 (8%)  | 10          | 35  |
| 19  | T     | 139/140 (99%)  | 128 (92%) | 11 (8%)  | 11          | 36  |
| 20  | U     | 89/114 (78%)   | 87 (98%)  | 2 (2%)   | 45          | 65  |
| 21  | V     | 101/107 (94%)  | 88 (87%)  | 13 (13%) | 4           | 21  |
| 22  | W     | 86/126 (68%)   | 86 (100%) | 0        | 100         | 100 |
| 23  | X     | 106/134 (79%)  | 100 (94%) | 6 (6%)   | 18          | 45  |
| 24  | Y     | 124/135 (92%)  | 117 (94%) | 7 (6%)   | 19          | 46  |
| 25  | Z     | 117/118 (99%)  | 113 (97%) | 4 (3%)   | 32          | 58  |
| 26  | a     | 119/120 (99%)  | 116 (98%) | 3 (2%)   | 42          | 63  |
| 27  | b     | 84/184 (46%)   | 81 (96%)  | 3 (4%)   | 31          | 57  |
| 28  | c     | 84/98 (86%)    | 77 (92%)  | 7 (8%)   | 10          | 35  |
| 29  | d     | 98/110 (89%)   | 86 (88%)  | 12 (12%) | 5           | 22  |
| 30  | e     | 114/121 (94%)  | 103 (90%) | 11 (10%) | 8           | 30  |
| 31  | f     | 88/89 (99%)    | 81 (92%)  | 7 (8%)   | 11          | 36  |
| 32  | g     | 98/100 (98%)   | 90 (92%)  | 8 (8%)   | 10          | 35  |

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| Mol | Chain | Analysed       | Rotameric | Outliers | Percentiles |     |
|-----|-------|----------------|-----------|----------|-------------|-----|
| 33  | h     | 109/110 (99%)  | 105 (96%) | 4 (4%)   | 30          | 56  |
| 34  | i     | 86/89 (97%)    | 81 (94%)  | 5 (6%)   | 18          | 45  |
| 35  | j     | 73/80 (91%)    | 68 (93%)  | 5 (7%)   | 14          | 41  |
| 36  | k     | 64/65 (98%)    | 61 (95%)  | 3 (5%)   | 23          | 50  |
| 37  | l     | 47/48 (98%)    | 46 (98%)  | 1 (2%)   | 47          | 66  |
| 38  | m     | 48/90 (53%)    | 45 (94%)  | 3 (6%)   | 16          | 43  |
| 39  | n     | 24/24 (100%)   | 22 (92%)  | 2 (8%)   | 10          | 35  |
| 40  | o     | 92/94 (98%)    | 87 (95%)  | 5 (5%)   | 20          | 47  |
| 41  | p     | 74/75 (99%)    | 71 (96%)  | 3 (4%)   | 27          | 53  |
| 42  | r     | 108/121 (89%)  | 95 (88%)  | 13 (12%) | 5           | 23  |
| 43  | s     | 164/258 (64%)  | 158 (96%) | 6 (4%)   | 30          | 56  |
| 44  | t     | 126/137 (92%)  | 122 (97%) | 4 (3%)   | 34          | 59  |
| 45  | 1     | 6/6 (100%)     | 6 (100%)  | 0        | 100         | 100 |
| 52  | AA    | 180/245 (74%)  | 161 (89%) | 19 (11%) | 6           | 27  |
| 53  | BB    | 194/231 (84%)  | 174 (90%) | 20 (10%) | 7           | 28  |
| 54  | CC    | 187/225 (83%)  | 172 (92%) | 15 (8%)  | 11          | 36  |
| 55  | DD    | 190/202 (94%)  | 172 (90%) | 18 (10%) | 8           | 31  |
| 56  | EE    | 224/225 (100%) | 208 (93%) | 16 (7%)  | 13          | 39  |
| 57  | FF    | 158/170 (93%)  | 151 (96%) | 7 (4%)   | 25          | 51  |
| 58  | GG    | 207/218 (95%)  | 187 (90%) | 20 (10%) | 8           | 30  |
| 59  | HH    | 165/174 (95%)  | 151 (92%) | 14 (8%)  | 10          | 34  |
| 60  | II    | 178/180 (99%)  | 166 (93%) | 12 (7%)  | 15          | 41  |
| 61  | JJ    | 161/168 (96%)  | 142 (88%) | 19 (12%) | 5           | 23  |
| 62  | KK    | 87/136 (64%)   | 82 (94%)  | 5 (6%)   | 18          | 45  |
| 63  | LL    | 130/142 (92%)  | 112 (86%) | 18 (14%) | 3           | 19  |
| 64  | MM    | 99/108 (92%)   | 86 (87%)  | 13 (13%) | 4           | 20  |
| 65  | NN    | 130/131 (99%)  | 117 (90%) | 13 (10%) | 7           | 29  |
| 66  | OO    | 106/130 (82%)  | 99 (93%)  | 7 (7%)   | 15          | 42  |
| 67  | PP    | 109/130 (84%)  | 98 (90%)  | 11 (10%) | 7           | 28  |
| 68  | QQ    | 117/121 (97%)  | 108 (92%) | 9 (8%)   | 12          | 37  |
| 69  | RR    | 119/121 (98%)  | 109 (92%) | 10 (8%)  | 10          | 34  |

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| Mol | Chain | Analysed          | Rotameric  | Outliers | Percentiles |    |
|-----|-------|-------------------|------------|----------|-------------|----|
| 70  | SS    | 125/132 (95%)     | 109 (87%)  | 16 (13%) | 4           | 21 |
| 71  | TT    | 111/115 (96%)     | 102 (92%)  | 9 (8%)   | 11          | 35 |
| 72  | UU    | 92/107 (86%)      | 83 (90%)   | 9 (10%)  | 7           | 30 |
| 73  | VV    | 67/67 (100%)      | 63 (94%)   | 4 (6%)   | 17          | 44 |
| 74  | WW    | 112/113 (99%)     | 102 (91%)  | 10 (9%)  | 9           | 33 |
| 75  | XX    | 113/115 (98%)     | 105 (93%)  | 8 (7%)   | 13          | 39 |
| 76  | YY    | 107/112 (96%)     | 91 (85%)   | 16 (15%) | 3           | 17 |
| 77  | ZZ    | 66/103 (64%)      | 58 (88%)   | 8 (12%)  | 5           | 22 |
| 78  | aa    | 88/98 (90%)       | 75 (85%)   | 13 (15%) | 3           | 17 |
| 79  | bb    | 75/76 (99%)       | 66 (88%)   | 9 (12%)  | 5           | 23 |
| 80  | cc    | 55/62 (89%)       | 49 (89%)   | 6 (11%)  | 6           | 26 |
| 81  | dd    | 48/49 (98%)       | 46 (96%)   | 2 (4%)   | 26          | 52 |
| 82  | ee    | 46/106 (43%)      | 39 (85%)   | 7 (15%)  | 3           | 16 |
| 83  | ff    | 61/140 (44%)      | 55 (90%)   | 6 (10%)  | 7           | 30 |
| 84  | gg    | 272/275 (99%)     | 257 (94%)  | 15 (6%)  | 19          | 46 |
| 86  | ii    | 326/353 (92%)     | 310 (95%)  | 16 (5%)  | 22          | 49 |
| 87  | jj    | 358/608 (59%)     | 331 (92%)  | 27 (8%)  | 12          | 38 |
| All | All   | 10733/12306 (87%) | 9907 (92%) | 826 (8%) | 14          | 37 |

5 of 826 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 55  | DD    | 146 | ARG  |
| 63  | LL    | 85  | THR  |
| 87  | jj    | 264 | VAL  |
| 56  | EE    | 66  | MET  |
| 55  | DD    | 142 | LEU  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 161 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 65  | NN    | 90  | HIS  |
| 84  | gg    | 64  | HIS  |
| 66  | OO    | 83  | GLN  |
| 73  | VV    | 49  | GLN  |

*Continued on next page...*

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 86  | ii    | 216 | GLN  |

### 5.3.3 RNA ⓘ

| Mol | Chain | Analysed        | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 46  | 2     | 74/76 (97%)     | 15 (20%)          | 0               |
| 47  | 3     | 72/75 (96%)     | 21 (29%)          | 1 (1%)          |
| 48  | 5     | 3511/3543 (99%) | 899 (25%)         | 182 (5%)        |
| 49  | 7     | 119/120 (99%)   | 13 (10%)          | 1 (0%)          |
| 50  | 8     | 149/156 (95%)   | 38 (25%)          | 6 (4%)          |
| 51  | 9     | 1683/1869 (90%) | 444 (26%)         | 85 (5%)         |
| 85  | hh    | 7/8 (87%)       | 4 (57%)           | 0               |
| All | All   | 5615/5847 (96%) | 1434 (25%)        | 275 (4%)        |

5 of 1434 RNA backbone outliers are listed below:

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

5 of 275 RNA pucker outliers are listed below:

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 51  | 9     | 688  | U    |
| 51  | 9     | 875  | A    |
| 51  | 9     | 1581 | C    |
| 48  | 5     | 2068 | C    |
| 48  | 5     | 1986 | U    |

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

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry

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

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

| Mol | Type | Chain | Res | Link | Bond lengths |      |             | Bond angles |      |             |
|-----|------|-------|-----|------|--------------|------|-------------|-------------|------|-------------|
|     |      |       |     |      | Counts       | RMSZ | # $ Z  > 2$ | Counts      | RMSZ | # $ Z  > 2$ |
| 90  | GCP  | jj    | 700 | 88   | 32,34,34     | 1.50 | 7 (21%)     | 49,54,54    | 1.73 | 7 (14%)     |

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

| Mol | Type | Chain | Res | Link | Chirals | Torsions   | Rings   |
|-----|------|-------|-----|------|---------|------------|---------|
| 90  | GCP  | jj    | 700 | 88   | -       | 3/19/38/38 | 0/3/3/3 |

The worst 5 of 7 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms  | Z    | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|--------|------|-------------|----------|
| 90  | jj    | 700 | GCP  | C5-C4  | 3.35 | 1.48        | 1.38     |
| 90  | jj    | 700 | GCP  | PG-O3G | 3.08 | 1.61        | 1.55     |
| 90  | jj    | 700 | GCP  | PG-O2G | 2.90 | 1.61        | 1.55     |
| 90  | jj    | 700 | GCP  | PB-O3A | 2.57 | 1.61        | 1.58     |
| 90  | jj    | 700 | GCP  | PB-O2B | 2.23 | 1.61        | 1.56     |

The worst 5 of 7 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms    | Z     | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|-------|-------------|----------|
| 90  | jj    | 700 | GCP  | C5-C4-N3 | -6.04 | 118.78      | 128.39   |
| 90  | jj    | 700 | GCP  | C2-N3-C4 | 4.87  | 120.68      | 112.30   |
| 90  | jj    | 700 | GCP  | N9-C4-N3 | 4.38  | 134.71      | 125.95   |
| 90  | jj    | 700 | GCP  | C6-C5-N7 | 3.21  | 136.14      | 130.29   |
| 90  | jj    | 700 | GCP  | C4-C5-N7 | -2.71 | 106.37      | 110.67   |

There are no chirality outliers.

All (3) torsion outliers are listed below:

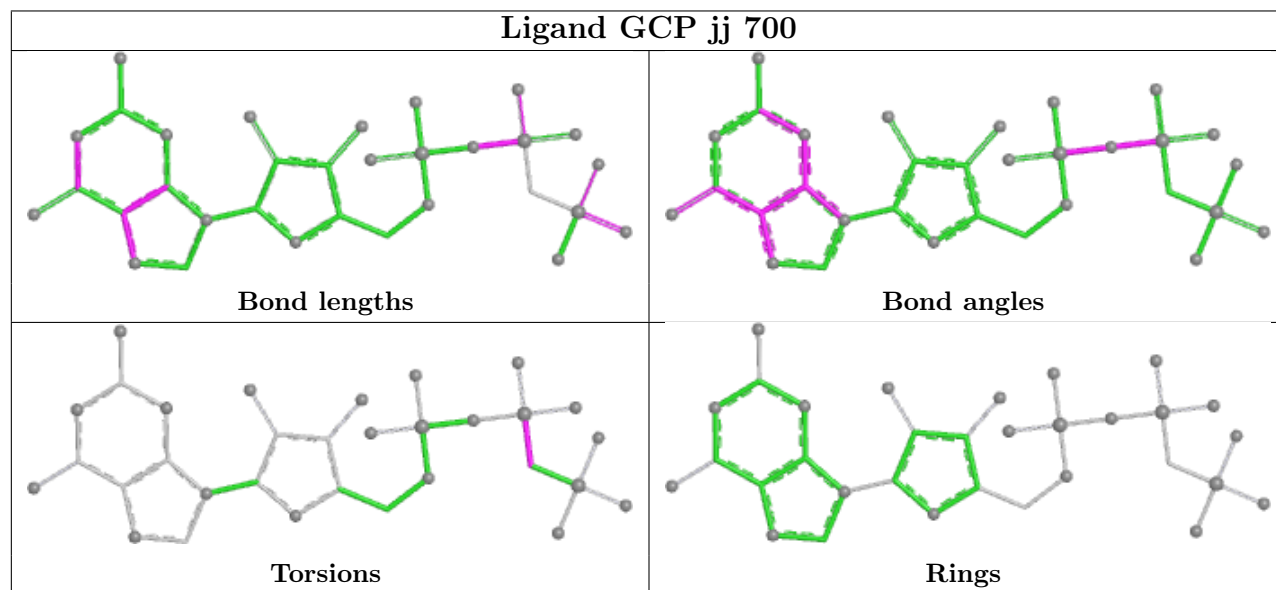
| Mol | Chain | Res | Type | Atoms         |
|-----|-------|-----|------|---------------|
| 90  | jj    | 700 | GCP  | PG-C3B-PB-O1B |
| 90  | jj    | 700 | GCP  | PG-C3B-PB-O3A |
| 90  | jj    | 700 | GCP  | PG-C3B-PB-O2B |

There are no ring outliers.

1 monomer is involved in 1 short contact:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 90  | jj    | 700 | GCP  | 1       | 0            |

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

The following chains have linkage breaks:

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

The worst 5 of 53 chain breaks are listed below:

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

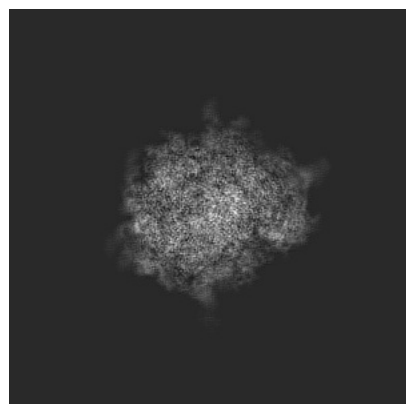
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4137. These allow visual inspection of the internal detail of the map and identification of artifacts.

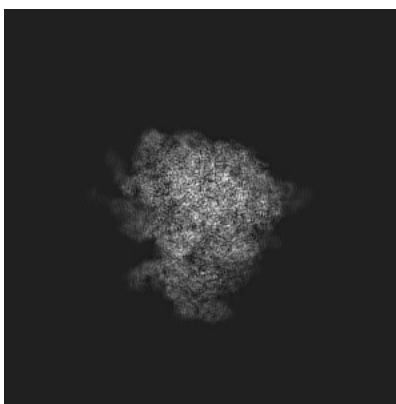
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

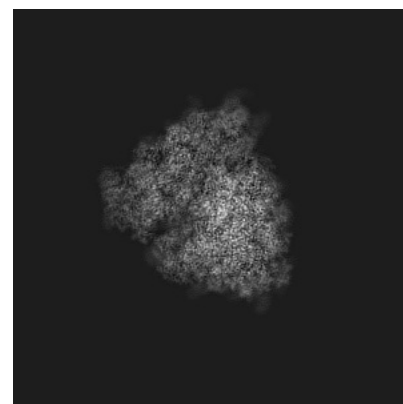
#### 6.1.1 Primary map



X

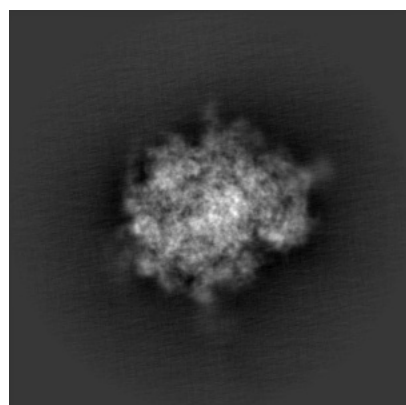


Y

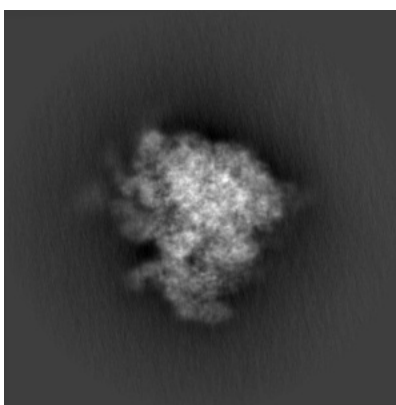


Z

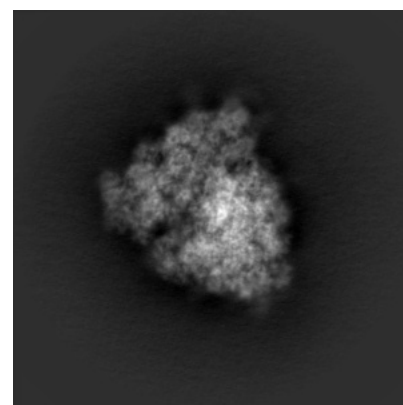
#### 6.1.2 Raw map



X



Y

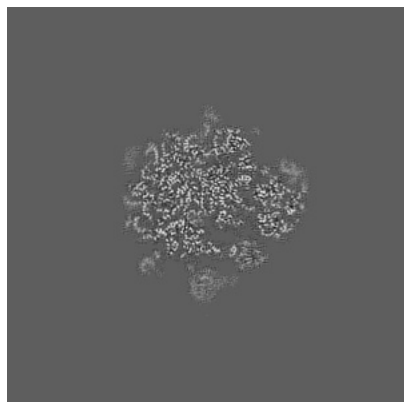


Z

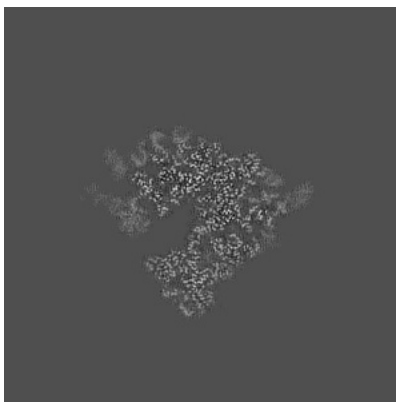
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

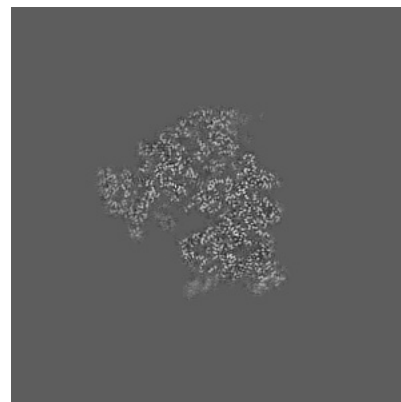
### 6.2.1 Primary map



X Index: 210

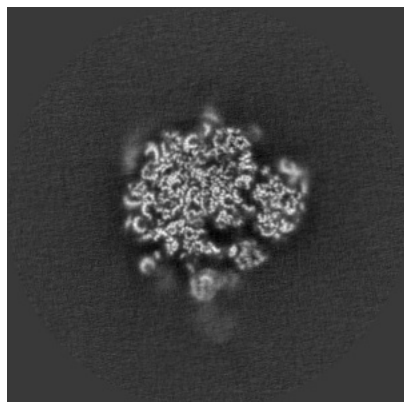


Y Index: 210

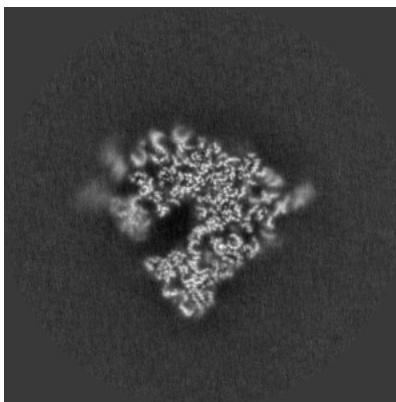


Z Index: 210

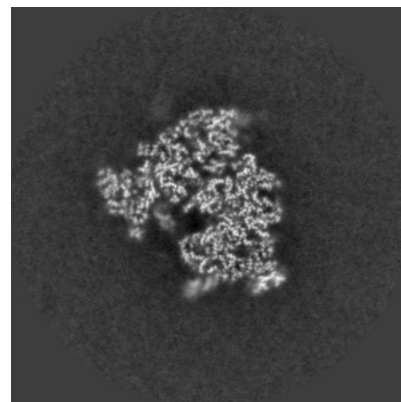
### 6.2.2 Raw map



X Index: 210



Y Index: 210

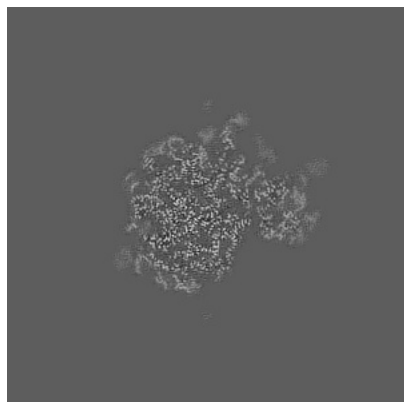


Z Index: 210

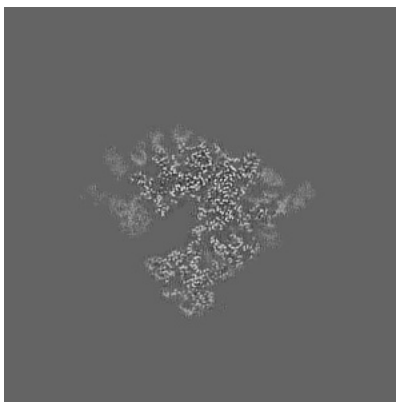
The images above show central slices of the map in three orthogonal directions.

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

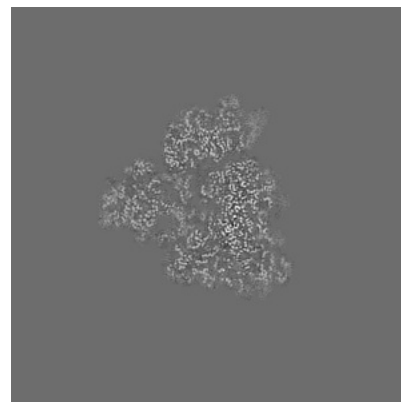
### 6.3.1 Primary map



X Index: 233

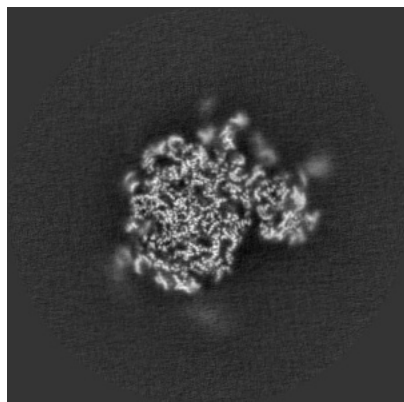


Y Index: 211

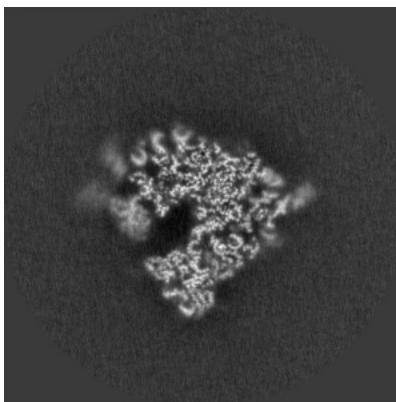


Z Index: 195

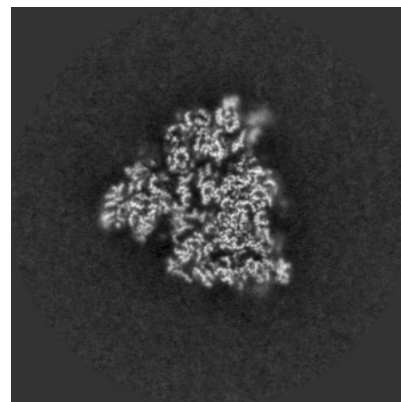
### 6.3.2 Raw map



X Index: 233



Y Index: 211

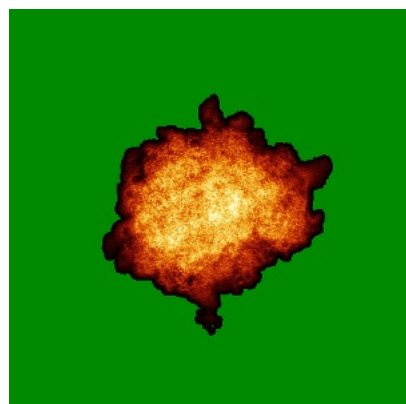


Z Index: 198

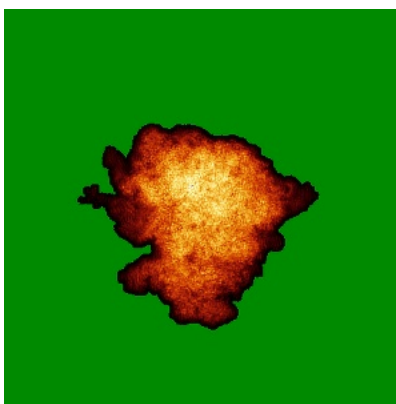
The images above show the largest variance slices of the map in three orthogonal directions.

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

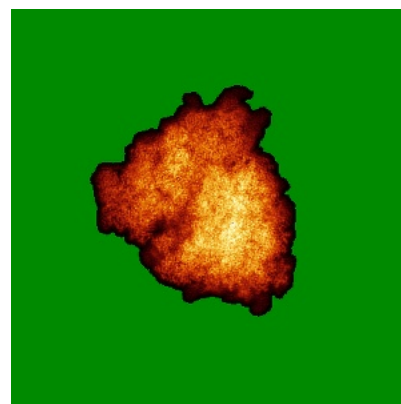
### 6.4.1 Primary map



X

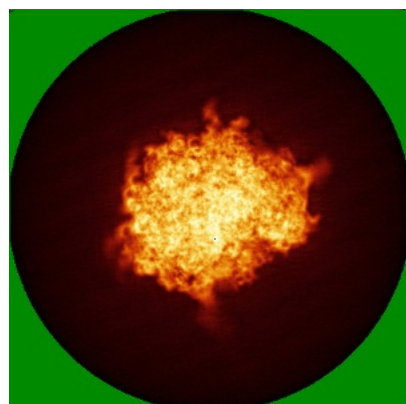


Y

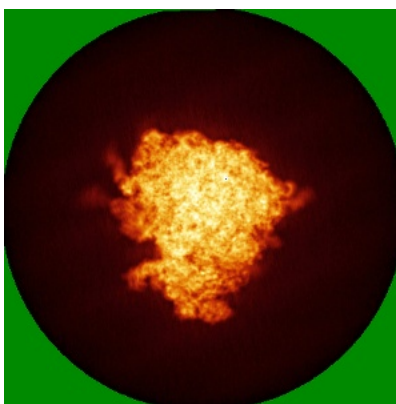


Z

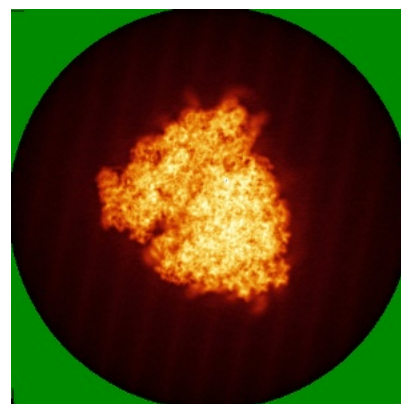
### 6.4.2 Raw map



X



Y

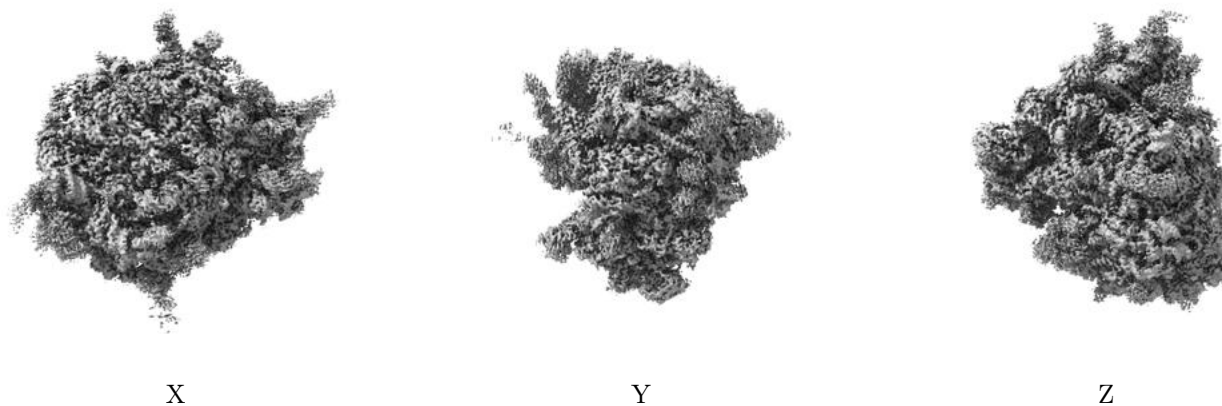


Z

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 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

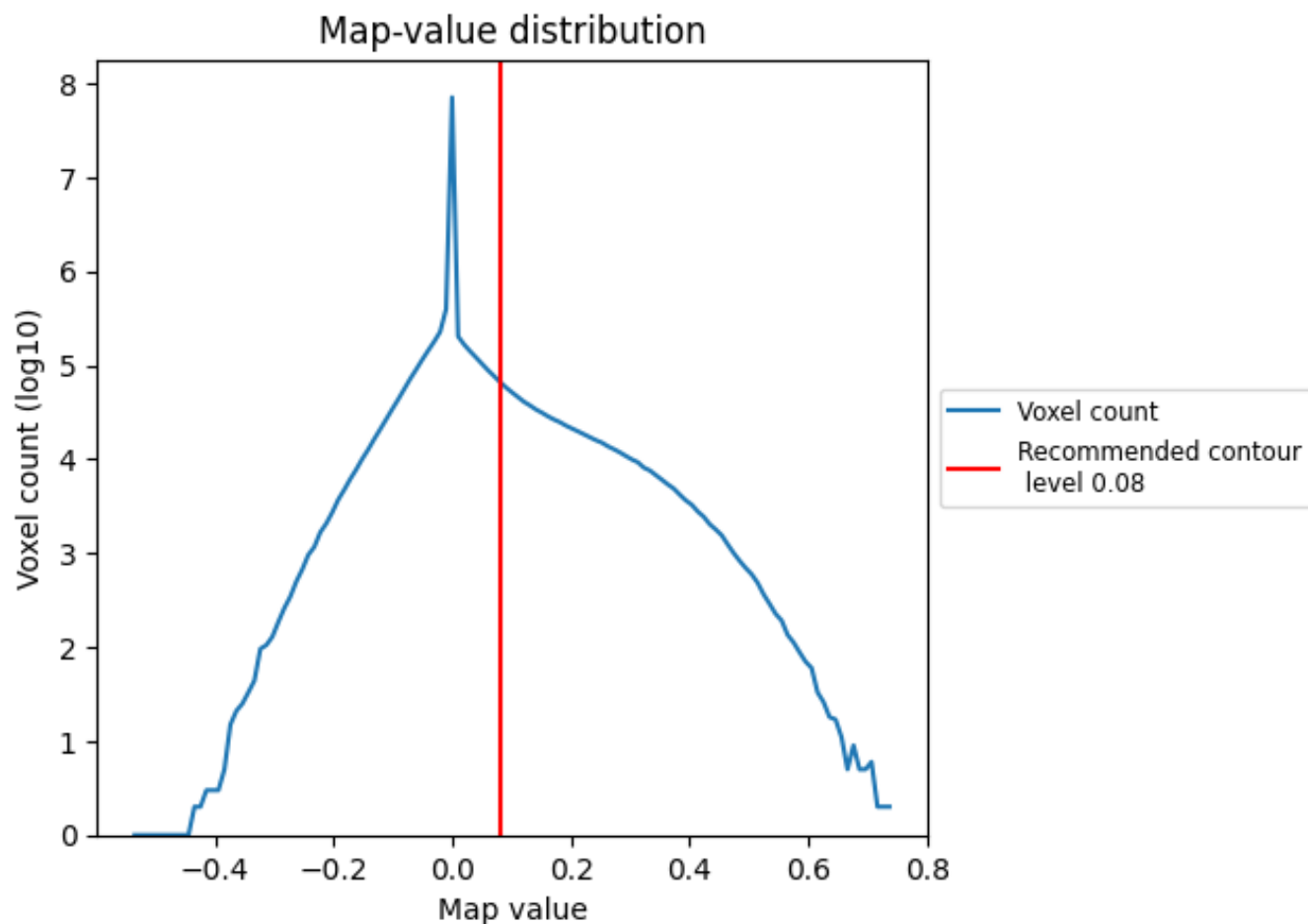
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

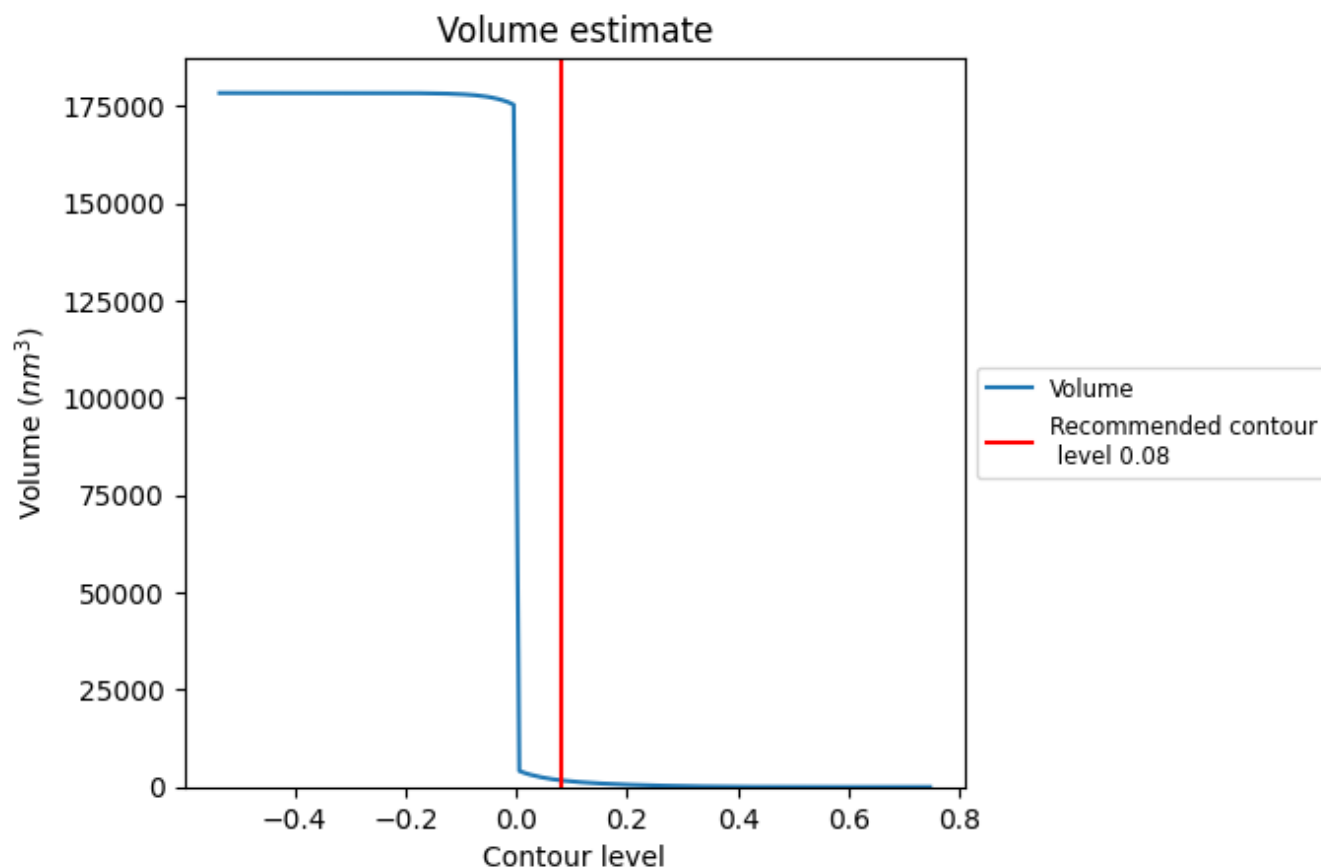
This section contains the results of statistical analysis of the map.

### 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.

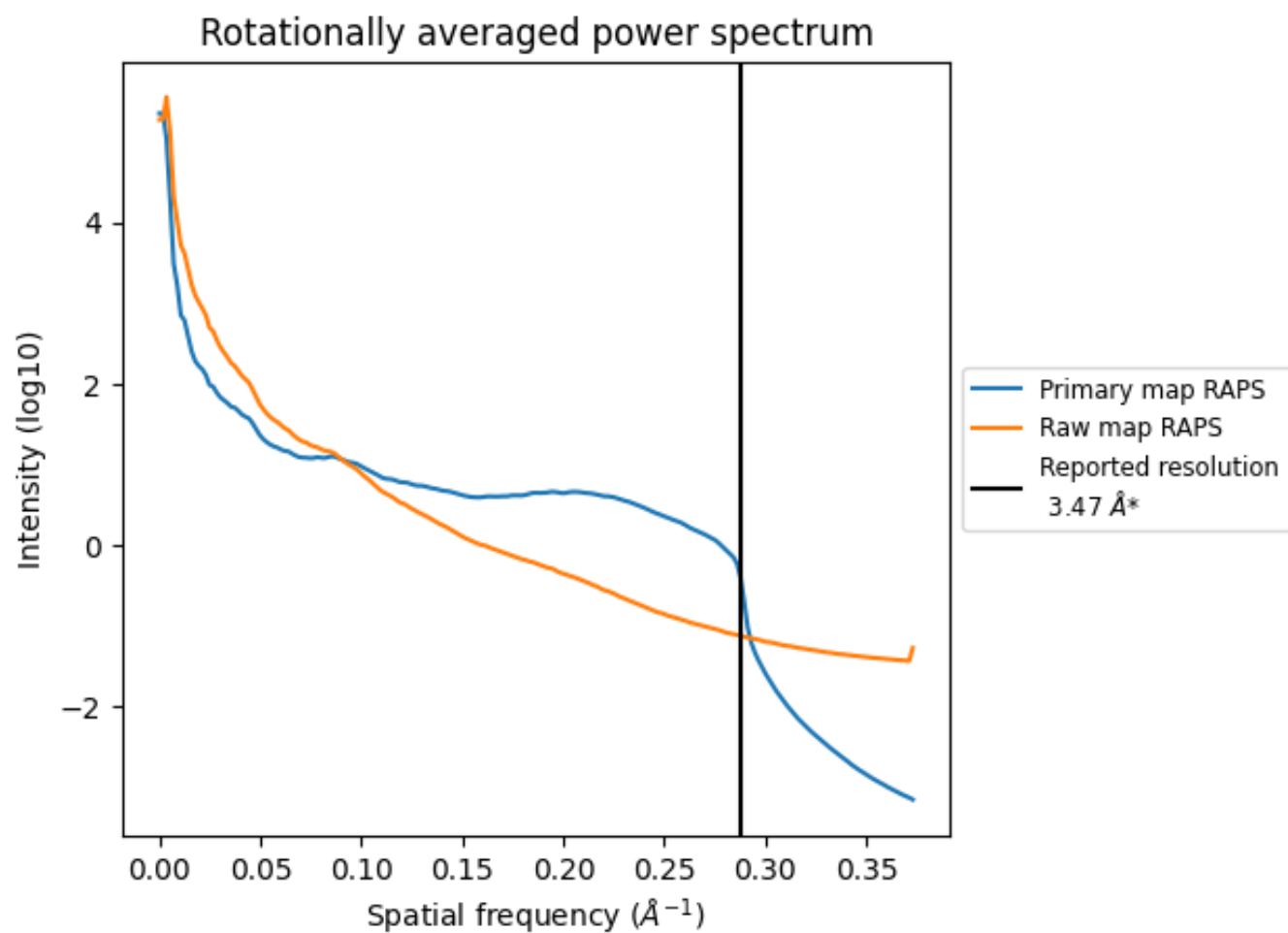
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1722 nm<sup>3</sup>; this corresponds to an approximate mass of 1556 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 ⓘ

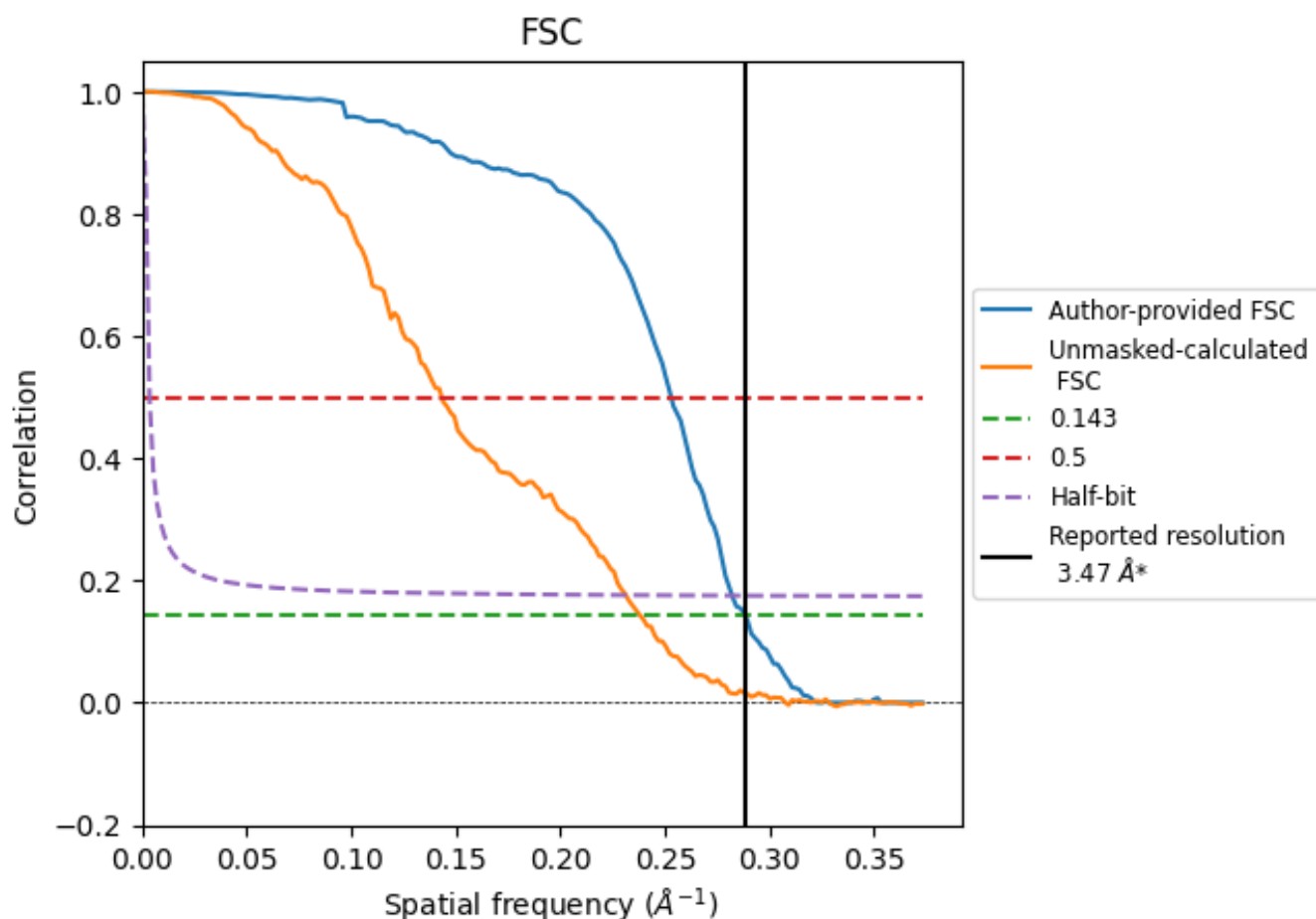


\*Reported resolution corresponds to spatial frequency of  $0.288 \text{ \AA}^{-1}$

## 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 0.288 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

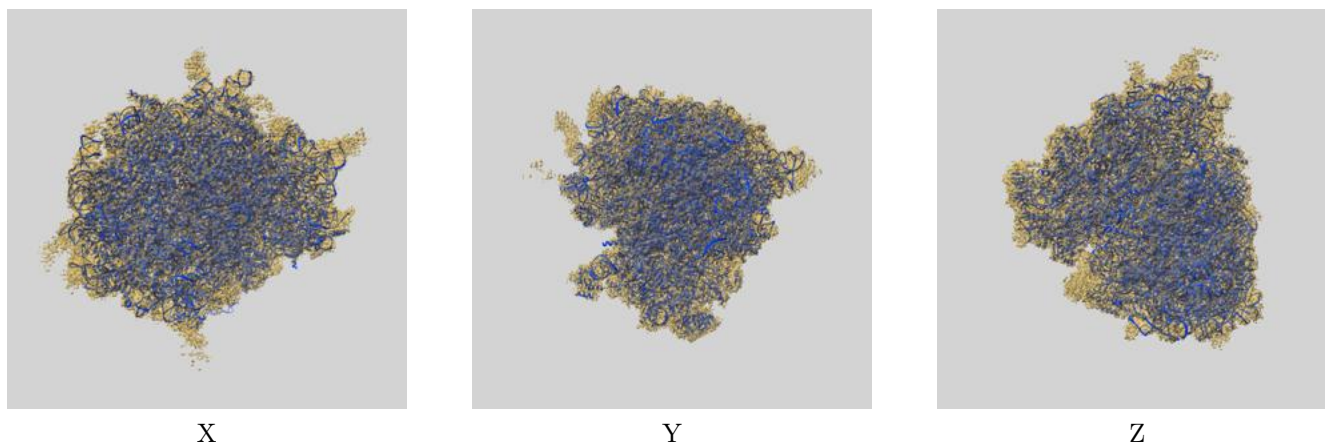
| Resolution estimate (Å)   | Estimation criterion (FSC cut-off) |      |          |
|---------------------------|------------------------------------|------|----------|
|                           | 0.143                              | 0.5  | Half-bit |
| Reported by author        | 3.47                               | -    | -        |
| Author-provided FSC curve | 3.47                               | 3.95 | 3.54     |
| Unmasked-calculated*      | 4.20                               | 6.98 | 4.32     |

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.20 differs from the reported value 3.47 by more than 10 %

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

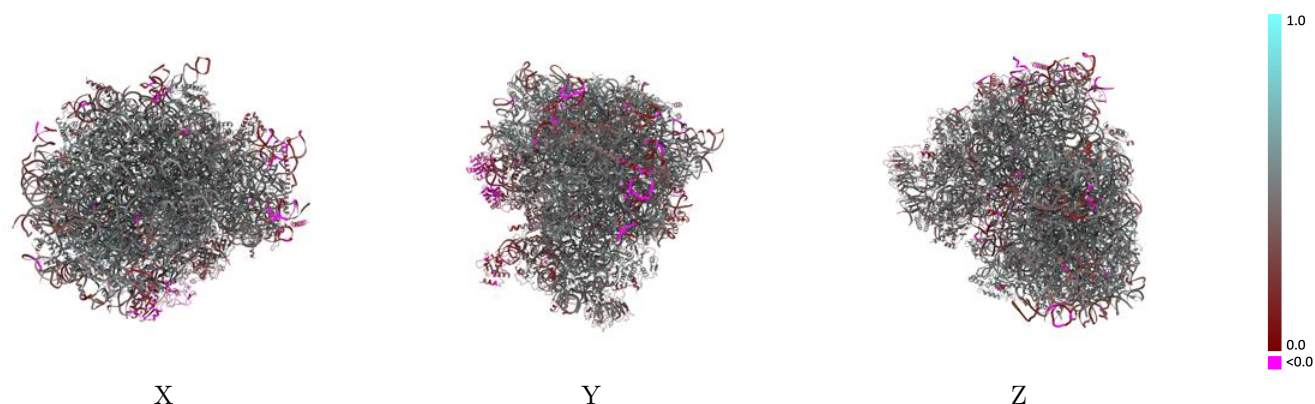
This section contains information regarding the fit between EMDB map EMD-4137 and PDB model 5LZZ. Per-residue inclusion information can be found in section [3](#) on page [24](#).

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



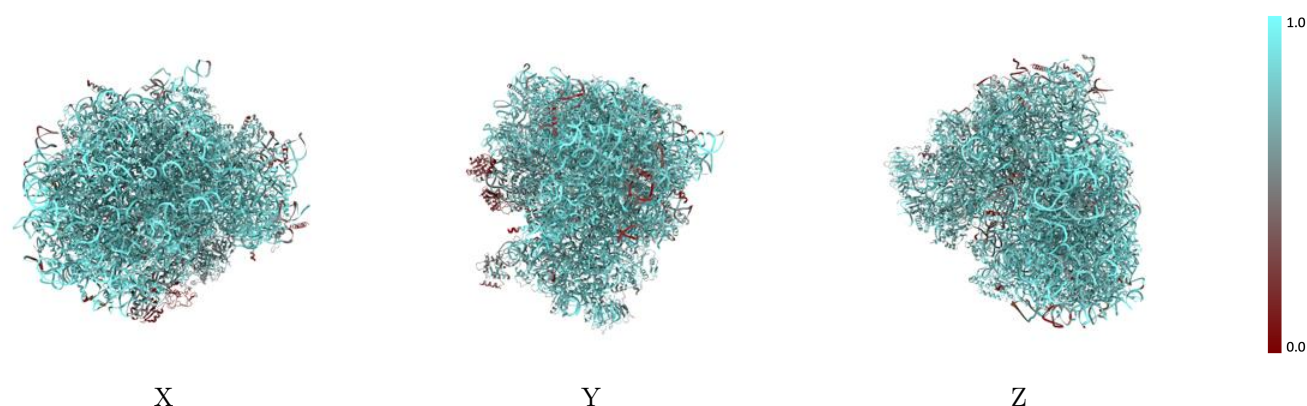
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



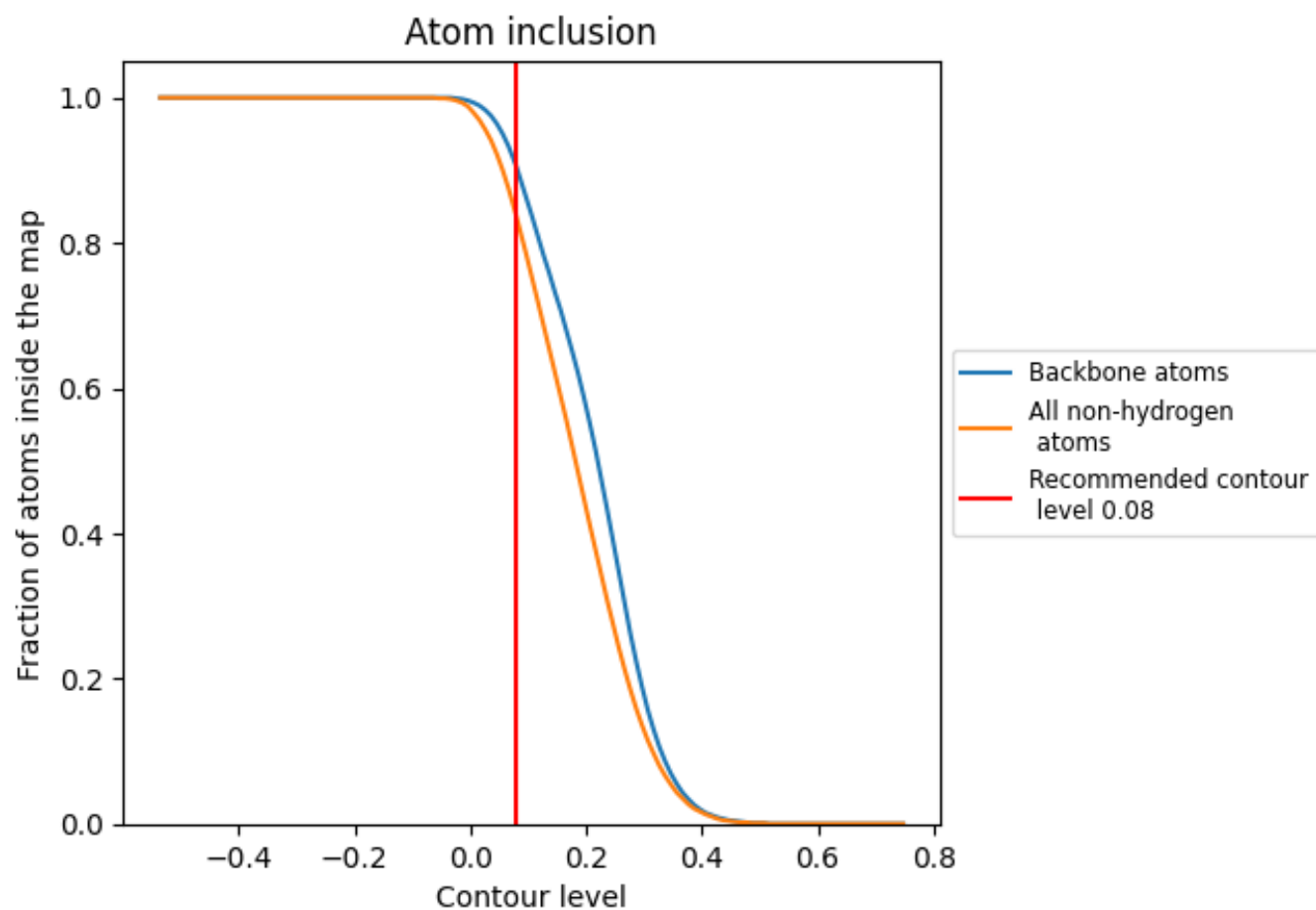
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.08).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 84% 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 (0.08) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion                                                                             | Q-score                                                                                    |
|-------|--------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|
| All   |  0.8350   |  0.4460   |
| 1     |  0.4490   |  0.3290   |
| 2     |  0.8300   |  0.4290   |
| 3     |  0.5840   |  0.2260   |
| 5     |  0.8920   |  0.4490   |
| 7     |  0.9390   |  0.4940   |
| 8     |  0.8980   |  0.4490   |
| 9     |  0.8790   |  0.4310   |
| A     |  0.8530   |  0.5150   |
| AA    |  0.7930   |  0.4570   |
| B     |  0.8560   |  0.5110   |
| BB    |  0.7820   |  0.4670   |
| C     |  0.8520   |  0.5060   |
| CC    |  0.8060   |  0.4810   |
| D     |  0.8370  |  0.4780  |
| DD    |  0.7470 |  0.4350 |
| E     |  0.8450 |  0.4890 |
| EE    |  0.7990 |  0.4750 |
| F     |  0.8520 |  0.5180 |
| FF    |  0.7620 |  0.4480 |
| G     |  0.7640 |  0.4410 |
| GG    |  0.7380 |  0.3920 |
| H     |  0.8260 |  0.4940 |
| HH    |  0.7000 |  0.4040 |
| I     |  0.8310 |  0.5080 |
| II    |  0.7870 |  0.4610 |
| J     |  0.8210 |  0.4720 |
| JJ    |  0.8210 |  0.4670 |
| KK    |  0.7630 |  0.4020 |
| L     |  0.8150 |  0.4760 |
| LL    |  0.8000 |  0.4810 |
| M     |  0.8390 |  0.4900 |
| MM    |  0.4840 |  0.1950 |
| N     |  0.8500 |  0.5180 |
| NN    |  0.8130 |  0.4850 |



*Continued on next page...*

*Continued from previous page...*

| Chain | Atom inclusion                                                                             | Q-score                                                                                    |
|-------|--------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|
| O     |  0.8500   |  0.5100   |
| OO    |  0.8140   |  0.4840   |
| P     |  0.8490   |  0.5110   |
| PP    |  0.7380   |  0.4060   |
| Q     |  0.8430   |  0.5100   |
| QQ    |  0.7960   |  0.4620   |
| R     |  0.7950   |  0.4600   |
| RR    |  0.7580   |  0.4370   |
| S     |  0.8620   |  0.5210   |
| SS    |  0.7710   |  0.4240   |
| T     |  0.8210   |  0.4920   |
| TT    |  0.8100   |  0.4360   |
| U     |  0.7940   |  0.4370   |
| UU    |  0.7460   |  0.4290   |
| V     |  0.8130   |  0.5150   |
| VV    |  0.8100   |  0.4750   |
| W     |  0.6790   |  0.3720   |
| WW    |  0.8440  |  0.5080  |
| X     |  0.8010 |  0.4830 |
| XX    |  0.8010 |  0.5020 |
| Y     |  0.8300 |  0.4960 |
| YY    |  0.7960 |  0.4470 |
| Z     |  0.8540 |  0.4880 |
| ZZ    |  0.7020 |  0.3930 |
| a     |  0.8460 |  0.5160 |
| aa    |  0.8080 |  0.4770 |
| b     |  0.7340 |  0.4180 |
| bb    |  0.7500 |  0.4340 |
| c     |  0.7940 |  0.4640 |
| cc    |  0.7210 |  0.4510 |
| d     |  0.8100 |  0.4820 |
| dd    |  0.8460 |  0.4950 |
| e     |  0.8470 |  0.5140 |
| ee    |  0.7250 |  0.4270 |
| f     |  0.8650 |  0.5260 |
| ff    |  0.5620 |  0.2600 |
| g     |  0.8120 |  0.4920 |
| gg    |  0.7550 |  0.4020 |
| h     |  0.8030 |  0.4760 |
| hh    |  0.1480 |  0.2260 |
| i     |  0.8100 |  0.4640 |
| ii    |  0.6220 |  0.3820 |

*Continued on next page...*

*Continued from previous page...*

| Chain | Atom inclusion                                                                           | Q-score                                                                                  |
|-------|------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------|
| j     |  0.8680 |  0.5140 |
| jj    |  0.6420 |  0.3630 |
| k     |  0.7500 |  0.4310 |
| l     |  0.8410 |  0.4970 |
| m     |  0.8490 |  0.5040 |
| n     |  0.6740 |  0.4700 |
| o     |  0.8090 |  0.5040 |
| p     |  0.7980 |  0.4900 |
| r     |  0.8750 |  0.5190 |
| s     |  0.2300 |  0.0810 |
| t     |  0.1440 |  0.0370 |