



Full wwPDB EM Validation Report ⓘ

Apr 7, 2025 – 01:43 PM EDT

PDB ID : 8UJD / pdb_00008ujd
EMDB ID : EMD-42319
Title : In situ human 60S ribosome with eIF6
Authors : Wei, Z.; Yong, X.
Deposited on : 2023-10-11
Resolution : 2.96 Å(reported)

This is a Full wwPDB EM Validation 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 ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

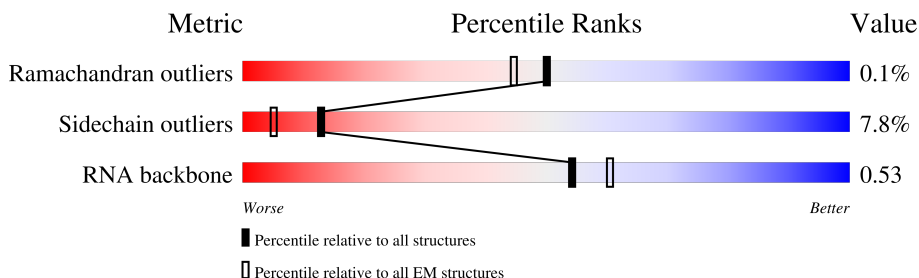
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.96 Å.

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



| Metric | Whole archive (#Entries) | EM structures (#Entries) |
|-----------------------|-----------------------------|-----------------------------|
| Ramachandran outliers | 207382 | 16835 |
| Sidechain outliers | 206894 | 16415 |
| RNA backbone | 6643 | 2191 |

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 $\leq 5\%$. 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 | LW | 118 | |
| 2 | L5 | 5070 | |
| 3 | L7 | 120 | |
| 4 | L8 | 156 | |
| 5 | LA | 248 | |
| 6 | LB | 402 | |
| 7 | LC | 368 | |
| 8 | LD | 293 | |

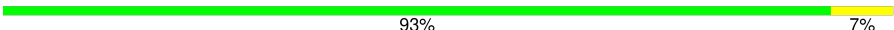

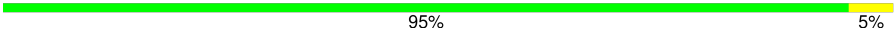





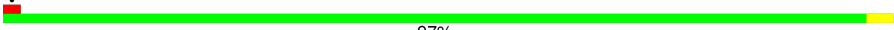


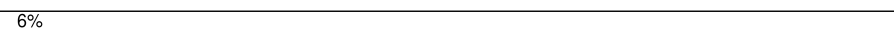

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 9 | LE | 242 | |
| 10 | LF | 225 | |
| 11 | LG | 241 | |
| 12 | LH | 190 | |
| 13 | LI | 213 | |
| 14 | LJ | 176 | |
| 15 | LL | 210 | |
| 16 | LM | 139 | |
| 17 | LN | 203 | |
| 18 | LO | 201 | |
| 19 | LP | 153 | |
| 20 | LQ | 187 | |
| 21 | LR | 187 | |
| 22 | LS | 175 | |
| 23 | LT | 159 | |
| 24 | LU | 101 | |
| 25 | LV | 131 | |
| 26 | LX | 120 | |
| 27 | LY | 134 | |
| 28 | LZ | 135 | |
| 29 | La | 147 | |
| 30 | Lb | 121 | |
| 31 | Lc | 98 | |
| 32 | Ld | 107 | |
| 33 | Le | 128 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|---|
| 34 | Lf | 109 |  93% 7% |
| 35 | Lg | 114 |  89% 11% |
| 36 | Lh | 122 |  95% 5% |
| 37 | Li | 102 |  92% 8% |
| 38 | Lj | 86 |  93% 7% |
| 39 | Lk | 69 |  87% 13% |
| 40 | Ll | 50 |  92% 8% |
| 41 | Lm | 52 |  96% 4% |
| 42 | Lo | 105 |  97% 3% |
| 43 | Lp | 91 |  92% 8% |
| 44 | Lr | 125 |  82% 18% |
| 45 | P | 225 |  6% 86% 14% |
| 46 | CA | 356 |  43% 94% 6% |

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 141127 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 Ribosomal protein L24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 1 | LW | 63 | Total | C | N | O | S | 0 | 0 |
| | | | 528 | 337 | 103 | 85 | 3 | | |

There are 6 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|----------------|
| LW | ? | - | SER | deletion | UNP A0A994J4A5 |
| LW | ? | - | GLU | deletion | UNP A0A994J4A5 |
| LW | ? | - | GLU | deletion | UNP A0A994J4A5 |
| LW | ? | - | ILE | deletion | UNP A0A994J4A5 |
| LW | ? | - | GLN | deletion | UNP A0A994J4A5 |
| LW | ? | - | LYS | deletion | UNP A0A994J4A5 |

- Molecule 2 is a RNA chain called 28S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|-------|-------|------|---------|-------|
| 2 | L5 | 3649 | Total | C | N | O | P | 0 | 0 |
| | | | 78229 | 34837 | 14317 | 25427 | 3648 | | |

- Molecule 3 is a RNA chain called 5S rRNA [Homo sapiens].

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 3 | L7 | 120 | Total | C | N | O | P | 0 | 0 |
| | | | 2561 | 1141 | 456 | 844 | 120 | | |

- Molecule 4 is a RNA chain called 5.8S rRNA [Homo sapiens].

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|------|-----|---------|-------|
| 4 | L8 | 156 | Total | C | N | O | P | 0 | 0 |
| | | | 3314 | 1480 | 585 | 1094 | 155 | | |

- Molecule 5 is a protein called 60S ribosomal protein L8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 5 | LA | 248 | Total | C | N | O | S | 0 | 0 |
| | | | 1898 | 1189 | 389 | 314 | 6 | | |

- Molecule 6 is a protein called Large ribosomal subunit protein uL3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 6 | LB | 402 | Total | C | N | O | S | 0 | 0 |
| | | | 3238 | 2060 | 608 | 556 | 14 | | |

- Molecule 7 is a protein called 60S ribosomal protein L4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 7 | LC | 368 | Total | C | N | O | S | 0 | 0 |
| | | | 2927 | 1840 | 583 | 489 | 15 | | |

- Molecule 8 is a protein called Large ribosomal subunit protein uL18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 8 | LD | 293 | Total | C | N | O | S | 0 | 0 |
| | | | 2382 | 1507 | 434 | 427 | 14 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 9 | LE | 236 | Total | C | N | O | S | 0 | 0 |
| | | | 1904 | 1222 | 361 | 317 | 4 | | |

- Molecule 10 is a protein called 60S ribosomal protein L7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 10 | LF | 225 | Total | C | N | O | S | 0 | 0 |
| | | | 1870 | 1202 | 358 | 301 | 9 | | |

- Molecule 11 is a protein called 60S ribosomal protein L7a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 11 | LG | 241 | Total | C | N | O | S | 0 | 0 |
| | | | 1927 | 1228 | 371 | 324 | 4 | | |

- Molecule 12 is a protein called 60S ribosomal protein L9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 12 | LH | 190 | Total | C | N | O | S | 0 | 0 |
| | | | 1518 | 956 | 284 | 272 | 6 | | |

- Molecule 13 is a protein called Ribosomal protein uL16-like.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 13 | LI | 202 | Total | C | N | O | S | 0 | 0 |
| | | | 1634 | 1037 | 314 | 269 | 14 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 14 | LJ | 176 | Total | C | N | O | S | 0 | 0 |
| | | | 1410 | 888 | 263 | 253 | 6 | | |

- Molecule 15 is a protein called Large ribosomal subunit protein eL13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 15 | LL | 210 | Total | C | N | O | S | 0 | 0 |
| | | | 1701 | 1064 | 352 | 281 | 4 | | |

- Molecule 16 is a protein called 60S ribosomal protein L14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 16 | LM | 139 | Total | C | N | O | S | 0 | 0 |
| | | | 1138 | 730 | 218 | 183 | 7 | | |

- Molecule 17 is a protein called 60S ribosomal protein L15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 17 | LN | 203 | Total | C | N | O | S | 0 | 0 |
| | | | 1701 | 1072 | 359 | 266 | 4 | | |

- Molecule 18 is a protein called 60S ribosomal protein L13a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 18 | LO | 201 | Total | C | N | O | S | 0 | 0 |
| | | | 1650 | 1063 | 321 | 261 | 5 | | |

- Molecule 19 is a protein called 60S ribosomal protein L17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 19 | LP | 153 | Total | C | N | O | S | 0 | 0 |
| | | | 1242 | 776 | 241 | 216 | 9 | | |

- Molecule 20 is a protein called 60S ribosomal protein L18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 20 | LQ | 187 | Total | C | N | O | S | 0 | 0 |
| | | | 1513 | 944 | 314 | 250 | 5 | | |

- Molecule 21 is a protein called 60S ribosomal protein L19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 21 | LR | 153 | Total | C | N | O | S | 0 | 0 |
| | | | 1281 | 799 | 276 | 197 | 9 | | |

- Molecule 22 is a protein called 60S ribosomal protein L18a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 22 | LS | 175 | Total | C | N | O | S | 0 | 0 |
| | | | 1453 | 925 | 283 | 235 | 10 | | |

- Molecule 23 is a protein called 60S ribosomal protein L21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 23 | LT | 159 | Total | C | N | O | S | 0 | 0 |
| | | | 1298 | 823 | 252 | 217 | 6 | | |

- Molecule 24 is a protein called Heparin-binding protein HBp15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 24 | LU | 101 | Total | C | N | O | S | 0 | 0 |
| | | | 825 | 529 | 144 | 150 | 2 | | |

- Molecule 25 is a protein called 60S ribosomal protein L23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 25 | LV | 131 | Total | C | N | O | S | 0 | 0 |
| | | | 979 | 618 | 184 | 172 | 5 | | |

- Molecule 26 is a protein called 60S ribosomal protein L23a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 26 | LX | 120 | Total | C | N | O | S | 0 | 0 |
| | | | 985 | 630 | 185 | 169 | 1 | | |

- Molecule 27 is a protein called 60S ribosomal protein L26.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 27 | LY | 134 | Total | C | N | O | S | 0 | 0 |
| | | | 1115 | 700 | 226 | 186 | 3 | | |

- Molecule 28 is a protein called 60S ribosomal protein L27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 28 | LZ | 135 | Total | C | N | O | S | 0 | 0 |
| | | | 1107 | 714 | 208 | 182 | 3 | | |

- Molecule 29 is a protein called 60S ribosomal protein L27a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 29 | La | 147 | Total | C | N | O | S | 0 | 0 |
| | | | 1162 | 736 | 237 | 186 | 3 | | |

- Molecule 30 is a protein called Large ribosomal subunit protein eL29.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 30 | Lb | 109 | Total | C | N | O | S | 0 | 0 |
| | | | 876 | 546 | 189 | 137 | 4 | | |

- Molecule 31 is a protein called 60S ribosomal protein L30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 31 | Lc | 98 | Total | C | N | O | S | 0 | 0 |
| | | | 764 | 485 | 135 | 138 | 6 | | |

- Molecule 32 is a protein called 60S ribosomal protein L31.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 32 | Ld | 107 | Total | C | N | O | S | 0 | 0 |
| | | | 888 | 560 | 171 | 155 | 2 | | |

- Molecule 33 is a protein called 60S ribosomal protein L32.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 33 | Le | 128 | Total | C | N | O | S | 0 | 0 |
| | | | 1053 | 667 | 216 | 165 | 5 | | |

- Molecule 34 is a protein called 60S ribosomal protein L35a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 34 | Lf | 109 | Total | C | N | O | S | 0 | 0 |
| | | | 876 | 555 | 174 | 144 | 3 | | |

- Molecule 35 is a protein called 60S ribosomal protein L34.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 35 | Lg | 114 | Total | C | N | O | S | 0 | 0 |
| | | | 906 | 566 | 187 | 147 | 6 | | |

- Molecule 36 is a protein called 60S ribosomal protein L35.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 36 | Lh | 122 | Total | C | N | O | S | 0 | 0 |
| | | | 1015 | 641 | 205 | 168 | 1 | | |

- Molecule 37 is a protein called 60S ribosomal protein L36.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 37 | Li | 102 | Total | C | N | O | S | 0 | 0 |
| | | | 832 | 521 | 177 | 129 | 5 | | |

- Molecule 38 is a protein called 60S ribosomal protein L37.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 38 | Lj | 86 | Total | C | N | O | S | 0 | 0 |
| | | | 705 | 434 | 155 | 111 | 5 | | |

- Molecule 39 is a protein called 60S ribosomal protein L38.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 39 | Lk | 69 | Total | C | N | O | S | 0 | 0 |
| | | | 569 | 366 | 103 | 99 | 1 | | |

- Molecule 40 is a protein called 60S ribosomal protein L39.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 40 | Ll | 50 | Total | C | N | O | S | 0 | 0 |
| | | | 444 | 281 | 98 | 64 | 1 | | |

- Molecule 41 is a protein called Large ribosomal subunit protein eL40.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 41 | Lm | 52 | Total | C | N | O | S | 0 | 0 |
| | | | 429 | 266 | 90 | 67 | 6 | | |

- Molecule 42 is a protein called 60S ribosomal protein L36a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 42 | Lo | 105 | Total | C | N | O | S | 0 | 0 |
| | | | 862 | 542 | 175 | 139 | 6 | | |

- Molecule 43 is a protein called 60S ribosomal protein L37a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 43 | Lp | 91 | Total | C | N | O | S | 0 | 0 |
| | | | 708 | 445 | 136 | 120 | 7 | | |

- Molecule 44 is a protein called 60S ribosomal protein L28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 44 | Lr | 125 | Total | C | N | O | S | 0 | 0 |
| | | | 1002 | 622 | 207 | 168 | 5 | | |

- Molecule 45 is a protein called Eukaryotic translation initiation factor 6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 45 | P | 225 | Total | C | N | O | S | 0 | 0 |
| | | | 1712 | 1065 | 295 | 340 | 12 | | |

- Molecule 46 is a protein called Proliferation-associated protein 2G4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 46 | CA | 354 | Total | C | N | O | S | 4 | 0 |
| | | | 2764 | 1744 | 475 | 528 | 17 | | |

- Molecule 47 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

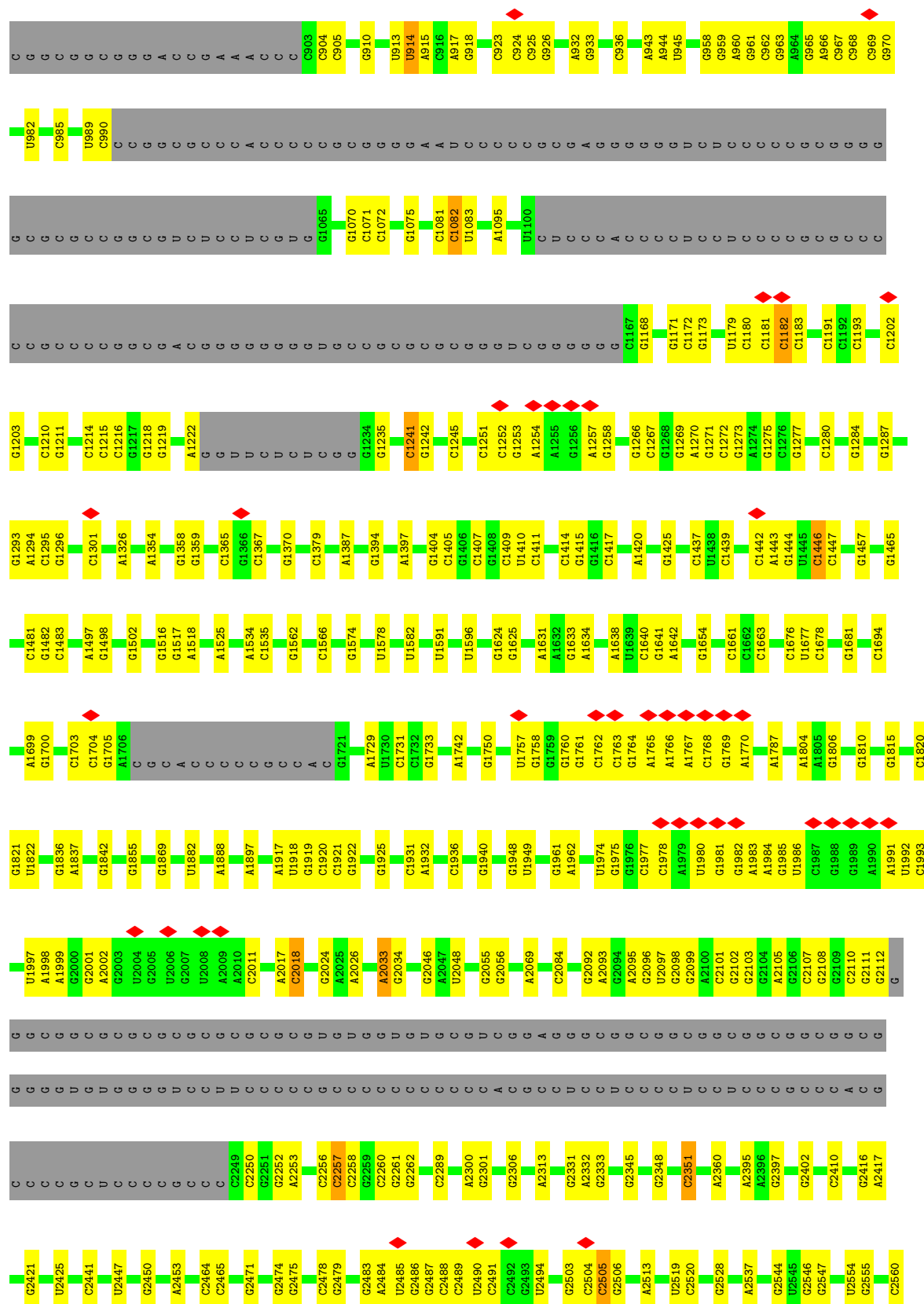
| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|--------------|-----------|---------|
| 47 | L5 | 214 | Total 214 | Mg 214 | 0 |
| 47 | L7 | 3 | Total 3 | Mg 3 | 0 |
| 47 | L8 | 4 | Total 4 | Mg 4 | 0 |
| 47 | LA | 1 | Total 1 | Mg 1 | 0 |
| 47 | LP | 1 | Total 1 | Mg 1 | 0 |
| 47 | LV | 1 | Total 1 | Mg 1 | 0 |
| 47 | Le | 1 | Total 1 | Mg 1 | 0 |
| 47 | Lg | 1 | Total 1 | Mg 1 | 0 |

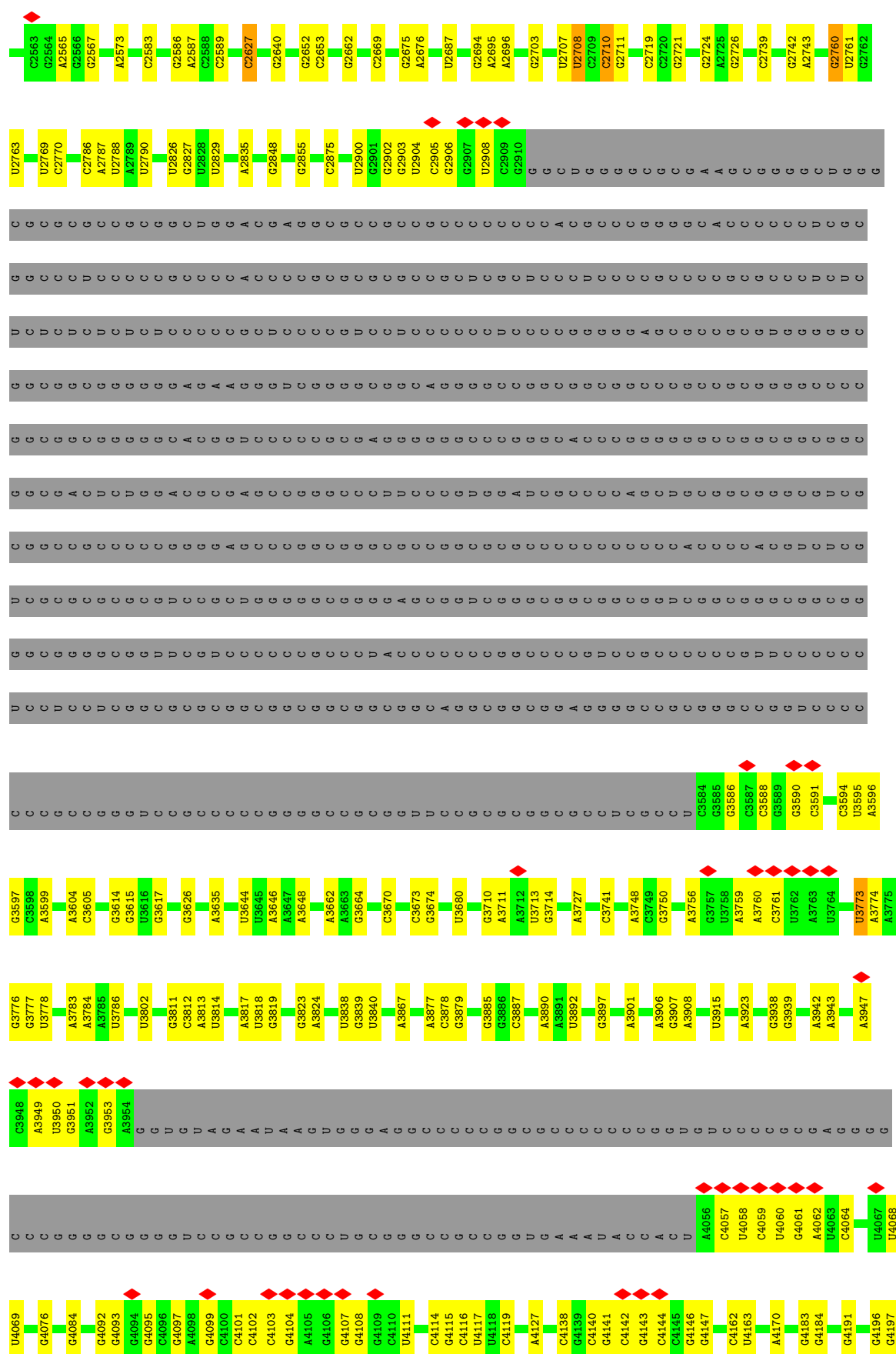
- Molecule 48 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

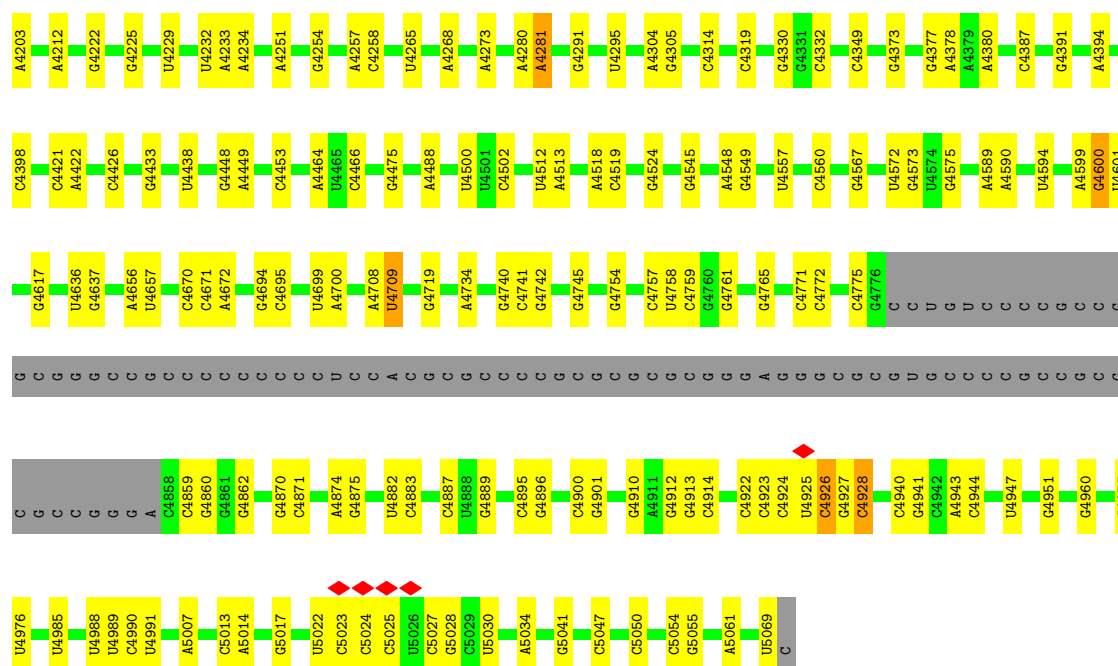
| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|------------|---------|---------|
| 48 | Lg | 1 | Total 1 | Zn 1 | 0 |
| 48 | Lj | 1 | Total 1 | Zn 1 | 0 |
| 48 | Lm | 1 | Total 1 | Zn 1 | 0 |
| 48 | Lo | 1 | Total 1 | Zn 1 | 0 |
| 48 | Lp | 1 | Total 1 | Zn 1 | 0 |

- Molecule 49 is water.

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|------------|--------|---------|
| 49 | P | 1 | Total 1 | O 1 | 0 |

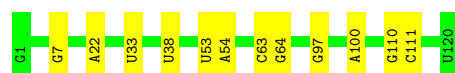






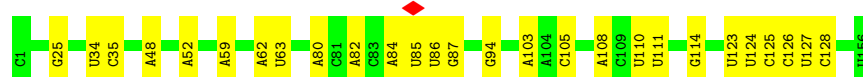
- Molecule 3: 5S rRNA [Homo sapiens]

Chain L7: 90% 10%



- Molecule 4: 5.8S rRNA [Homo sapiens]

Chain L8: 83% 17%



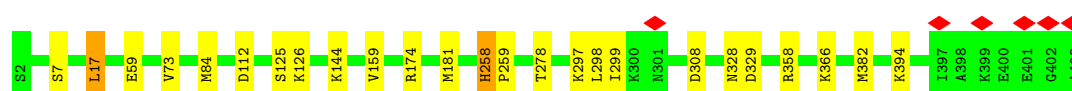
- Molecule 5: 60S ribosomal protein L8

Chain LA: 94% 5%



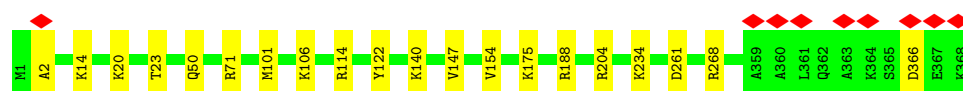
- Molecule 6: Large ribosomal subunit protein uL3

Chain LB: 94% 6%



- Molecule 7: 60S ribosomal protein L4

Chain LC:  95% 5%




- Molecule 8: Large ribosomal subunit protein uL18

Chain LD:  91% 9%



- Molecule 9: 60S ribosomal protein L6

Chain LE:  6% 90% 7%



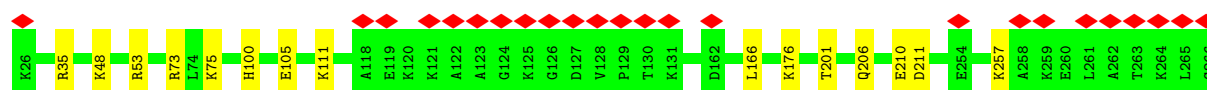
- Molecule 10: 60S ribosomal protein L7

Chain LF:  95% 5%



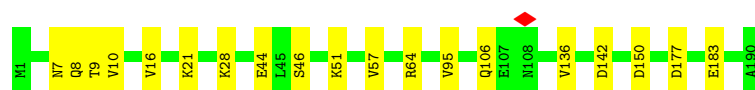
- Molecule 11: 60S ribosomal protein L7a

Chain LG:  10% 94% 6%



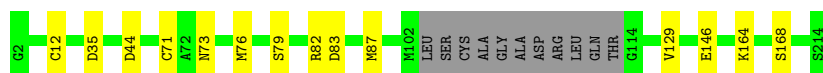
- Molecule 12: 60S ribosomal protein L9

Chain LH:  90% 10%

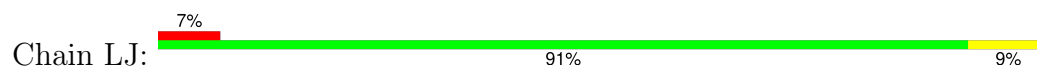


- Molecule 13: Ribosomal protein uL16-like

Chain LI:  88% 7% 5%



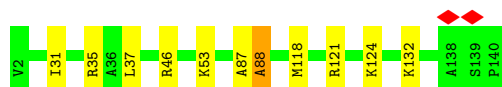
- Molecule 14: 60S ribosomal protein L11



- Molecule 15: Large ribosomal subunit protein eL13



- Molecule 16: 60S ribosomal protein L14



- Molecule 17: 60S ribosomal protein L15



- Molecule 18: 60S ribosomal protein L13a



- Molecule 19: 60S ribosomal protein L17




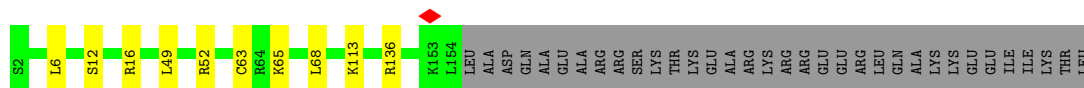
- Molecule 20: 60S ribosomal protein L18

Chain LQ:  95% 5%



- Molecule 21: 60S ribosomal protein L19

Chain LR:  76% 5% 18%



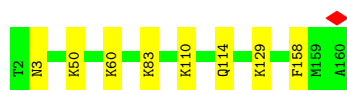
- Molecule 22: 60S ribosomal protein L18a

Chain LS:  97%




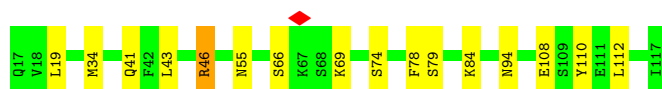
- Molecule 23: 60S ribosomal protein L21

Chain LT:  95% 5%



- Molecule 24: Heparin-binding protein HBp15

Chain LU:  84% 15%



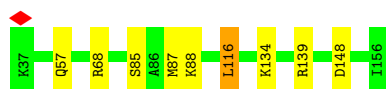
- Molecule 25: 60S ribosomal protein L23

Chain LV:  96%



- Molecule 26: 60S ribosomal protein L23a

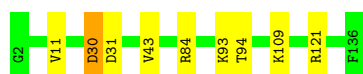
Chain LX:  92% 7%



• Molecule 27: 60S ribosomal protein L26

Chain LY:  93% 7%


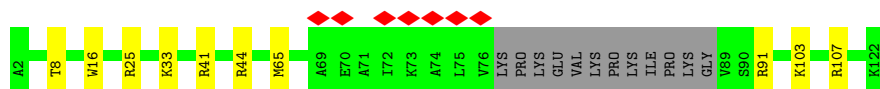
• Molecule 28: 60S ribosomal protein L27

Chain LZ:  93% 6%

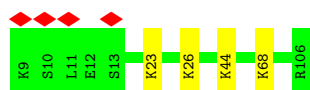
• Molecule 29: 60S ribosomal protein L27a

Chain La:  97%

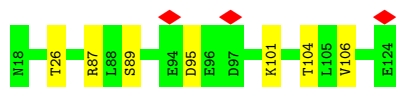
• Molecule 30: Large ribosomal subunit protein eL29

Chain Lb:  6% 82% 8% 10%

• Molecule 31: 60S ribosomal protein L30

Chain Lc:  96%

• Molecule 32: 60S ribosomal protein L31

Chain Ld:  93% 7%

• Molecule 33: 60S ribosomal protein L32

Chain Le:  93% 7%



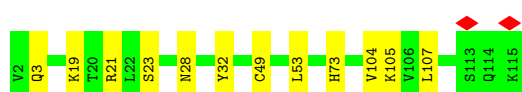
- Molecule 34: 60S ribosomal protein L35a

Chain Lf: 93% 7%



- Molecule 35: 60S ribosomal protein L34

Chain Lg: 89% 11%



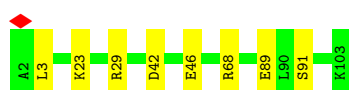
- Molecule 36: 60S ribosomal protein L35

Chain Lh: 95% 5%



- Molecule 37: 60S ribosomal protein L36

Chain Li: 92% 8%



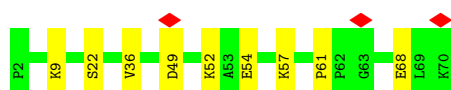
- Molecule 38: 60S ribosomal protein L37

Chain Lj: 93% 7%



- Molecule 39: 60S ribosomal protein L38

Chain Lk: 87% 13%



- Molecule 40: 60S ribosomal protein L39

Chain Ll: 92% 8%



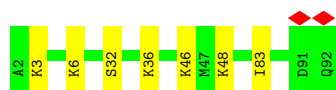
- Molecule 41: Large ribosomal subunit protein eL40



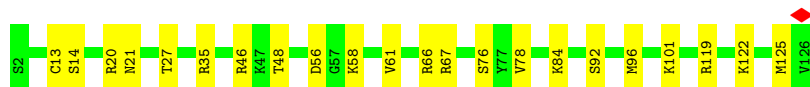
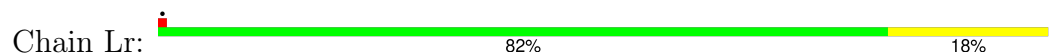
- Molecule 42: 60S ribosomal protein L36a



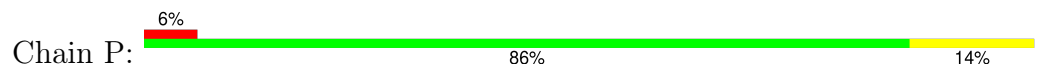
- Molecule 43: 60S ribosomal protein L37a



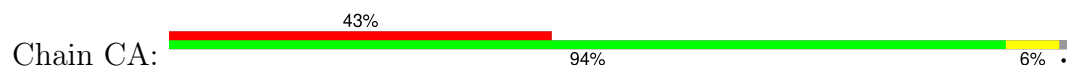
- Molecule 44: 60S ribosomal protein L28

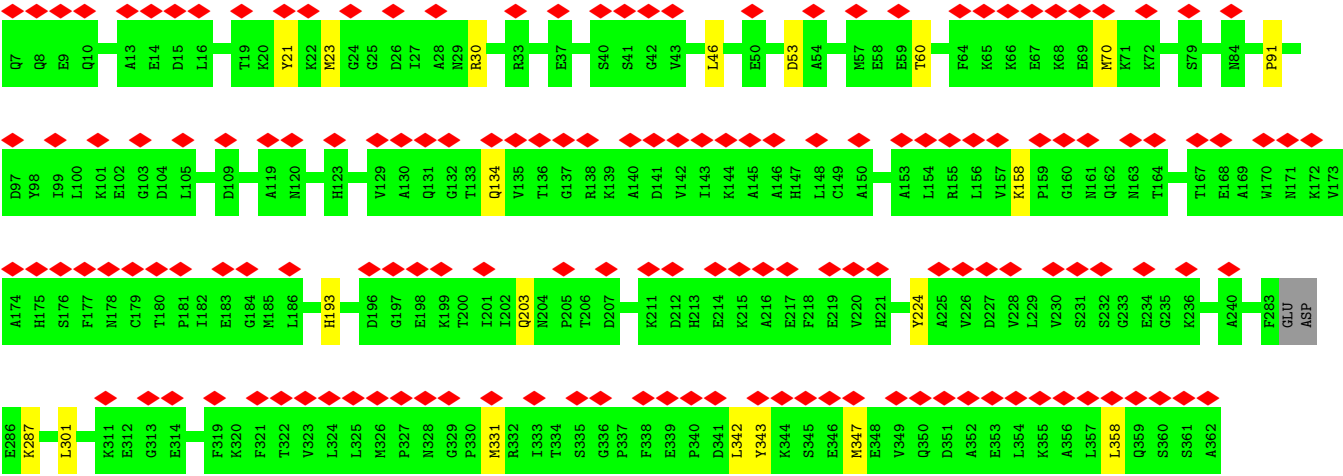


- Molecule 45: Eukaryotic translation initiation factor 6



- Molecule 46: Proliferation-associated protein 2G4





4 Experimental information

| Property | Value | Source |
|--------------------------------------|---------------------------|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 132478 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | NONE | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 50 | Depositor |
| Minimum defocus (nm) | 1200 | Depositor |
| Maximum defocus (nm) | 2500 | Depositor |
| Magnification | Not provided | |
| Image detector | GATAN K3 (6k x 4k) | Depositor |
| Maximum map value | 0.629 | Depositor |
| Minimum map value | -0.281 | Depositor |
| Average map value | -0.000 | Depositor |
| Map value standard deviation | 0.022 | Depositor |
| Recommended contour level | 0.065 | Depositor |
| Map size (\AA) | 546.816, 546.816, 546.816 | wwPDB |
| Map dimensions | 512, 512, 512 | wwPDB |
| Map angles ($^\circ$) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (\AA) | 1.068, 1.068, 1.068 | 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

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 | LW | 0.32 | 0/541 | 0.60 | 0/720 |
| 2 | L5 | 0.50 | 0/87512 | 0.87 | 104/136518 (0.1%) |
| 3 | L7 | 0.48 | 0/2861 | 0.81 | 0/4459 |
| 4 | L8 | 0.50 | 0/3701 | 0.81 | 2/5766 (0.0%) |
| 5 | LA | 0.35 | 0/1936 | 0.63 | 1/2596 (0.0%) |
| 6 | LB | 0.34 | 0/3306 | 0.60 | 2/4424 (0.0%) |
| 7 | LC | 0.33 | 0/2981 | 0.59 | 1/4002 (0.0%) |
| 8 | LD | 0.32 | 0/2428 | 0.56 | 1/3252 (0.0%) |
| 9 | LE | 0.31 | 0/1942 | 0.60 | 0/2606 |
| 10 | LF | 0.35 | 0/1905 | 0.58 | 0/2539 |
| 11 | LG | 0.32 | 0/1960 | 0.56 | 0/2637 |
| 12 | LH | 0.33 | 0/1537 | 0.61 | 1/2066 (0.0%) |
| 13 | LI | 0.33 | 0/1673 | 0.59 | 0/2233 |
| 14 | LJ | 0.31 | 0/1433 | 0.65 | 0/1915 |
| 15 | LL | 0.34 | 0/1732 | 0.65 | 2/2315 (0.1%) |
| 16 | LM | 0.33 | 0/1161 | 0.57 | 0/1554 |
| 17 | LN | 0.35 | 0/1746 | 0.60 | 0/2338 |
| 18 | LO | 0.34 | 0/1682 | 0.57 | 0/2250 |
| 19 | LP | 0.33 | 0/1268 | 0.54 | 0/1701 |
| 20 | LQ | 0.35 | 0/1537 | 0.63 | 1/2052 (0.0%) |
| 21 | LR | 0.30 | 0/1296 | 0.62 | 1/1713 (0.1%) |
| 22 | LS | 0.36 | 0/1493 | 0.61 | 1/2003 (0.0%) |
| 23 | LT | 0.36 | 0/1326 | 0.61 | 0/1770 |
| 24 | LU | 0.38 | 0/839 | 0.72 | 1/1126 (0.1%) |
| 25 | LV | 0.34 | 0/993 | 0.59 | 0/1332 |
| 26 | LX | 0.32 | 0/1002 | 0.59 | 1/1345 (0.1%) |
| 27 | LY | 0.34 | 0/1132 | 0.59 | 0/1504 |
| 28 | LZ | 0.33 | 0/1130 | 0.59 | 1/1507 (0.1%) |
| 29 | La | 0.34 | 0/1191 | 0.54 | 0/1591 |
| 30 | Lb | 0.27 | 0/889 | 0.58 | 0/1175 |
| 31 | Lc | 0.36 | 0/774 | 0.62 | 0/1038 |
| 32 | Ld | 0.33 | 0/903 | 0.59 | 0/1216 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|----------|-------------|-------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 33 | Le | 0.36 | 0/1071 | 0.61 | 0/1429 |
| 34 | Lf | 0.37 | 0/895 | 0.62 | 0/1198 |
| 35 | Lg | 0.34 | 0/916 | 0.63 | 0/1220 |
| 36 | Lh | 0.30 | 0/1023 | 0.59 | 0/1351 |
| 37 | Li | 0.29 | 0/843 | 0.62 | 0/1115 |
| 38 | Lj | 0.35 | 0/720 | 0.62 | 0/952 |
| 39 | Lk | 0.34 | 0/575 | 0.71 | 1/761 (0.1%) |
| 40 | Ll | 0.30 | 0/454 | 0.61 | 0/599 |
| 41 | Lm | 0.30 | 0/435 | 0.54 | 0/575 |
| 42 | Lo | 0.32 | 0/876 | 0.59 | 0/1156 |
| 43 | Lp | 0.33 | 0/718 | 0.57 | 0/953 |
| 44 | Lr | 0.32 | 0/1017 | 0.59 | 0/1364 |
| 45 | P | 0.32 | 0/1736 | 0.68 | 1/2362 (0.0%) |
| 46 | CA | 0.29 | 0/2810 | 0.64 | 3/3780 (0.1%) |
| All | All | 0.44 | 0/151899 | 0.78 | 125/224078 (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 |
|-----|-------|---------------------|---------------------|
| 5 | LA | 0 | 1 |
| 6 | LB | 0 | 2 |
| 15 | LL | 0 | 1 |
| 16 | LM | 0 | 2 |
| 18 | LO | 0 | 1 |
| 24 | LU | 0 | 1 |
| 34 | Lf | 0 | 3 |
| 38 | Lj | 0 | 1 |
| All | All | 0 | 12 |

There are no bond length outliers.

All (125) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|-----------|--------|-------------|----------|
| 46 | CA | 91 | PRO | CA-N-CD | -12.06 | 94.61 | 111.50 |
| 2 | L5 | 485 | C | C2-N1-C1' | 11.09 | 131.00 | 118.80 |
| 15 | LL | 134 | PRO | CA-N-CD | -10.56 | 96.71 | 111.50 |
| 2 | L5 | 2710 | C | N1-C2-O2 | 10.32 | 125.09 | 118.90 |
| 2 | L5 | 2710 | C | C2-N1-C1' | 9.21 | 128.93 | 118.80 |
| 2 | L5 | 654 | C | N1-C2-O2 | 8.99 | 124.30 | 118.90 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|------------|-------|-------------|----------|
| 12 | LH | 142 | ASP | CB-CG-OD2 | 8.57 | 126.01 | 118.30 |
| 2 | L5 | 485 | C | C6-N1-C1' | -8.45 | 110.66 | 120.80 |
| 2 | L5 | 4138 | C | N3-C2-O2 | -8.44 | 116.00 | 121.90 |
| 2 | L5 | 2257 | C | C2-N1-C1' | 8.39 | 128.03 | 118.80 |
| 2 | L5 | 2257 | C | N1-C2-O2 | 8.37 | 123.92 | 118.90 |
| 2 | L5 | 456 | C | O4'-C1'-N1 | 8.31 | 114.85 | 108.20 |
| 2 | L5 | 456 | C | N3-C2-O2 | -7.96 | 116.33 | 121.90 |
| 2 | L5 | 1414 | C | N1-C2-O2 | 7.92 | 123.65 | 118.90 |
| 2 | L5 | 1414 | C | N3-C2-O2 | -7.89 | 116.38 | 121.90 |
| 2 | L5 | 2710 | C | N3-C2-O2 | -7.86 | 116.40 | 121.90 |
| 24 | LU | 43 | LEU | CA-CB-CG | 7.74 | 133.10 | 115.30 |
| 2 | L5 | 1252 | C | N3-C2-O2 | -7.56 | 116.61 | 121.90 |
| 2 | L5 | 925 | C | N3-C2-O2 | -7.42 | 116.71 | 121.90 |
| 2 | L5 | 1082 | C | O4'-C1'-N1 | 7.41 | 114.13 | 108.20 |
| 2 | L5 | 490 | C | N3-C2-O2 | -7.37 | 116.74 | 121.90 |
| 2 | L5 | 925 | C | N1-C2-O2 | 7.30 | 123.28 | 118.90 |
| 2 | L5 | 209 | U | C2-N1-C1' | 7.14 | 126.27 | 117.70 |
| 2 | L5 | 1082 | C | N3-C2-O2 | -7.13 | 116.91 | 121.90 |
| 2 | L5 | 255 | C | N3-C2-O2 | -7.06 | 116.96 | 121.90 |
| 2 | L5 | 4709 | U | C2-N1-C1' | 7.01 | 126.12 | 117.70 |
| 2 | L5 | 100 | C | C2-N1-C1' | 6.95 | 126.44 | 118.80 |
| 2 | L5 | 175 | C | N3-C2-O2 | -6.95 | 117.04 | 121.90 |
| 2 | L5 | 1216 | C | C2-N1-C1' | 6.85 | 126.33 | 118.80 |
| 2 | L5 | 129 | C | N3-C2-O2 | -6.84 | 117.11 | 121.90 |
| 2 | L5 | 485 | C | N1-C2-O2 | 6.79 | 122.97 | 118.90 |
| 5 | LA | 228 | ASP | CB-CG-OD2 | 6.70 | 124.33 | 118.30 |
| 2 | L5 | 3773 | U | N3-C2-O2 | -6.66 | 117.54 | 122.20 |
| 2 | L5 | 4928 | C | N1-C2-O2 | 6.62 | 122.87 | 118.90 |
| 2 | L5 | 2410 | C | C2-N1-C1' | 6.55 | 126.01 | 118.80 |
| 2 | L5 | 4928 | C | C2-N1-C1' | 6.53 | 125.99 | 118.80 |
| 2 | L5 | 181 | C | C2-N1-C1' | 6.42 | 125.86 | 118.80 |
| 2 | L5 | 1191 | C | N3-C2-O2 | -6.42 | 117.41 | 121.90 |
| 2 | L5 | 2710 | C | C6-N1-C1' | -6.40 | 113.12 | 120.80 |
| 2 | L5 | 654 | C | C2-N1-C1' | 6.36 | 125.79 | 118.80 |
| 4 | L8 | 128 | C | C2-N1-C1' | 6.28 | 125.71 | 118.80 |
| 6 | LB | 299 | ILE | CG1-CB-CG2 | -6.28 | 97.59 | 111.40 |
| 2 | L5 | 3741 | C | N3-C2-O2 | -6.26 | 117.52 | 121.90 |
| 2 | L5 | 753 | C | N1-C2-O2 | 6.23 | 122.64 | 118.90 |
| 2 | L5 | 2257 | C | N3-C2-O2 | -6.20 | 117.56 | 121.90 |
| 2 | L5 | 4926 | C | N1-C2-O2 | 6.18 | 122.61 | 118.90 |
| 45 | P | 131 | ASP | CB-CG-OD2 | 6.17 | 123.86 | 118.30 |
| 2 | L5 | 2257 | C | C6-N1-C1' | -6.16 | 113.41 | 120.80 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|------------|-------|-------------|----------|
| 2 | L5 | 181 | C | N1-C2-O2 | 6.16 | 122.59 | 118.90 |
| 2 | L5 | 753 | C | C2-N1-C1' | 6.12 | 125.53 | 118.80 |
| 2 | L5 | 4926 | C | C2-N1-C1' | 6.08 | 125.49 | 118.80 |
| 2 | L5 | 4924 | C | N3-C2-O2 | -6.08 | 117.64 | 121.90 |
| 2 | L5 | 3773 | U | C2-N1-C1' | 6.07 | 124.98 | 117.70 |
| 2 | L5 | 4147 | G | C5-C6-O6 | 6.05 | 132.23 | 128.60 |
| 7 | LC | 2 | ALA | C-N-CA | 6.03 | 136.78 | 121.70 |
| 2 | L5 | 3773 | U | N1-C2-O2 | 6.03 | 127.02 | 122.80 |
| 15 | LL | 134 | PRO | N-CD-CG | -5.94 | 94.29 | 103.20 |
| 2 | L5 | 485 | C | C5-C6-N1 | 5.93 | 123.97 | 121.00 |
| 2 | L5 | 1241 | C | C2-N1-C1' | 5.88 | 125.27 | 118.80 |
| 2 | L5 | 2710 | C | C6-N1-C2 | -5.88 | 117.95 | 120.30 |
| 28 | LZ | 30 | ASP | CB-CG-OD1 | 5.87 | 123.58 | 118.30 |
| 2 | L5 | 4147 | G | N1-C6-O6 | -5.86 | 116.39 | 119.90 |
| 2 | L5 | 1216 | C | N1-C2-O2 | 5.83 | 122.40 | 118.90 |
| 2 | L5 | 1245 | C | C2-N1-C1' | 5.76 | 125.14 | 118.80 |
| 2 | L5 | 417 | G | O4'-C1'-N9 | 5.72 | 112.78 | 108.20 |
| 2 | L5 | 4426 | C | C2-N1-C1' | 5.70 | 125.07 | 118.80 |
| 39 | Lk | 61 | PRO | CA-N-CD | -5.70 | 103.53 | 111.50 |
| 2 | L5 | 4758 | U | C2-N1-C1' | 5.63 | 124.46 | 117.70 |
| 2 | L5 | 753 | C | N3-C2-O2 | -5.60 | 117.98 | 121.90 |
| 2 | L5 | 1241 | C | N1-C2-O2 | 5.60 | 122.26 | 118.90 |
| 2 | L5 | 255 | C | N1-C2-O2 | 5.58 | 122.25 | 118.90 |
| 2 | L5 | 2760 | G | P-O3'-C3' | 5.57 | 126.39 | 119.70 |
| 8 | LD | 235 | MET | CA-CB-CG | 5.55 | 122.73 | 113.30 |
| 2 | L5 | 4502 | C | N1-C2-O2 | 5.54 | 122.22 | 118.90 |
| 2 | L5 | 1663 | C | C2-N1-C1' | 5.54 | 124.89 | 118.80 |
| 2 | L5 | 1082 | C | P-O3'-C3' | 5.52 | 126.33 | 119.70 |
| 2 | L5 | 2528 | G | C4-N9-C1' | 5.50 | 133.65 | 126.50 |
| 2 | L5 | 2262 | G | C4-N9-C1' | 5.47 | 133.61 | 126.50 |
| 46 | CA | 301 | LEU | CA-CB-CG | 5.46 | 127.86 | 115.30 |
| 22 | LS | 112 | ASP | CB-CG-OD2 | 5.43 | 123.18 | 118.30 |
| 2 | L5 | 2627 | C | C2-N1-C1' | 5.42 | 124.76 | 118.80 |
| 2 | L5 | 2627 | C | N1-C2-O2 | 5.39 | 122.14 | 118.90 |
| 2 | L5 | 4709 | U | C6-N1-C1' | -5.39 | 113.65 | 121.20 |
| 26 | LX | 116 | LEU | CA-CB-CG | 5.39 | 127.69 | 115.30 |
| 2 | L5 | 654 | C | N3-C2-O2 | -5.38 | 118.13 | 121.90 |
| 2 | L5 | 654 | C | C6-N1-C1' | -5.38 | 114.35 | 120.80 |
| 2 | L5 | 489 | C | N1-C2-O2 | 5.36 | 122.11 | 118.90 |
| 2 | L5 | 4107 | G | N3-C4-C5 | -5.36 | 125.92 | 128.60 |
| 2 | L5 | 209 | U | C6-N1-C1' | -5.35 | 113.71 | 121.20 |
| 2 | L5 | 1251 | C | N1-C2-O2 | 5.35 | 122.11 | 118.90 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|------------|-------|-------------|----------|
| 2 | L5 | 2708 | U | C2-N1-C1' | 5.35 | 124.12 | 117.70 |
| 2 | L5 | 2708 | U | N1-C2-O2 | 5.34 | 126.54 | 122.80 |
| 2 | L5 | 4281 | A | O4'-C1'-N9 | 5.33 | 112.47 | 108.20 |
| 2 | L5 | 1081 | C | N1-C2-O2 | 5.30 | 122.08 | 118.90 |
| 2 | L5 | 4107 | G | C4-N9-C1' | 5.29 | 133.38 | 126.50 |
| 2 | L5 | 4928 | C | N3-C2-O2 | -5.28 | 118.20 | 121.90 |
| 2 | L5 | 661 | C | N3-C2-O2 | -5.28 | 118.21 | 121.90 |
| 2 | L5 | 914 | U | P-O3'-C3' | 5.24 | 125.99 | 119.70 |
| 2 | L5 | 664 | G | C5-C6-O6 | 5.24 | 131.74 | 128.60 |
| 2 | L5 | 100 | C | N3-C2-O2 | -5.23 | 118.24 | 121.90 |
| 2 | L5 | 1082 | C | C6-N1-C2 | -5.23 | 118.21 | 120.30 |
| 21 | LR | 68 | LEU | CA-CB-CG | 5.23 | 127.32 | 115.30 |
| 2 | L5 | 100 | C | N1-C2-O2 | 5.21 | 122.03 | 118.90 |
| 46 | CA | 358 | LEU | CA-CB-CG | 5.21 | 127.28 | 115.30 |
| 2 | L5 | 4600 | G | P-O3'-C3' | 5.18 | 125.91 | 119.70 |
| 2 | L5 | 3773 | U | O4'-C1'-N1 | 5.18 | 112.34 | 108.20 |
| 20 | LQ | 28 | LEU | CA-CB-CG | 5.18 | 127.20 | 115.30 |
| 2 | L5 | 2018 | C | C5-C6-N1 | 5.16 | 123.58 | 121.00 |
| 2 | L5 | 2505 | C | N1-C2-O2 | 5.15 | 121.99 | 118.90 |
| 2 | L5 | 2710 | C | C5-C6-N1 | 5.14 | 123.57 | 121.00 |
| 2 | L5 | 4107 | G | N3-C4-N9 | 5.14 | 129.08 | 126.00 |
| 2 | L5 | 3741 | C | N1-C2-O2 | 5.12 | 121.97 | 118.90 |
| 2 | L5 | 2033 | A | P-O3'-C3' | 5.11 | 125.84 | 119.70 |
| 2 | L5 | 4138 | C | N1-C2-O2 | 5.10 | 121.96 | 118.90 |
| 6 | LB | 259 | PRO | CA-N-CD | -5.09 | 104.37 | 111.50 |
| 2 | L5 | 2528 | G | N3-C4-C5 | -5.09 | 126.06 | 128.60 |
| 2 | L5 | 1182 | C | C2-N1-C1' | 5.08 | 124.39 | 118.80 |
| 2 | L5 | 1241 | C | N3-C2-O2 | -5.08 | 118.35 | 121.90 |
| 2 | L5 | 2351 | C | C2-N1-C1' | 5.07 | 124.38 | 118.80 |
| 2 | L5 | 672 | C | C2-N1-C1' | 5.06 | 124.36 | 118.80 |
| 2 | L5 | 2528 | G | N3-C4-N9 | 5.05 | 129.03 | 126.00 |
| 2 | L5 | 4887 | C | N1-C2-O2 | 5.05 | 121.93 | 118.90 |
| 4 | L8 | 128 | C | C6-N1-C1' | -5.02 | 114.77 | 120.80 |
| 2 | L5 | 1446 | C | N1-C2-O2 | 5.02 | 121.91 | 118.90 |
| 2 | L5 | 209 | U | N1-C2-O2 | 5.01 | 126.31 | 122.80 |

There are no chirality outliers.

All (12) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 5 | LA | 13 | GLY | Peptide |
| 6 | LB | 17 | LEU | Peptide |

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| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 6 | LB | 258 | HIS | Peptide |
| 15 | LL | 154 | VAL | Peptide |
| 16 | LM | 87 | ALA | Peptide |
| 16 | LM | 88 | ALA | Peptide |
| 18 | LO | 110 | PRO | Peptide |
| 24 | LU | 46 | ARG | Peptide |
| 34 | Lf | 103 | VAL | Peptide |
| 34 | Lf | 106 | TYR | Peptide |
| 34 | Lf | 79 | GLY | Peptide |
| 38 | Lj | 39 | TYR | 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 | Percentiles | |
|-----|-------|----------------|-----------|----------|----------|-------------|-----|
| 1 | LW | 61/118 (52%) | 55 (90%) | 6 (10%) | 0 | 100 | 100 |
| 5 | LA | 246/248 (99%) | 220 (89%) | 26 (11%) | 0 | 100 | 100 |
| 6 | LB | 400/402 (100%) | 371 (93%) | 29 (7%) | 0 | 100 | 100 |
| 7 | LC | 366/368 (100%) | 340 (93%) | 26 (7%) | 0 | 100 | 100 |
| 8 | LD | 291/293 (99%) | 274 (94%) | 17 (6%) | 0 | 100 | 100 |
| 9 | LE | 232/242 (96%) | 209 (90%) | 23 (10%) | 0 | 100 | 100 |
| 10 | LF | 223/225 (99%) | 214 (96%) | 9 (4%) | 0 | 100 | 100 |
| 11 | LG | 239/241 (99%) | 223 (93%) | 16 (7%) | 0 | 100 | 100 |
| 12 | LH | 188/190 (99%) | 174 (93%) | 14 (7%) | 0 | 100 | 100 |
| 13 | LI | 198/213 (93%) | 187 (94%) | 11 (6%) | 0 | 100 | 100 |
| 14 | LJ | 174/176 (99%) | 159 (91%) | 15 (9%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 15 | LL | 208/210 (99%) | 193 (93%) | 15 (7%) | 0 | 100 | 100 |
| 16 | LM | 137/139 (99%) | 126 (92%) | 10 (7%) | 1 (1%) | 19 | 41 |
| 17 | LN | 201/203 (99%) | 189 (94%) | 11 (6%) | 1 (0%) | 25 | 50 |
| 18 | LO | 199/201 (99%) | 191 (96%) | 8 (4%) | 0 | 100 | 100 |
| 19 | LP | 151/153 (99%) | 143 (95%) | 8 (5%) | 0 | 100 | 100 |
| 20 | LQ | 185/187 (99%) | 178 (96%) | 7 (4%) | 0 | 100 | 100 |
| 21 | LR | 149/187 (80%) | 144 (97%) | 5 (3%) | 0 | 100 | 100 |
| 22 | LS | 173/175 (99%) | 161 (93%) | 12 (7%) | 0 | 100 | 100 |
| 23 | LT | 157/159 (99%) | 144 (92%) | 13 (8%) | 0 | 100 | 100 |
| 24 | LU | 99/101 (98%) | 80 (81%) | 19 (19%) | 0 | 100 | 100 |
| 25 | LV | 129/131 (98%) | 122 (95%) | 7 (5%) | 0 | 100 | 100 |
| 26 | LX | 118/120 (98%) | 117 (99%) | 1 (1%) | 0 | 100 | 100 |
| 27 | LY | 132/134 (98%) | 127 (96%) | 5 (4%) | 0 | 100 | 100 |
| 28 | LZ | 133/135 (98%) | 127 (96%) | 6 (4%) | 0 | 100 | 100 |
| 29 | La | 145/147 (99%) | 136 (94%) | 9 (6%) | 0 | 100 | 100 |
| 30 | Lb | 105/121 (87%) | 99 (94%) | 6 (6%) | 0 | 100 | 100 |
| 31 | Lc | 96/98 (98%) | 89 (93%) | 7 (7%) | 0 | 100 | 100 |
| 32 | Ld | 105/107 (98%) | 97 (92%) | 8 (8%) | 0 | 100 | 100 |
| 33 | Le | 126/128 (98%) | 118 (94%) | 8 (6%) | 0 | 100 | 100 |
| 34 | Lf | 107/109 (98%) | 97 (91%) | 9 (8%) | 1 (1%) | 14 | 35 |
| 35 | Lg | 112/114 (98%) | 111 (99%) | 1 (1%) | 0 | 100 | 100 |
| 36 | Lh | 120/122 (98%) | 117 (98%) | 3 (2%) | 0 | 100 | 100 |
| 37 | Li | 100/102 (98%) | 94 (94%) | 6 (6%) | 0 | 100 | 100 |
| 38 | Lj | 84/86 (98%) | 78 (93%) | 6 (7%) | 0 | 100 | 100 |
| 39 | Lk | 67/69 (97%) | 62 (92%) | 5 (8%) | 0 | 100 | 100 |
| 40 | Ll | 48/50 (96%) | 47 (98%) | 1 (2%) | 0 | 100 | 100 |
| 41 | Lm | 50/52 (96%) | 49 (98%) | 1 (2%) | 0 | 100 | 100 |
| 42 | Lo | 103/105 (98%) | 99 (96%) | 4 (4%) | 0 | 100 | 100 |
| 43 | Lp | 89/91 (98%) | 84 (94%) | 5 (6%) | 0 | 100 | 100 |
| 44 | Lr | 123/125 (98%) | 115 (94%) | 8 (6%) | 0 | 100 | 100 |
| 45 | P | 223/225 (99%) | 209 (94%) | 12 (5%) | 2 (1%) | 14 | 35 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-----------------|------------|----------|----------|-------------|-----|
| 46 | CA | 350/356 (98%) | 330 (94%) | 20 (6%) | 0 | 100 | 100 |
| All | All | 6942/7158 (97%) | 6499 (94%) | 438 (6%) | 5 (0%) | 50 | 72 |

All (5) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 45 | P | 201 | ASP |
| 17 | LN | 124 | ASP |
| 16 | LM | 88 | ALA |
| 45 | P | 32 | GLU |
| 34 | Lf | 107 | PRO |

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 | LW | 55/97 (57%) | 49 (89%) | 6 (11%) | 5 | 15 |
| 5 | LA | 190/190 (100%) | 177 (93%) | 13 (7%) | 13 | 32 |
| 6 | LB | 348/348 (100%) | 325 (93%) | 23 (7%) | 14 | 33 |
| 7 | LC | 306/306 (100%) | 287 (94%) | 19 (6%) | 15 | 36 |
| 8 | LD | 246/247 (100%) | 220 (89%) | 26 (11%) | 5 | 16 |
| 9 | LE | 209/215 (97%) | 191 (91%) | 18 (9%) | 8 | 23 |
| 10 | LF | 194/194 (100%) | 183 (94%) | 11 (6%) | 17 | 39 |
| 11 | LG | 203/205 (99%) | 188 (93%) | 15 (7%) | 11 | 28 |
| 12 | LH | 169/169 (100%) | 151 (89%) | 18 (11%) | 5 | 15 |
| 13 | LI | 172/180 (96%) | 158 (92%) | 14 (8%) | 9 | 24 |
| 14 | LJ | 148/148 (100%) | 133 (90%) | 15 (10%) | 6 | 18 |
| 15 | LL | 176/176 (100%) | 163 (93%) | 13 (7%) | 11 | 28 |
| 16 | LM | 118/118 (100%) | 109 (92%) | 9 (8%) | 11 | 27 |
| 17 | LN | 171/171 (100%) | 159 (93%) | 12 (7%) | 12 | 31 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-----------------|------------|----------|-------------|----|
| 18 | LO | 173/173 (100%) | 167 (96%) | 6 (4%) | 31 | 56 |
| 19 | LP | 134/134 (100%) | 123 (92%) | 11 (8%) | 9 | 24 |
| 20 | LQ | 164/164 (100%) | 154 (94%) | 10 (6%) | 15 | 36 |
| 21 | LR | 137/166 (82%) | 128 (93%) | 9 (7%) | 14 | 33 |
| 22 | LS | 156/156 (100%) | 152 (97%) | 4 (3%) | 41 | 65 |
| 23 | LT | 139/139 (100%) | 131 (94%) | 8 (6%) | 17 | 38 |
| 24 | LU | 91/91 (100%) | 76 (84%) | 15 (16%) | 2 | 4 |
| 25 | LV | 101/101 (100%) | 96 (95%) | 5 (5%) | 20 | 44 |
| 26 | LX | 108/108 (100%) | 99 (92%) | 9 (8%) | 9 | 24 |
| 27 | LY | 124/124 (100%) | 115 (93%) | 9 (7%) | 11 | 29 |
| 28 | LZ | 117/117 (100%) | 108 (92%) | 9 (8%) | 10 | 27 |
| 29 | La | 120/120 (100%) | 116 (97%) | 4 (3%) | 33 | 58 |
| 30 | Lb | 88/101 (87%) | 78 (89%) | 10 (11%) | 4 | 14 |
| 31 | Lc | 83/83 (100%) | 79 (95%) | 4 (5%) | 21 | 46 |
| 32 | Ld | 98/98 (100%) | 91 (93%) | 7 (7%) | 12 | 31 |
| 33 | Le | 114/114 (100%) | 105 (92%) | 9 (8%) | 10 | 25 |
| 34 | Lf | 88/88 (100%) | 84 (96%) | 4 (4%) | 23 | 48 |
| 35 | Lg | 98/98 (100%) | 86 (88%) | 12 (12%) | 4 | 12 |
| 36 | Lh | 109/109 (100%) | 103 (94%) | 6 (6%) | 18 | 41 |
| 37 | Li | 86/86 (100%) | 78 (91%) | 8 (9%) | 7 | 20 |
| 38 | Lj | 73/73 (100%) | 68 (93%) | 5 (7%) | 13 | 32 |
| 39 | Lk | 64/64 (100%) | 56 (88%) | 8 (12%) | 3 | 11 |
| 40 | Ll | 47/47 (100%) | 43 (92%) | 4 (8%) | 8 | 23 |
| 41 | Lm | 48/48 (100%) | 46 (96%) | 2 (4%) | 25 | 50 |
| 42 | Lo | 93/93 (100%) | 90 (97%) | 3 (3%) | 34 | 59 |
| 43 | Lp | 74/74 (100%) | 67 (90%) | 7 (10%) | 7 | 19 |
| 44 | Lr | 109/109 (100%) | 87 (80%) | 22 (20%) | 1 | 2 |
| 45 | P | 195/195 (100%) | 165 (85%) | 30 (15%) | 2 | 6 |
| 46 | CA | 303/305 (99%) | 286 (94%) | 17 (6%) | 17 | 40 |
| All | All | 6039/6142 (98%) | 5570 (92%) | 469 (8%) | 13 | 26 |

All (469) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | LW | 8 | PHE |
| 1 | LW | 20 | ARG |
| 1 | LW | 32 | LEU |
| 1 | LW | 49 | ILE |
| 1 | LW | 55 | TYR |
| 1 | LW | 60 | LYS |
| 5 | LA | 54 | ARG |
| 5 | LA | 102 | LEU |
| 5 | LA | 115 | CYS |
| 5 | LA | 139 | HIS |
| 5 | LA | 146 | THR |
| 5 | LA | 154 | SER |
| 5 | LA | 155 | LYS |
| 5 | LA | 169 | VAL |
| 5 | LA | 207 | VAL |
| 5 | LA | 221 | LYS |
| 5 | LA | 223 | SER |
| 5 | LA | 228 | ASP |
| 5 | LA | 243 | THR |
| 6 | LB | 7 | SER |
| 6 | LB | 17 | LEU |
| 6 | LB | 59 | GLU |
| 6 | LB | 73 | VAL |
| 6 | LB | 84 | MET |
| 6 | LB | 112 | ASP |
| 6 | LB | 125 | SER |
| 6 | LB | 126 | LYS |
| 6 | LB | 144 | LYS |
| 6 | LB | 159 | VAL |
| 6 | LB | 174 | ARG |
| 6 | LB | 181 | MET |
| 6 | LB | 258 | HIS |
| 6 | LB | 278 | THR |
| 6 | LB | 297 | LYS |
| 6 | LB | 298 | LEU |
| 6 | LB | 308 | ASP |
| 6 | LB | 328 | ASN |
| 6 | LB | 329 | ASP |
| 6 | LB | 358 | ARG |
| 6 | LB | 366 | LYS |
| 6 | LB | 382 | MET |
| 6 | LB | 394 | LYS |
| 7 | LC | 14 | LYS |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 7 | LC | 20 | LYS |
| 7 | LC | 23 | THR |
| 7 | LC | 50 | GLN |
| 7 | LC | 71 | ARG |
| 7 | LC | 101 | MET |
| 7 | LC | 106 | LYS |
| 7 | LC | 114 | ARG |
| 7 | LC | 122 | TYR |
| 7 | LC | 140 | LYS |
| 7 | LC | 147 | VAL |
| 7 | LC | 154 | VAL |
| 7 | LC | 175 | LYS |
| 7 | LC | 188 | ARG |
| 7 | LC | 204 | ARG |
| 7 | LC | 234 | LYS |
| 7 | LC | 261 | ASP |
| 7 | LC | 268 | ARG |
| 7 | LC | 366 | ASP |
| 8 | LD | 48 | LYS |
| 8 | LD | 50 | ARG |
| 8 | LD | 51 | MET |
| 8 | LD | 68 | ARG |
| 8 | LD | 72 | ASP |
| 8 | LD | 86 | TYR |
| 8 | LD | 89 | LYS |
| 8 | LD | 115 | MET |
| 8 | LD | 126 | THR |
| 8 | LD | 132 | VAL |
| 8 | LD | 136 | ASP |
| 8 | LD | 152 | ARG |
| 8 | LD | 171 | LEU |
| 8 | LD | 189 | GLU |
| 8 | LD | 194 | VAL |
| 8 | LD | 206 | ASP |
| 8 | LD | 232 | THR |
| 8 | LD | 235 | MET |
| 8 | LD | 236 | MET |
| 8 | LD | 259 | LYS |
| 8 | LD | 261 | VAL |
| 8 | LD | 268 | ARG |
| 8 | LD | 270 | LYS |
| 8 | LD | 276 | LYS |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 8 | LD | 286 | SER |
| 8 | LD | 289 | ARG |
| 9 | LE | 45 | SER |
| 9 | LE | 51 | VAL |
| 9 | LE | 74 | SER |
| 9 | LE | 88 | VAL |
| 9 | LE | 100 | LYS |
| 9 | LE | 128 | HIS |
| 9 | LE | 183 | ARG |
| 9 | LE | 187 | ARG |
| 9 | LE | 191 | GLN |
| 9 | LE | 199 | THR |
| 9 | LE | 202 | ASP |
| 9 | LE | 210 | LYS |
| 9 | LE | 221 | LYS |
| 9 | LE | 236 | GLU |
| 9 | LE | 240 | TYR |
| 9 | LE | 260 | LYS |
| 9 | LE | 267 | LEU |
| 9 | LE | 273 | SER |
| 10 | LF | 27 | GLU |
| 10 | LF | 32 | ARG |
| 10 | LF | 33 | LEU |
| 10 | LF | 86 | GLU |
| 10 | LF | 171 | ASP |
| 10 | LF | 174 | LEU |
| 10 | LF | 178 | SER |
| 10 | LF | 189 | ASP |
| 10 | LF | 200 | ARG |
| 10 | LF | 236 | ARG |
| 10 | LF | 248 | ASN |
| 11 | LG | 35 | ARG |
| 11 | LG | 48 | LYS |
| 11 | LG | 53 | ARG |
| 11 | LG | 73 | ARG |
| 11 | LG | 75 | LYS |
| 11 | LG | 100 | HIS |
| 11 | LG | 105 | GLU |
| 11 | LG | 111 | LYS |
| 11 | LG | 166 | LEU |
| 11 | LG | 176 | LYS |
| 11 | LG | 201 | THR |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 11 | LG | 206 | GLN |
| 11 | LG | 210 | GLU |
| 11 | LG | 211 | ASP |
| 11 | LG | 257 | LYS |
| 12 | LH | 7 | ASN |
| 12 | LH | 8 | GLN |
| 12 | LH | 9 | THR |
| 12 | LH | 10 | VAL |
| 12 | LH | 16 | VAL |
| 12 | LH | 21 | LYS |
| 12 | LH | 28 | LYS |
| 12 | LH | 44 | GLU |
| 12 | LH | 46 | SER |
| 12 | LH | 51 | LYS |
| 12 | LH | 57 | VAL |
| 12 | LH | 64 | ARG |
| 12 | LH | 95 | VAL |
| 12 | LH | 106 | GLN |
| 12 | LH | 136 | VAL |
| 12 | LH | 150 | ASP |
| 12 | LH | 177 | ASP |
| 12 | LH | 183 | GLU |
| 13 | LI | 12 | CYS |
| 13 | LI | 35 | ASP |
| 13 | LI | 44 | ASP |
| 13 | LI | 71 | CYS |
| 13 | LI | 73 | ASN |
| 13 | LI | 76 | MET |
| 13 | LI | 79 | SER |
| 13 | LI | 82 | ARG |
| 13 | LI | 83 | ASP |
| 13 | LI | 87 | MET |
| 13 | LI | 129 | VAL |
| 13 | LI | 146 | GLU |
| 13 | LI | 164 | LYS |
| 13 | LI | 168 | SER |
| 14 | LJ | 29 | SER |
| 14 | LJ | 51 | SER |
| 14 | LJ | 58 | ARG |
| 14 | LJ | 60 | PHE |
| 14 | LJ | 65 | ASN |
| 14 | LJ | 72 | CYS |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 14 | LJ | 94 | LEU |
| 14 | LJ | 95 | ARG |
| 14 | LJ | 97 | ASN |
| 14 | LJ | 104 | ASN |
| 14 | LJ | 115 | LEU |
| 14 | LJ | 119 | TYR |
| 14 | LJ | 125 | ILE |
| 14 | LJ | 143 | ASP |
| 14 | LJ | 166 | PHE |
| 15 | LL | 19 | GLN |
| 15 | LL | 52 | SER |
| 15 | LL | 64 | VAL |
| 15 | LL | 67 | HIS |
| 15 | LL | 70 | VAL |
| 15 | LL | 98 | VAL |
| 15 | LL | 103 | ARG |
| 15 | LL | 109 | SER |
| 15 | LL | 115 | GLN |
| 15 | LL | 124 | LEU |
| 15 | LL | 144 | LEU |
| 15 | LL | 162 | LYS |
| 15 | LL | 175 | ASN |
| 16 | LM | 31 | ILE |
| 16 | LM | 35 | ARG |
| 16 | LM | 37 | LEU |
| 16 | LM | 46 | ARG |
| 16 | LM | 53 | LYS |
| 16 | LM | 118 | MET |
| 16 | LM | 121 | ARG |
| 16 | LM | 124 | LYS |
| 16 | LM | 132 | LYS |
| 17 | LN | 5 | LYS |
| 17 | LN | 18 | VAL |
| 17 | LN | 41 | ARG |
| 17 | LN | 67 | ARG |
| 17 | LN | 75 | VAL |
| 17 | LN | 80 | THR |
| 17 | LN | 100 | SER |
| 17 | LN | 110 | CYS |
| 17 | LN | 126 | THR |
| 17 | LN | 153 | LYS |
| 17 | LN | 182 | HIS |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 17 | LN | 187 | SER |
| 18 | LO | 27 | VAL |
| 18 | LO | 100 | ASP |
| 18 | LO | 127 | VAL |
| 18 | LO | 145 | VAL |
| 18 | LO | 169 | ARG |
| 18 | LO | 170 | LYS |
| 19 | LP | 13 | LYS |
| 19 | LP | 18 | ARG |
| 19 | LP | 24 | VAL |
| 19 | LP | 57 | CYS |
| 19 | LP | 58 | VAL |
| 19 | LP | 69 | ARG |
| 19 | LP | 76 | TRP |
| 19 | LP | 96 | LYS |
| 19 | LP | 100 | SER |
| 19 | LP | 142 | SER |
| 19 | LP | 152 | GLU |
| 20 | LQ | 3 | VAL |
| 20 | LQ | 19 | LYS |
| 20 | LQ | 28 | LEU |
| 20 | LQ | 62 | SER |
| 20 | LQ | 82 | VAL |
| 20 | LQ | 98 | LEU |
| 20 | LQ | 124 | ASP |
| 20 | LQ | 150 | ARG |
| 20 | LQ | 168 | ARG |
| 20 | LQ | 180 | ARG |
| 21 | LR | 6 | LEU |
| 21 | LR | 12 | SER |
| 21 | LR | 16 | ARG |
| 21 | LR | 49 | LEU |
| 21 | LR | 52 | ARG |
| 21 | LR | 63 | CYS |
| 21 | LR | 65 | LYS |
| 21 | LR | 113 | LYS |
| 21 | LR | 136 | ARG |
| 22 | LS | 57 | SER |
| 22 | LS | 85 | ASP |
| 22 | LS | 154 | LEU |
| 22 | LS | 168 | THR |
| 23 | LT | 3 | ASN |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 23 | LT | 50 | LYS |
| 23 | LT | 60 | LYS |
| 23 | LT | 83 | LYS |
| 23 | LT | 110 | LYS |
| 23 | LT | 114 | GLN |
| 23 | LT | 129 | LYS |
| 23 | LT | 158 | PHE |
| 24 | LU | 19 | LEU |
| 24 | LU | 34 | MET |
| 24 | LU | 41 | GLN |
| 24 | LU | 46 | ARG |
| 24 | LU | 55 | ASN |
| 24 | LU | 66 | SER |
| 24 | LU | 69 | LYS |
| 24 | LU | 74 | SER |
| 24 | LU | 78 | PHE |
| 24 | LU | 79 | SER |
| 24 | LU | 84 | LYS |
| 24 | LU | 94 | ASN |
| 24 | LU | 108 | GLU |
| 24 | LU | 110 | TYR |
| 24 | LU | 112 | LEU |
| 25 | LV | 17 | SER |
| 25 | LV | 48 | ARG |
| 25 | LV | 100 | ASP |
| 25 | LV | 112 | MET |
| 25 | LV | 115 | SER |
| 26 | LX | 57 | GLN |
| 26 | LX | 68 | ARG |
| 26 | LX | 85 | SER |
| 26 | LX | 87 | MET |
| 26 | LX | 88 | LYS |
| 26 | LX | 116 | LEU |
| 26 | LX | 134 | LYS |
| 26 | LX | 139 | ARG |
| 26 | LX | 148 | ASP |
| 27 | LY | 10 | ASP |
| 27 | LY | 12 | SER |
| 27 | LY | 66 | GLN |
| 27 | LY | 74 | TYR |
| 27 | LY | 84 | ARG |
| 27 | LY | 108 | ARG |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 27 | LY | 115 | ARG |
| 27 | LY | 120 | GLU |
| 27 | LY | 124 | LYS |
| 28 | LZ | 11 | VAL |
| 28 | LZ | 30 | ASP |
| 28 | LZ | 31 | ASP |
| 28 | LZ | 43 | VAL |
| 28 | LZ | 84 | ARG |
| 28 | LZ | 93 | LYS |
| 28 | LZ | 94 | THR |
| 28 | LZ | 109 | LYS |
| 28 | LZ | 121 | ARG |
| 29 | La | 77 | LYS |
| 29 | La | 93 | ASN |
| 29 | La | 103 | VAL |
| 29 | La | 106 | SER |
| 30 | Lb | 8 | THR |
| 30 | Lb | 16 | TRP |
| 30 | Lb | 25 | ARG |
| 30 | Lb | 33 | LYS |
| 30 | Lb | 41 | ARG |
| 30 | Lb | 44 | ARG |
| 30 | Lb | 65 | MET |
| 30 | Lb | 91 | ARG |
| 30 | Lb | 103 | LYS |
| 30 | Lb | 107 | ARG |
| 31 | Lc | 23 | LYS |
| 31 | Lc | 26 | LYS |
| 31 | Lc | 44 | LYS |
| 31 | Lc | 68 | LYS |
| 32 | Ld | 26 | THR |
| 32 | Ld | 87 | ARG |
| 32 | Ld | 89 | SER |
| 32 | Ld | 95 | ASP |
| 32 | Ld | 101 | LYS |
| 32 | Ld | 104 | THR |
| 32 | Ld | 106 | VAL |
| 33 | Le | 17 | THR |
| 33 | Le | 25 | SER |
| 33 | Le | 32 | LYS |
| 33 | Le | 33 | ARG |
| 33 | Le | 57 | ASN |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 33 | Le | 76 | LYS |
| 33 | Le | 102 | ASN |
| 33 | Le | 109 | LYS |
| 33 | Le | 126 | ASN |
| 34 | Lf | 19 | ARG |
| 34 | Lf | 33 | VAL |
| 34 | Lf | 37 | ASP |
| 34 | Lf | 95 | LYS |
| 35 | Lg | 3 | GLN |
| 35 | Lg | 19 | LYS |
| 35 | Lg | 21 | ARG |
| 35 | Lg | 23 | SER |
| 35 | Lg | 28 | ASN |
| 35 | Lg | 32 | TYR |
| 35 | Lg | 49 | CYS |
| 35 | Lg | 53 | LEU |
| 35 | Lg | 73 | HIS |
| 35 | Lg | 104 | VAL |
| 35 | Lg | 105 | LYS |
| 35 | Lg | 107 | LEU |
| 36 | Lh | 42 | SER |
| 36 | Lh | 87 | LYS |
| 36 | Lh | 98 | HIS |
| 36 | Lh | 102 | LEU |
| 36 | Lh | 109 | ARG |
| 36 | Lh | 116 | LEU |
| 37 | Li | 3 | LEU |
| 37 | Li | 23 | LYS |
| 37 | Li | 29 | ARG |
| 37 | Li | 42 | ASP |
| 37 | Li | 46 | GLU |
| 37 | Li | 68 | ARG |
| 37 | Li | 89 | GLU |
| 37 | Li | 91 | SER |
| 38 | Lj | 6 | SER |
| 38 | Lj | 7 | SER |
| 38 | Lj | 31 | LYS |
| 38 | Lj | 85 | LYS |
| 38 | Lj | 87 | LYS |
| 39 | Lk | 9 | LYS |
| 39 | Lk | 22 | SER |
| 39 | Lk | 36 | VAL |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 39 | Lk | 49 | ASP |
| 39 | Lk | 52 | LYS |
| 39 | Lk | 54 | GLU |
| 39 | Lk | 57 | LYS |
| 39 | Lk | 68 | GLU |
| 40 | Ll | 8 | ARG |
| 40 | Ll | 21 | ARG |
| 40 | Ll | 37 | TYR |
| 40 | Ll | 47 | THR |
| 41 | Lm | 83 | ARG |
| 41 | Lm | 119 | ASN |
| 42 | Lo | 32 | SER |
| 42 | Lo | 77 | CYS |
| 42 | Lo | 83 | LEU |
| 43 | Lp | 3 | LYS |
| 43 | Lp | 6 | LYS |
| 43 | Lp | 32 | SER |
| 43 | Lp | 36 | LYS |
| 43 | Lp | 46 | LYS |
| 43 | Lp | 48 | LYS |
| 43 | Lp | 83 | ILE |
| 44 | Lr | 13 | CYS |
| 44 | Lr | 14 | SER |
| 44 | Lr | 20 | ARG |
| 44 | Lr | 21 | ASN |
| 44 | Lr | 27 | THR |
| 44 | Lr | 35 | ARG |
| 44 | Lr | 46 | ARG |
| 44 | Lr | 48 | THR |
| 44 | Lr | 56 | ASP |
| 44 | Lr | 58 | LYS |
| 44 | Lr | 61 | VAL |
| 44 | Lr | 66 | ARG |
| 44 | Lr | 67 | ARG |
| 44 | Lr | 76 | SER |
| 44 | Lr | 78 | VAL |
| 44 | Lr | 84 | LYS |
| 44 | Lr | 92 | SER |
| 44 | Lr | 96 | MET |
| 44 | Lr | 101 | LYS |
| 44 | Lr | 119 | ARG |
| 44 | Lr | 122 | LYS |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 44 | Lr | 125 | MET |
| 45 | P | 1 | MET |
| 45 | P | 11 | CYS |
| 45 | P | 18 | LYS |
| 45 | P | 19 | LEU |
| 45 | P | 26 | VAL |
| 45 | P | 28 | ILE |
| 45 | P | 31 | SER |
| 45 | P | 48 | VAL |
| 45 | P | 61 | ARG |
| 45 | P | 62 | MET |
| 45 | P | 64 | VAL |
| 45 | P | 74 | ASN |
| 45 | P | 78 | ASP |
| 45 | P | 85 | ARG |
| 45 | P | 95 | ARG |
| 45 | P | 96 | ARG |
| 45 | P | 116 | LEU |
| 45 | P | 118 | HIS |
| 45 | P | 120 | ASP |
| 45 | P | 121 | LEU |
| 45 | P | 123 | ARG |
| 45 | P | 162 | HIS |
| 45 | P | 164 | LYS |
| 45 | P | 175 | SER |
| 45 | P | 177 | LEU |
| 45 | P | 179 | VAL |
| 45 | P | 188 | ARG |
| 45 | P | 197 | MET |
| 45 | P | 201 | ASP |
| 45 | P | 209 | ASP |
| 46 | CA | 21 | TYR |
| 46 | CA | 23 | MET |
| 46 | CA | 30 | ARG |
| 46 | CA | 46 | LEU |
| 46 | CA | 53 | ASP |
| 46 | CA | 60 | THR |
| 46 | CA | 70 | MET |
| 46 | CA | 134 | GLN |
| 46 | CA | 158 | LYS |
| 46 | CA | 193 | HIS |
| 46 | CA | 203 | GLN |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 46 | CA | 224 | TYR |
| 46 | CA | 287 | LYS |
| 46 | CA | 331 | MET |
| 46 | CA | 342 | LEU |
| 46 | CA | 343 | TYR |
| 46 | CA | 347 | MET |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 6 | LB | 167 | GLN |
| 6 | LB | 315 | ASN |
| 7 | LC | 310 | HIS |
| 8 | LD | 17 | GLN |
| 11 | LG | 46 | GLN |
| 13 | LI | 147 | HIS |
| 15 | LL | 175 | ASN |
| 17 | LN | 8 | GLN |
| 21 | LR | 134 | ASN |
| 45 | P | 68 | HIS |
| 45 | P | 145 | GLN |

5.3.3 RNA ⓘ

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 2 | L5 | 3638/5070 (71%) | 768 (21%) | 18 (0%) |
| 3 | L7 | 119/120 (99%) | 12 (10%) | 0 |
| 4 | L8 | 155/156 (99%) | 26 (16%) | 0 |
| All | All | 3912/5346 (73%) | 806 (20%) | 18 (0%) |

All (806) RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2 | L5 | 2 | G |
| 2 | L5 | 17 | A |
| 2 | L5 | 25 | A |
| 2 | L5 | 26 | C |
| 2 | L5 | 30 | C |
| 2 | L5 | 39 | A |
| 2 | L5 | 42 | A |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2 | L5 | 48 | G |
| 2 | L5 | 56 | A |
| 2 | L5 | 59 | A |
| 2 | L5 | 64 | A |
| 2 | L5 | 65 | A |
| 2 | L5 | 66 | A |
| 2 | L5 | 69 | A |
| 2 | L5 | 73 | A |
| 2 | L5 | 91 | G |
| 2 | L5 | 104 | G |
| 2 | L5 | 108 | A |
| 2 | L5 | 109 | G |
| 2 | L5 | 110 | C |
| 2 | L5 | 119 | G |
| 2 | L5 | 120 | A |
| 2 | L5 | 132 | G |
| 2 | L5 | 133 | C |
| 2 | L5 | 134 | G |
| 2 | L5 | 135 | G |
| 2 | L5 | 136 | C |
| 2 | L5 | 152 | U |
| 2 | L5 | 159 | C |
| 2 | L5 | 165 | A |
| 2 | L5 | 172 | C |
| 2 | L5 | 183 | C |
| 2 | L5 | 184 | U |
| 2 | L5 | 185 | C |
| 2 | L5 | 187 | U |
| 2 | L5 | 188 | G |
| 2 | L5 | 200 | U |
| 2 | L5 | 201 | C |
| 2 | L5 | 209 | U |
| 2 | L5 | 210 | C |
| 2 | L5 | 216 | C |
| 2 | L5 | 218 | A |
| 2 | L5 | 220 | C |
| 2 | L5 | 234 | G |
| 2 | L5 | 237 | G |
| 2 | L5 | 253 | G |
| 2 | L5 | 255 | C |
| 2 | L5 | 256 | G |
| 2 | L5 | 261 | G |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2 | L5 | 264 | C |
| 2 | L5 | 265 | C |
| 2 | L5 | 266 | C |
| 2 | L5 | 267 | G |
| 2 | L5 | 269 | G |
| 2 | L5 | 276 | C |
| 2 | L5 | 278 | G |
| 2 | L5 | 280 | G |
| 2 | L5 | 297 | U |
| 2 | L5 | 306 | A |
| 2 | L5 | 315 | G |
| 2 | L5 | 316 | U |
| 2 | L5 | 340 | C |
| 2 | L5 | 350 | C |
| 2 | L5 | 373 | G |
| 2 | L5 | 387 | G |
| 2 | L5 | 388 | A |
| 2 | L5 | 407 | A |
| 2 | L5 | 409 | G |
| 2 | L5 | 410 | A |
| 2 | L5 | 411 | G |
| 2 | L5 | 412 | G |
| 2 | L5 | 413 | G |
| 2 | L5 | 415 | G |
| 2 | L5 | 431 | G |
| 2 | L5 | 432 | U |
| 2 | L5 | 433 | A |
| 2 | L5 | 449 | C |
| 2 | L5 | 450 | G |
| 2 | L5 | 452 | A |
| 2 | L5 | 453 | G |
| 2 | L5 | 454 | U |
| 2 | L5 | 456 | C |
| 2 | L5 | 457 | G |
| 2 | L5 | 467 | U |
| 2 | L5 | 472 | C |
| 2 | L5 | 485 | C |
| 2 | L5 | 486 | C |
| 2 | L5 | 489 | C |
| 2 | L5 | 493 | G |
| 2 | L5 | 494 | U |
| 2 | L5 | 497 | G |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2 | L5 | 498 | C |
| 2 | L5 | 499 | G |
| 2 | L5 | 500 | G |
| 2 | L5 | 501 | C |
| 2 | L5 | 502 | C |
| 2 | L5 | 503 | C |
| 2 | L5 | 504 | G |
| 2 | L5 | 505 | G |
| 2 | L5 | 509 | A |
| 2 | L5 | 510 | U |
| 2 | L5 | 512 | U |
| 2 | L5 | 513 | U |
| 2 | L5 | 514 | U |
| 2 | L5 | 517 | C |
| 2 | L5 | 518 | G |
| 2 | L5 | 643 | C |
| 2 | L5 | 644 | G |
| 2 | L5 | 646 | G |
| 2 | L5 | 653 | U |
| 2 | L5 | 654 | C |
| 2 | L5 | 655 | C |
| 2 | L5 | 656 | C |
| 2 | L5 | 657 | C |
| 2 | L5 | 659 | G |
| 2 | L5 | 666 | G |
| 2 | L5 | 667 | A |
| 2 | L5 | 668 | C |
| 2 | L5 | 669 | C |
| 2 | L5 | 673 | C |
| 2 | L5 | 685 | C |
| 2 | L5 | 686 | A |
| 2 | L5 | 687 | U |
| 2 | L5 | 696 | C |
| 2 | L5 | 703 | G |
| 2 | L5 | 704 | C |
| 2 | L5 | 706 | C |
| 2 | L5 | 708 | G |
| 2 | L5 | 731 | G |
| 2 | L5 | 738 | C |
| 2 | L5 | 739 | G |
| 2 | L5 | 742 | G |
| 2 | L5 | 747 | A |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 2 | L5 | 757 | G |
| 2 | L5 | 759 | G |
| 2 | L5 | 904 | C |
| 2 | L5 | 905 | C |
| 2 | L5 | 910 | G |
| 2 | L5 | 913 | U |
| 2 | L5 | 914 | U |
| 2 | L5 | 915 | A |
| 2 | L5 | 917 | A |
| 2 | L5 | 918 | G |
| 2 | L5 | 923 | C |
| 2 | L5 | 924 | C |
| 2 | L5 | 926 | G |
| 2 | L5 | 932 | A |
| 2 | L5 | 933 | G |
| 2 | L5 | 936 | C |
| 2 | L5 | 943 | A |
| 2 | L5 | 944 | A |
| 2 | L5 | 945 | U |
| 2 | L5 | 958 | G |
| 2 | L5 | 959 | G |
| 2 | L5 | 960 | A |
| 2 | L5 | 961 | G |
| 2 | L5 | 962 | C |
| 2 | L5 | 963 | G |
| 2 | L5 | 965 | G |
| 2 | L5 | 966 | A |
| 2 | L5 | 967 | C |
| 2 | L5 | 968 | C |
| 2 | L5 | 969 | C |
| 2 | L5 | 970 | G |
| 2 | L5 | 982 | U |
| 2 | L5 | 985 | C |
| 2 | L5 | 989 | U |
| 2 | L5 | 990 | C |
| 2 | L5 | 1070 | G |
| 2 | L5 | 1071 | C |
| 2 | L5 | 1072 | C |
| 2 | L5 | 1075 | G |
| 2 | L5 | 1082 | C |
| 2 | L5 | 1083 | U |
| 2 | L5 | 1095 | A |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 2 | L5 | 1168 | G |
| 2 | L5 | 1171 | G |
| 2 | L5 | 1172 | C |
| 2 | L5 | 1173 | G |
| 2 | L5 | 1179 | U |
| 2 | L5 | 1180 | C |
| 2 | L5 | 1181 | C |
| 2 | L5 | 1182 | C |
| 2 | L5 | 1183 | C |
| 2 | L5 | 1193 | C |
| 2 | L5 | 1202 | C |
| 2 | L5 | 1203 | G |
| 2 | L5 | 1210 | C |
| 2 | L5 | 1211 | G |
| 2 | L5 | 1214 | C |
| 2 | L5 | 1215 | C |
| 2 | L5 | 1218 | G |
| 2 | L5 | 1219 | G |
| 2 | L5 | 1222 | A |
| 2 | L5 | 1235 | G |
| 2 | L5 | 1241 | C |
| 2 | L5 | 1242 | G |
| 2 | L5 | 1253 | G |
| 2 | L5 | 1254 | A |
| 2 | L5 | 1257 | A |
| 2 | L5 | 1258 | G |
| 2 | L5 | 1266 | G |
| 2 | L5 | 1267 | C |
| 2 | L5 | 1269 | G |
| 2 | L5 | 1270 | A |
| 2 | L5 | 1271 | G |
| 2 | L5 | 1272 | C |
| 2 | L5 | 1273 | G |
| 2 | L5 | 1275 | G |
| 2 | L5 | 1277 | G |
| 2 | L5 | 1280 | C |
| 2 | L5 | 1284 | G |
| 2 | L5 | 1287 | G |
| 2 | L5 | 1293 | G |
| 2 | L5 | 1294 | A |
| 2 | L5 | 1295 | C |
| 2 | L5 | 1296 | G |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 2 | L5 | 1301 | C |
| 2 | L5 | 1326 | A |
| 2 | L5 | 1354 | A |
| 2 | L5 | 1358 | G |
| 2 | L5 | 1359 | G |
| 2 | L5 | 1365 | C |
| 2 | L5 | 1367 | C |
| 2 | L5 | 1370 | G |
| 2 | L5 | 1379 | C |
| 2 | L5 | 1387 | A |
| 2 | L5 | 1394 | G |
| 2 | L5 | 1397 | A |
| 2 | L5 | 1404 | G |
| 2 | L5 | 1405 | C |
| 2 | L5 | 1407 | C |
| 2 | L5 | 1409 | C |
| 2 | L5 | 1410 | U |
| 2 | L5 | 1411 | C |
| 2 | L5 | 1415 | G |
| 2 | L5 | 1417 | C |
| 2 | L5 | 1420 | A |
| 2 | L5 | 1425 | G |
| 2 | L5 | 1437 | C |
| 2 | L5 | 1439 | C |
| 2 | L5 | 1442 | C |
| 2 | L5 | 1443 | A |
| 2 | L5 | 1444 | G |
| 2 | L5 | 1446 | C |
| 2 | L5 | 1447 | C |
| 2 | L5 | 1457 | G |
| 2 | L5 | 1465 | G |
| 2 | L5 | 1481 | C |
| 2 | L5 | 1482 | G |
| 2 | L5 | 1483 | C |
| 2 | L5 | 1497 | A |
| 2 | L5 | 1498 | G |
| 2 | L5 | 1502 | G |
| 2 | L5 | 1516 | G |
| 2 | L5 | 1517 | G |
| 2 | L5 | 1518 | A |
| 2 | L5 | 1525 | A |
| 2 | L5 | 1534 | A |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 2 | L5 | 1535 | C |
| 2 | L5 | 1562 | G |
| 2 | L5 | 1566 | C |
| 2 | L5 | 1574 | G |
| 2 | L5 | 1578 | U |
| 2 | L5 | 1582 | U |
| 2 | L5 | 1591 | U |
| 2 | L5 | 1596 | U |
| 2 | L5 | 1624 | G |
| 2 | L5 | 1625 | G |
| 2 | L5 | 1631 | A |
| 2 | L5 | 1633 | G |
| 2 | L5 | 1634 | A |
| 2 | L5 | 1638 | A |
| 2 | L5 | 1640 | C |
| 2 | L5 | 1641 | G |
| 2 | L5 | 1642 | A |
| 2 | L5 | 1654 | G |
| 2 | L5 | 1661 | C |
| 2 | L5 | 1676 | C |
| 2 | L5 | 1677 | U |
| 2 | L5 | 1678 | C |
| 2 | L5 | 1681 | G |
| 2 | L5 | 1694 | C |
| 2 | L5 | 1699 | A |
| 2 | L5 | 1700 | G |
| 2 | L5 | 1703 | C |
| 2 | L5 | 1704 | C |
| 2 | L5 | 1705 | G |
| 2 | L5 | 1729 | A |
| 2 | L5 | 1731 | C |
| 2 | L5 | 1733 | G |
| 2 | L5 | 1742 | A |
| 2 | L5 | 1750 | G |
| 2 | L5 | 1757 | U |
| 2 | L5 | 1758 | G |
| 2 | L5 | 1760 | G |
| 2 | L5 | 1761 | G |
| 2 | L5 | 1762 | C |
| 2 | L5 | 1763 | C |
| 2 | L5 | 1764 | G |
| 2 | L5 | 1765 | A |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 2 | L5 | 1766 | A |
| 2 | L5 | 1767 | A |
| 2 | L5 | 1768 | C |
| 2 | L5 | 1769 | G |
| 2 | L5 | 1770 | A |
| 2 | L5 | 1787 | A |
| 2 | L5 | 1804 | A |
| 2 | L5 | 1806 | G |
| 2 | L5 | 1810 | G |
| 2 | L5 | 1815 | G |
| 2 | L5 | 1820 | C |
| 2 | L5 | 1821 | G |
| 2 | L5 | 1822 | U |
| 2 | L5 | 1836 | G |
| 2 | L5 | 1837 | A |
| 2 | L5 | 1842 | G |
| 2 | L5 | 1855 | G |
| 2 | L5 | 1869 | G |
| 2 | L5 | 1882 | U |
| 2 | L5 | 1888 | A |
| 2 | L5 | 1897 | A |
| 2 | L5 | 1917 | A |
| 2 | L5 | 1918 | U |
| 2 | L5 | 1919 | G |
| 2 | L5 | 1920 | C |
| 2 | L5 | 1921 | C |
| 2 | L5 | 1922 | G |
| 2 | L5 | 1925 | G |
| 2 | L5 | 1931 | C |
| 2 | L5 | 1932 | A |
| 2 | L5 | 1936 | C |
| 2 | L5 | 1940 | G |
| 2 | L5 | 1948 | G |
| 2 | L5 | 1949 | U |
| 2 | L5 | 1961 | G |
| 2 | L5 | 1962 | A |
| 2 | L5 | 1974 | U |
| 2 | L5 | 1975 | G |
| 2 | L5 | 1978 | C |
| 2 | L5 | 1980 | U |
| 2 | L5 | 1981 | G |
| 2 | L5 | 1982 | G |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 2 | L5 | 1983 | A |
| 2 | L5 | 1984 | A |
| 2 | L5 | 1985 | G |
| 2 | L5 | 1986 | U |
| 2 | L5 | 1991 | A |
| 2 | L5 | 1992 | U |
| 2 | L5 | 1993 | C |
| 2 | L5 | 1997 | U |
| 2 | L5 | 1998 | A |
| 2 | L5 | 1999 | A |
| 2 | L5 | 2001 | G |
| 2 | L5 | 2002 | A |
| 2 | L5 | 2011 | C |
| 2 | L5 | 2017 | A |
| 2 | L5 | 2018 | C |
| 2 | L5 | 2024 | G |
| 2 | L5 | 2026 | A |
| 2 | L5 | 2033 | A |
| 2 | L5 | 2034 | G |
| 2 | L5 | 2046 | G |
| 2 | L5 | 2048 | U |
| 2 | L5 | 2055 | G |
| 2 | L5 | 2056 | G |
| 2 | L5 | 2069 | A |
| 2 | L5 | 2084 | C |
| 2 | L5 | 2092 | G |
| 2 | L5 | 2093 | A |
| 2 | L5 | 2095 | A |
| 2 | L5 | 2096 | G |
| 2 | L5 | 2097 | U |
| 2 | L5 | 2098 | G |
| 2 | L5 | 2099 | G |
| 2 | L5 | 2101 | C |
| 2 | L5 | 2102 | G |
| 2 | L5 | 2103 | G |
| 2 | L5 | 2105 | A |
| 2 | L5 | 2107 | C |
| 2 | L5 | 2108 | G |
| 2 | L5 | 2110 | C |
| 2 | L5 | 2111 | G |
| 2 | L5 | 2112 | G |
| 2 | L5 | 2250 | C |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 2 | L5 | 2252 | G |
| 2 | L5 | 2253 | A |
| 2 | L5 | 2256 | C |
| 2 | L5 | 2257 | C |
| 2 | L5 | 2258 | C |
| 2 | L5 | 2260 | C |
| 2 | L5 | 2261 | G |
| 2 | L5 | 2289 | C |
| 2 | L5 | 2300 | A |
| 2 | L5 | 2301 | G |
| 2 | L5 | 2306 | G |
| 2 | L5 | 2313 | A |
| 2 | L5 | 2331 | G |
| 2 | L5 | 2332 | A |
| 2 | L5 | 2333 | G |
| 2 | L5 | 2345 | G |
| 2 | L5 | 2348 | G |
| 2 | L5 | 2351 | C |
| 2 | L5 | 2360 | A |
| 2 | L5 | 2395 | A |
| 2 | L5 | 2397 | G |
| 2 | L5 | 2402 | G |
| 2 | L5 | 2417 | A |
| 2 | L5 | 2421 | G |
| 2 | L5 | 2425 | U |
| 2 | L5 | 2441 | C |
| 2 | L5 | 2447 | U |
| 2 | L5 | 2450 | G |
| 2 | L5 | 2453 | A |
| 2 | L5 | 2464 | C |
| 2 | L5 | 2465 | C |
| 2 | L5 | 2471 | G |
| 2 | L5 | 2474 | G |
| 2 | L5 | 2475 | G |
| 2 | L5 | 2478 | C |
| 2 | L5 | 2479 | G |
| 2 | L5 | 2483 | G |
| 2 | L5 | 2484 | A |
| 2 | L5 | 2485 | U |
| 2 | L5 | 2486 | G |
| 2 | L5 | 2487 | G |
| 2 | L5 | 2488 | C |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 2 | L5 | 2489 | C |
| 2 | L5 | 2490 | U |
| 2 | L5 | 2491 | C |
| 2 | L5 | 2494 | U |
| 2 | L5 | 2503 | G |
| 2 | L5 | 2504 | C |
| 2 | L5 | 2505 | C |
| 2 | L5 | 2506 | G |
| 2 | L5 | 2513 | A |
| 2 | L5 | 2519 | U |
| 2 | L5 | 2520 | C |
| 2 | L5 | 2537 | A |
| 2 | L5 | 2544 | G |
| 2 | L5 | 2546 | G |
| 2 | L5 | 2547 | G |
| 2 | L5 | 2554 | U |
| 2 | L5 | 2555 | G |
| 2 | L5 | 2560 | C |
| 2 | L5 | 2565 | A |
| 2 | L5 | 2567 | G |
| 2 | L5 | 2573 | A |
| 2 | L5 | 2583 | C |
| 2 | L5 | 2586 | G |
| 2 | L5 | 2587 | A |
| 2 | L5 | 2589 | C |
| 2 | L5 | 2627 | C |
| 2 | L5 | 2640 | G |
| 2 | L5 | 2652 | G |
| 2 | L5 | 2653 | C |
| 2 | L5 | 2662 | G |
| 2 | L5 | 2669 | C |
| 2 | L5 | 2675 | G |
| 2 | L5 | 2676 | A |
| 2 | L5 | 2687 | U |
| 2 | L5 | 2694 | G |
| 2 | L5 | 2695 | A |
| 2 | L5 | 2696 | A |
| 2 | L5 | 2703 | G |
| 2 | L5 | 2707 | U |
| 2 | L5 | 2708 | U |
| 2 | L5 | 2710 | C |
| 2 | L5 | 2711 | G |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 2 | L5 | 2719 | C |
| 2 | L5 | 2721 | G |
| 2 | L5 | 2724 | G |
| 2 | L5 | 2726 | G |
| 2 | L5 | 2739 | C |
| 2 | L5 | 2742 | G |
| 2 | L5 | 2743 | A |
| 2 | L5 | 2761 | U |
| 2 | L5 | 2763 | U |
| 2 | L5 | 2769 | U |
| 2 | L5 | 2770 | C |
| 2 | L5 | 2787 | A |
| 2 | L5 | 2788 | U |
| 2 | L5 | 2790 | U |
| 2 | L5 | 2826 | U |
| 2 | L5 | 2827 | G |
| 2 | L5 | 2829 | U |
| 2 | L5 | 2835 | A |
| 2 | L5 | 2848 | G |
| 2 | L5 | 2855 | G |
| 2 | L5 | 2875 | C |
| 2 | L5 | 2900 | U |
| 2 | L5 | 2902 | G |
| 2 | L5 | 2903 | G |
| 2 | L5 | 2904 | U |
| 2 | L5 | 2905 | C |
| 2 | L5 | 2906 | G |
| 2 | L5 | 2908 | U |
| 2 | L5 | 3586 | G |
| 2 | L5 | 3588 | C |
| 2 | L5 | 3590 | G |
| 2 | L5 | 3591 | C |
| 2 | L5 | 3594 | C |
| 2 | L5 | 3595 | U |
| 2 | L5 | 3596 | A |
| 2 | L5 | 3597 | G |
| 2 | L5 | 3599 | A |
| 2 | L5 | 3604 | A |
| 2 | L5 | 3605 | C |
| 2 | L5 | 3615 | G |
| 2 | L5 | 3617 | G |
| 2 | L5 | 3626 | G |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 2 | L5 | 3635 | A |
| 2 | L5 | 3644 | U |
| 2 | L5 | 3646 | A |
| 2 | L5 | 3648 | A |
| 2 | L5 | 3662 | A |
| 2 | L5 | 3664 | G |
| 2 | L5 | 3670 | C |
| 2 | L5 | 3673 | C |
| 2 | L5 | 3674 | G |
| 2 | L5 | 3680 | U |
| 2 | L5 | 3710 | G |
| 2 | L5 | 3711 | A |
| 2 | L5 | 3713 | U |
| 2 | L5 | 3714 | G |
| 2 | L5 | 3727 | A |
| 2 | L5 | 3748 | A |
| 2 | L5 | 3750 | G |
| 2 | L5 | 3756 | A |
| 2 | L5 | 3759 | A |
| 2 | L5 | 3760 | A |
| 2 | L5 | 3761 | C |
| 2 | L5 | 3773 | U |
| 2 | L5 | 3774 | A |
| 2 | L5 | 3776 | G |
| 2 | L5 | 3777 | G |
| 2 | L5 | 3778 | U |
| 2 | L5 | 3783 | A |
| 2 | L5 | 3784 | A |
| 2 | L5 | 3786 | U |
| 2 | L5 | 3802 | U |
| 2 | L5 | 3811 | G |
| 2 | L5 | 3812 | C |
| 2 | L5 | 3813 | A |
| 2 | L5 | 3814 | U |
| 2 | L5 | 3817 | A |
| 2 | L5 | 3818 | U |
| 2 | L5 | 3819 | G |
| 2 | L5 | 3823 | G |
| 2 | L5 | 3824 | A |
| 2 | L5 | 3838 | U |
| 2 | L5 | 3839 | G |
| 2 | L5 | 3840 | U |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 2 | L5 | 3867 | A |
| 2 | L5 | 3877 | A |
| 2 | L5 | 3878 | C |
| 2 | L5 | 3879 | G |
| 2 | L5 | 3885 | G |
| 2 | L5 | 3887 | C |
| 2 | L5 | 3890 | A |
| 2 | L5 | 3892 | U |
| 2 | L5 | 3897 | G |
| 2 | L5 | 3901 | A |
| 2 | L5 | 3906 | A |
| 2 | L5 | 3907 | G |
| 2 | L5 | 3908 | A |
| 2 | L5 | 3915 | U |
| 2 | L5 | 3923 | A |
| 2 | L5 | 3938 | G |
| 2 | L5 | 3939 | G |
| 2 | L5 | 3942 | A |
| 2 | L5 | 3943 | A |
| 2 | L5 | 3947 | A |
| 2 | L5 | 3949 | A |
| 2 | L5 | 3950 | U |
| 2 | L5 | 3951 | G |
| 2 | L5 | 3953 | G |
| 2 | L5 | 4057 | C |
| 2 | L5 | 4058 | U |
| 2 | L5 | 4059 | C |
| 2 | L5 | 4060 | U |
| 2 | L5 | 4061 | G |
| 2 | L5 | 4062 | A |
| 2 | L5 | 4064 | C |
| 2 | L5 | 4068 | U |
| 2 | L5 | 4069 | U |
| 2 | L5 | 4076 | G |
| 2 | L5 | 4084 | G |
| 2 | L5 | 4092 | G |
| 2 | L5 | 4093 | G |
| 2 | L5 | 4095 | G |
| 2 | L5 | 4097 | G |
| 2 | L5 | 4099 | G |
| 2 | L5 | 4101 | C |
| 2 | L5 | 4102 | C |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 2 | L5 | 4103 | C |
| 2 | L5 | 4104 | G |
| 2 | L5 | 4108 | G |
| 2 | L5 | 4111 | U |
| 2 | L5 | 4114 | C |
| 2 | L5 | 4115 | G |
| 2 | L5 | 4116 | C |
| 2 | L5 | 4117 | U |
| 2 | L5 | 4119 | C |
| 2 | L5 | 4127 | A |
| 2 | L5 | 4140 | C |
| 2 | L5 | 4141 | G |
| 2 | L5 | 4142 | C |
| 2 | L5 | 4143 | G |
| 2 | L5 | 4144 | C |
| 2 | L5 | 4146 | G |
| 2 | L5 | 4162 | C |
| 2 | L5 | 4163 | U |
| 2 | L5 | 4170 | A |
| 2 | L5 | 4183 | G |
| 2 | L5 | 4184 | G |
| 2 | L5 | 4191 | G |
| 2 | L5 | 4196 | G |
| 2 | L5 | 4197 | G |
| 2 | L5 | 4203 | A |
| 2 | L5 | 4212 | A |
| 2 | L5 | 4222 | G |
| 2 | L5 | 4225 | G |
| 2 | L5 | 4229 | U |
| 2 | L5 | 4232 | U |
| 2 | L5 | 4233 | A |
| 2 | L5 | 4234 | A |
| 2 | L5 | 4251 | A |
| 2 | L5 | 4254 | G |
| 2 | L5 | 4257 | A |
| 2 | L5 | 4258 | C |
| 2 | L5 | 4265 | U |
| 2 | L5 | 4268 | A |
| 2 | L5 | 4273 | A |
| 2 | L5 | 4280 | A |
| 2 | L5 | 4281 | A |
| 2 | L5 | 4291 | G |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 2 | L5 | 4295 | U |
| 2 | L5 | 4304 | A |
| 2 | L5 | 4305 | G |
| 2 | L5 | 4314 | C |
| 2 | L5 | 4319 | C |
| 2 | L5 | 4330 | G |
| 2 | L5 | 4332 | C |
| 2 | L5 | 4349 | C |
| 2 | L5 | 4373 | G |
| 2 | L5 | 4377 | G |
| 2 | L5 | 4378 | A |
| 2 | L5 | 4380 | A |
| 2 | L5 | 4387 | C |
| 2 | L5 | 4391 | G |
| 2 | L5 | 4394 | A |
| 2 | L5 | 4398 | C |
| 2 | L5 | 4421 | C |
| 2 | L5 | 4422 | A |
| 2 | L5 | 4433 | G |
| 2 | L5 | 4438 | U |
| 2 | L5 | 4448 | G |
| 2 | L5 | 4449 | A |
| 2 | L5 | 4453 | C |
| 2 | L5 | 4464 | A |
| 2 | L5 | 4466 | C |
| 2 | L5 | 4475 | G |
| 2 | L5 | 4488 | A |
| 2 | L5 | 4500 | U |
| 2 | L5 | 4512 | U |
| 2 | L5 | 4513 | A |
| 2 | L5 | 4518 | A |
| 2 | L5 | 4519 | C |
| 2 | L5 | 4524 | G |
| 2 | L5 | 4545 | G |
| 2 | L5 | 4548 | A |
| 2 | L5 | 4549 | G |
| 2 | L5 | 4557 | U |
| 2 | L5 | 4560 | C |
| 2 | L5 | 4567 | G |
| 2 | L5 | 4572 | U |
| 2 | L5 | 4573 | G |
| 2 | L5 | 4575 | G |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 2 | L5 | 4589 | A |
| 2 | L5 | 4590 | A |
| 2 | L5 | 4594 | U |
| 2 | L5 | 4599 | A |
| 2 | L5 | 4600 | G |
| 2 | L5 | 4601 | U |
| 2 | L5 | 4617 | G |
| 2 | L5 | 4636 | U |
| 2 | L5 | 4637 | G |
| 2 | L5 | 4656 | A |
| 2 | L5 | 4657 | U |
| 2 | L5 | 4670 | C |
| 2 | L5 | 4671 | C |
| 2 | L5 | 4672 | A |
| 2 | L5 | 4694 | G |
| 2 | L5 | 4695 | C |
| 2 | L5 | 4700 | A |
| 2 | L5 | 4708 | A |
| 2 | L5 | 4709 | U |
| 2 | L5 | 4719 | G |
| 2 | L5 | 4734 | A |
| 2 | L5 | 4740 | G |
| 2 | L5 | 4741 | C |
| 2 | L5 | 4742 | G |
| 2 | L5 | 4745 | G |
| 2 | L5 | 4754 | G |
| 2 | L5 | 4757 | C |
| 2 | L5 | 4759 | C |
| 2 | L5 | 4761 | G |
| 2 | L5 | 4765 | G |
| 2 | L5 | 4771 | C |
| 2 | L5 | 4772 | C |
| 2 | L5 | 4775 | C |
| 2 | L5 | 4859 | C |
| 2 | L5 | 4860 | G |
| 2 | L5 | 4862 | G |
| 2 | L5 | 4870 | G |
| 2 | L5 | 4871 | C |
| 2 | L5 | 4874 | A |
| 2 | L5 | 4875 | G |
| 2 | L5 | 4882 | U |
| 2 | L5 | 4883 | C |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 2 | L5 | 4889 | G |
| 2 | L5 | 4895 | C |
| 2 | L5 | 4896 | G |
| 2 | L5 | 4900 | C |
| 2 | L5 | 4901 | G |
| 2 | L5 | 4910 | G |
| 2 | L5 | 4912 | G |
| 2 | L5 | 4914 | C |
| 2 | L5 | 4922 | C |
| 2 | L5 | 4923 | C |
| 2 | L5 | 4925 | U |
| 2 | L5 | 4926 | C |
| 2 | L5 | 4927 | G |
| 2 | L5 | 4928 | C |
| 2 | L5 | 4940 | C |
| 2 | L5 | 4941 | G |
| 2 | L5 | 4943 | A |
| 2 | L5 | 4944 | C |
| 2 | L5 | 4947 | U |
| 2 | L5 | 4951 | G |
| 2 | L5 | 4960 | G |
| 2 | L5 | 4975 | G |
| 2 | L5 | 4976 | U |
| 2 | L5 | 4985 | U |
| 2 | L5 | 4988 | U |
| 2 | L5 | 4989 | U |
| 2 | L5 | 4990 | C |
| 2 | L5 | 4991 | U |
| 2 | L5 | 5007 | A |
| 2 | L5 | 5013 | C |
| 2 | L5 | 5014 | A |
| 2 | L5 | 5017 | G |
| 2 | L5 | 5022 | U |
| 2 | L5 | 5023 | C |
| 2 | L5 | 5024 | C |
| 2 | L5 | 5025 | C |
| 2 | L5 | 5027 | C |
| 2 | L5 | 5028 | G |
| 2 | L5 | 5030 | U |
| 2 | L5 | 5034 | A |
| 2 | L5 | 5041 | G |
| 2 | L5 | 5047 | C |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 2 | L5 | 5050 | C |
| 2 | L5 | 5054 | C |
| 2 | L5 | 5055 | G |
| 2 | L5 | 5061 | A |
| 2 | L5 | 5069 | U |
| 3 | L7 | 7 | G |
| 3 | L7 | 22 | A |
| 3 | L7 | 33 | U |
| 3 | L7 | 38 | U |
| 3 | L7 | 53 | U |
| 3 | L7 | 54 | A |
| 3 | L7 | 63 | C |
| 3 | L7 | 64 | G |
| 3 | L7 | 97 | G |
| 3 | L7 | 100 | A |
| 3 | L7 | 110 | G |
| 3 | L7 | 111 | C |
| 4 | L8 | 25 | G |
| 4 | L8 | 34 | U |
| 4 | L8 | 35 | C |
| 4 | L8 | 48 | A |
| 4 | L8 | 52 | A |
| 4 | L8 | 59 | A |
| 4 | L8 | 62 | A |
| 4 | L8 | 63 | U |
| 4 | L8 | 80 | A |
| 4 | L8 | 82 | A |
| 4 | L8 | 84 | A |
| 4 | L8 | 85 | U |
| 4 | L8 | 86 | U |
| 4 | L8 | 87 | G |
| 4 | L8 | 94 | G |
| 4 | L8 | 103 | A |
| 4 | L8 | 105 | C |
| 4 | L8 | 108 | A |
| 4 | L8 | 110 | U |
| 4 | L8 | 111 | U |
| 4 | L8 | 114 | G |
| 4 | L8 | 123 | U |
| 4 | L8 | 124 | U |
| 4 | L8 | 125 | C |
| 4 | L8 | 126 | C |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 4 | L8 | 127 | U |

All (18) RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 2 | L5 | 265 | C |
| 2 | L5 | 406 | C |
| 2 | L5 | 493 | G |
| 2 | L5 | 914 | U |
| 2 | L5 | 1082 | C |
| 2 | L5 | 1633 | G |
| 2 | L5 | 1977 | C |
| 2 | L5 | 2033 | A |
| 2 | L5 | 2416 | G |
| 2 | L5 | 2485 | U |
| 2 | L5 | 2675 | G |
| 2 | L5 | 2760 | G |
| 2 | L5 | 2786 | C |
| 2 | L5 | 3614 | G |
| 2 | L5 | 3673 | C |
| 2 | L5 | 4600 | G |
| 2 | L5 | 4699 | U |
| 2 | L5 | 4913 | G |

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 231 ligands modelled in this entry, 231 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](#)

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 21 | LR | 1 |

All chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1 | LR | 134:ASN | C | 135:LYS | N | 2.96 |

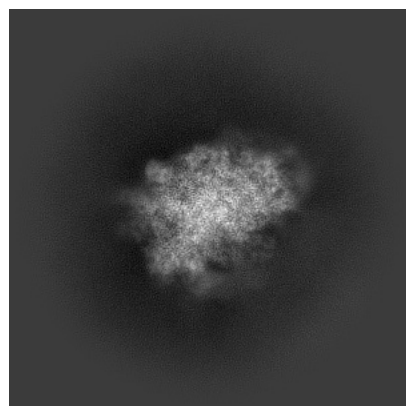
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42319. These allow visual inspection of the internal detail of the map and identification of artifacts.

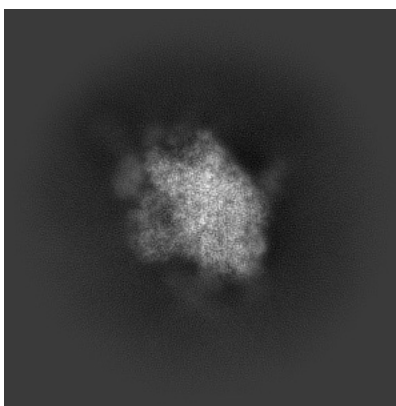
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

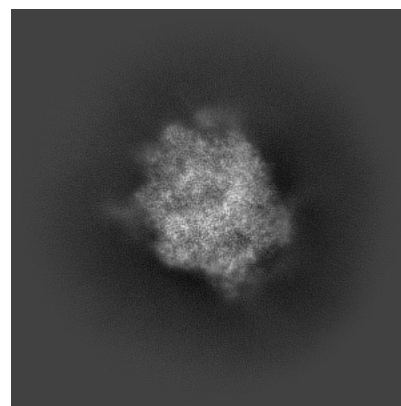
6.1.1 Primary map



X

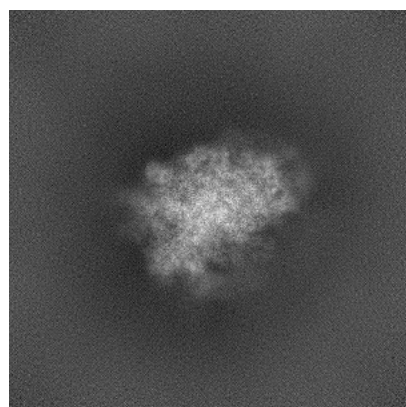


Y

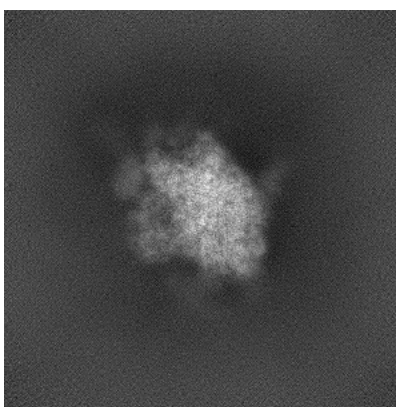


Z

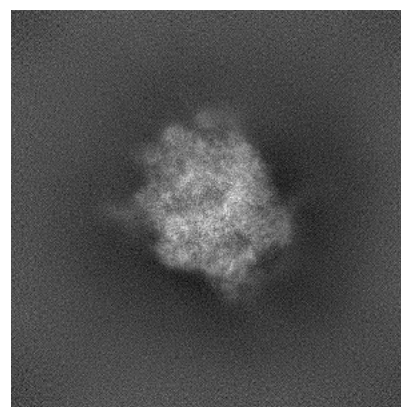
6.1.2 Raw map



X



Y

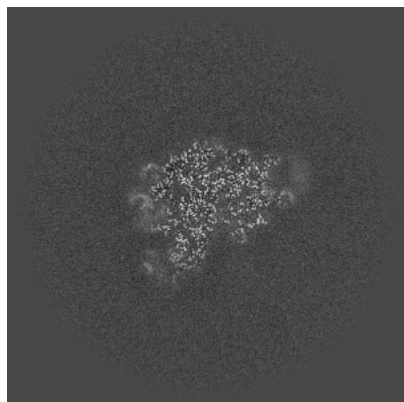


Z

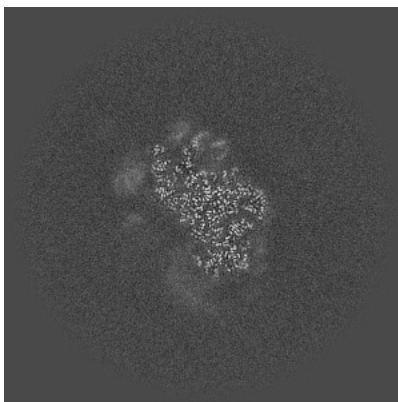
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

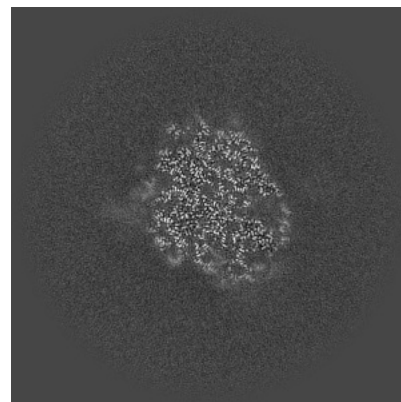
6.2.1 Primary map



X Index: 256

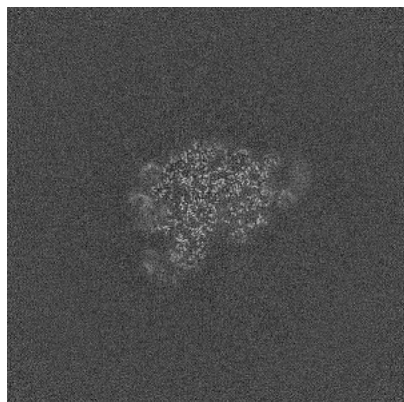


Y Index: 256

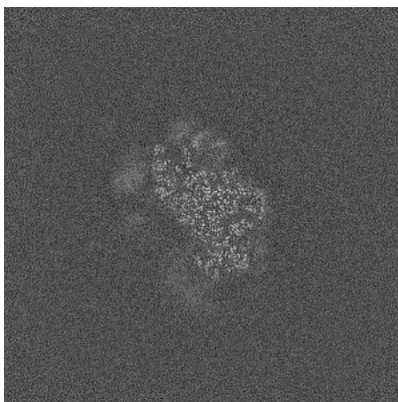


Z Index: 256

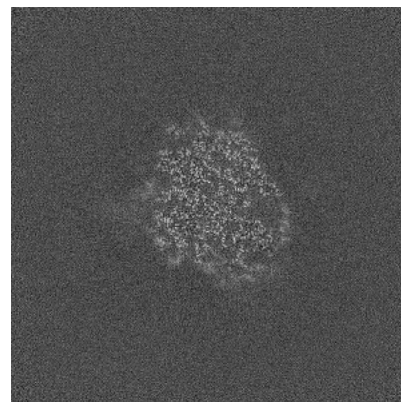
6.2.2 Raw map



X Index: 256



Y Index: 256

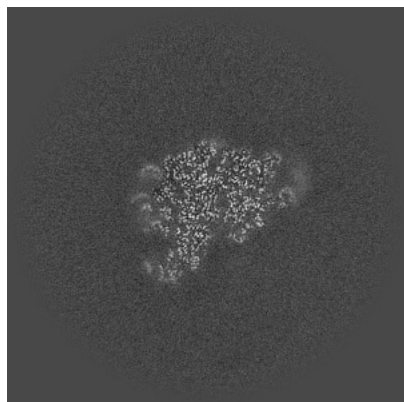


Z Index: 256

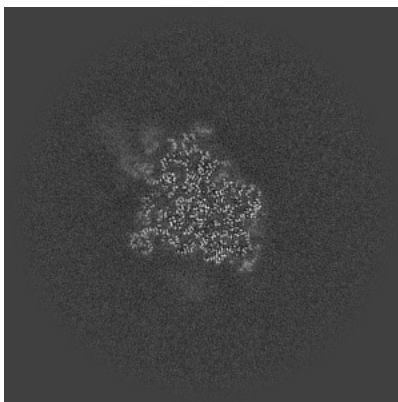
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

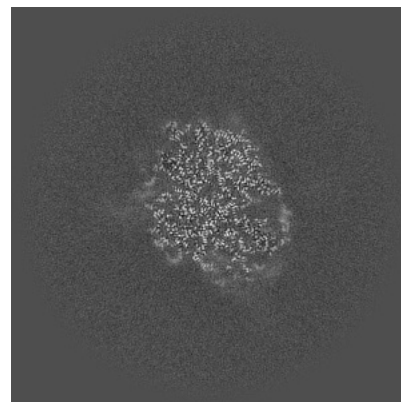
6.3.1 Primary map



X Index: 253

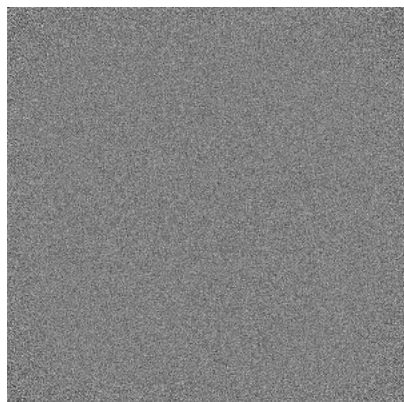


Y Index: 233

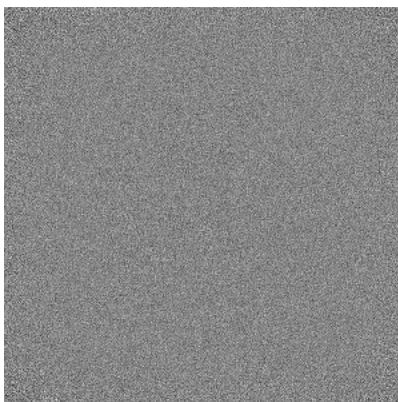


Z Index: 258

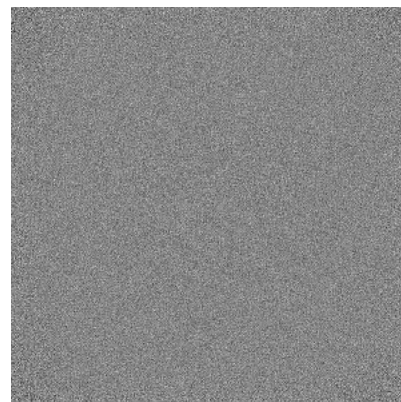
6.3.2 Raw map



X Index: 0



Y Index: 0

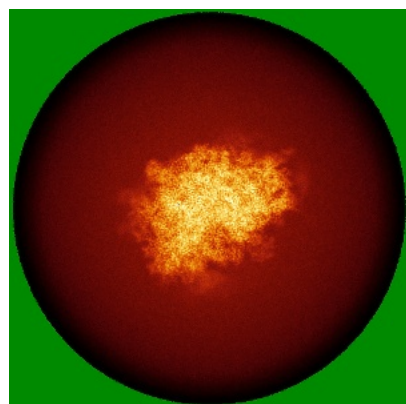


Z Index: 0

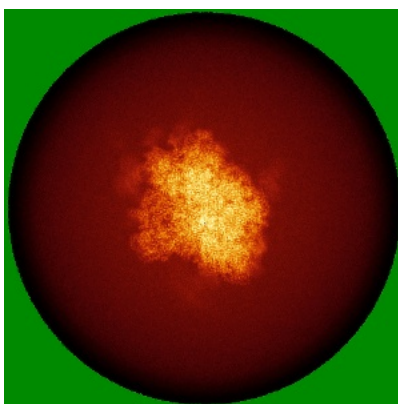
The images above show the largest variance slices of the map in three orthogonal directions.

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

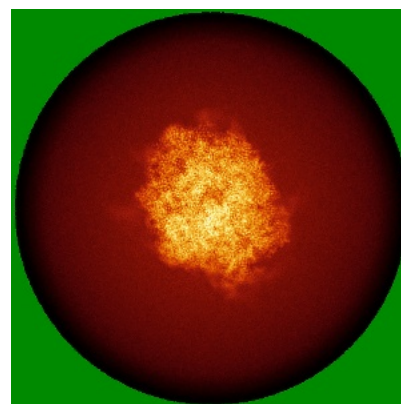
6.4.1 Primary map



X

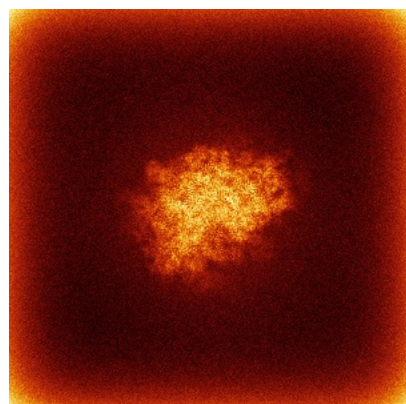


Y

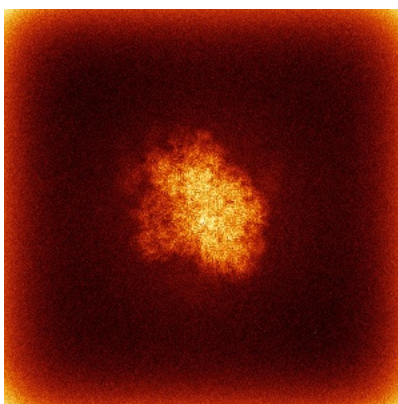


Z

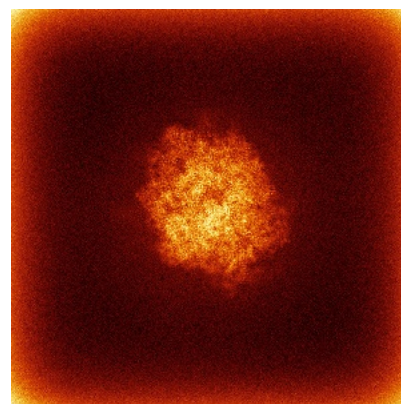
6.4.2 Raw map



X



Y

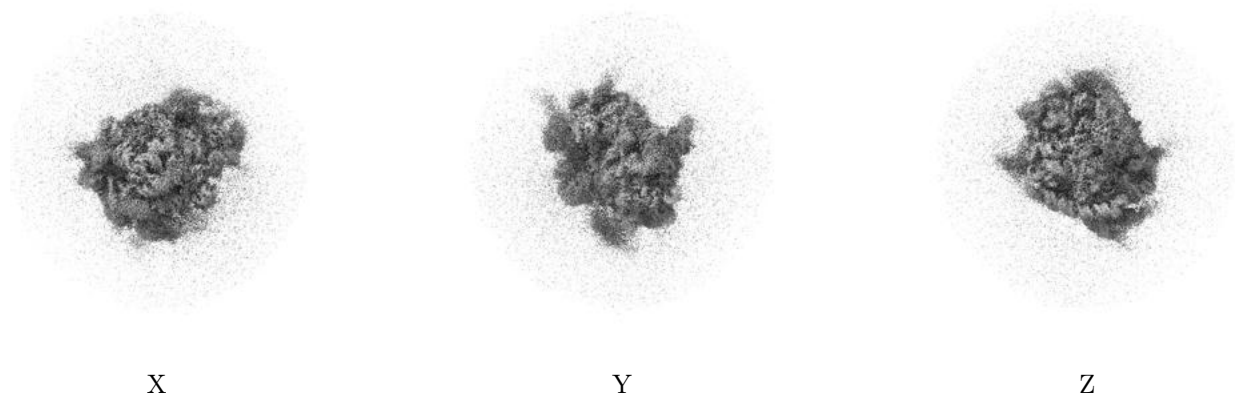


Z

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.

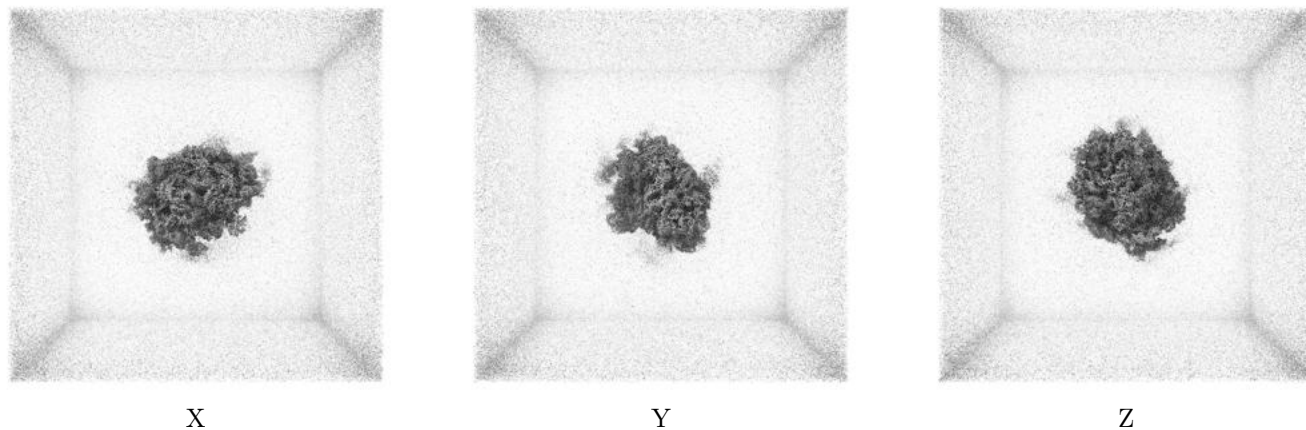
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.065. 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.

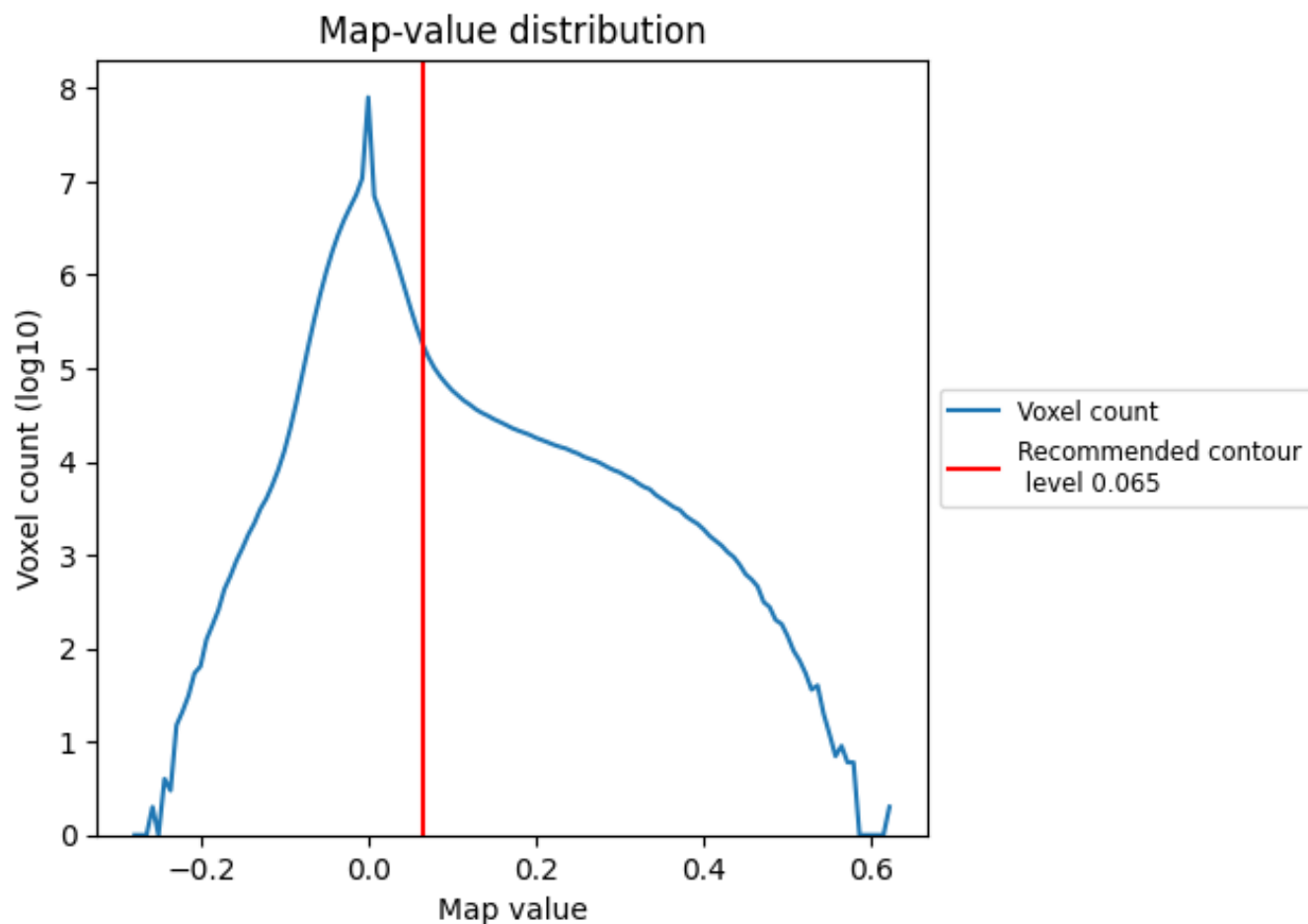
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

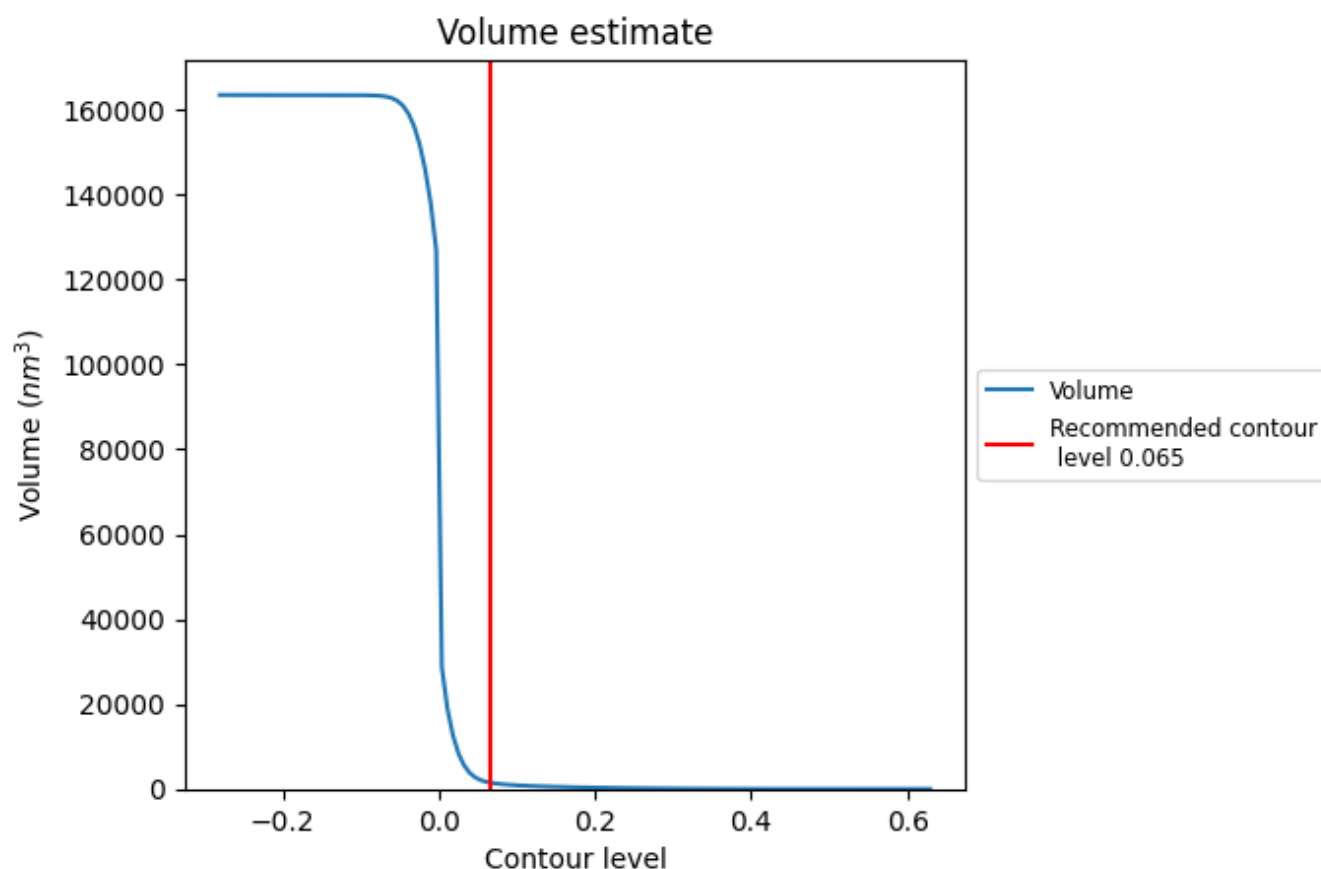
This section contains the results of statistical analysis of the map.

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.

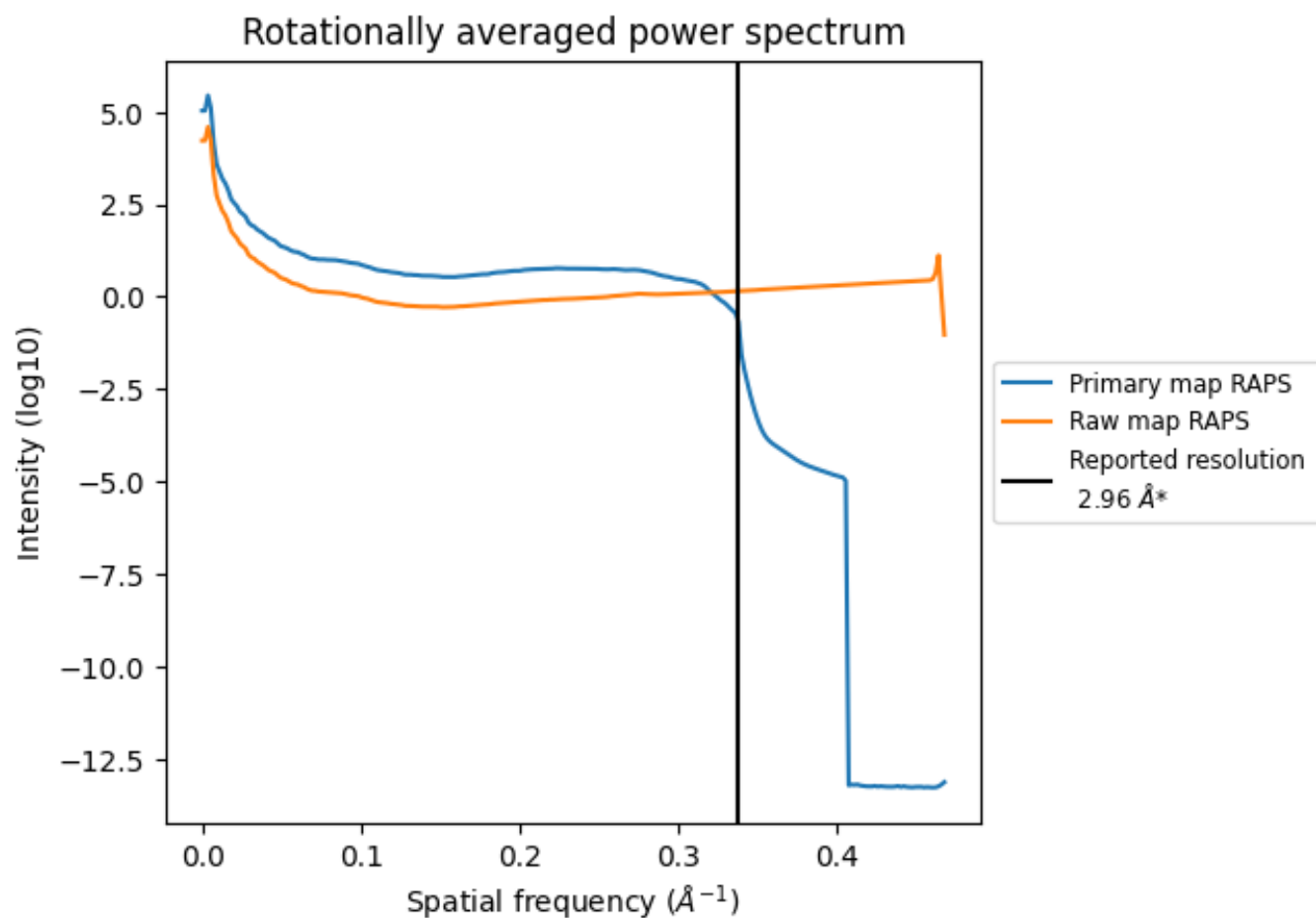
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1513 nm³; this corresponds to an approximate mass of 1366 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 ⓘ

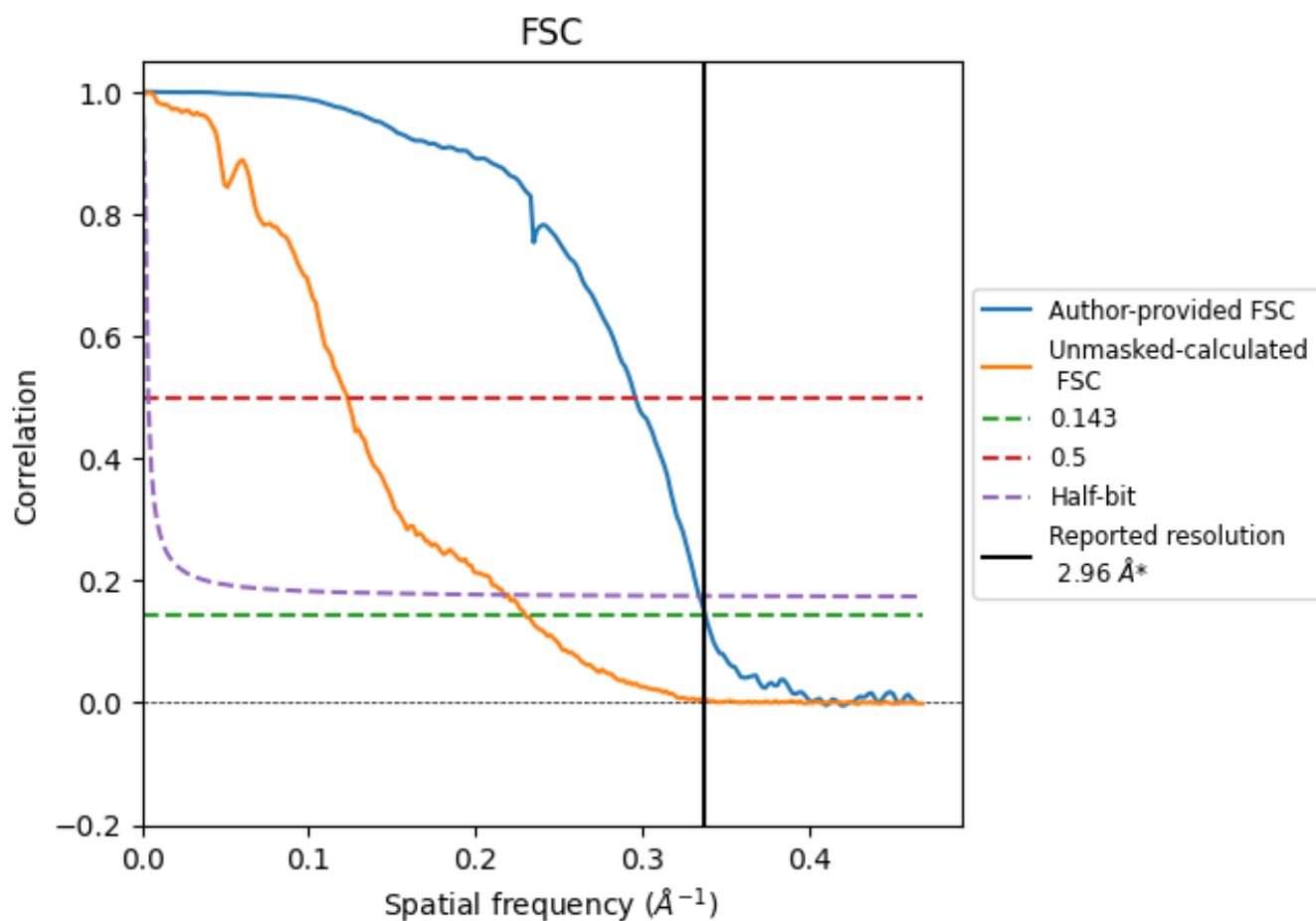


*Reported resolution corresponds to spatial frequency of 0.338 Å⁻¹

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 0.338 Å⁻¹

8.2 Resolution estimates [i](#)

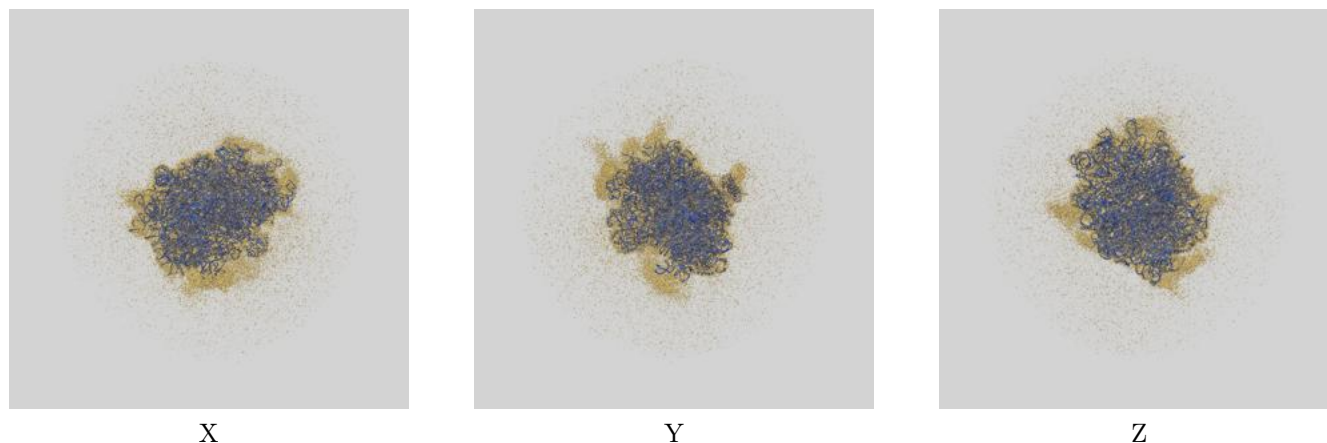
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---------------------------|------------------------------------|------|----------|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 2.96 | - | - |
| Author-provided FSC curve | 2.96 | 3.38 | 2.99 |
| Unmasked-calculated* | 4.35 | 8.13 | 4.61 |

*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 4.35 differs from the reported value 2.96 by more than 10 %

9 Map-model fit [i](#)

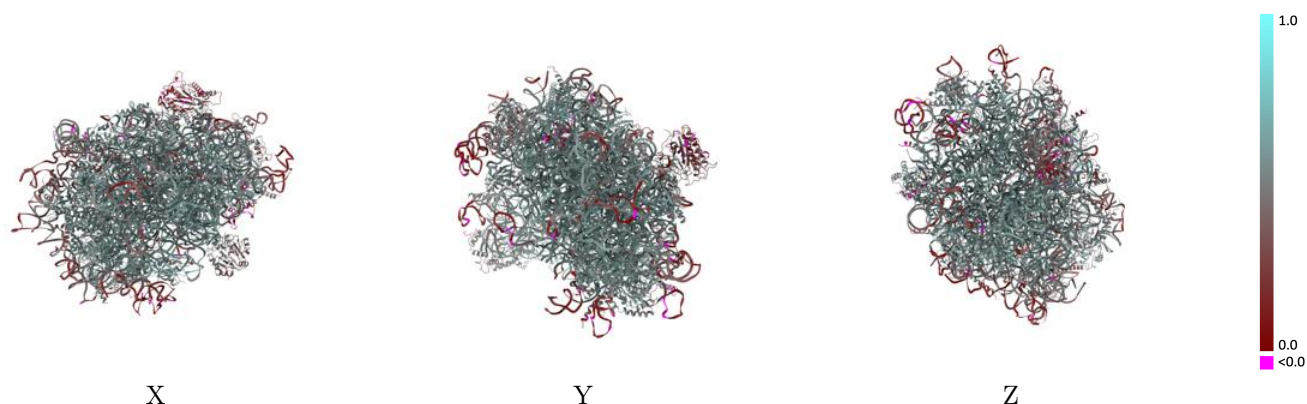
This section contains information regarding the fit between EMDB map EMD-42319 and PDB model 8UJD. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



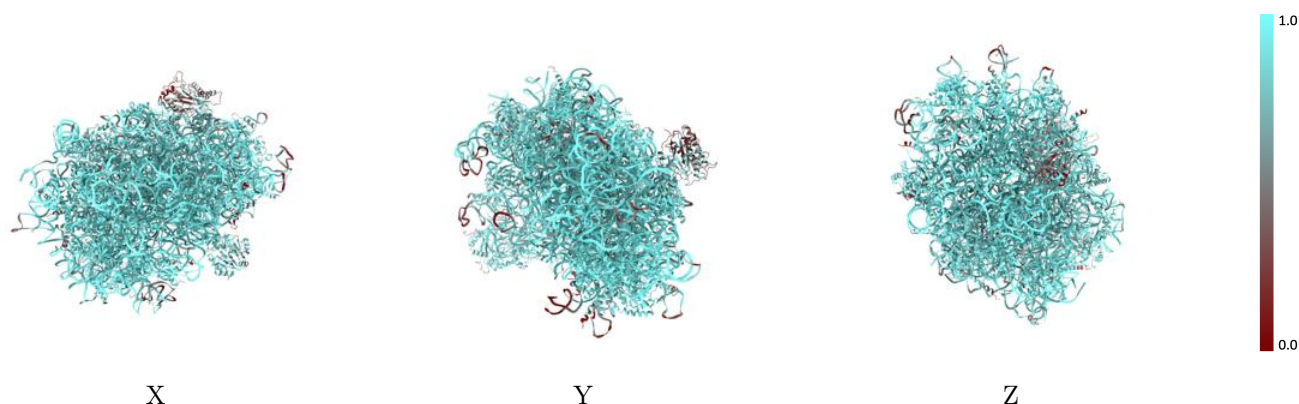
The images above show the 3D surface view of the map at the recommended contour level 0.065 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



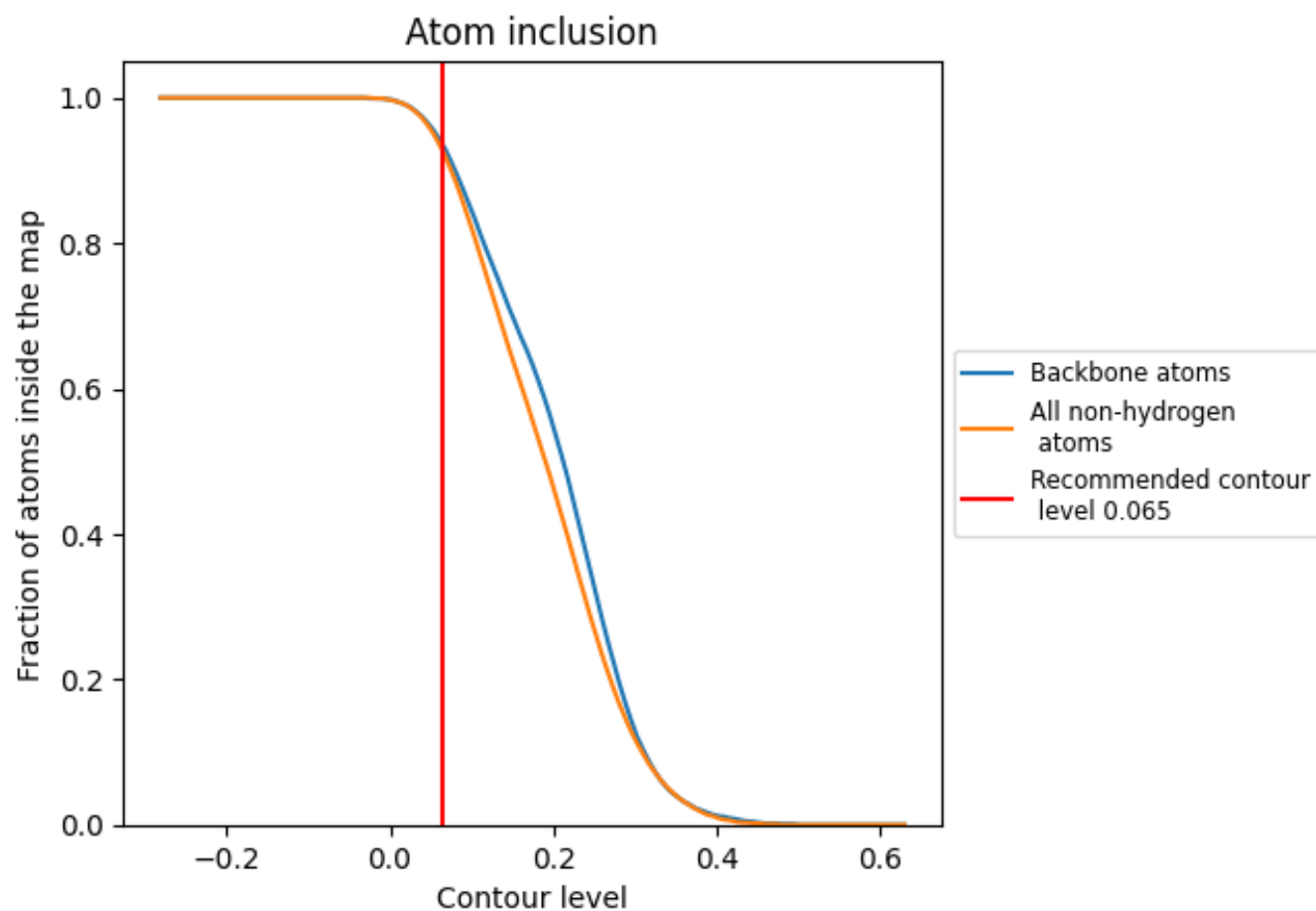
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.065).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 93% 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 (0.065) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|--|--|
| All |  0.9260 |  0.5160 |
| CA |  0.4860 |  0.2980 |
| L5 |  0.9400 |  0.5010 |
| L7 |  0.9910 |  0.5520 |
| L8 |  0.9650 |  0.5360 |
| LA |  0.9620 |  0.5800 |
| LB |  0.9380 |  0.5690 |
| LC |  0.9400 |  0.5670 |
| LD |  0.9220 |  0.5260 |
| LE |  0.8790 |  0.5140 |
| LF |  0.9650 |  0.5720 |
| LG |  0.8640 |  0.5080 |
| LH |  0.9230 |  0.5520 |
| LI |  0.9230 |  0.5640 |
| LJ |  0.8280 |  0.4470 |
| LL |  0.9090 |  0.5420 |
| LM |  0.9400 |  0.5540 |
| LN |  0.9820 |  0.5930 |
| LO |  0.9530 |  0.5700 |
| LP |  0.9580 |  0.5880 |
| LQ |  0.9660 |  0.5880 |
| LR |  0.9430 |  0.5530 |
| LS |  0.9670 |  0.5850 |
| LT |  0.9360 |  0.5520 |
| LU |  0.8600 |  0.4300 |
| LV |  0.9410 |  0.5640 |
| LW |  0.4640 |  0.1810 |
| LX |  0.9290 |  0.5620 |
| LY |  0.9470 |  0.5700 |
| LZ |  0.9440 |  0.5490 |
| La |  0.9680 |  0.5900 |
| Lb |  0.8940 |  0.5210 |
| Lc |  0.9120 |  0.5260 |
| Ld |  0.9370 |  0.5460 |
| Le |  0.9770 |  0.5910 |



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Continued from previous page...

| Chain | Atom inclusion | Q-score |
|-------|--|--|
| Lf |  0.9660 |  0.5890 |
| Lg |  0.9320 |  0.5570 |
| Lh |  0.9350 |  0.5550 |
| Li |  0.9260 |  0.5470 |
| Lj |  0.9730 |  0.5790 |
| Lk |  0.8580 |  0.5030 |
| Ll |  0.9570 |  0.5770 |
| Lm |  0.9350 |  0.5730 |
| Lo |  0.9310 |  0.5640 |
| Lp |  0.9420 |  0.5610 |
| Lr |  0.9550 |  0.5760 |
| P |  0.7620 |  0.4140 |