



## wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 11:36 AM UTC

PDB ID : 3J0O / pdb\_00003j0o  
EMDB ID : EMD-5327  
Title : Core of mammalian 80S pre-ribosome in complex with tRNAs fitted to a 9A cryo-EM map: classic PRE state 2  
Authors : Budkevich, T.; Giesebrecht, J.; Altman, R.; Munro, J.; Mielke, T.; Nierhaus, K.; Blanchard, S.; Spahn, C.M.  
Deposited on : 2011-10-05  
Resolution : 9.00 Å(reported)  
Based on initial models : 2WDK, 3O58, 2XZM

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

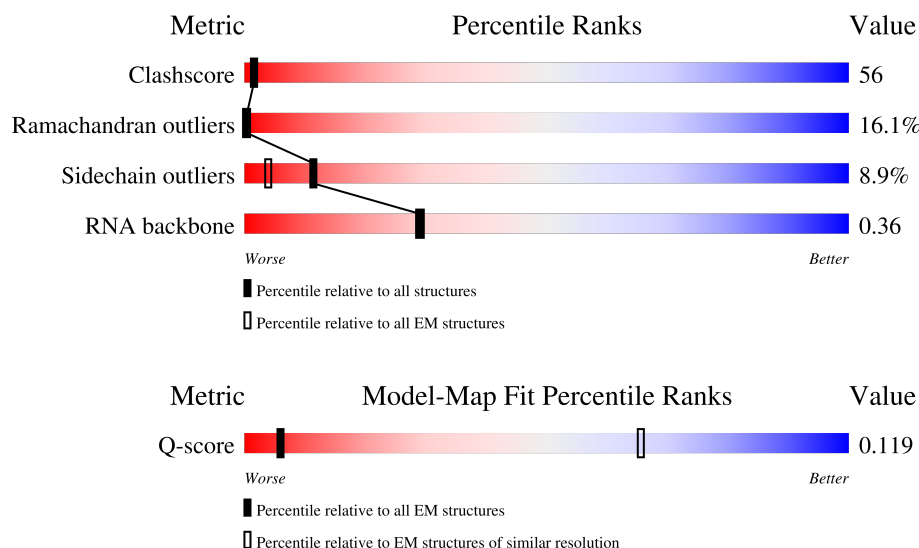
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 9.00 Å.

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



| Metric                | Whole archive<br>(#Entries) | EM structures<br>(#Entries) | Similar EM resolution<br>(#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|-----------------------------|----------------------------------------------------------|
| Clashscore            | 229148                      | 23984                       | -                                                        |
| Ramachandran outliers | 224038                      | 23583                       | -                                                        |
| Sidechain outliers    | 223484                      | 23102                       | -                                                        |
| RNA backbone          | 8273                        | 3508                        | -                                                        |
| Q-score               | -                           | 25397                       | 257 ( 8.50 - 9.50 )                                      |

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

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1   | a     | 48     |                  |
| 2   | b     | 12     |                  |
| 3   | c     | 17     |                  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 4   | d     | 7      |                  |
| 5   | e     | 4      |                  |
| 6   | E     | 5      |                  |
| 7   | f     | 21     |                  |
| 8   | g     | 31     |                  |
| 9   | G     | 13     |                  |
| 10  | h     | 111    |                  |
| 11  | T     | 192    |                  |
| 12  | K     | 140    |                  |
| 13  | L     | 141    |                  |
| 14  | X     | 68     |                  |
| 15  | S     | 125    |                  |
| 16  | 2     | 112    |                  |
| 17  | 3     | 12     |                  |
| 18  | 4     | 14     |                  |
| 19  | 5     | 6      |                  |
| 20  | 6     | 19     |                  |
| 21  | 7     | 50     |                  |
| 22  | 8     | 20     |                  |
| 23  | B     | 213    |                  |
| 24  | F     | 95     |                  |
| 25  | V     | 76     |                  |
| 25  | W     | 76     |                  |
| 25  | Y     | 76     |                  |
| 26  | v     | 3      |                  |

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| Mol | Chain | Length | Quality of chain                                   |
|-----|-------|--------|----------------------------------------------------|
| 26  | y     | 3      | <div><div></div><div>33%</div><div>67%</div></div> |
| 27  | w     | 2      | <div><div></div><div>100%</div></div>              |

## 2 Entry composition

There are 27 unique types of molecules in this entry. The entry contains 22450 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 40S ribosomal RNA fragment.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 1   | a     | 48       | Total | C   | N   | O   | P  | 0       | 0     |
|     |       |          | 1029  | 459 | 190 | 332 | 48 |         |       |

- Molecule 2 is a RNA chain called 40S ribosomal RNA fragment.

| Mol | Chain | Residues | Atoms |     |    |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|----|---------|-------|
| 2   | b     | 12       | Total | C   | N  | O  | P  | 0       | 0     |
|     |       |          | 260   | 116 | 49 | 83 | 12 |         |       |

- Molecule 3 is a RNA chain called 40S ribosomal RNA fragment.

| Mol | Chain | Residues | Atoms |     |    |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|-----|----|---------|-------|
| 3   | c     | 17       | Total | C   | N  | O   | P  | 0       | 0     |
|     |       |          | 362   | 162 | 66 | 117 | 17 |         |       |

- Molecule 4 is a RNA chain called 40S ribosomal RNA fragment.

| Mol | Chain | Residues | Atoms |    |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|---|---------|-------|
| 4   | d     | 7        | Total | C  | N  | O  | P | 0       | 0     |
|     |       |          | 155   | 69 | 33 | 46 | 7 |         |       |

- Molecule 5 is a RNA chain called 40S ribosomal RNA fragment.

| Mol | Chain | Residues | Atoms |    |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|---|---------|-------|
| 5   | e     | 4        | Total | C  | N  | O  | P | 0       | 0     |
|     |       |          | 84    | 38 | 16 | 26 | 4 |         |       |

- Molecule 6 is a RNA chain called 40S ribosomal RNA fragment.

| Mol | Chain | Residues | Atoms |    |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|---|---------|-------|
| 6   | E     | 5        | Total | C  | N  | O  | P | 0       | 0     |
|     |       |          | 100   | 45 | 13 | 37 | 5 |         |       |

- Molecule 7 is a RNA chain called 40S ribosomal RNA fragment.

| Mol | Chain | Residues | Atoms |     |    |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|-----|----|---------|-------|
| 7   | f     | 21       | Total | C   | N  | O   | P  | 0       | 0     |
|     |       |          | 452   | 200 | 79 | 152 | 21 |         |       |

- Molecule 8 is a RNA chain called 40S ribosomal RNA fragment.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 8   | g     | 31       | Total | C   | N   | O   | P  | 0       | 0     |
|     |       |          | 660   | 295 | 118 | 216 | 31 |         |       |

- Molecule 9 is a RNA chain called 40S ribosomal RNA fragment.

| Mol | Chain | Residues | Atoms |     |    |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|----|---------|-------|
| 9   | G     | 13       | Total | C   | N  | O  | P  | 0       | 0     |
|     |       |          | 276   | 123 | 49 | 91 | 13 |         |       |

- Molecule 10 is a RNA chain called 40S ribosomal RNA fragment.

| Mol | Chain | Residues | Atoms |      |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 10  | h     | 111      | Total | C    | N   | O   | P   | 0       | 0     |
|     |       |          | 2368  | 1060 | 431 | 766 | 111 |         |       |

- Molecule 11 is a protein called Ribosomal protein S5.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 11  | T     | 192      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1520  | 961 | 281 | 270 | 8 |         |       |

- Molecule 12 is a protein called Ribosomal protein S14.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 12  | K     | 140      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1063  | 654 | 206 | 197 | 6 |         |       |

- Molecule 13 is a protein called Ribosomal protein S23.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 13  | L     | 141      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1097  | 691 | 221 | 180 | 5 |         |       |

- Molecule 14 is a protein called Ribosomal protein S30.

| Mol | Chain | Residues | Atoms |     |     |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 14  | X     | 68       | Total | C   | N   | O  | S | 0       | 0     |
|     |       |          | 554   | 350 | 113 | 90 | 1 |         |       |

- Molecule 15 is a protein called Ribosomal protein S15.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 15  | S     | 125      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 985   | 632 | 173 | 176 | 4 |         |       |

- Molecule 16 is a RNA chain called 60S ribosomal RNA fragment.

| Mol | Chain | Residues | Atoms |      |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 16  | 2     | 112      | Total | C    | N   | O   | P   | 0       | 0     |
|     |       |          | 2392  | 1070 | 435 | 775 | 112 |         |       |

- Molecule 17 is a RNA chain called 60S ribosomal RNA fragment.

| Mol | Chain | Residues | Atoms |     |    |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|----|---------|-------|
| 17  | 3     | 12       | Total | C   | N  | O  | P  | 0       | 0     |
|     |       |          | 259   | 116 | 50 | 81 | 12 |         |       |

- Molecule 18 is a RNA chain called 60S ribosomal RNA fragment.

| Mol | Chain | Residues | Atoms |     |    |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|----|---------|-------|
| 18  | 4     | 14       | Total | C   | N  | O  | P  | 0       | 0     |
|     |       |          | 306   | 135 | 59 | 98 | 14 |         |       |

- Molecule 19 is a RNA chain called 60S ribosomal RNA fragment.

| Mol | Chain | Residues | Atoms |    |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|---|---------|-------|
| 19  | 5     | 6        | Total | C  | N  | O  | P | 0       | 0     |
|     |       |          | 127   | 57 | 23 | 41 | 6 |         |       |

- Molecule 20 is a RNA chain called 60S ribosomal RNA fragment.

| Mol | Chain | Residues | Atoms |     |    |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|-----|----|---------|-------|
| 20  | 6     | 19       | Total | C   | N  | O   | P  | 0       | 0     |
|     |       |          | 417   | 187 | 88 | 123 | 19 |         |       |

- Molecule 21 is a RNA chain called 60S ribosomal RNA fragment.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 21  | 7     | 50       | Total | C   | N   | O   | P  | 0       | 0     |
|     |       |          | 1054  | 471 | 173 | 360 | 50 |         |       |

- Molecule 22 is a RNA chain called 60S ribosomal RNA fragment.

| Mol | Chain | Residues | Atoms |     |    |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|-----|----|---------|-------|
| 22  | 8     | 20       | Total | C   | N  | O   | P  | 0       | 0     |
|     |       |          | 431   | 192 | 80 | 139 | 20 |         |       |

- Molecule 23 is a protein called Ribosomal protein L10a.

| Mol | Chain | Residues | Atoms |     |     |     |  | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|-------|
| 23  | B     | 213      | Total | C   | N   | O   |  | 0       | 0     |
|     |       |          | 1055  | 629 | 213 | 213 |  |         |       |

- Molecule 24 is a protein called Ribosomal protein L36a.

| Mol | Chain | Residues | Atoms |     |    |    |  | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|--|---------|-------|
| 24  | F     | 95       | Total | C   | N  | O  |  | 0       | 0     |
|     |       |          | 467   | 277 | 95 | 95 |  |         |       |

- Molecule 25 is a RNA chain called tRNA.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 25  | Y     | 75       | Total | C   | N   | O   | P  | 0       | 0     |
|     |       |          | 1597  | 713 | 285 | 525 | 74 |         |       |
| 25  | V     | 75       | Total | C   | N   | O   | P  | 0       | 0     |
|     |       |          | 1597  | 713 | 285 | 525 | 74 |         |       |
| 25  | W     | 76       | Total | C   | N   | O   | P  | 0       | 0     |
|     |       |          | 1619  | 723 | 290 | 531 | 75 |         |       |

- Molecule 26 is a RNA chain called mRNA fragment.

| Mol | Chain | Residues | Atoms |    |   |    |   | AltConf | Trace |
|-----|-------|----------|-------|----|---|----|---|---------|-------|
| 26  | y     | 3        | Total | C  | N | O  | P | 0       | 0     |
|     |       |          | 60    | 27 | 7 | 23 | 3 |         |       |
| 26  | v     | 3        | Total | C  | N | O  | P | 0       | 0     |
|     |       |          | 60    | 27 | 7 | 23 | 3 |         |       |

- Molecule 27 is a RNA chain called mRNA fragment.

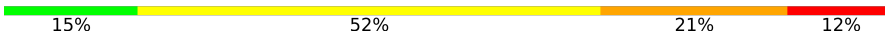


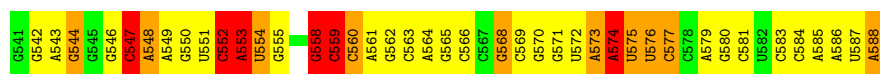
| Mol | Chain | Residues | Atoms |    |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|---|---------|-------|
|     |       |          | Total | C  | N  | O  | P |         |       |
| 27  | w     | 2        | 44    | 20 | 10 | 12 | 2 | 0       | 0     |

### 3 Residue-property plots

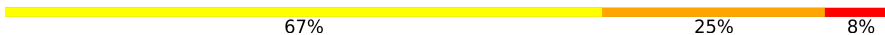
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: 40S ribosomal RNA fragment

Chain a: 



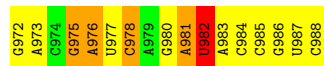
- Molecule 2: 40S ribosomal RNA fragment

Chain b: 

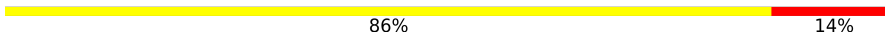


- Molecule 3: 40S ribosomal RNA fragment

Chain c: 



- Molecule 4: 40S ribosomal RNA fragment

Chain d: 



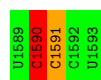
- Molecule 5: 40S ribosomal RNA fragment

Chain e: 



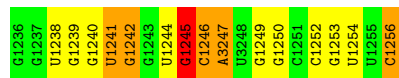
- Molecule 6: 40S ribosomal RNA fragment

Chain E: 



• Molecule 7: 40S ribosomal RNA fragment

Chain f: 29% 43% 24% 5%



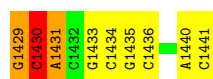
• Molecule 8: 40S ribosomal RNA fragment

Chain g: 6% 68% 19% 6%



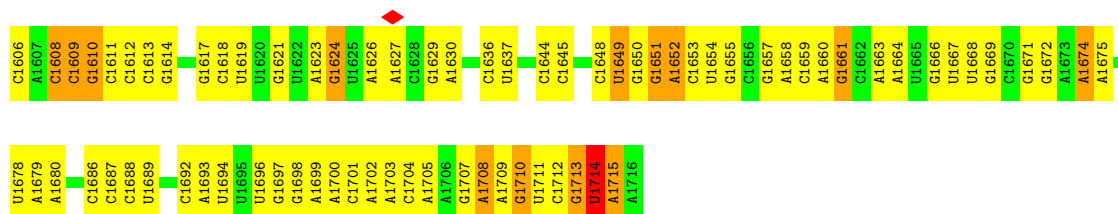
• Molecule 9: 40S ribosomal RNA fragment

Chain G: 31% 46% 15% 8%



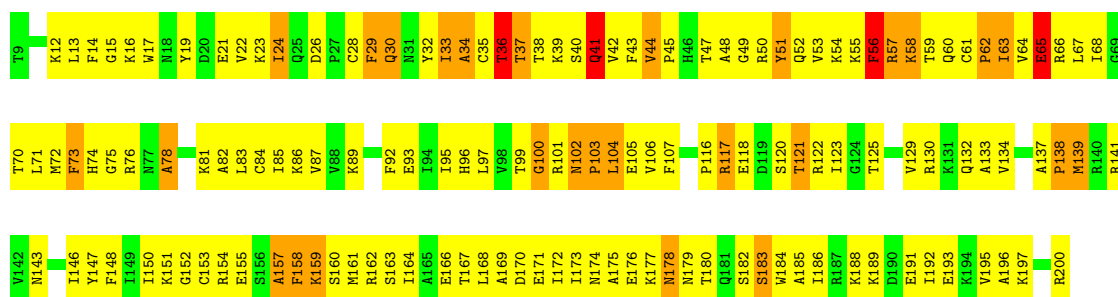
• Molecule 10: 40S ribosomal RNA fragment

Chain h: 33% 54% 12%

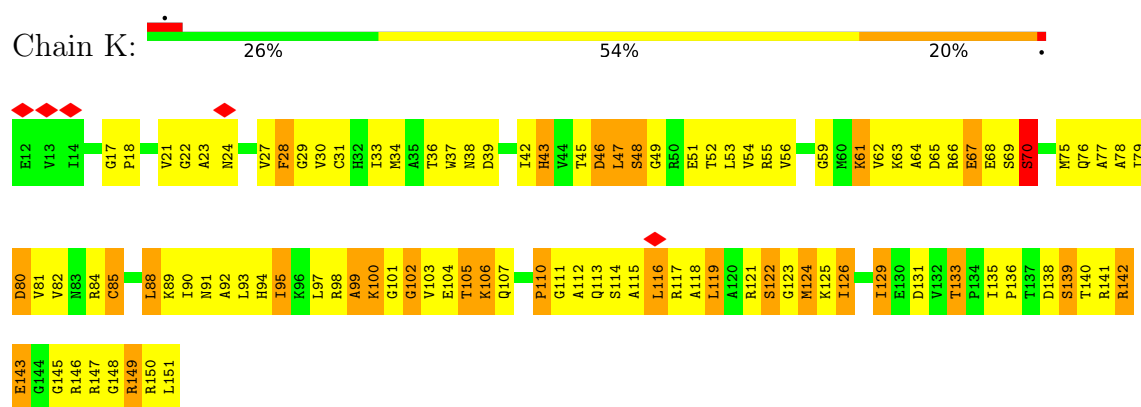


• Molecule 11: Ribosomal protein S5

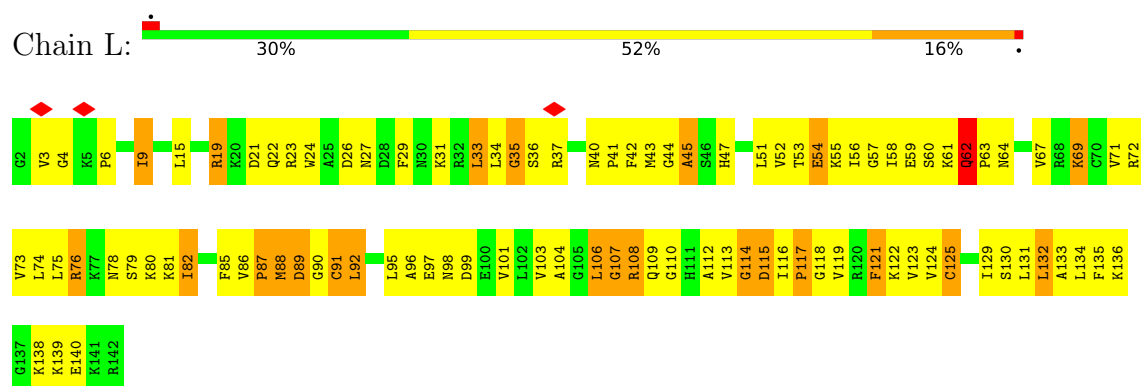
Chain T: 24% 59% 14%



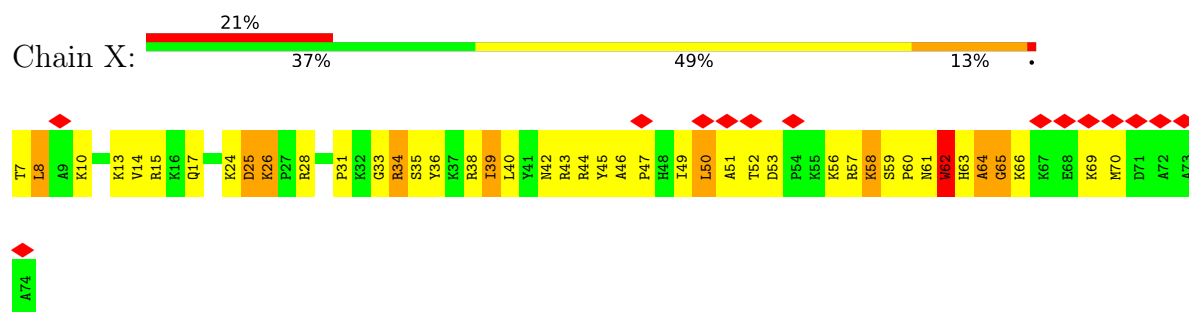
• Molecule 12: Ribosomal protein S14



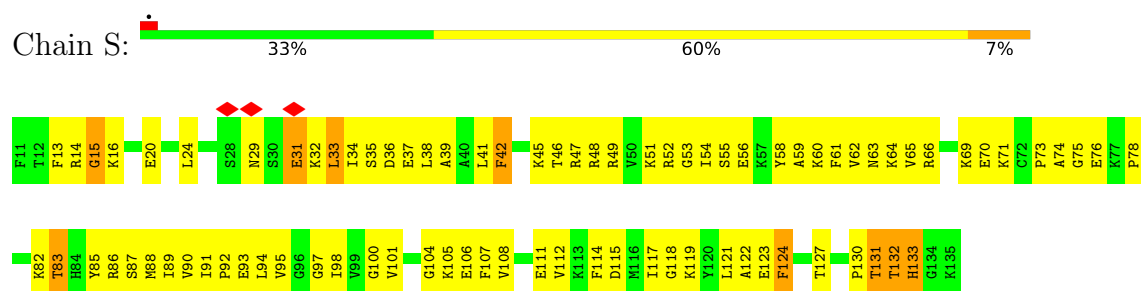
- Molecule 13: Ribosomal protein S23



- Molecule 14: Ribosomal protein S30



- Molecule 15: Ribosomal protein S15



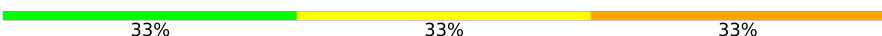
- Molecule 16: 60S ribosomal RNA fragment



G2194 G2195 G2196 G2197 G2198 G2199 G2200 G2201 G2202 G2203 G2204 G2205 G2206 G2207 G2208 G2209 G2210 G2211 G2212 G2213 G2214 G2215 G2216 G2217 G2218 G2219 G2220 G2221 G2222 G2223 G2224 G2225 G2226 G2227 G2228 G2229 G2230 G2231 G2232 G2233 G2234 G2235 G2236 G2237 G2238 G2239 G2240 G2241 G2242 G2243 G2244 G2245 G2246 G2247 G2248 G2249 G2250 G2251 G2252 G2253

U2254 A2255 A2256 A2257 U2258 A2259 U2260 A2261 A2262 A2263 A2264 A2265 U2266 A2267 U2268 U2269 A2270 A2271 A2272 G2273 G2274 A2275 A2276 G2277 G2278 A2279 A2280 A2281 U2282 A2283 G2284 A2285 U2286 G2287 G2288 A2289 G2290 A2291 U2292 A2293 U2294 A2295 A2296 U2297 U2298 A2299 G2300 U2301 G2302 A2303 G2304 G2305

- Molecule 17: 60S ribosomal RNA fragment

Chain 3:  33% 33% 33%

G2477 G2478 G2479 U2482 G2483 A2484 A2485 A2486 U2487 A2488

- Molecule 18: 60S ribosomal RNA fragment

Chain 4:  71% 29%

G2614 G2615 G2616 U2617 G2618 G2619 G2620 G2621 G2622 G2623 G2624 A2625 A2626 G2627

- Molecule 19: 60S ribosomal RNA fragment

Chain 5:  17% 17% 67%

G2653 G2654 U2655 A2656 A2657 G2658

- Molecule 20: 60S ribosomal RNA fragment

Chain 6:  32% 68%

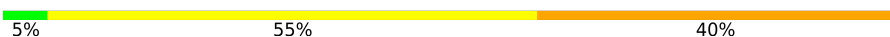
A2689 G2690 A2691 A2692 G2693 A2694 A2695 A2696 A2697 G2698 G2699 G2700 U2701 A2702 A2703 A2704 A2705 G2706 G2707

- Molecule 21: 60S ribosomal RNA fragment

Chain 7:  44% 54%

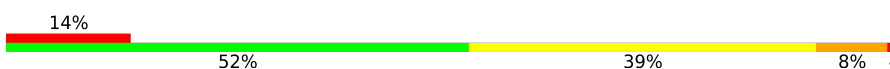
G2824 G2825 U2826 U2827 G2828 U2829 G2830 G2831 G2832 A2833 G2834 U2835 G2836 A2837 A2838 G2839 G2840 G2841 U2842 U2843 G2844 A2845 U2846 A2847 G2848 G2849 G2850 A2851 G2852 A2853 U2854 U2855 G2856 G2857 U2858 U2859 U2860 U2861 U2862 G2863 A2864 U2865 U2866 G2867 U2868 U2869 G2870 G2871 A2872 U2873

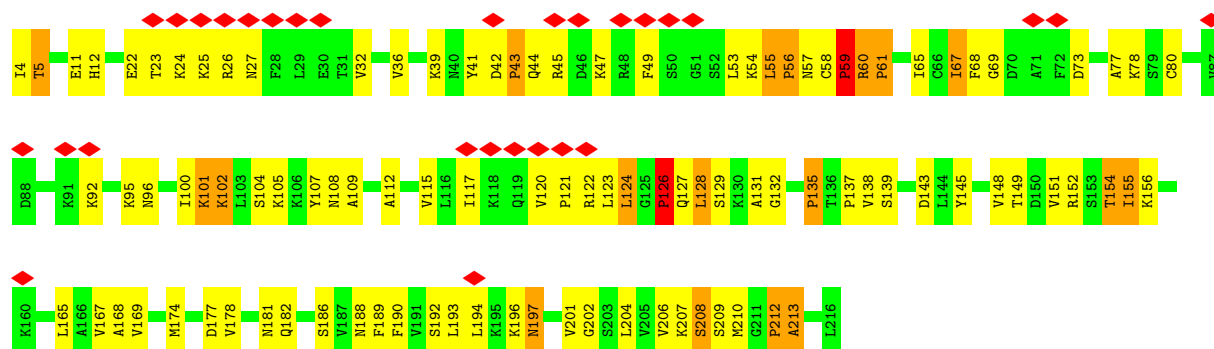
- Molecule 22: 60S ribosomal RNA fragment

Chain 8:  5% 55% 40%

G2957 A2958 G2959 G2960 G2961 U2962 G2963 U2964 G2965 U2966 A2967 G2968 A2969 G2970 A2971 G2972 G2973 U2974 U2975 A2976

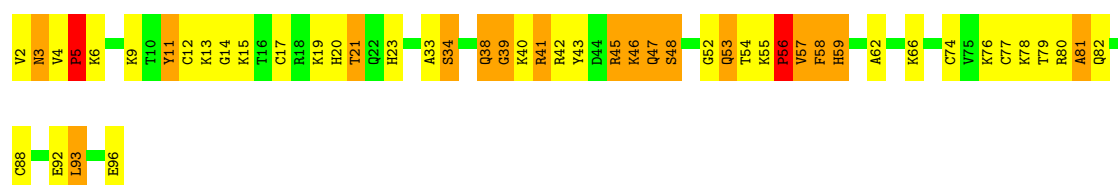
- Molecule 23: Ribosomal protein L10a

Chain B:  14% 52% 39% 8%



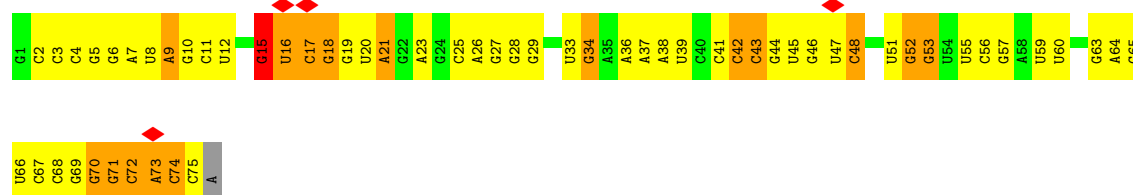
• Molecule 24: Ribosomal protein L36a

Chain F: 47% 33% 18% .



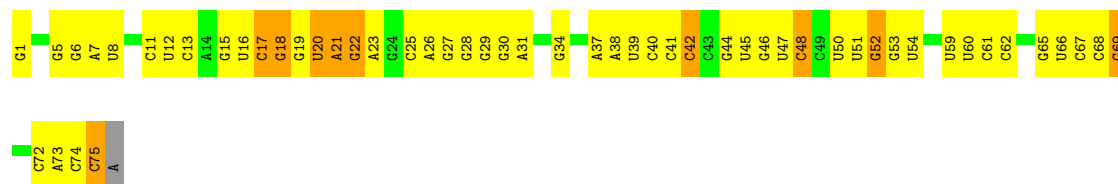
• Molecule 25: tRNA

Chain Y: 5% 21% 55% 21% ..



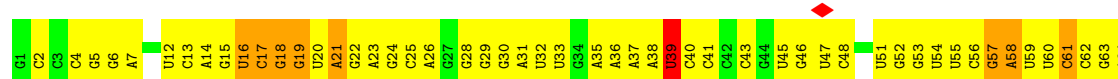
• Molecule 25: tRNA

Chain V: 28% 58% 13% .



• Molecule 25: tRNA

Chain W: 20% 66% 13% .





- Molecule 26: mRNA fragment

Chain y: 33% 67%



- Molecule 26: mRNA fragment

Chain v: 67% 33%



- Molecule 27: mRNA fragment

Chain w: 100%

There are no outlier residues recorded for this chain.

## 4 Experimental information

| Property                             | Value                                                                | Source    |
|--------------------------------------|----------------------------------------------------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE                                                      | Depositor |
| Imposed symmetry                     | POINT, C1                                                            | Depositor |
| Number of particles used             | 81946                                                                | Depositor |
| Resolution determination method      | Not provided                                                         |           |
| CTF correction method                | CTF CORRECTION OF EACH DEFOCUS GROUP VOLUME PRIOR TO BACK PROJECTION | Depositor |
| Microscope                           | FEI POLARA 300                                                       | Depositor |
| Voltage (kV)                         | 300                                                                  | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 20                                                                   | Depositor |
| Minimum defocus (nm)                 | 2000                                                                 | Depositor |
| Maximum defocus (nm)                 | 4000                                                                 | Depositor |
| Magnification                        | 65520                                                                | Depositor |
| Image detector                       | KODAK SO-163 FILM                                                    | Depositor |
| Maximum map value                    | 21309.771                                                            | Depositor |
| Minimum map value                    | -5197.505                                                            | Depositor |
| Average map value                    | 340.467                                                              | Depositor |
| Map value standard deviation         | 1535.379                                                             | Depositor |
| Recommended contour level            | 1000                                                                 | Depositor |
| Map size ( $\text{\AA}$ )            | 453.6, 453.6, 453.6                                                  | wwPDB     |
| Map dimensions                       | 180, 180, 180                                                        | wwPDB     |
| Map angles ( $^\circ$ )              | 90.0, 90.0, 90.0                                                     | wwPDB     |
| Pixel spacing ( $\text{\AA}$ )       | 2.52, 2.52, 2.52                                                     | Depositor |



## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

| Mol | Chain | Bond lengths |             | Bond angles |                 |
|-----|-------|--------------|-------------|-------------|-----------------|
|     |       | RMSZ         | $\# Z  > 5$ | RMSZ        | $\# Z  > 5$     |
| 1   | a     | 0.55         | 0/1151      | 0.98        | 6/1793 (0.3%)   |
| 2   | b     | 0.41         | 0/291       | 0.83        | 1/452 (0.2%)    |
| 3   | c     | 0.46         | 0/404       | 0.93        | 3/627 (0.5%)    |
| 4   | d     | 0.42         | 0/174       | 0.94        | 1/270 (0.4%)    |
| 5   | e     | 0.41         | 0/93        | 0.72        | 0/142           |
| 6   | E     | 0.41         | 0/109       | 1.04        | 1/166 (0.6%)    |
| 7   | f     | 0.47         | 0/504       | 0.91        | 3/785 (0.4%)    |
| 8   | g     | 0.50         | 0/737       | 0.95        | 4/1146 (0.3%)   |
| 9   | G     | 0.44         | 0/307       | 0.93        | 2/476 (0.4%)    |
| 10  | h     | 0.38         | 0/2650      | 0.70        | 2/4127 (0.0%)   |
| 11  | T     | 0.54         | 0/1546      | 1.15        | 12/2079 (0.6%)  |
| 12  | K     | 0.53         | 0/1078      | 1.09        | 9/1452 (0.6%)   |
| 13  | L     | 0.53         | 0/1114      | 1.06        | 4/1485 (0.3%)   |
| 14  | X     | 0.47         | 0/566       | 1.18        | 5/753 (0.7%)    |
| 15  | S     | 0.45         | 0/1003      | 1.03        | 6/1342 (0.4%)   |
| 16  | 2     | 0.58         | 0/2677      | 0.64        | 0/4170          |
| 17  | 3     | 0.11         | 0/290       | 0.24        | 0/450           |
| 18  | 4     | 0.38         | 0/342       | 0.51        | 0/533           |
| 19  | 5     | 0.39         | 0/141       | 0.54        | 0/217           |
| 20  | 6     | 0.70         | 0/470       | 0.80        | 0/732           |
| 21  | 7     | 0.58         | 0/1174      | 0.74        | 3/1825 (0.2%)   |
| 22  | 8     | 0.76         | 0/482       | 0.64        | 0/750           |
| 23  | B     | 0.51         | 0/1054      | 1.05        | 12/1468 (0.8%)  |
| 24  | F     | 0.66         | 0/466       | 1.04        | 3/646 (0.5%)    |
| 25  | V     | 0.40         | 0/1784      | 0.68        | 0/2780          |
| 25  | W     | 0.44         | 0/1809      | 0.61        | 0/2819          |
| 25  | Y     | 0.50         | 0/1784      | 0.68        | 2/2780 (0.1%)   |
| 26  | v     | 0.40         | 0/65        | 0.70        | 0/98            |
| 26  | y     | 0.44         | 0/65        | 0.54        | 0/98            |
| 27  | w     | 0.42         | 0/49        | 0.62        | 0/74            |
| All | All   | 0.50         | 0/24379     | 0.84        | 79/36535 (0.2%) |

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected

by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 1   | a     | 0                   | 4                   |
| 4   | d     | 0                   | 1                   |
| 6   | E     | 0                   | 1                   |
| 8   | g     | 0                   | 2                   |
| 9   | G     | 0                   | 1                   |
| 10  | h     | 0                   | 2                   |
| 25  | W     | 0                   | 2                   |
| All | All   | 0                   | 13                  |

There are no bond length outliers.

The worst 5 of 79 bond angle outliers are listed below:

| Mol | Chain | Res  | Type | Atoms      | Z     | Observed(°) | Ideal(°) |
|-----|-------|------|------|------------|-------|-------------|----------|
| 11  | T     | 36   | THR  | N-CA-C     | 10.62 | 123.93      | 111.71   |
| 15  | S     | 131  | THR  | N-CA-C     | 9.81  | 125.24      | 109.24   |
| 10  | h     | 1714 | U    | N1-C1'-C2' | 9.06  | 125.60      | 112.00   |
| 11  | T     | 73   | PHE  | N-CA-C     | 8.95  | 124.26      | 113.16   |
| 14  | X     | 58   | LYS  | N-CA-C     | 8.92  | 122.12      | 110.43   |

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

| Mol | Chain | Res  | Type | Group     |
|-----|-------|------|------|-----------|
| 1   | a     | 547  | C    | Sidechain |
| 1   | a     | 558  | G    | Sidechain |
| 1   | a     | 559  | C    | Sidechain |
| 1   | a     | 574  | A    | Sidechain |
| 4   | d     | 1545 | A    | Sidechain |

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

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

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1   | a     | 1029  | 0        | 521      | 73      | 0            |
| 2   | b     | 260   | 0        | 130      | 31      | 0            |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 3   | c     | 362   | 0        | 185      | 23      | 0            |
| 4   | d     | 155   | 0        | 78       | 6       | 0            |
| 5   | e     | 84    | 0        | 45       | 2       | 0            |
| 6   | E     | 100   | 0        | 54       | 7       | 0            |
| 7   | f     | 452   | 0        | 226      | 27      | 0            |
| 8   | g     | 660   | 0        | 335      | 49      | 0            |
| 9   | G     | 276   | 0        | 141      | 18      | 0            |
| 10  | h     | 2368  | 0        | 1197     | 162     | 0            |
| 11  | T     | 1520  | 0        | 1569     | 198     | 0            |
| 12  | K     | 1063  | 0        | 1088     | 130     | 0            |
| 13  | L     | 1097  | 0        | 1169     | 118     | 0            |
| 14  | X     | 554   | 0        | 604      | 58      | 0            |
| 15  | S     | 985   | 0        | 1026     | 103     | 0            |
| 16  | 2     | 2392  | 0        | 1208     | 448     | 0            |
| 17  | 3     | 259   | 0        | 131      | 13      | 0            |
| 18  | 4     | 306   | 0        | 154      | 63      | 0            |
| 19  | 5     | 127   | 0        | 66       | 25      | 0            |
| 20  | 6     | 417   | 0        | 209      | 78      | 0            |
| 21  | 7     | 1054  | 0        | 532      | 175     | 0            |
| 22  | 8     | 431   | 0        | 216      | 50      | 0            |
| 23  | B     | 1055  | 0        | 453      | 34      | 0            |
| 24  | F     | 467   | 0        | 208      | 33      | 0            |
| 25  | V     | 1597  | 0        | 807      | 94      | 0            |
| 25  | W     | 1619  | 0        | 821      | 120     | 0            |
| 25  | Y     | 1597  | 0        | 811      | 95      | 0            |
| 26  | v     | 60    | 0        | 31       | 23      | 0            |
| 26  | y     | 60    | 0        | 31       | 14      | 0            |
| 27  | w     | 44    | 0        | 23       | 0       | 0            |
| All | All   | 22450 | 0        | 14069    | 2044    | 0            |

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 56.

The worst 5 of 2044 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1          | Atom-2         | Interatomic distance (Å) | Clash overlap (Å) |
|-----------------|----------------|--------------------------|-------------------|
| 10:h:1609:C:C6  | 25:V:34:G:C6   | 1.84                     | 1.50              |
| 19:5:2657:A:C2  | 20:6:2694:A:N3 | 1.73                     | 1.45              |
| 10:h:1609:C:C1' | 26:v:18:C:N4   | 1.76                     | 1.44              |
| 10:h:1709:A:OP1 | 26:y:20:U:C5'  | 1.64                     | 1.41              |
| 18:4:2619:G:OP1 | 21:7:2866:U:C6 | 1.79                     | 1.35              |

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

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

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

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

| Mol | Chain | Analysed      | Favoured  | Allowed   | Outliers  | Percentiles |    |
|-----|-------|---------------|-----------|-----------|-----------|-------------|----|
| 11  | T     | 190/192 (99%) | 141 (74%) | 33 (17%)  | 16 (8%)   | 0           | 9  |
| 12  | K     | 138/140 (99%) | 96 (70%)  | 28 (20%)  | 14 (10%)  | 0           | 7  |
| 13  | L     | 139/141 (99%) | 106 (76%) | 17 (12%)  | 16 (12%)  | 0           | 5  |
| 14  | X     | 66/68 (97%)   | 48 (73%)  | 12 (18%)  | 6 (9%)    | 0           | 8  |
| 15  | S     | 123/125 (98%) | 91 (74%)  | 25 (20%)  | 7 (6%)    | 1           | 14 |
| 23  | B     | 211/213 (99%) | 76 (36%)  | 67 (32%)  | 68 (32%)  | 0           | 0  |
| 24  | F     | 93/95 (98%)   | 37 (40%)  | 28 (30%)  | 28 (30%)  | 0           | 0  |
| All | All   | 960/974 (99%) | 595 (62%) | 210 (22%) | 155 (16%) | 0           | 2  |

5 of 155 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 11  | T     | 56  | PHE  |
| 11  | T     | 60  | GLN  |
| 11  | T     | 63  | ILE  |
| 11  | T     | 75  | GLY  |
| 11  | T     | 158 | PHE  |

### 5.3.2 Protein sidechains [i](#)

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 |    |
|-----|-------|----------------|-----------|----------|-------------|----|
| 11  | T     | 163/163 (100%) | 146 (90%) | 17 (10%) | 7           | 22 |
| 12  | K     | 112/112 (100%) | 96 (86%)  | 16 (14%) | 3           | 13 |
| 13  | L     | 113/113 (100%) | 103 (91%) | 10 (9%)  | 9           | 28 |
| 14  | X     | 57/57 (100%)   | 55 (96%)  | 2 (4%)   | 32          | 53 |
| 15  | S     | 105/105 (100%) | 101 (96%) | 4 (4%)   | 29          | 50 |
| All | All   | 550/550 (100%) | 501 (91%) | 49 (9%)  | 11          | 28 |

5 of 49 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 12  | K     | 117 | ARG  |
| 13  | L     | 33  | LEU  |
| 12  | K     | 119 | LEU  |
| 12  | K     | 149 | ARG  |
| 13  | L     | 69  | LYS  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 15  | S     | 29  | ASN  |
| 14  | X     | 42  | ASN  |
| 13  | L     | 47  | HIS  |
| 14  | X     | 17  | GLN  |
| 12  | K     | 43  | HIS  |

### 5.3.3 RNA ⓘ

| Mol | Chain | Analysed      | Backbone Outliers | Pucker Outliers |
|-----|-------|---------------|-------------------|-----------------|
| 1   | a     | 47/48 (97%)   | 16 (34%)          | 0               |
| 10  | h     | 110/111 (99%) | 12 (10%)          | 0               |
| 16  | 2     | 111/112 (99%) | 55 (49%)          | 9 (8%)          |
| 17  | 3     | 11/12 (91%)   | 6 (54%)           | 1 (9%)          |
| 18  | 4     | 13/14 (92%)   | 5 (38%)           | 1 (7%)          |
| 19  | 5     | 5/6 (83%)     | 4 (80%)           | 1 (20%)         |
| 2   | b     | 11/12 (91%)   | 4 (36%)           | 0               |
| 20  | 6     | 18/19 (94%)   | 13 (72%)          | 1 (5%)          |
| 21  | 7     | 49/50 (98%)   | 29 (59%)          | 5 (10%)         |
| 22  | 8     | 19/20 (95%)   | 8 (42%)           | 0               |
| 25  | V     | 74/76 (97%)   | 15 (20%)          | 0               |

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| Mol | Chain | Analysed      | Backbone Outliers | Pucker Outliers |
|-----|-------|---------------|-------------------|-----------------|
| 25  | W     | 75/76 (98%)   | 13 (17%)          | 0               |
| 25  | Y     | 74/76 (97%)   | 20 (27%)          | 1 (1%)          |
| 26  | v     | 2/3 (66%)     | 0                 | 0               |
| 26  | y     | 2/3 (66%)     | 0                 | 0               |
| 27  | w     | 1/2 (50%)     | 0                 | 0               |
| 3   | c     | 16/17 (94%)   | 4 (25%)           | 0               |
| 4   | d     | 6/7 (85%)     | 2 (33%)           | 0               |
| 5   | e     | 3/4 (75%)     | 0                 | 0               |
| 6   | E     | 4/5 (80%)     | 1 (25%)           | 1 (25%)         |
| 7   | f     | 20/21 (95%)   | 5 (25%)           | 0               |
| 8   | g     | 30/31 (96%)   | 8 (26%)           | 0               |
| 9   | G     | 12/13 (92%)   | 2 (16%)           | 1 (8%)          |
| All | All   | 713/738 (96%) | 222 (31%)         | 21 (2%)         |

5 of 222 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | a     | 544 | G    |
| 1   | a     | 547 | C    |
| 1   | a     | 548 | A    |
| 1   | a     | 552 | C    |
| 1   | a     | 553 | A    |

5 of 21 RNA pucker outliers are listed below:

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 20  | 6     | 2699 | G    |
| 21  | 7     | 2851 | A    |
| 25  | Y     | 15   | G    |
| 21  | 7     | 2859 | U    |
| 21  | 7     | 2850 | 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](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

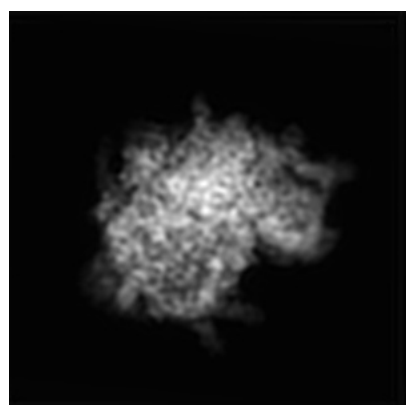
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5327. These allow visual inspection of the internal detail of the map and identification of artifacts.

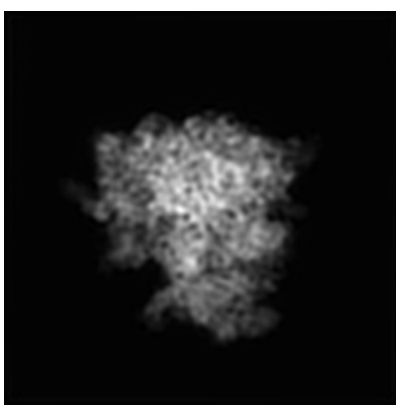
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

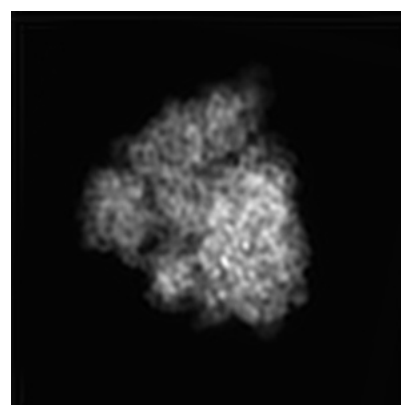
#### 6.1.1 Primary map



X



Y

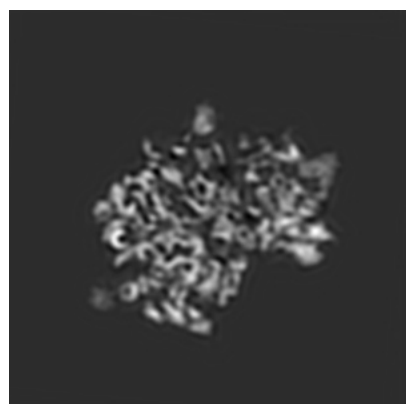


Z

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

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

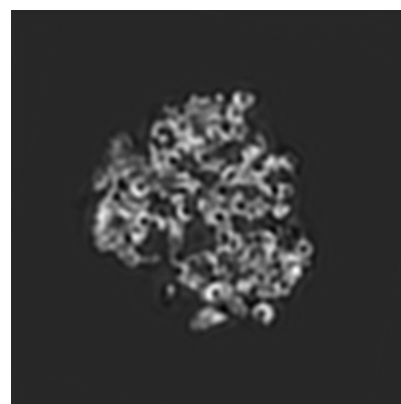
#### 6.2.1 Primary map



X Index: 90



Y Index: 90



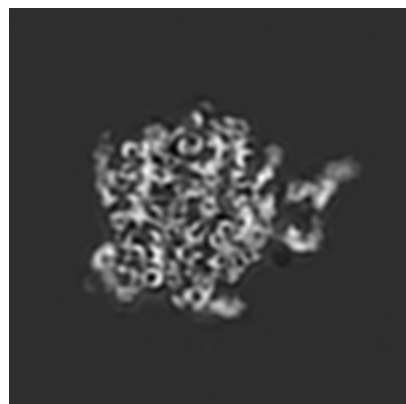
Z Index: 90



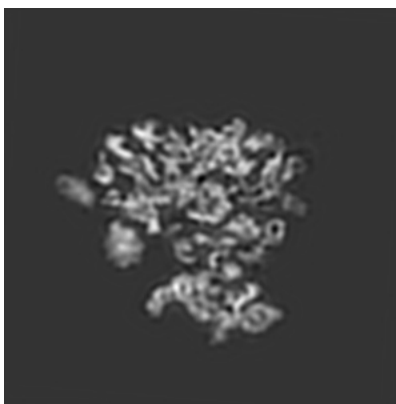
The images above show central slices of the map in three orthogonal directions.

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

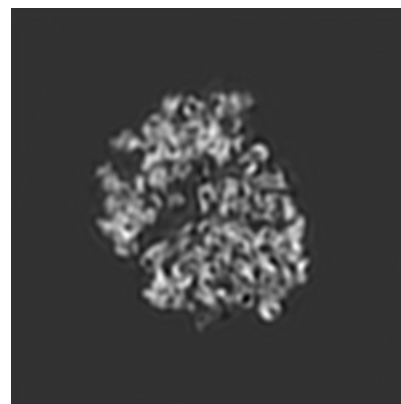
### 6.3.1 Primary map



X Index: 108



Y Index: 91

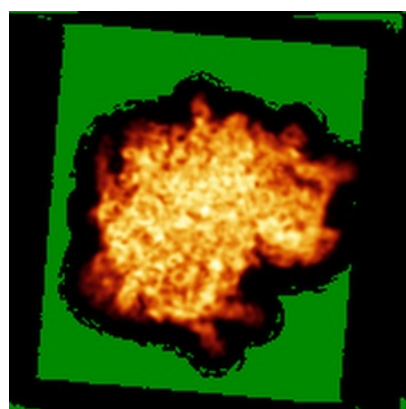


Z Index: 84

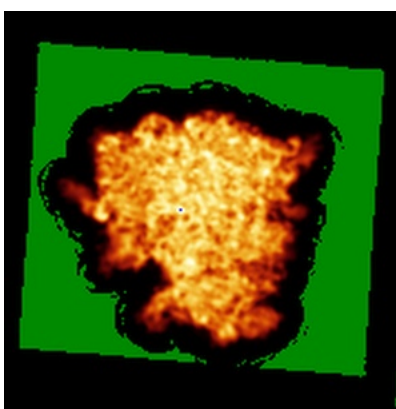
The images above show the largest variance slices of the map in three orthogonal directions.

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

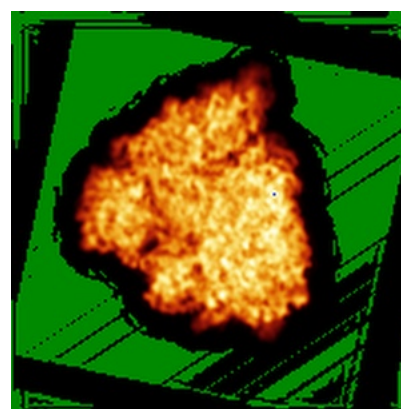
### 6.4.1 Primary map



X



Y



Z

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

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

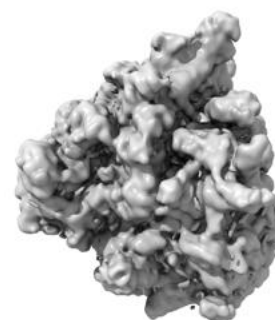
### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1000.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

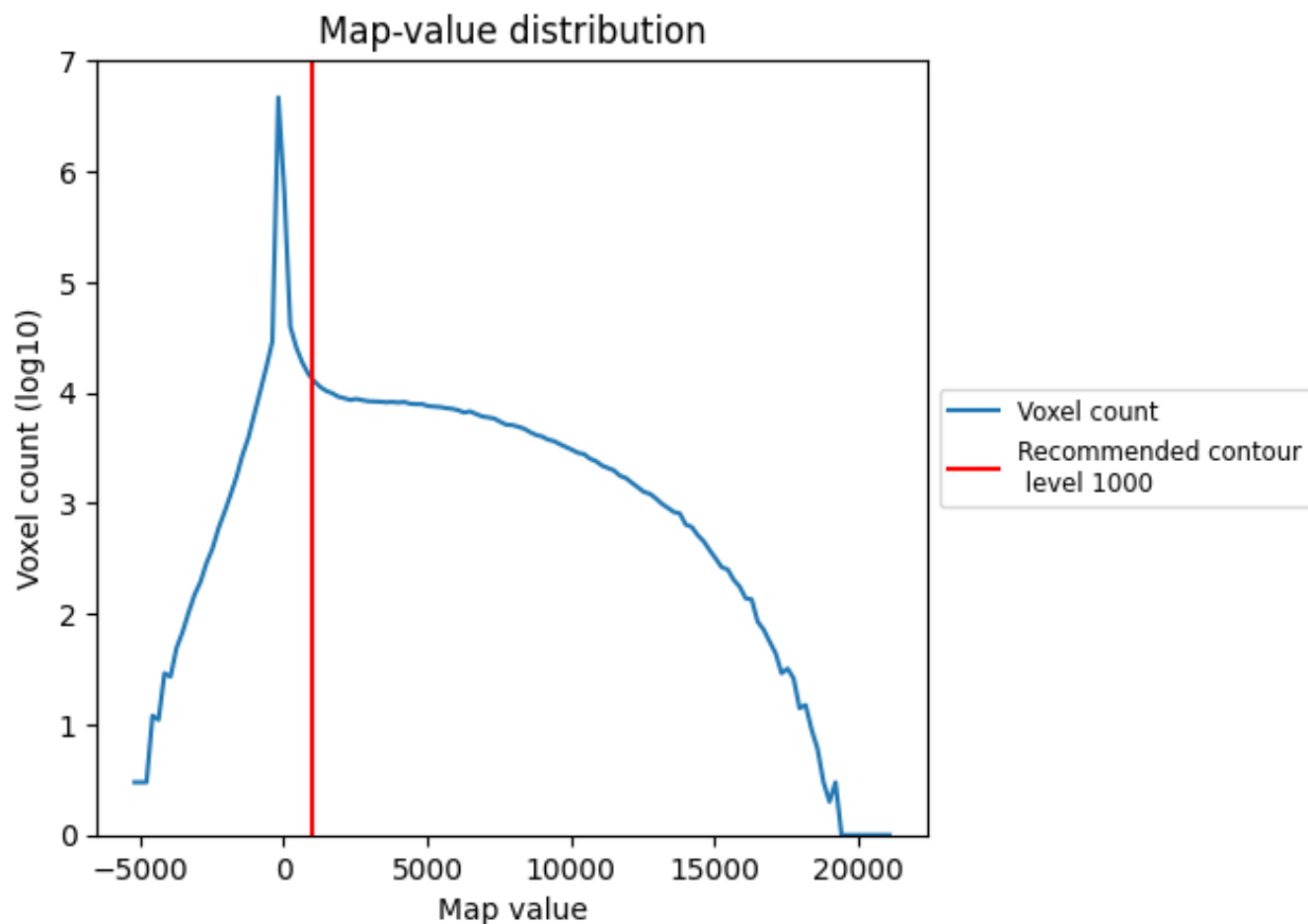
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

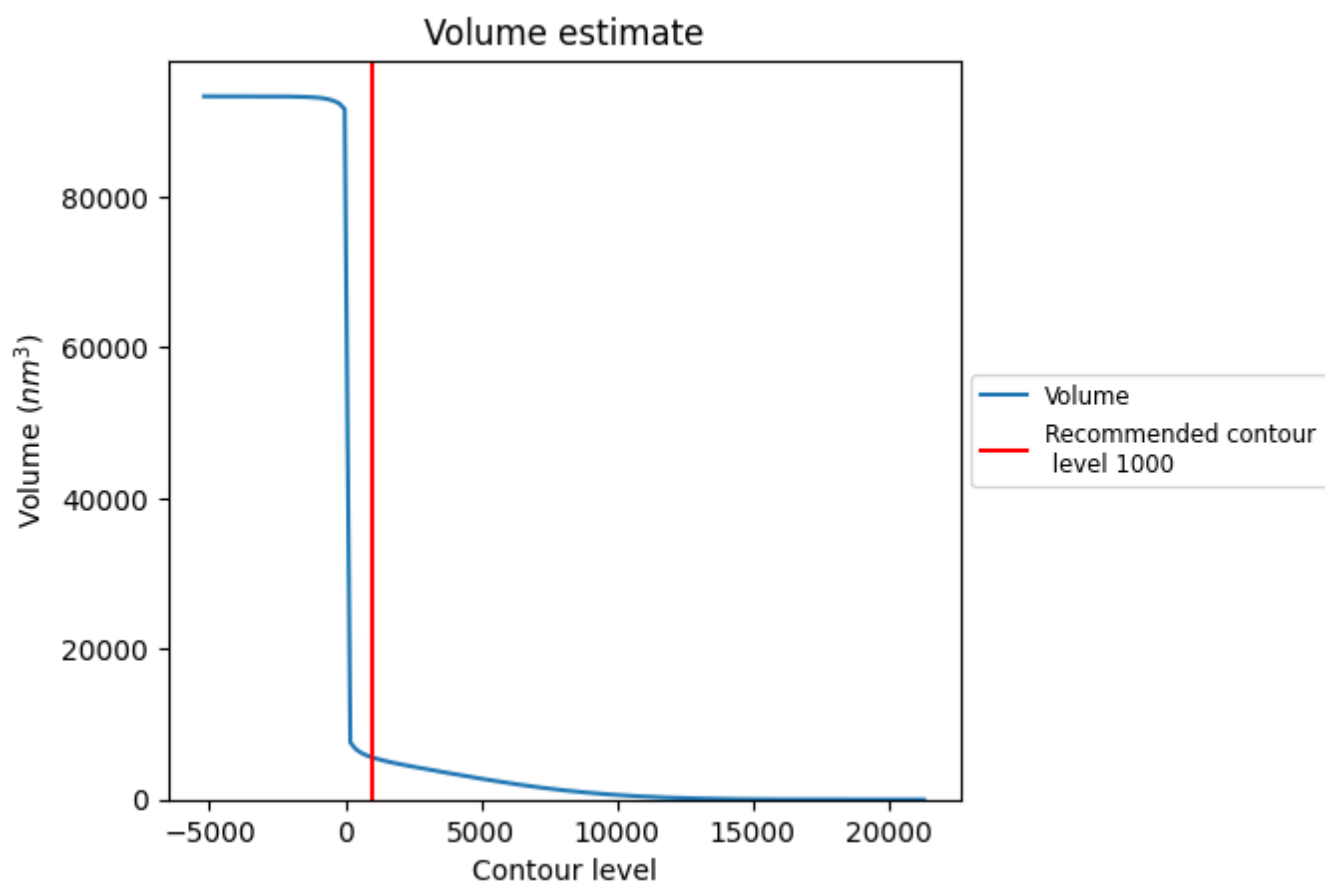
This section contains the results of statistical analysis of the map.

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



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

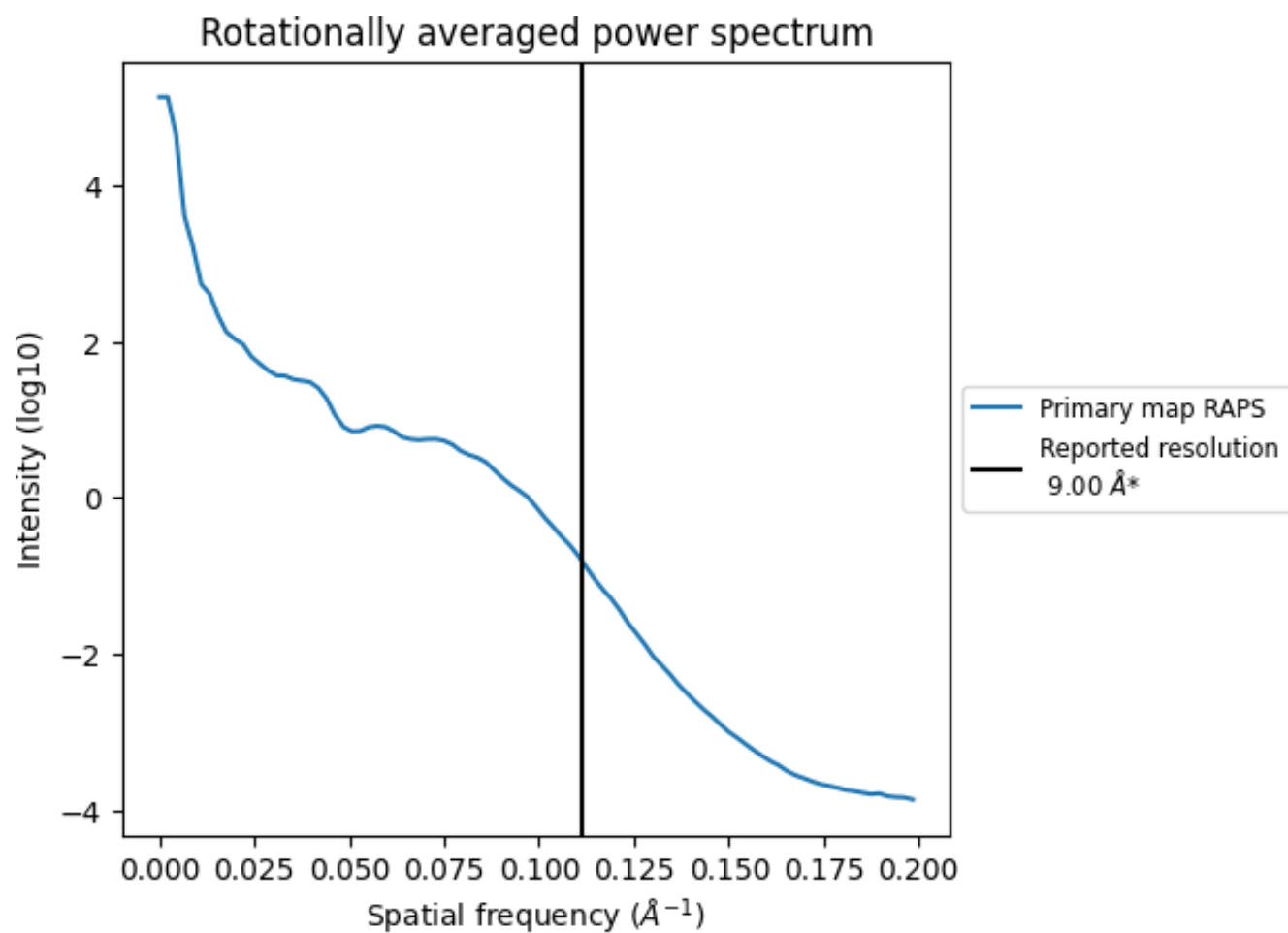
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5581  $\text{nm}^3$ ; this corresponds to an approximate mass of 5042 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 0.111 Å<sup>-1</sup>

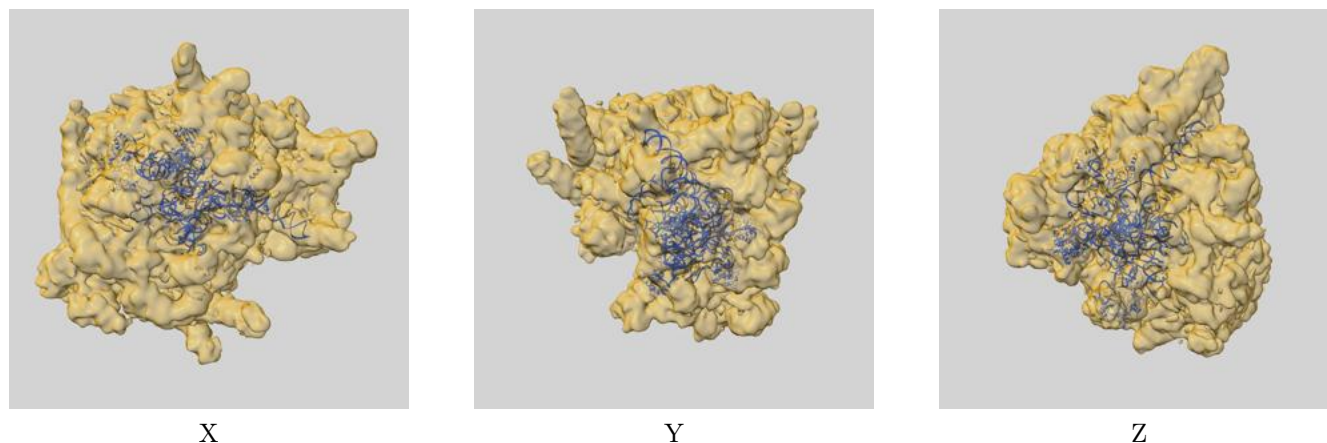
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

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

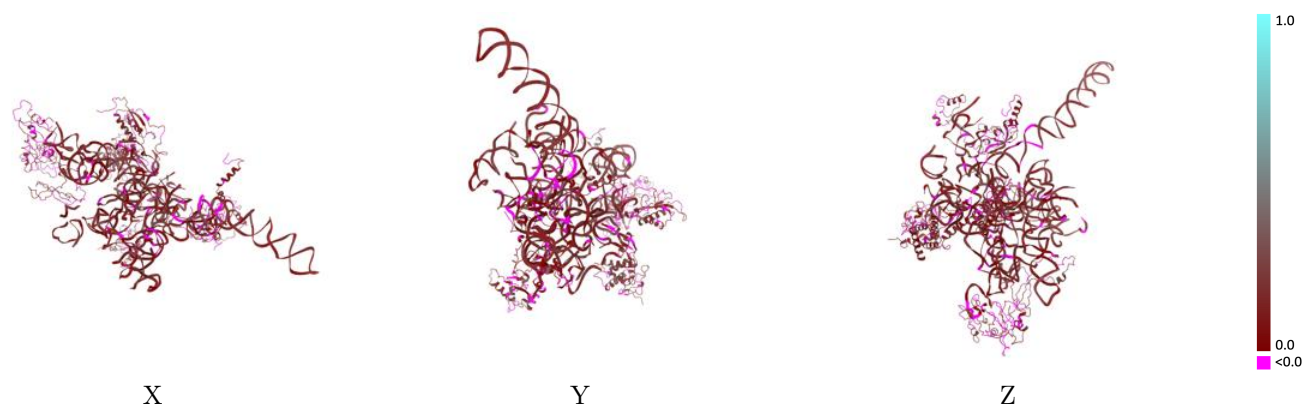
This section contains information regarding the fit between EMDB map EMD-5327 and PDB model 3J0O. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

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



The images above show the 3D surface view of the map at the recommended contour level 1000.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



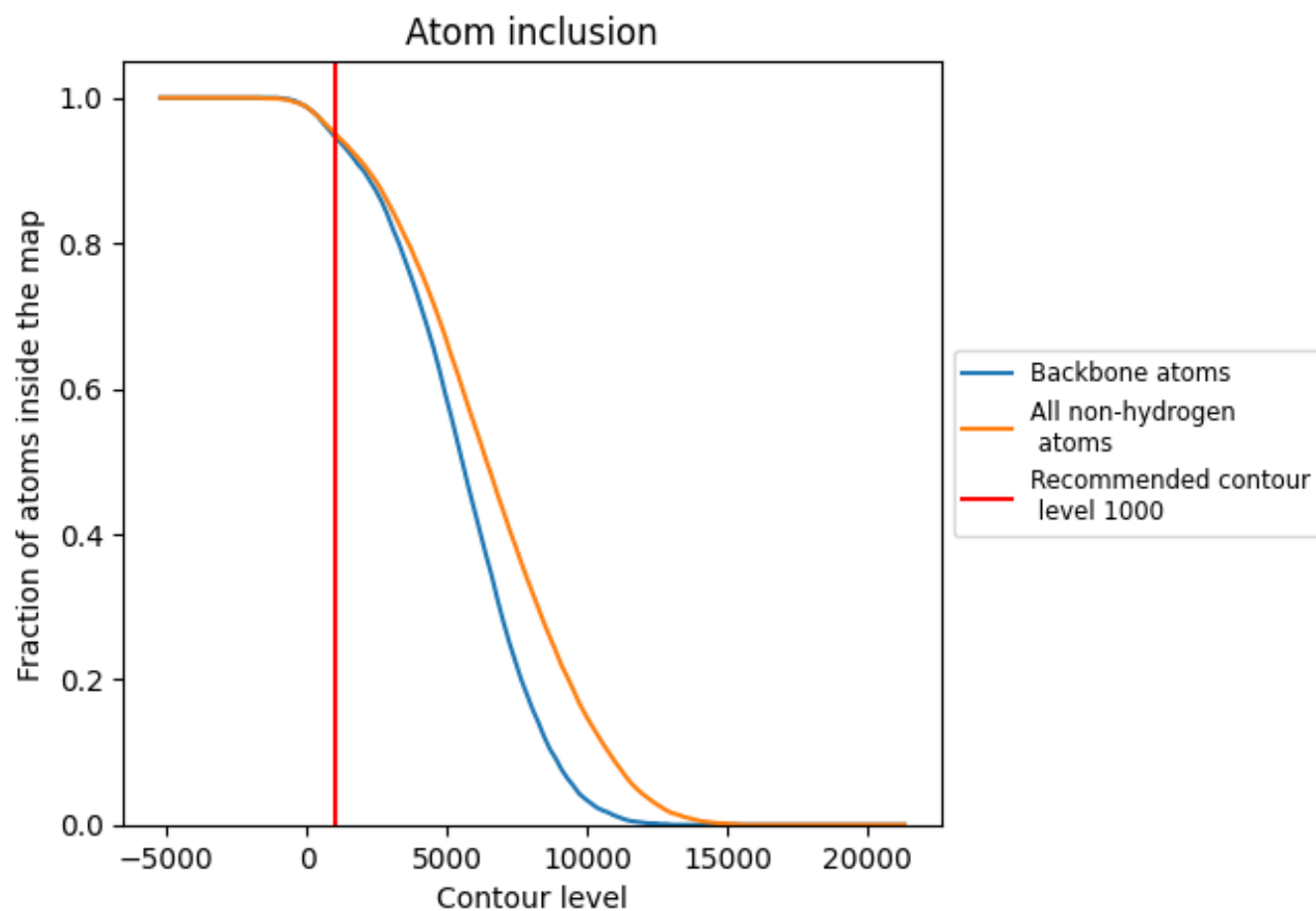
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.



## 9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 95% 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 (1000) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion                                                                             | Q-score                                                                                    |
|-------|--------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|
| All   |  0.9520   |  0.1190   |
| 2     |  0.9840   |  0.1500   |
| 3     |  1.0000   |  0.1050   |
| 4     |  0.9970   |  0.1530   |
| 5     |  1.0000   |  0.1680   |
| 6     |  1.0000   |  0.1770   |
| 7     |  0.9970   |  0.1520   |
| 8     |  0.9930   |  0.1590   |
| B     |  0.8500   |  0.0350   |
| E     |  1.0000   |  0.1290   |
| F     |  0.9910   |  0.1210   |
| G     |  1.0000   |  0.1720   |
| K     |  0.9240   |  0.0840   |
| L     |  0.9110   |  0.0570   |
| S     |  0.9530  |  0.0910  |
| T     |  0.9760 |  0.1050 |
| V     |  0.9630 |  0.1400 |
| W     |  0.9490 |  0.1190 |
| X     |  0.7440 |  0.0440 |
| Y     |  0.8770 |  0.1200 |
| a     |  0.9960 |  0.1350 |
| b     |  0.9960 |  0.1440 |
| c     |  0.9860 |  0.1360 |
| d     |  1.0000 |  0.1320 |
| e     |  1.0000 |  0.1310 |
| f     |  0.9980 |  0.1380 |
| g     |  1.0000 |  0.1320 |
| h     |  0.9450 |  0.1310 |
| v     |  1.0000 |  0.1860 |
| w     |  0.8640 |  0.0260 |
| y     |  1.0000 |  0.0860 |

