

wwPDB EM Validation Summary Report (i)

Dec 1, 2021 - 06:50 pm GMT

| PDB ID | : | 70HQ |
|------------------------|---|--|
| EMDB ID | : | EMD-12905 |
| Title | : | Nog1-TAP associated immature ribosomal particle population C from S. cere- |
| | | visiae |
| Authors | : | Milkereit, P.; Poell, G. |
| Deposited on | : | 2021-05-11 |
| Resolution | : | 3.10 Å(reported) |
| Based on initial model | : | 3JCT |

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

We welcome your comments at *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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

| EMDB validation analysis | : | $0.0.0.{ m dev}97$ |
|--------------------------------|---|--|
| MolProbity | : | 4.02b-467 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.23.2 |

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 3.10 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 | $egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$ | ${f EM\ structures}\ (\#{ m Entries})$ |
|-----------------------|--|--|
| Ramachandran outliers | 154571 | 4023 |
| Sidechain outliers | 154315 | 3826 |
| RNA backbone | 4643 | 859 |

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 >=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 <=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 o | of chain | | |
|-----|-------|--------|----------|------------|-----------|----------|-----|-------|
| 1 | 1 | 3396 | - | | 70% | | 20% | 10% |
| 2 | 2 | 158 | | | 82% | | | 18% • |
| 3 | 3 | 121 | | | 84% | | | 16% |
| 4 | 5 | 120 | | 35% 41% | • | 58% | | |
| 5 | 6 | 232 | 18% | 10% | | 72% | | |
| 6 | А | 254 | 7% | | 83% | | | 17% |
| 7 | В | 387 | — | | 98% | | | · |
| 8 | С | 362 | | | 98% | | | • |



| Mol | Chain | Length | Quality of chain | |
|-----|-------|--------|------------------|-------|
| 9 | D | 297 | 41% | • 12% |
| 10 | F | 176 | • | 110/ |
| 10 | | 170 | 88% | • 11% |
| 11 | F | 244 | 90% | • 9% |
| 12 | G | 256 | 90% | • 9% |
| 13 | Н | 191 | • 99% | • |
| 14 | J | 174 | 8% | ••• |
| 15 | K | 376 | 6 5% • 33 | % |
| 16 | L | 199 | <u>6%</u> 92% | • 6% |
| 17 | М | 138 | 99% | · |
| 18 | Ν | 204 | 98% | • |
| 19 | Ο | 199 | 98% | |
| 20 | Р | 184 | 94% | • • |
| 21 | Q | 186 | 72% | 28% |
| 22 | R | 189 | 81% | 17% |
| 23 | S | 172 | 97% | •• |
| 24 | Т | 160 | 71% | 28% |
| 25 | U | 121 | 81% | 17% |
| 26 | V | 137 | 99% | |
| 27 | W | 236 | 96% | |
| 28 | X | 142 | 97% | •• |
| 29 | Y | 127 | 98% | •• |
| 30 | Z | 136 | 98% | •• |
| 31 | a | 149 | 62% · 38% |) |
| 32 | b | 647 | 9% 81% · | 17% |
| 33 | с | 105 | 91% | • 8% |

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• 7%

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 Mol
 Chain
 Length
 Quality of chain

 34
 d
 113
 91%

 35
 e
 130
 96%

 36
 f
 107
 98%

| 35 | е | 130 | 96% | •• |
|------|-----|-----------|----------------|--------|
| 36 | f | 107 | 98% | •• |
| 37 | ď | 191 | 7% | 70/ |
| - 51 | g | 121 | 93% | 1% |
| 38 | h | 120 | 98% | •• |
| 39 | i | 100 | 97% | |
| 40 | i | 88 | 97% | 5% • |
| 10 | J | | 14% | 570 - |
| 41 | k | 78 | 99% | · |
| 42 | 1 | 51 | 96% | |
| 49 | | 196 | 16% | |
| 45 | III | 480 | 93% | • 5% |
| 44 | n | 605 | 60% | 39% |
| 45 | О | 220 | 59% • | 40% |
| 16 | | 0.0 | <u></u> | |
| 40 | р | 92 | 98% | •• |
| 47 | q | 455 | 32% 68% | |
| 48 | r | 261 | 85% | • 12% |
| | | | •••••• | |
| 49 | S | 520 | 10% 90% 15% | |
| 50 | t | 322 | 87% | •• 11% |
| 51 | 11 | 100 | 9% | 250/ |
| - 51 | u | 199 | 74% 38% | 25% |
| 52 | v | 344 | 83% | 17% |
| 53 | 337 | 203 | 40% | 10% |
| - 00 | vv | 200 | 25% | • 10% |
| 54 | x | 515 | 80% | • 20% |
| 55 | у | 245 | 98% | · |
| 56 | 7 | 106 | 23% | |
| | | 1 1 1 1 1 | • | |



2 Entry composition (i)

There are 58 unique types of molecules in this entry. The entry contains 264865 atoms, of which 115934 are hydrogens and 0 are deuteriums.

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

• Molecule 1 is a RNA chain called 25S rRNA.

| Mol | Chain | Residues | | | AltConf | Trace | | | | |
|-----|-------|----------|----------------|------------|------------|------------|------------|-----------|---|---|
| 1 | 1 | 3053 | Total 98146 | C 29178 | H 32819 | N 11796 | O 21300 | Р 3053 | 0 | 0 |

• Molecule 2 is a RNA chain called 5.8S rRNA.

| Mol | Chain | Residues | | | AltConf | Trace | | | | |
|-----|-------|----------|---------------|-----------|-----------|----------|-----------|----------|---|---|
| 2 | 2 | 158 | Total 5048 | C 1500 | Н 1695 | N 586 | O 1109 | Р 158 | 0 | 0 |

• Molecule 3 is a RNA chain called 5S rRNA.

| Mol | Chain | Residues | | | AltConf | Trace | | | | |
|-----|-------|----------|-------|------|---------|-------|-----|-----|---|---|
| 3 | 2 | 191 | Total | С | Η | Ν | 0 | Р | 0 | 0 |
| 5 | 5 | 121 | 3883 | 1152 | 1304 | 461 | 845 | 121 | 0 | 0 |

• Molecule 4 is a protein called rRNA-processing protein CGR1.

| Mol | Chain | Residues | | ŀ | AltConf | Trace | | | | |
|-----|-------|----------|--------------|----------|----------|---------|---------|--------|---|---|
| 4 | 5 | 51 | Total 927 | C 280 | Н 475 | N 86 | O 85 | S 1 | 0 | 0 |

• Molecule 5 is a RNA chain called ITS2.

| Mol | Chain | Residues | | | AltConf | Trace | | | | |
|-----|-------|----------|---------------|----------|----------|----------|----------|---------|---|---|
| 5 | 6 | 65 | Total 2061 | C 614 | Н 691 | N 228 | 0 463 | Р 65 | 0 | 0 |

• Molecule 6 is a protein called 60S ribosomal protein L2-A.

| Mol | Chain | Residues | | | AltConf | Trace | | | | |
|-----|-------|----------|---------------|-----------|-----------|----------|----------|--------|---|---|
| 6 | А | 212 | Total 3314 | C 1021 | Н 1684 | N 325 | 0 283 | S 1 | 0 | 0 |



• Molecule 7 is a protein called 60S ribosomal protein L3.

| Mol | Chain | Residues | | | Atoms | 5 | | | AltConf | Trace |
|-----|-------|----------|---------------|-----------|-----------|----------|----------|--------|---------|-------|
| 7 | В | 386 | Total 6247 | C 1956 | Н 3166 | N 584 | O 533 | S 8 | 0 | 0 |

• Molecule 8 is a protein called 60S ribosomal protein L4-A.

| Mol | Chain | Residues | | | Atoms | 5 | | | AltConf | Trace |
|-----|-------|----------|---------------|-----------|-----------|----------|----------|--------|---------|-------|
| 8 | С | 361 | Total 5613 | C 1730 | Н 2864 | N 522 | 0 494 | S 3 | 0 | 0 |

• Molecule 9 is a protein called 60S ribosomal protein L5.

| Mol | Chain | Residues | | | Atoms | 5 | | | AltConf | Trace |
|-----|-------|----------|---------------|-----------|-----------|----------|----------|-----------------|---------|-------|
| 9 | D | 261 | Total 4178 | C 1335 | Н 2066 | N 372 | 0 403 | ${ m S} { m 2}$ | 0 | 0 |

• Molecule 10 is a protein called 60S ribosomal protein L6-A.

| Mol | Chain | Residues | | | Atom | S | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|-----------|----------|----------|--------|---------|-------|
| 10 | Е | 156 | Total 2567 | C 800 | Н 1328 | N 222 | 0 216 | S 1 | 0 | 0 |

• Molecule 11 is a protein called 60S ribosomal protein L7-A.

| Mol | Chain | Residues | | | Atom | 5 | | | AltConf | Trace |
|-----|-------|----------|---------------|-----------|-----------|----------|----------|--------|---------|-------|
| 11 | F | 222 | Total 3647 | C 1151 | Н 1863 | N 324 | O 308 | S 1 | 0 | 0 |

• Molecule 12 is a protein called 60S ribosomal protein L8-A.

| Mol | Chain | Residues | | | Atoms | 5 | | | AltConf | Trace |
|-----|-------|----------|---------------|-----------|-----------|----------|----------|-----------------|---------|-------|
| 12 | G | 233 | Total 3726 | C 1159 | H 1909 | N 326 | O 329 | ${ m S} { m 3}$ | 0 | 0 |

• Molecule 13 is a protein called 60S ribosomal protein L9-A.

| Mol | Chain | Residues | | | Atom | S | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|-----------|----------|----------|---------------|---------|-------|
| 13 | Н | 191 | Total 3105 | C 963 | H 1587 | N 274 | 0 277 | ${S \over 4}$ | 0 | 0 |

• Molecule 14 is a protein called 60S ribosomal protein L11-A.



| Mol | Chain | Residues | | | Atom | IS | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|-----------|----------|----------|---------------|---------|-------|
| 14 | J | 169 | Total 2737 | C 847 | Н 1384 | N 253 | O 249 | $\frac{S}{4}$ | 0 | 0 |

• Molecule 15 is a protein called Proteasome-interacting protein CIC1.

| Mol | Chain | Residues | | | Atom | 5 | | | AltConf | Trace |
|-----|-------|----------|---------------|-----------|-----------|----------|----------|-----------------|---------|-------|
| 15 | К | 252 | Total 4153 | C 1312 | Н 2121 | N 336 | O 381 | ${ m S} { m 3}$ | 0 | 0 |

• Molecule 16 is a protein called 60S ribosomal protein L13-A.

| Mol | Chain | Residues | | A | AltConf | Trace | | | |
|-----|-------|----------|---------------|----------|-----------|----------|----------|---|---|
| 16 | L | 187 | Total 3057 | C 934 | Н 1558 | N 307 | O 258 | 0 | 0 |

• Molecule 17 is a protein called 60S ribosomal protein L14-A.

| Mol | Chain | Residues | | | Atom | .s | | | AltConf | Trace |
|-----|-------|----------|---------------|--|-----------|----------|----------|-----------------|---------|-------|
| 17 | М | 137 | Total 2214 | $\begin{array}{c} \mathrm{C} \\ 678 \end{array}$ | Н 1155 | N 200 | O 179 | ${ m S} { m 2}$ | 0 | 0 |

• Molecule 18 is a protein called 60S ribosomal protein L15-A.

| Mol | Chain | Residues | | | Atoms | 5 | | | AltConf | Trace |
|-----|-------|----------|---------------|-----------|-----------|----------|----------|--------|---------|-------|
| 18 | Ν | 203 | Total 3500 | C 1077 | Н 1780 | N 361 | 0 281 | S 1 | 0 | 0 |

• Molecule 19 is a protein called 60S ribosomal protein L16-A.

| Mol | Chain | Residues | | | | AltConf | Trace | | | |
|-----|-------|----------|---------------|-----------|-----------|----------|----------|--------|---|---|
| 19 | Ο | 197 | Total 3215 | C 1003 | Н 1660 | N 289 | O 262 | S 1 | 0 | 0 |

• Molecule 20 is a protein called 60S ribosomal protein L17-A.

| Mol | Chain | Residues | | A | Atoms | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|-----------|----------|----------|---------|-------|
| 20 | Р | 177 | Total 2845 | C 871 | Н 1443 | N 280 | O 251 | 0 | 0 |

• Molecule 21 is a protein called 60S ribosomal protein L18-A.



| Mol | Chain | Residues | | | Atom | S | | | AltConf | Trace |
|-----|-------|----------|---------------|--|-----------|----------|----------|--------|---------|-------|
| 21 | Q | 134 | Total 2151 | $\begin{array}{c} \mathrm{C} \\ 659 \end{array}$ | Н 1116 | N 196 | O 179 | S 1 | 0 | 0 |

• Molecule 22 is a protein called 60S ribosomal protein L19-A.

| Mol | Chain | Residues | | A | Atoms | | Atoms | | | | | |
|-----|-------|----------|---------------|----------|-----------|----------|----------|---|---|--|--|--|
| 22 | R | 156 | Total 2601 | C 781 | Н 1343 | N 265 | O 212 | 0 | 0 | | | |

• Molecule 23 is a protein called 60S ribosomal protein L20-A.

| Mol | Chain | Residues | | | Atom | S | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|-----------|----------|----------|-----------------|---------|-------|
| 23 | S | 171 | Total 2913 | C 925 | Н 1476 | N 266 | O 243 | ${ m S} { m 3}$ | 0 | 0 |

• Molecule 24 is a protein called 60S ribosomal protein L21-A.

| Mol | Chain | Residues | | | Aton | ıs | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|----------|----------|----------|-----------------|---------|-------|
| 24 | Т | 116 | Total 1902 | C 584 | Н 978 | N 176 | 0 161 | ${ m S} { m 3}$ | 0 | 0 |

• Molecule 25 is a protein called 60S ribosomal protein L22-A.

| Mol | Chain | Residues | | Α | toms | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|----------|----------|----------|---------|-------|
| 25 | U | 101 | Total 1617 | C 519 | Н 816 | N 131 | 0 151 | 0 | 0 |

• Molecule 26 is a protein called 60S ribosomal protein L23-A.

| Mol | Chain | Residues | | | Atom | .s | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|-----------|----------|----------|----------|---------|-------|
| 26 | V | 136 | Total 2052 | C 628 | Н 1049 | N 189 | 0 179 | ${f S}7$ | 0 | 0 |

• Molecule 27 is a protein called Ribosome assembly factor MRT4.

| Mol | Chain | Residues | | | Atom | 5 | | | AltConf | Trace |
|-----|-------|----------|---------------|-----------|-----------|----------|----------|--------|---------|-------|
| 27 | W | 234 | Total 3806 | C 1194 | Н 1921 | N 323 | O 362 | S 6 | 0 | 0 |

• Molecule 28 is a protein called 60S ribosomal protein L25.



| Mol | Chain | Residues | | | Atom | IS | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|-----------|----------|----------|-----------------|---------|-------|
| 28 | Х | 141 | Total 2288 | C 705 | Н 1188 | N 196 | O 197 | ${ m S} { m 2}$ | 0 | 0 |

• Molecule 29 is a protein called 60S ribosomal protein L26-A.

| Mol | Chain | Residues | | A | toms | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|-----------|----------|----------|---------|-------|
| 29 | Y | 126 | Total 2075 | C 625 | Н 1082 | N 192 | O 176 | 0 | 0 |

• Molecule 30 is a protein called 60S ribosomal protein L27-A.

| Mol | Chain | Residues | | A | AltConf | Trace | | | |
|-----|-------|----------|---------------|----------|-----------|----------|----------|---|---|
| 30 | Ζ | 135 | Total 2248 | C 710 | Н 1156 | N 202 | O 180 | 0 | 0 |

• Molecule 31 is a protein called 60S ribosomal protein L28.

| Mol | Chain | Residues | | | Aton | ıs | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|----------|----------|----------|--------|---------|-------|
| 31 | a | 93 | Total 1512 | C 479 | Н 777 | N 130 | 0 125 | S 1 | 0 | 0 |

• Molecule 32 is a protein called Nucleolar GTP-binding protein 1.

| Mol | Chain | Residues | | | Atom | S | | | AltConf | Trace |
|-----|-------|----------|---------------|-----------|-----------|----------|----------|---------|---------|-------|
| 32 | b | 537 | Total 8784 | C 2760 | Н 4427 | N 763 | 0 811 | S 23 | 0 | 0 |

• Molecule 33 is a protein called 60S ribosomal protein L30.

| Mol | Chain | Residues | | | Aton | ns | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|----------|----------|----------|--------|---------|-------|
| 33 | С | 97 | Total 1541 | C 479 | Н 798 | N 124 | 0 139 | S 1 | 0 | 0 |

• Molecule 34 is a protein called 60S ribosomal protein L31-A.

| Mol | Chain | Residues | | | AltConf | Trace | | | | |
|-----|-------|----------|---------------|----------|----------|----------|----------|--------|---|---|
| 34 | d | 105 | Total 1761 | С 544 | Н 905 | N 163 | 0 148 | S 1 | 0 | 0 |

• Molecule 35 is a protein called 60S ribosomal protein L32.



| Mol | Chain | Residues | | | Atom | IS | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|-----------|----------|----------|--------|---------|-------|
| 35 | е | 127 | Total 2112 | С 647 | Н 1092 | N 205 | O 167 | S 1 | 0 | 0 |

• Molecule 36 is a protein called 60S ribosomal protein L33-A.

| Mol | Chain | Residues | | | Aton | ıs | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|----------|----------|----------|--------|---------|-------|
| 36 | f | 106 | Total 1731 | C 540 | Н 881 | N 165 | 0 144 | S 1 | 0 | 0 |

• Molecule 37 is a protein called 60S ribosomal protein L34-A.

| Mol | Chain | Residues | | | AltConf | Trace | | | | |
|-----|-------|----------|---------------|----------|----------|----------|----------|---------------|---|---|
| 37 | g | 112 | Total 1831 | C 546 | Н 950 | N 179 | 0 152 | $\frac{S}{4}$ | 0 | 0 |

• Molecule 38 is a protein called 60S ribosomal protein L35-A.

| Mol | Chain | Residues | | | Atom | s | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|-----------|----------|----------|--------|---------|-------|
| 38 | h | 119 | Total 2048 | C 615 | Н 1079 | N 186 | 0 167 | S 1 | 0 | 0 |

• Molecule 39 is a protein called 60S ribosomal protein L36-A.

| Mol | Chain | Residues | | | Atom | ns | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|----------|----------|----------|-----------------|---------|-------|
| 39 | i | 99 | Total 1621 | C 481 | Н 850 | N 156 | O 132 | ${ m S} { m 2}$ | 0 | 0 |

• Molecule 40 is a protein called 60S ribosomal protein L37-A.

| Mol | Chain | Residues | | | Atom | ns | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|----------|----------|----------|----------------|---------|-------|
| 40 | j | 85 | Total 1348 | C 408 | Н 678 | N 146 | 0 111 | ${ m S}{ m 5}$ | 0 | 0 |

• Molecule 41 is a protein called 60S ribosomal protein L38.

| Mol | Chain | Residues | | A | AltConf | Trace | | | |
|-----|-------|----------|---------------|----------|----------|----------|----------|---|---|
| 41 | k | 77 | Total 1295 | C 391 | Н 683 | N 115 | O 106 | 0 | 0 |

• Molecule 42 is a protein called 60S ribosomal protein L39.



| Mol | Chain | Residues | | ŀ | Atom | s | | | AltConf | Trace |
|-----|-------|----------|--------------|----------|----------|---------|---------|---------------|---------|-------|
| 42 | 1 | 50 | Total 912 | С 272 | Н 476 | N 97 | O 65 | ${S \over 2}$ | 0 | 0 |

• Molecule 43 is a protein called Nucleolar GTP-binding protein 2.

| Mol | Chain | Residues | | | Atoms | 5 | | | AltConf | Trace |
|-----|-------|----------|---------------|-----------|-----------|----------|----------|--------|---------|-------|
| 43 | m | 461 | Total 7508 | C 2350 | Н 3788 | N 675 | O 686 | S 9 | 0 | 0 |

• Molecule 44 is a protein called Pescadillo homolog.

| Mol | Chain | Residues | | | Atom | s | | | AltConf | Trace |
|-----|-------|----------|---------------|-----------|-----------|----------|----------|---------|---------|-------|
| 44 | n | 371 | Total 6139 | C 1963 | Н 3109 | N 523 | 0 534 | S 10 | 0 | 0 |

• Molecule 45 is a protein called Ribosome biogenesis protein 15.

| Mol | Chain | Residues | | | Atom | .s | | | AltConf | Trace |
|-----|-------|----------|-------|----------|-----------|----------|-----|--------|---------|-------|
| 45 | 0 | 133 | Total | C 716 | H 1160 | N 109 | 0 | S 4 | 0 | 0 |
| | | | 2207 | 110 | 1100 | 190 | 169 | 4 | | |

• Molecule 46 is a protein called 60S ribosomal protein L43-A.

| Mol | Chain | Residues | | | Aton | ns | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|----------|----------|----------|--------|---------|-------|
| 46 | р | 91 | Total 1434 | C 429 | Н 740 | N 138 | 0 121 | S 6 | 0 | 0 |

• Molecule 47 is a protein called Ribosome biogenesis protein NOP53.

| Mol | Chain | Residues | | | Atom | s | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|-----------|----------|----------|--------|---------|-------|
| 47 | q | 147 | Total 2501 | C 778 | Н 1268 | N 222 | O 232 | S 1 | 0 | 0 |

• Molecule 48 is a protein called Ribosome biogenesis protein NSA2.

| Mol | Chain | Residues | | | Atom | 5 | | | AltConf | Trace |
|-----|-------|----------|---------------|-----------|-----------|----------|----------|------------|---------|-------|
| 48 | r | 230 | Total 3827 | C 1177 | Н 1967 | N 352 | 0 324 | ${f S}{7}$ | 0 | 0 |

• Molecule 49 is a protein called Nuclear GTP-binding protein NUG1.



| Mol | Chain | Residues | | ŀ | Atom | s | | | AltConf | Trace |
|-----|-------|----------|--------------|----------|----------|---------|---------|---------------|---------|-------|
| 49 | s | 53 | Total 935 | С 274 | Н 499 | N 90 | O 70 | ${S \over 2}$ | 0 | 0 |

• Molecule 50 is a protein called Ribosome biogenesis protein RLP7.

| Mol | Chain | Residues | | | Atom | S | | | AltConf | Trace |
|-----|-------|----------|---------------|-----------|-----------|----------|----------|-----------------|---------|-------|
| 50 | t | 287 | Total 4762 | C 1459 | Н 2456 | N 427 | 0 417 | ${ m S} { m 3}$ | 0 | 0 |

• Molecule 51 is a protein called Ribosome biogenesis protein RLP24.

| Mol | Chain | Residues | | | Atom | .s | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|-----------|----------|----------|--------|---------|-------|
| 51 | u | 150 | Total 2582 | C 793 | Н 1317 | N 253 | O 210 | S 9 | 0 | 0 |

• Molecule 52 is a protein called Ribosome biogenesis protein RPF2.

| Mol | Chain | Residues | | | Atom | s | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|--------------|---------|-------|
| 59 | 17 | 287 | Total | С | Η | Ν | 0 | \mathbf{S} | 0 | 0 |
| 52 | v | 201 | 4718 | 1482 | 2400 | 408 | 412 | 16 | 0 | 0 |

• Molecule 53 is a protein called Regulator of ribosome biosynthesis.

| Mol | Chain | Residues | | | Atom | S | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|-----------|----------|----------|----------------|---------|-------|
| 53 | W | 182 | Total 2960 | C 911 | H 1512 | N 261 | 0 271 | ${ m S}{ m 5}$ | 0 | 0 |

• Molecule 54 is a protein called Ribosome assembly protein 4.

| Mol | Chain | Residues | | | Atom | .s | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|--------------|---------|-------|
| 54 | v | /12 | Total | С | Η | Ν | Ο | \mathbf{S} | 0 | 0 |
| 04 | X | 410 | 6438 | 2030 | 3207 | 583 | 598 | 20 | | U |

• Molecule 55 is a protein called Eukaryotic translation initiation factor 6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|---|-----------|-----------|----------|----------|------------|-------|---|
| 55 | У | 244 | $\begin{array}{c} \text{Total} \\ 3685 \end{array}$ | C 1146 | Н 1836 | N 319 | 0 377 | ${f S}{7}$ | 0 | 0 |

• Molecule 56 is a protein called UPF0642 protein YBL028C.



| Mol | Chain | Residues | Atoms | | | | AltConf | Trace | |
|-----|-------|----------|--------------|----------|----------|---------|---------|-------|---|
| 56 | Z | 46 | Total 772 | C 228 | Н 402 | N 75 | O 67 | 0 | 0 |

• Molecule 57 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | AltConf |
|-----|-------|----------|-----------------|---------|
| 57 | b | 1 | Total Mg 1 1 | 0 |
| 57 | m | 1 | Total Mg 1 1 | 0 |

• Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | AltConf |
|-----|-------|----------|-----------------|---------|
| 58 | j | 1 | Total Zn 1 1 | 0 |
| 58 | р | 1 | Total Zn 1 1 | 0 |
| 58 | u | 1 | Total Zn 1 1 | 0 |



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.



 \bullet Molecule 1: 25S rRNA









• Molecule 2: 5.8S rRNA

| Chain 2: | | 82% | | 18% • | I |
|--|---|---|---|---|---|
| A1 616 134 035 639 639 A59 A59 | G63 A71 A71 A72 A71 A71 A72 C83 C83 C83 C83 C83 C83 C83 C83 C83 C83 | U90 695 U100 A104 A105 C106 | A111 U112 U113 G116 G116 G124 G123 G124 U125 A126 | C151 U158 | |
| • Molecule 3: 58 | S rRNA | | | | |
| Chain 3: | | 84% | | 16% | |
| G1 67 422 427 427 652 052 053 | U54 464 465 465 472 476 673 476 677 | 685 691 492 495 4102 4102 | A104 A104 G112 C13 U121 U121 | | |
| • Molecule 4: rF | NA-processing p | protein CGR1 | | | |
| Chain 5: | 35% 41% | · | 58% | | 1 |
| MET VAL VAL ASN GLU GLV GLU SER ALA ALA | LYS GLY THR PRO VAL SER CLY CLY UAL TYR LYS ALA | OLU LYS THR PRO PRO LEU ALA ALA ALA ALA ALA VAL | VAL VAL IVS IVS IVS IVS IVS IVS IVS IVS IVS VA2 K47 | K48 Q49 K50 R51 L52 E53 D54 K55 | 456 757 758 758 759 759 760 761 761 762 762 |
| A71 | N/2 473 A74 176 176 177 L79 K80 K80 K80 | R82 R83 E84 K85 K85 E87 E87 B87 B89 B89 E88 | H91 92 6LU 6LU ARG LEU ALA ALA MET MET HIS | ALA LYS LYS VAL GLU ARG ARG ARG ARG | GLU LYS ARG ARG ARG ALA LYS CLU GLU GLU ARG |
| • Molecule 5: IT | TS2 | | | | |
| Chain 6: 189 | % 10% | | 72% | | |
| C1 C2 C5 C5 C5 A8 A8 V1 4 U1 5 U1 5 C1 7 C1 7 C1 7 C1 7 C1 7 C1 7 C1 7 C1 7 | 023 424 434 637 040 041 652 | A53 A54 A55 A55 A55 C59 C59 C59 C59 C59 C59 C59 C59 C59 C | 00000 4 000 | A U Q U U U U U U U U U U U U U U U U U | |
| A A Q A Q A Q D D D D O | 000000000000000000000000000000000000000 | 4 U U D 4 D 4 A D U U | 4 4 0 D 4 0 0 0 D 0 0 | | |
| < < こし い こ い い つ つ し < < | A A C C C C C C C C C C | 0004000400 | 004400DD4D0 | ७ द 🗅 द द ७ द द ७ - | < ひ く ひ じ |
| のしつしょののののすべい | A A G G C C C C C C C C C C C C C C C C | | | | |
| • Molecule 6: 60 | S ribosomal prot | tein L2-A | | | |
| Chain A: | | 83% | | 17% | |
| MET G2 I5 R6 K28 L32 | A78 A78 E143 V202 A203 M204 | N205 P206 V207 V207 H209 P210 H211 G212 G212 | GLY ASN ASN ASN ALS CLN CLN ALZ ALZ ALZ | TILE SER ARG CLY ALA VAL SER SER CLN GLN | LYS ALA GLY LEU TLE ALA ALA ALA ARG ARG ARG |



GLY LEU LEU ARG GLY SER CLN LYS THR GLN ASP

 \bullet Molecule 7: 60S ribosomal protein L3



| • Molecule 12: | 60S ribosomal protein L8-A | |
|---|---|---|
| Chain G: | 90% | 9% |
| MET ALA ALA GLY CJY CYS LYS VAL ALA ALA ALA ALA PRO | PHE GLY ALA ALA ALA SER THR LIYS SER ARG ARG ARG CI CI CI CI CI CI CI CI CI CI CI CI CI | R249 A250 K251 N252 S253 D254 S255 A256 |
| • Molecule 13: | 60S ribosomal protein L9-A | |
| Chain H: | 99% | |
| M1 S73 N157 E189 D190 | | |
| • Molecule 14: | 60S ribosomal protein L11-A | |
| Chain J: | 95% | |
| MET SER ALA ALA ALA Q6 N7 L30 T31 | R32 K75 K75 R82 S1114 S1120 G121 1122 G121 C122 F163 K174 K174 | |
| • Molecule 15: | Proteasome-interacting protein CIC1 | |
| Chain K: | 65% · 33% | _ |
| MET ALA LYS SFR SFR SFR SFR LYS SFR THR | PRO VAL SER PRO FRO FRO FRO FRO FRO FRO FRO FRO FRO F | F101 F106 K119 |
| K133 | P235 ◆ N262 N262 P235 P233 P262 P235 P235 P235 P235 P235 P235 P235 P23 | GLU TILE ALA ASN PRO SER SER CLU CLU CLU |
| SER ILE PHE SER LYS GLN ASN ASN ALA LYS | LYS SER SER SER CUU CUU CUU CUU CUU CUU CUU CUU CUU CU | |
| • Molecule 16: | 60S ribosomal protein L13-A | |
| Chain L: | 92% | 6% |
| MET ALA ILE SER LYS ASN LEU F P 19 F 10 | R55 V63 V63 V63 V63 1147 A190 A191 A194 A194 A193 E194 A193 E194 A193 LYS LYS LYS | |
| • Molecule 17: | 60S ribosomal protein L14-A | |
| Chain M: | 99% | |





- Molecule 18: 60S ribosomal protein L15-A Chain N: 98% • Molecule 19: 60S ribosomal protein L16-A Chain O: 98% • Molecule 20: 60S ribosomal protein L17-A Chain P: 94% VAL ALA LYS ALA ALA ALA GLU • Molecule 21: 60S ribosomal protein L18-A Chain Q: 72% 28% MET GLY TILE HIS HIS HIS SER LYS GLN HIS SER ARG GLY SER HIS GLY • Molecule 22: 60S ribosomal protein L19-A Chain R: 81% 17% GLU GLU GLU GLU LLEU LLEU LLYS ARG ARG ALA ARG ALA ARG ALA ARG CLU VAL LLEU LLEU LLEU LLEU LLEU LLEU ALA • Molecule 23: 60S ribosomal protein L20-A Chain S: • • 97%
- Molecule 24: 60S ribosomal protein L21-A



| 20% | % | | | | |
|--|--|--|--------------------------|--------------------------|-----|
| Chain T: | 71% | • 28% | 6 | | |
| MET GLY LYS SER HIS GLY CLY ARG ARG SER ARG ARG ARG ARG ARG | MET PHE ALA ARP ARP ARP ALA ALA ALA ALA CLY CLY CLEU CLEU CLEU CLEU CLEU CLEU CLEU CLEU | M45 GLY SER ILF CLN CLN CLN GLY M52 P53 P53 F56 | V63 V64 V67 T68 | K69 S70 S71 V72 | I76 |
| NT7 KT8 MT9 VAL GLY ASN R83 R83 R83 F84 E86 E86 | R85 L89 R92 R92 E94 A125 E137 S138 E137 S138 E144 K139 | P165 | | | |
| • Molecule 25: 60 | 0S ribosomal protein L22-A | | | | |
| Chain U: | 81% | • | 17% | | |
| MET ALA ALA ALA ARO ARO CLYS CLYS CLYS CLYS CLYS CLYS CLYS CLYS | NE2 NF2 K70 K70 K70 CUU CUU CUU CUU CUU CUU CUU CUU CUU CU | | | | |
| • Molecule 26: 60 | 0S ribosomal protein L23-A | | | | |
| Chain V: | 99% | | •• | | |
| MET S2 G3 K71 M74 V137 | | | | | |
| • Molecule 27: R | ibosome assembly factor MRT | `4 | | | |
| Chain W: | 96% | | • • | | |
| M1 P2 R3 R3 R3 R3 P2 V10 M60 | C96 127 K130 E139 E139 D154 N167 K168 K168 K168 K168 K168 K168 K168 CU | | | | |
| • Molecule 28: 60 | 0S ribosomal protein L25 | | | | |
| Chain X: | 97% | | | | |
| MET A2 P3 S4 K12 K25 K25 L40 | K45 M73 N137 1142 | | | | |
| • Molecule 29: 60 | 0S ribosomal protein L26-A | | | | |
| Chain Y: | 98% | | | | |
| MET A2 Y74 E83 E127 | | | | | |
| • Molecule 30: 60 | 0S ribosomal protein L27-A | | | | |
| Chain Z: | 98% | | | | |
| | W O R PROTEI | | | | |



| • | Molecule | 31: | 60S | ribosomal | protein L28 | 3 |
|---|----------|-----|-----|-----------|-------------|---|
|---|----------|-----|-----|-----------|-------------|---|

| Chain a: | 62% | • 38% | - |
|---|--|--|---|
| MET PRO SER ARG PHE LYS THR ARG LYS HIS ARG CLY | VILS VILS SER ALA ALA GLY GLY GLY GLY HTS HTS HTS CLY CLY CLY ARG CLY ARG CLY ARG CLY | MLLI MLA GLY GLY GLY GLN GLN HIS HIS HIS ASP ASP ASP ASP TYR TYR TYR TYR TYR PPRO GLY GLY | LYS V AL G 57 Y 60 |
| 895 A 149 | | | |
| • Molecule 32: Nu | cleolar GTP-binding prote | ein 1 | |
| Chain b: | 81% | • 17% | - |
| M1 Q2 W5 P9 P9 P73 K202 | E230 | L348 K349 S350 G351 S352 R353 R355 R355 R355 R355 K360 K360 R356 R360 R360 R360 R360 S70 | 6471 W427 W427 W432 K439 M470 SER ASP ASP GLU GLU |
| E476 D479 D479 5482 5484 5485 V486 D487 D487 | K492 E491 K492 M498 M498 M493 R403 A503 A503 A504 A504 | K516 A517 1518 M519 P520 P520 F525 K525 F525 K526 S527 K526 S527 K526 K526 K526 K526 K525 K526 K526 K526 | M64.2 SER ALA ALA ALA ALA ALA ALA ALA ALA ALA AL |
| LYS ASN ASN ARG ARG GLU GLU GLU GLV SER ASP VAL VAL VAL | ALT ASP ASP ALA ALA ALA ALA THR THR THR CLU CLU ASN CLU ASN CLU ASN CLU ASN CLU ASN CLU ASN CLU ASN ACA ALA ALA ALA ALA ALA ALA ALA ALA ALA | ARG LEU LEU ASP ASP ASP CLY ALA ASP ASP ASP ASP ASP ASP ASP ASP ASP AS | GLU ARG ARG GLU ARG ASN |
| ARG HIS CLYS CLY GLN GLN GLN GLN GLU ASP ASP ASP ASN ASN | SER LEU LEU LEU LEU LEU PHE CIY CIY CIY CIY CIY CIY CIY CIY CIY CIY | | |
| • Molecule 33: 609 | 5 ribosomal protein L30 | | |
| Chain c: | 91% | • 8% | - |
| MET ALA PALO VAL LYS SER GLU GLU M11 110 110 110 110 | ♦ B B | | |
| • Molecule 34: 605 | 5 ribosomal protein L31-A | | |
| Chain d: | 91% | • 7% | - |
| MET ALA ALA GIY LEU LYS D6 K26 B2 E81 E82 | E83 | | |
| • Molecule 35: 608 | S ribosomal protein L32 | | |
| Chain e: | 96% | | |



••

7%

••

..

5%•

•

| MET H21 GLU GLU GLU |
|--|
| • Molecule 36: 60S ribosomal protein L33-A |
| Chain f: 98% |
| NET NATION AND A CONTRACT OF A |
| • Molecule 37: 60S ribosomal protein L34-A |
| Chain g: 93% |
| MET A2 A2 A2 A1 A111 A111 A112 A112 CYS CYS CYS CYS CYS CYS CYS CYS CYS CYS |
| \bullet Molecule 38: 60S ribosomal protein L35-A |
| Chain h: 98% |
| |
| • Molecule 39: 60S ribosomal protein L36-A |
| Chain i: 97% |
| MET 12 X 53 X 53 H100 H100 |
| \bullet Molecule 40: 60S ribosomal protein L37-A |
| Chain j: 92% |
| MET G2 R25 P40 A16 A16 A1A A1A |
| • Molecule 41: 60S ribosomal protein L38 |
| Chain k: 99% |
| MET A2 F3 F3 K29 A34 G35 K29 A62 C5 F C5 C5 C5 C5 C5 C5 C5 C5 C5 C5 C5 C5 C5 |

• Molecule 42: 60S ribosomal protein L39











• Molecule 52: Ribosome biogenesis protein RPF2







• Molecule 56: UPF0642 protein YBL028C





4 Experimental information (i)

| Property | Value | Source |
|------------------------------------|---------------------------------|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, C1 | Depositor |
| Number of particles used | 34162 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE | Depositor |
| | CORRECTION | |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose $(e^-/\text{\AA}^2)$ | 84.67 | Depositor |
| Minimum defocus (nm) | Not provided | |
| Maximum defocus (nm) | Not provided | |
| Magnification | Not provided | |
| Image detector | FEI FALCON III (4k x 4k) | Depositor |
| Maximum map value | 0.165 | Depositor |
| Minimum map value | -0.045 | Depositor |
| Average map value | -0.000 | Depositor |
| Map value standard deviation | 0.008 | Depositor |
| Recommended contour level | 0.021 | Depositor |
| Map size (Å) | 425.40002, 425.40002, 425.40002 | wwPDB |
| Map dimensions | 400, 400, 400 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.0635, 1.0635, 1.0635 | Depositor |



5 Model quality (i)

5.1 Standard geometry (i)

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

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).

| Mal | Chain | Bond | lengths | Bond angles | | |
|-----|---------|------|---------------------|-------------|---------------------|--|
| | Ullaili | RMSZ | # Z > 5 | RMSZ | # Z > 5 | |
| 1 | 1 | 0.16 | 0/73123 | 0.74 | 30/113993~(0.0%) | |
| 2 | 2 | 0.16 | 0/3746 | 0.76 | 2/5832~(0.0%) | |
| 3 | 3 | 0.15 | 0/2883 | 0.75 | 1/4491~(0.0%) | |
| 4 | 5 | 0.25 | 0/455 | 0.35 | 0/596 | |
| 5 | 6 | 0.17 | 0/1527 | 0.77 | 3/2371~(0.1%) | |
| 6 | А | 0.24 | 0/1662 | 0.44 | 0/2236 | |
| 7 | В | 0.24 | 0/3152 | 0.43 | 0/4239 | |
| 8 | С | 0.24 | 0/2801 | 0.42 | 0/3792 | |
| 9 | D | 0.24 | 0/2158 | 0.40 | 0/2910 | |
| 10 | Е | 0.25 | 0/1260 | 0.42 | 0/1694 | |
| 11 | F | 0.25 | 0/1821 | 0.41 | 0/2451 | |
| 12 | G | 0.25 | 0/1849 | 0.42 | 0/2495 | |
| 13 | Н | 0.24 | 0/1539 | 0.43 | 0/2073 | |
| 14 | J | 0.24 | 0/1374 | 0.43 | 0/1842 | |
| 15 | Κ | 0.24 | 0/2066 | 0.42 | 0/2789 | |
| 16 | L | 0.24 | 0/1524 | 0.43 | 0/2046 | |
| 17 | М | 0.23 | 0/1074 | 0.41 | 0/1446 | |
| 18 | Ν | 0.26 | 0/1757 | 0.43 | 0/2354 | |
| 19 | 0 | 0.25 | 0/1585 | 0.39 | 0/2128 | |
| 20 | Р | 0.24 | 0/1424 | 0.42 | 0/1911 | |
| 21 | Q | 0.25 | 0/1050 | 0.41 | 0/1419 | |
| 22 | R | 0.23 | 0/1275 | 0.39 | 0/1702 | |
| 23 | S | 0.24 | 0/1473 | 0.42 | 0/1980 | |
| 24 | Т | 0.25 | 0/937 | 0.44 | 0/1256 | |
| 25 | U | 0.25 | 0/817 | 0.42 | 0/1108 | |
| 26 | V | 0.25 | 0/1018 | 0.42 | 0/1369 | |
| 27 | W | 0.24 | 0/1918 | 0.42 | 0/2586 | |
| 28 | X | 0.24 | $0/1\overline{116}$ | 0.41 | $0/1\overline{503}$ | |
| 29 | Y | 0.24 | 0/1004 | 0.40 | 0/1341 | |
| 30 | Z | 0.26 | 0/1118 | 0.43 | 0/1497 | |
| 31 | a | 0.25 | 0/751 | 0.40 | 0/1013 | |
| 32 | b | 0.24 | 0/4435 | 0.40 | 0/5971 | |



| Mal | Chain | Bond | lengths | E | Bond angles |
|-----|-------|------|----------|------|------------------|
| | Unain | RMSZ | # Z > 5 | RMSZ | # Z > 5 |
| 33 | с | 0.24 | 0/751 | 0.40 | 0/1008 |
| 34 | d | 0.23 | 0/870 | 0.41 | 0/1168 |
| 35 | е | 0.23 | 0/1041 | 0.41 | 0/1394 |
| 36 | f | 0.25 | 0/868 | 0.45 | 0/1168 |
| 37 | g | 0.23 | 0/891 | 0.40 | 0/1191 |
| 38 | h | 0.24 | 0/978 | 0.38 | 0/1301 |
| 39 | i | 0.23 | 0/778 | 0.38 | 0/1034 |
| 40 | j | 0.25 | 0/685 | 0.41 | 0/908 |
| 41 | k | 0.26 | 0/618 | 0.44 | 0/826 |
| 42 | 1 | 0.23 | 0/443 | 0.41 | 0/588 |
| 43 | m | 0.24 | 0/3794 | 0.43 | 0/5108 |
| 44 | n | 0.24 | 0/3101 | 0.40 | 0/4187 |
| 45 | 0 | 0.24 | 0/1129 | 0.40 | 0/1502 |
| 46 | р | 0.24 | 0/701 | 0.45 | 0/934 |
| 47 | q | 0.23 | 0/1254 | 0.42 | 0/1675 |
| 48 | r | 0.24 | 0/1892 | 0.44 | 0/2528 |
| 49 | s | 0.25 | 0/440 | 0.40 | 0/573 |
| 50 | t | 0.24 | 0/2333 | 0.43 | 0/3128 |
| 51 | u | 0.25 | 0/1287 | 0.40 | 0/1711 |
| 52 | V | 0.25 | 0/2361 | 0.42 | 0/3153 |
| 53 | W | 0.24 | 0/1471 | 0.40 | 0/1980 |
| 54 | X | 0.23 | 0/3313 | 0.42 | 0/4490 |
| 55 | У | 0.23 | 0/1872 | 0.44 | 0/2548 |
| 56 | Z | 0.24 | 0/371 | 0.34 | 0/489 |
| All | All | 0.20 | 0/158934 | 0.62 | 36/231026~(0.0%) |

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

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 11 | F | 0 | 1 |
| 30 | Ζ | 0 | 1 |
| 32 | b | 0 | 1 |
| 43 | m | 0 | 1 |
| 50 | t | 0 | 2 |
| All | All | 0 | 6 |

There are no bond length outliers.

The worst 5 of 36 bond angle outliers are listed below:



| Mol | Chain | Res | Type | Atoms | Z | $Observed(^{o})$ | $Ideal(^{o})$ |
|-----|-------|------|------|-----------|-------|------------------|---------------|
| 1 | 1 | 2376 | G | OP1-P-OP2 | -6.80 | 109.39 | 119.60 |
| 1 | 1 | 1082 | U | OP1-P-OP2 | -6.79 | 109.41 | 119.60 |
| 2 | 2 | 1 | А | OP1-P-OP2 | -6.79 | 109.41 | 119.60 |
| 1 | 1 | 2501 | U | OP1-P-OP2 | -6.78 | 109.43 | 119.60 |
| 5 | 6 | 1 | С | OP1-P-OP2 | -6.77 | 109.45 | 119.60 |

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 11 | F | 158 | LYS | Peptide |
| 30 | Ζ | 104 | PRO | Peptide |
| 32 | b | 369 | ARG | Peptide |
| 43 | m | 77 | TRP | Peptide |
| 50 | t | 220 | ASN | Peptide |

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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 | Perce | ntiles |
|-----|-------|---------------|-----------|---------|----------|-------|--------|
| 4 | 5 | 49/120~(41%) | 49 (100%) | 0 | 0 | 100 | 100 |
| 6 | А | 210/254~(83%) | 199 (95%) | 11 (5%) | 0 | 100 | 100 |
| 7 | В | 384/387~(99%) | 358~(93%) | 26 (7%) | 0 | 100 | 100 |
| 8 | С | 359/362~(99%) | 336 (94%) | 23~(6%) | 0 | 100 | 100 |
| 9 | D | 257/297~(86%) | 246~(96%) | 11 (4%) | 0 | 100 | 100 |
| 10 | Е | 152/176~(86%) | 145 (95%) | 7 (5%) | 0 | 100 | 100 |
| 11 | F | 220/244~(90%) | 210 (96%) | 9 (4%) | 1 (0%) | 29 | 64 |



| a 1 | c | | |
|-----------|------|----------|------|
| Continued | trom | previous | page |
| | 9 | 1 | 1 0 |

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Perce | ntiles |
|-----|-------|---------------|------------|----------|----------|-------|--------|
| 12 | G | 231/256~(90%) | 212 (92%) | 19 (8%) | 0 | 100 | 100 |
| 13 | Н | 189/191~(99%) | 177 (94%) | 12~(6%) | 0 | 100 | 100 |
| 14 | J | 167/174~(96%) | 152 (91%) | 15~(9%) | 0 | 100 | 100 |
| 15 | Κ | 248/376~(66%) | 231~(93%) | 17 (7%) | 0 | 100 | 100 |
| 16 | L | 185/199~(93%) | 174 (94%) | 10 (5%) | 1 (0%) | 29 | 64 |
| 17 | М | 135/138~(98%) | 132 (98%) | 3 (2%) | 0 | 100 | 100 |
| 18 | Ν | 201/204 (98%) | 187 (93%) | 13 (6%) | 1 (0%) | 29 | 64 |
| 19 | Ο | 195/199~(98%) | 194 (100%) | 1 (0%) | 0 | 100 | 100 |
| 20 | Р | 173/184 (94%) | 168 (97%) | 5 (3%) | 0 | 100 | 100 |
| 21 | Q | 132/186~(71%) | 131 (99%) | 1 (1%) | 0 | 100 | 100 |
| 22 | R | 154/189~(82%) | 147 (96%) | 7 (4%) | 0 | 100 | 100 |
| 23 | S | 169/172~(98%) | 160 (95%) | 9(5%) | 0 | 100 | 100 |
| 24 | Т | 110/160~(69%) | 98 (89%) | 12 (11%) | 0 | 100 | 100 |
| 25 | U | 99/121~(82%) | 95 (96%) | 4 (4%) | 0 | 100 | 100 |
| 26 | V | 134/137~(98%) | 129 (96%) | 5 (4%) | 0 | 100 | 100 |
| 27 | W | 232/236~(98%) | 219 (94%) | 12 (5%) | 1 (0%) | 34 | 69 |
| 28 | Х | 139/142~(98%) | 133 (96%) | 6 (4%) | 0 | 100 | 100 |
| 29 | Y | 124/127~(98%) | 122 (98%) | 2 (2%) | 0 | 100 | 100 |
| 30 | Ζ | 133/136~(98%) | 123 (92%) | 10 (8%) | 0 | 100 | 100 |
| 31 | a | 91/149~(61%) | 86 (94%) | 5 (6%) | 0 | 100 | 100 |
| 32 | b | 533/647~(82%) | 490 (92%) | 43 (8%) | 0 | 100 | 100 |
| 33 | с | 95/105~(90%) | 94 (99%) | 1 (1%) | 0 | 100 | 100 |
| 34 | d | 103/113~(91%) | 97 (94%) | 6 (6%) | 0 | 100 | 100 |
| 35 | е | 125/130~(96%) | 120 (96%) | 5 (4%) | 0 | 100 | 100 |
| 36 | f | 104/107~(97%) | 95 (91%) | 9 (9%) | 0 | 100 | 100 |
| 37 | g | 110/121 (91%) | 108 (98%) | 2 (2%) | 0 | 100 | 100 |
| 38 | h | 117/120~(98%) | 112 (96%) | 5 (4%) | 0 | 100 | 100 |
| 39 | i | 97/100~(97%) | 91 (94%) | 6 (6%) | 0 | 100 | 100 |
| 40 | j | 83/88~(94%) | 78 (94%) | 5 (6%) | 0 | 100 | 100 |
| 41 | k | 75/78~(96%) | 70 (93%) | 5 (7%) | 0 | 100 | 100 |
| 42 | 1 | 48/51 (94%) | 46 (96%) | 2 (4%) | 0 | 100 | 100 |



| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Perce | ntiles |
|-----|-------|------------------|------------|----------|----------|-------|--------|
| 43 | m | 457/486~(94%) | 420 (92%) | 36~(8%) | 1 (0%) | 47 | 79 |
| 44 | n | 365/605~(60%) | 340~(93%) | 25~(7%) | 0 | 100 | 100 |
| 45 | 0 | 131/220~(60%) | 123~(94%) | 8 (6%) | 0 | 100 | 100 |
| 46 | р | 89/92~(97%) | 80 (90%) | 9 (10%) | 0 | 100 | 100 |
| 47 | q | 143/455~(31%) | 130 (91%) | 13 (9%) | 0 | 100 | 100 |
| 48 | r | 224/261~(86%) | 199~(89%) | 25 (11%) | 0 | 100 | 100 |
| 49 | S | 49/520~(9%) | 46~(94%) | 3~(6%) | 0 | 100 | 100 |
| 50 | t | 283/322~(88%) | 261 (92%) | 20 (7%) | 2(1%) | 22 | 57 |
| 51 | u | 148/199~(74%) | 143~(97%) | 5(3%) | 0 | 100 | 100 |
| 52 | v | 283/344~(82%) | 270 (95%) | 13~(5%) | 0 | 100 | 100 |
| 53 | W | 178/203~(88%) | 174~(98%) | 4 (2%) | 0 | 100 | 100 |
| 54 | х | 409/515~(79%) | 391~(96%) | 18 (4%) | 0 | 100 | 100 |
| 55 | У | 242/245~(99%) | 229 (95%) | 13 (5%) | 0 | 100 | 100 |
| 56 | Z | 44/106~(42%) | 44 (100%) | 0 | 0 | 100 | 100 |
| All | All | 9407/11749~(80%) | 8864 (94%) | 536 (6%) | 7 (0%) | 54 | 83 |

Continued from previous page...

5 of 7 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 11 | F | 159 | GLN |
| 50 | t | 220 | ASN |
| 50 | t | 221 | GLU |
| 18 | Ν | 146 | ALA |
| 43 | m | 208 | SER |

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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 |
|-----|-------|---------------|------------|----------|-------------|
| 4 | 5 | 48/106~(45%) | 46 (96%) | 2(4%) | 30 62 |
| 6 | А | 166/196~(85%) | 166 (100%) | 0 | 100 100 |



Continued from previous page...

| Mol | Chain | Analysed | Rotameric | Outliers | Percentile | |
|-----|--------------|--------------------|------------|----------|------------|-----|
| 7 | В | 322/323~(100%) | 317~(98%) | 5(2%) | 62 | 84 |
| 8 | \mathbf{C} | 288/289~(100%) | 282~(98%) | 6 (2%) | 53 | 79 |
| 9 | D | 219/245~(89%) | 213~(97%) | 6 (3%) | 44 | 74 |
| 10 | Ε | 134/153~(88%) | 133 (99%) | 1 (1%) | 84 | 93 |
| 11 | F | 186/205~(91%) | 185 (100%) | 1 (0%) | 88 | 94 |
| 12 | G | 191/208~(92%) | 189 (99%) | 2 (1%) | 76 | 90 |
| 13 | Н | $171/171\ (100\%)$ | 169 (99%) | 2 (1%) | 71 | 88 |
| 14 | J | 147/150~(98%) | 144 (98%) | 3 (2%) | 55 | 80 |
| 15 | К | 233/346~(67%) | 227 (97%) | 6 (3%) | 46 | 74 |
| 16 | L | 149/159~(94%) | 147 (99%) | 2 (1%) | 69 | 87 |
| 17 | М | 108/109~(99%) | 108 (100%) | 0 | 100 | 100 |
| 18 | Ν | 175/176~(99%) | 172 (98%) | 3 (2%) | 60 | 83 |
| 19 | О | 160/162~(99%) | 159 (99%) | 1 (1%) | 86 | 94 |
| 20 | Р | 142/146~(97%) | 138 (97%) | 4 (3%) | 43 | 73 |
| 21 | Q | 110/151~(73%) | 110 (100%) | 0 | 100 | 100 |
| 22 | R | 129/154~(84%) | 126 (98%) | 3 (2%) | 50 | 77 |
| 23 | S | 155/156~(99%) | 151 (97%) | 4 (3%) | 46 | 74 |
| 24 | Т | 100/137~(73%) | 98~(98%) | 2 (2%) | 55 | 80 |
| 25 | U | 88/107~(82%) | 85~(97%) | 3 (3%) | 37 | 69 |
| 26 | V | 104/105~(99%) | 103 (99%) | 1 (1%) | 76 | 90 |
| 27 | W | 211/213~(99%) | 205~(97%) | 6 (3%) | 43 | 73 |
| 28 | Х | 117/118~(99%) | 114 (97%) | 3 (3%) | 46 | 74 |
| 29 | Y | 109/110~(99%) | 107 (98%) | 2(2%) | 59 | 82 |
| 30 | Z | 115/116~(99%) | 114 (99%) | 1 (1%) | 78 | 91 |
| 31 | a | 76/119~(64%) | 75~(99%) | 1 (1%) | 69 | 87 |
| 32 | b | 482/573~(84%) | 473 (98%) | 9 (2%) | 57 | 81 |
| 33 | с | 81/88 (92%) | 80 (99%) | 1 (1%) | 71 | 88 |
| 34 | d | 92/97~(95%) | 90 (98%) | 2 (2%) | 52 | 78 |
| 35 | е | 109/111~(98%) | 107 (98%) | 2 (2%) | 59 | 82 |
| 36 | f | 90/91~(99%) | 89 (99%) | 1 (1%) | 73 | 89 |
| 37 | g | 95/103~(92%) | 95 (100%) | 0 | 100 | 100 |



| Mol | Chain | Analysed | Rotameric | Outliers | Perce | ntiles |
|-----|-------|------------------|------------|----------|-------|--------|
| 38 | h | 104/105~(99%) | 103~(99%) | 1 (1%) | 76 | 90 |
| 39 | i | 81/82~(99%) | 79~(98%) | 2(2%) | 47 | 75 |
| 40 | j | 69/71~(97%) | 65~(94%) | 4 (6%) | 20 | 51 |
| 41 | k | 68/69~(99%) | 68 (100%) | 0 | 100 | 100 |
| 42 | 1 | 45/46~(98%) | 44 (98%) | 1 (2%) | 52 | 78 |
| 43 | m | 408/428~(95%) | 401 (98%) | 7 (2%) | 60 | 83 |
| 44 | n | 334/548~(61%) | 326~(98%) | 8 (2%) | 49 | 76 |
| 45 | 0 | 118/199~(59%) | 115 (98%) | 3 (2%) | 47 | 75 |
| 46 | р | 71/72~(99%) | 70~(99%) | 1 (1%) | 67 | 86 |
| 47 | q | 137/420~(33%) | 136 (99%) | 1 (1%) | 84 | 93 |
| 48 | r | 203/229~(89%) | 196~(97%) | 7 (3%) | 37 | 69 |
| 49 | s | 47/445 (11%) | 45 (96%) | 2 (4%) | 29 | 62 |
| 50 | t | 256/287~(89%) | 251 (98%) | 5 (2%) | 55 | 80 |
| 51 | u | 133/180 (74%) | 131 (98%) | 2 (2%) | 65 | 85 |
| 52 | V | 258/309~(84%) | 257 (100%) | 1 (0%) | 91 | 96 |
| 53 | W | 161/179~(90%) | 156 (97%) | 5 (3%) | 40 | 70 |
| 54 | x | 361/451~(80%) | 358~(99%) | 3 (1%) | 81 | 92 |
| 55 | У | 210/211 (100%) | 207~(99%) | 3 (1%) | 67 | 86 |
| 56 | Z | 40/95~(42%) | 39~(98%) | 1 (2%) | 47 | 75 |
| All | All | 8206/10119 (81%) | 8064 (98%) | 142 (2%) | 62 | 83 |

Continued from previous page...

 $5~{\rm of}~142$ residues with a non-rotameric side chain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 48 | r | 133 | MET |
| 48 | r | 210 | THR |
| 53 | W | 29 | PHE |
| 23 | S | 136 | LYS |
| 23 | S | 96 | ASP |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 32 | b | 356 | ASN |



Continued from previous page...

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 48 | r | 256 | ASN |
| 34 | d | 57 | GLN |
| 44 | n | 53 | ASN |
| 51 | u | 5 | GLN |

5.3.3 RNA (i)

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 1 | 1 | 3044/3396~(89%) | 615 (20%) | 78~(2%) |
| 2 | 2 | 157/158~(99%) | 27 (17%) | 2(1%) |
| 3 | 3 | 120/121~(99%) | 16 (13%) | 2(1%) |
| 5 | 6 | 64/232~(27%) | 21 (32%) | 5 (7%) |
| All | All | 3385/3907~(86%) | 679~(20%) | 87 (2%) |

5 of 679 RNA backbone outliers are listed below:

| Mol | Chain | \mathbf{Res} | Type |
|-----|-------|----------------|------|
| 1 | 1 | 2 | U |
| 1 | 1 | 13 | А |
| 1 | 1 | 14 | U |
| 1 | 1 | 26 | А |
| 1 | 1 | 40 | А |

5 of 87 RNA pucker outliers are listed below:

| Mol | Chain | \mathbf{Res} | Type |
|-----|-------|----------------|------|
| 1 | 1 | 2728 | G |
| 1 | 1 | 3195 | U |
| 1 | 1 | 2761 | G |
| 1 | 1 | 2868 | U |
| 1 | 1 | 3350 | С |

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.



5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis. There are no bond length outliers. There are no bond angle outliers. There are no chirality outliers. There are no torsion outliers. There are no ring outliers. No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-12905. 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



6.1.2 Raw map



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



6.2 Central slices (i)

6.2.1 Primary map



X Index: 200





Z Index: 200

6.2.2 Raw map



X Index: 200

Y Index: 200



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: 183





Z Index: 153

6.3.2 Raw map



X Index: 184

Y Index: 178



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



6.4 Orthogonal surface views (i)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.021. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

6.5 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 1666 nm^3 ; this corresponds to an approximate mass of 1505 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 (i)



*Reported resolution corresponds to spatial frequency of 0.323 ${\rm \AA}^{-1}$



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 0.323 $\mathrm{\AA^{-1}}$



8.2 Resolution estimates (i)

| $\begin{bmatrix} Bosolution ostimato (Å) \end{bmatrix}$ | Estimation criterion (FSC cut-off) | | |
|---|------------------------------------|------|----------|
| resolution estimate (A) | 0.143 | 0.5 | Half-bit |
| Reported by author | 3.10 | - | - |
| Author-provided FSC curve | 3.04 | 3.64 | 3.09 |
| Unmasked-calculated* | 3.98 | 8.26 | 4.11 |

*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 3.98 differs from the reported value 3.1 by more than 10 %



9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-12905 and PDB model 7OHQ. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.021 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 Atom inclusion (i)



At the recommended contour level, 94% of all backbone atoms, 87% of all non-hydrogen atoms, are inside the map.

