



wwPDB EM Validation Summary Report ⓘ

May 25, 2024 – 10:25 am BST

PDB ID : 8QZS
EMDB ID : EMD-18781
Title : Cryo-EM structure of the cross-exon B-like complex
Authors : Zhang, Z.; Kumar, V.; Dybkov, O.; Will, C.L.; Zhong, J.; Ludwig, S.; Urlaub, H.; Kastner, B.; Stark, H.; Luehrmann, R.
Deposited on : 2023-10-29
Resolution : 4.10 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

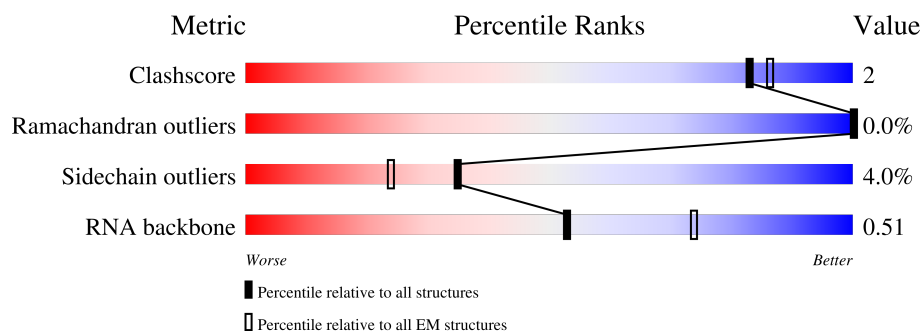
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.10 Å.

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



| Metric | Whole archive (#Entries) | EM structures (#Entries) |
|-----------------------|--------------------------|--------------------------|
| Clashscore | 158937 | 4297 |
| Ramachandran outliers | 154571 | 4023 |
| Sidechain outliers | 154315 | 3826 |
| RNA backbone | 4643 | 859 |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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 | 2335 | 95% . . |
| 2 | B | 2136 | 79% . 21% |
| 3 | 5 | 117 | 48% 32% 13% 7% |
| 4 | 2 | 188 | 32% 16% 48% |
| 5 | 6 | 106 | 32% 16% 8% 44% |
| 6 | 4 | 144 | 54% 38% 6% |
| 7 | C | 972 | 85% 14% |



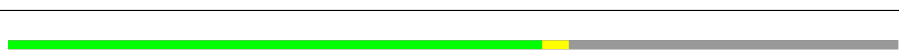
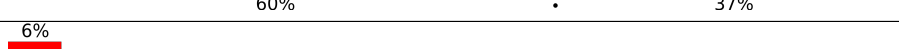





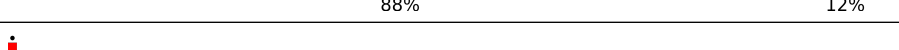
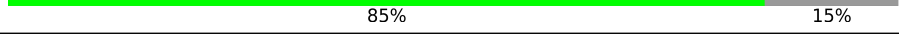
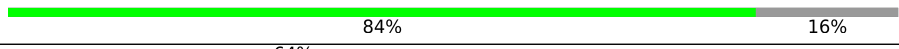
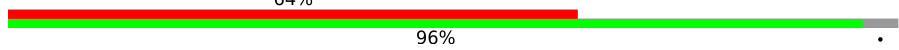
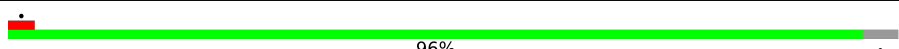







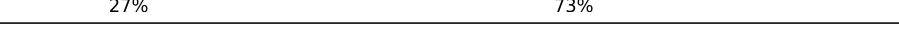



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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 8 | D | 142 | |
| 9 | E | 357 | |
| 10 | I | 312 | |
| 11 | M | 128 | |
| 12 | U | 565 | |
| 13 | W | 177 | |
| 14 | X | 376 | |
| 15 | Z | 15 | |
| 16 | 7 | 793 | |
| 17 | r | 199 | |
| 18 | B4 | 424 | |
| 19 | 8 | 464 | |
| 20 | 9 | 501 | |
| 21 | B2 | 895 | |
| 22 | B5 | 86 | |
| 23 | B3 | 1217 | |
| 24 | BP | 110 | |
| 25 | B1 | 1304 | |
| 26 | B6 | 125 | |
| 27 | 62 | 95 | |
| 28 | 63 | 102 | |
| 29 | 64 | 139 | |
| 30 | 65 | 91 | |
| 31 | 66 | 80 | |
| 32 | 67 | 103 | |

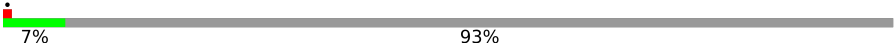
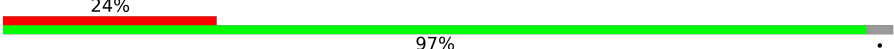
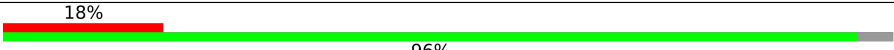


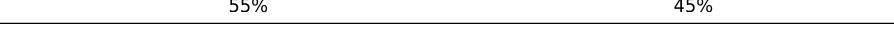
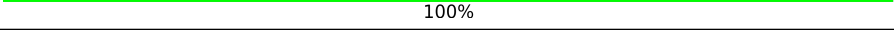

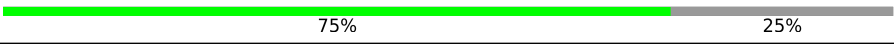


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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 33 | 68 | 96 |  |
| 34 | 22 | 118 |  |
| 34 | 42 | 118 |  |
| 34 | 52 | 118 |  |
| 35 | 2f | 86 |  |
| 35 | 4f | 86 |  |
| 35 | 5f | 86 |  |
| 36 | 2e | 92 |  |
| 36 | 4e | 92 |  |
| 36 | 5e | 92 |  |
| 37 | 2g | 76 |  |
| 37 | 4g | 76 |  |
| 37 | 5g | 76 |  |
| 38 | 23 | 126 |  |
| 38 | 43 | 126 |  |
| 38 | 53 | 126 |  |
| 39 | 2b | 240 |  |
| 39 | 4b | 240 |  |
| 39 | 5b | 240 |  |
| 40 | 21 | 119 |  |
| 40 | 41 | 119 |  |
| 40 | 51 | 119 |  |
| 41 | 2B | 225 |  |
| 42 | 2A | 255 |  |
| 43 | x | 557 |  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 43 | y | 557 |  |
| 44 | v | 513 |  |
| 44 | w | 513 |  |
| 45 | K | 439 |  |
| 46 | z1 | 11 |  |
| 47 | z2 | 4 |  |
| 48 | J | 683 |  |
| 49 | L | 499 |  |
| 50 | F | 522 |  |
| 51 | N | 941 |  |
| 52 | S | 800 |  |

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 86145 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 Pre-mRNA-processing-splicing factor 8.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|---------|-------|
| 1 | A | 2247 | Total | C | N | O | 0 | 0 |
| | | | 11389 | 6895 | 2247 | 2247 | | |

- Molecule 2 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|---------|-------|
| 2 | B | 1693 | Total | C | N | O | 0 | 0 |
| | | | 8538 | 5154 | 1693 | 1691 | | |

- Molecule 3 is a RNA chain called U5 snRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 3 | 5 | 109 | Total | C | N | O | P | 0 | 0 |
| | | | 2296 | 1028 | 383 | 776 | 109 | | |

- Molecule 4 is a RNA chain called U2 snRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 4 | 2 | 98 | Total | C | N | O | P | 0 | 0 |
| | | | 2071 | 926 | 349 | 698 | 98 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|-----------|
| 2 | 97 | A | G | conflict | GB 36516 |

- Molecule 5 is a RNA chain called U6 snRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 5 | 6 | 59 | Total | C | N | O | P | 0 | 0 |
| | | | 1251 | 558 | 230 | 404 | 59 | | |

- Molecule 6 is a RNA chain called U4 snRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 6 | 4 | 136 | Total | C | N | O | P | 0 | 0 |
| | | | 2881 | 1288 | 498 | 959 | 136 | | |

- Molecule 7 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 7 | C | 836 | Total | C | N | O | 0 | 0 |
| | | | 4223 | 2551 | 836 | 836 | | |

- Molecule 8 is a protein called Thioredoxin-like protein 4A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 8 | D | 141 | Total | C | N | O | 0 | 0 |
| | | | 708 | 426 | 141 | 141 | | |

- Molecule 9 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 9 | E | 299 | Total | C | N | O | 0 | 0 |
| | | | 1196 | 598 | 299 | 299 | | |

- Molecule 10 is a protein called Pre-mRNA-splicing factor 38A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 10 | I | 183 | Total | C | N | O | 0 | 0 |
| | | | 920 | 554 | 183 | 183 | | |

- Molecule 11 is a protein called NHP2-like protein 1, N-terminally processed.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 11 | M | 124 | Total | C | N | O | 0 | 0 |
| | | | 627 | 379 | 124 | 124 | | |

- Molecule 12 is a protein called Ubiquitin carboxyl-terminal hydrolase 39.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 12 | U | 456 | Total | C | N | O | 0 | 0 |
| | | | 2308 | 1396 | 456 | 456 | | |

- Molecule 13 is a protein called Peptidyl-prolyl cis-trans isomerase H.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 13 | W | 169 | Total | C | N | O | 0 | 0 |
| | | | 844 | 506 | 169 | 169 | | |

- Molecule 14 is a protein called WW domain-binding protein 4.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 14 | X | 80 | Total | C | N | O | 0 | 0 |
| | | | 403 | 243 | 80 | 80 | | |

- Molecule 15 is a RNA chain called Pre-mRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|-----|----|---------|-------|
| 15 | Z | 15 | Total | C | N | O | P | 0 | 0 |
| | | | 314 | 141 | 51 | 107 | 15 | | |

- Molecule 16 is a protein called Splicing factor 3A subunit 1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 16 | 7 | 204 | Total | C | N | O | 0 | 0 |
| | | | 1028 | 620 | 204 | 204 | | |

- Molecule 17 is a protein called Zinc finger matrin-type protein 2.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 17 | r | 114 | Total | C | N | O | 0 | 0 |
| | | | 568 | 340 | 114 | 114 | | |

- Molecule 18 is a protein called Splicing factor 3B subunit 4.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 18 | B4 | 78 | Total | C | N | O | 0 | 0 |
| | | | 391 | 235 | 78 | 78 | | |

- Molecule 19 is a protein called Splicing factor 3A subunit 2.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 19 | 8 | 144 | Total | C | N | O | 0 | 0 |
| | | | 729 | 441 | 144 | 144 | | |

- Molecule 20 is a protein called Splicing factor 3A subunit 3.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 20 | 9 | 350 | Total | C | N | O | 0 | 0 |
| | | | 1755 | 1055 | 350 | 350 | | |

- Molecule 21 is a protein called Splicing factor 3B subunit 2.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 21 | B2 | 208 | Total | C | N | O | 0 | 0 |
| | | | 1072 | 656 | 208 | 208 | | |

- Molecule 22 is a protein called Splicing factor 3B subunit 5.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 22 | B5 | 69 | Total | C | N | O | 0 | 0 |
| | | | 347 | 209 | 69 | 69 | | |

- Molecule 23 is a protein called Splicing factor 3B subunit 3.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|---------|-------|
| 23 | B3 | 1186 | Total | C | N | O | 0 | 0 |
| | | | 5969 | 3597 | 1186 | 1186 | | |

- Molecule 24 is a protein called PHD finger-like domain-containing protein 5A.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 24 | BP | 100 | Total | C | N | O | 0 | 0 |
| | | | 498 | 298 | 100 | 100 | | |

- Molecule 25 is a protein called Splicing factor 3B subunit 1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 25 | B1 | 870 | Total | C | N | O | 0 | 0 |
| | | | 4383 | 2643 | 870 | 870 | | |

- Molecule 26 is a protein called Splicing factor 3B subunit 6.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 26 | B6 | 90 | Total | C | N | O | 0 | 0 |
| | | | 455 | 275 | 90 | 90 | | |

- Molecule 27 is a protein called U6 snRNA-associated Sm-like protein LSm2.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 27 | 62 | 90 | Total | C | N | O | 0 | 0 |
| | | | 360 | 180 | 90 | 90 | | |

- Molecule 28 is a protein called U6 snRNA-associated Sm-like protein LSm3.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 28 | 63 | 74 | Total | C | N | O | 0 | 0 |
| | | | 296 | 148 | 74 | 74 | | |

- Molecule 29 is a protein called U6 snRNA-associated Sm-like protein LSm4.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 29 | 64 | 74 | Total | C | N | O | 0 | 0 |
| | | | 296 | 148 | 74 | 74 | | |

- Molecule 30 is a protein called U6 snRNA-associated Sm-like protein LSm5.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 30 | 65 | 72 | Total | C | N | O | 0 | 0 |
| | | | 288 | 144 | 72 | 72 | | |

- Molecule 31 is a protein called U6 snRNA-associated Sm-like protein LSm6.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 31 | 66 | 70 | Total | C | N | O | 0 | 0 |
| | | | 280 | 140 | 70 | 70 | | |

- Molecule 32 is a protein called U6 snRNA-associated Sm-like protein LSm7.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 32 | 67 | 65 | Total | C | N | O | 0 | 0 |
| | | | 260 | 130 | 65 | 65 | | |

- Molecule 33 is a protein called U6 snRNA-associated Sm-like protein LSm8.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 33 | 68 | 61 | Total | C | N | O | 0 | 0 |
| | | | 244 | 122 | 61 | 61 | | |

- Molecule 34 is a protein called Small nuclear ribonucleoprotein Sm D2.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 34 | 42 | 74 | Total | C | N | O | 0 | 0 |
| | | | 300 | 152 | 74 | 74 | | |
| 34 | 52 | 98 | Total | C | N | O | S | 0 |
| | | | 796 | 498 | 144 | 148 | 6 | 0 |
| 34 | 22 | 95 | Total | C | N | O | | 0 |
| | | | 482 | 292 | 95 | 95 | | 0 |

- Molecule 35 is a protein called Small nuclear ribonucleoprotein F.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|-----|---------|-------|
| 35 | 4f | 71 | Total | C | N | O | 0 | 0 |
| | | | 292 | 150 | 71 | 71 | | |
| 35 | 5f | 73 | Total | C | N | O | S | 0 |
| | | | 567 | 367 | 94 | 101 | 5 | 0 |
| 35 | 2f | 72 | Total | C | N | O | | 0 |
| | | | 359 | 215 | 72 | 72 | | 0 |

- Molecule 36 is a protein called Small nuclear ribonucleoprotein E.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 36 | 4e | 78 | Total | C | N | O | 0 | 0 |
| | | | 314 | 158 | 78 | 78 | | |
| 36 | 5e | 77 | Total | C | N | O | S | 0 |
| | | | 638 | 405 | 113 | 115 | 5 | 0 |
| 36 | 2e | 81 | Total | C | N | O | | 0 |
| | | | 403 | 241 | 81 | 81 | | 0 |

- Molecule 37 is a protein called Small nuclear ribonucleoprotein G.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 37 | 4g | 73 | Total | C | N | O | 0 | 0 |
| | | | 298 | 152 | 73 | 73 | | |
| 37 | 5g | 74 | Total | C | N | O | S | 0 |
| | | | 577 | 364 | 104 | 103 | 6 | 0 |
| 37 | 2g | 73 | Total | C | N | O | | 0 |
| | | | 364 | 218 | 73 | 73 | | 0 |

- Molecule 38 is a protein called Small nuclear ribonucleoprotein Sm D3.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 38 | 43 | 71 | Total | C | N | O | 0 | 0 |
| | | | 288 | 146 | 71 | 71 | | |

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| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 38 | 53 | 84 | Total | C | N | O | S | 0 | 0 |
| | | | 657 | 412 | 116 | 123 | 6 | | |
| 38 | 23 | 83 | Total | C | N | O | | 0 | 0 |
| | | | 415 | 249 | 83 | 83 | | | |

- Molecule 39 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 39 | 4b | 64 | Total | C | N | O | | 0 | 0 |
| | | | 256 | 128 | 64 | 64 | | | |
| 39 | 5b | 73 | Total | C | N | O | S | 0 | 0 |
| | | | 594 | 376 | 108 | 103 | 7 | | |
| 39 | 2b | 82 | Total | C | N | O | | 0 | 0 |
| | | | 413 | 249 | 82 | 82 | | | |

- Molecule 40 is a protein called Small nuclear ribonucleoprotein Sm D1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 40 | 41 | 82 | Total | C | N | O | | 0 | 0 |
| | | | 334 | 170 | 82 | 82 | | | |
| 40 | 51 | 81 | Total | C | N | O | S | 0 | 0 |
| | | | 641 | 408 | 112 | 118 | 3 | | |
| 40 | 21 | 80 | Total | C | N | O | | 0 | 0 |
| | | | 402 | 242 | 80 | 80 | | | |

- Molecule 41 is a protein called U2 small nuclear ribonucleoprotein B''.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 41 | 2B | 92 | Total | C | N | O | 0 | 0 |
| | | | 461 | 277 | 92 | 92 | | |

- Molecule 42 is a protein called U2 small nuclear ribonucleoprotein A'.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 42 | 2A | 162 | Total | C | N | O | 0 | 0 |
| | | | 816 | 492 | 162 | 162 | | |

- Molecule 43 is a protein called Protein Red.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 43 | x | 39 | Total | C | N | O | 0 | 0 |
| | | | 197 | 119 | 39 | 39 | | |
| 43 | y | 37 | Total | C | N | O | 0 | 0 |
| | | | 187 | 113 | 37 | 37 | | |

- Molecule 44 is a protein called WD40 repeat-containing protein SMU1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 44 | w | 495 | Total | C | N | O | 0 | 0 |
| | | | 2474 | 1484 | 495 | 495 | | |
| 44 | v | 496 | Total | C | N | O | 0 | 0 |
| | | | 2478 | 1486 | 496 | 496 | | |

- Molecule 45 is a protein called Microfibrillar-associated protein 1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 45 | K | 109 | Total | C | N | O | 0 | 0 |
| | | | 543 | 325 | 109 | 109 | | |

- Molecule 46 is a RNA chain called Oligo 1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|----|---------|-------|
| 46 | z1 | 11 | Total | C | N | O | P | 0 | 0 |
| | | | 239 | 107 | 46 | 75 | 11 | | |

- Molecule 47 is a RNA chain called Oligo 2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|---|---------|-------|
| 47 | z2 | 4 | Total | C | N | O | P | 0 | 0 |
| | | | 90 | 40 | 20 | 26 | 4 | | |

- Molecule 48 is a protein called U4/U6 small nuclear ribonucleoprotein Prp3.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 48 | J | 224 | Total | C | N | O | 0 | 0 |
| | | | 1125 | 677 | 224 | 224 | | |

- Molecule 49 is a protein called U4/U6 small nuclear ribonucleoprotein Prp31.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 49 | L | 376 | Total | C | N | O | 0 | 0 |
| | | | 1887 | 1135 | 376 | 376 | | |

- Molecule 50 is a protein called U4/U6 small nuclear ribonucleoprotein Prp4.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 50 | F | 404 | Total | C | N | O | 0 | 0 |
| | | | 2020 | 1212 | 404 | 404 | | |

- Molecule 51 is a protein called Pre-mRNA-processing factor 6.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 51 | N | 831 | Total | C | N | O | 0 | 0 |
| | | | 4192 | 2530 | 831 | 831 | | |

- Molecule 52 is a protein called U4/U6.U5 tri-snRNP-associated protein 1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 52 | S | 171 | Total | C | N | O | 0 | 0 |
| | | | 858 | 516 | 171 | 171 | | |



- MET
THR
GLU
ALA
D5
E61
P62
V128

[illegible]

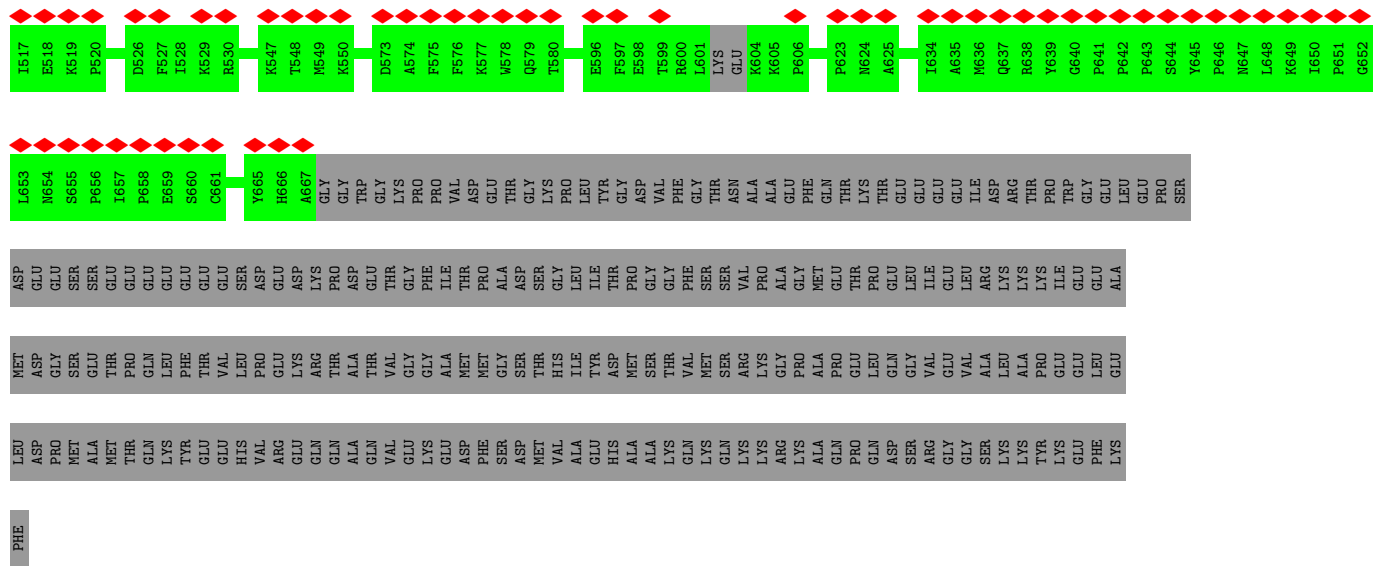
- Molecule 19: Splicing factor 3A subunit 2

[illegible]

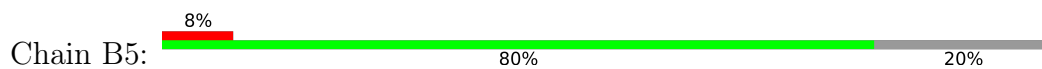
- Molecule 20: Splicing factor 3A subunit 3



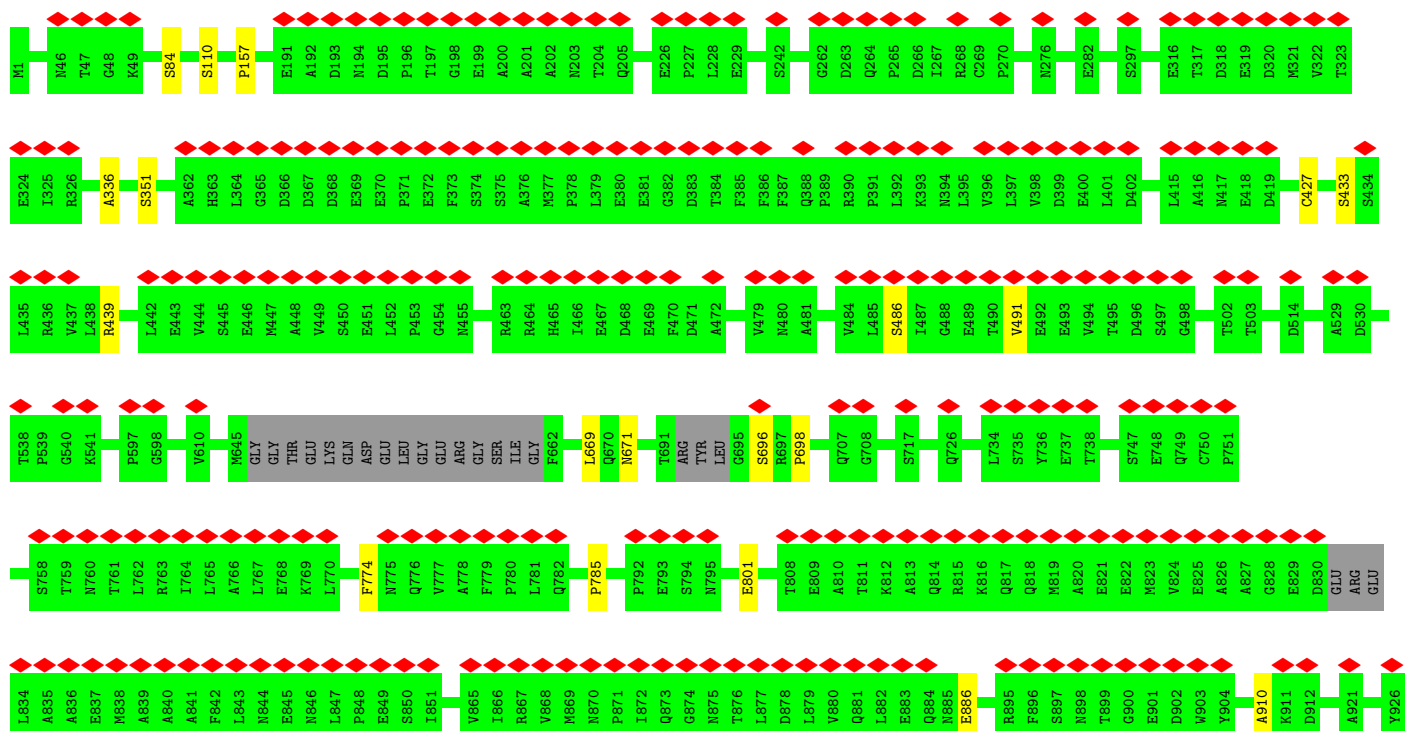
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| M1 | E2 | T3 | I4 | L5 | E6 | Q7 | Q8 | R9 | R10 | V11 | H12 | E13 | E14 | K15 | E16 | R17 | L18 | M19 | D20 | V21 | M22 | A23 | K24 | E25 | M26 | L27 | T28 | K29 | K30 | S31 | L32 | L33 | K34 | D35 | Q36 | Q37 | N38 | S39 | D40 | H41 | R42 | T43 | R44 | A45 | M46 | Q47 | D48 | R49 | Y50 | M51 | E52 | V53 | S54 | E55 | N56 | L57 | R58 | D59 | E60 |
|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|



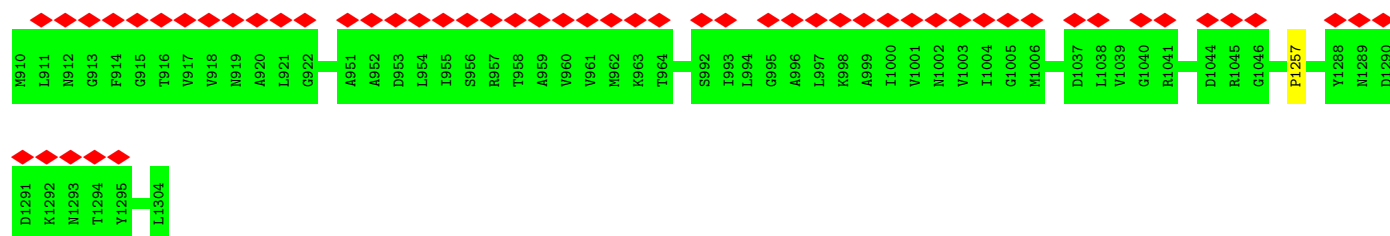
• Molecule 22: Splicing factor 3B subunit 5



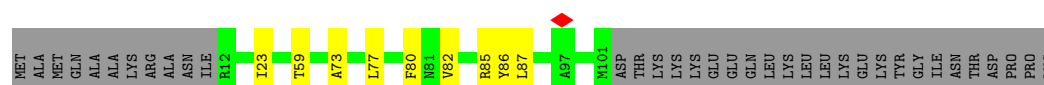
• Molecule 23: Splicing factor 3B subunit 3



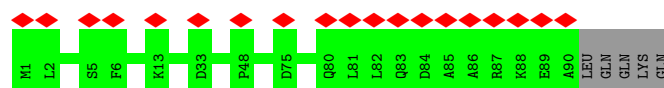




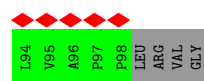
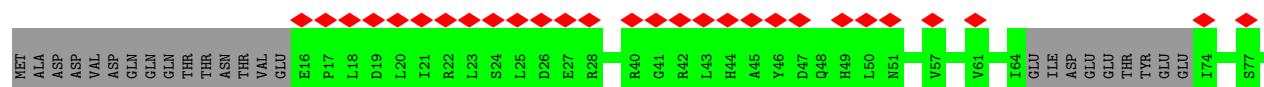
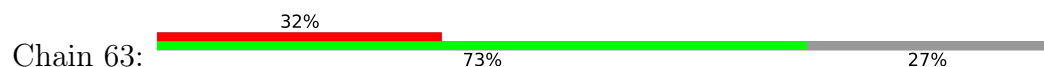
- Molecule 26: Splicing factor 3B subunit 6



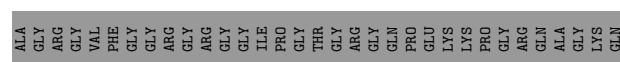
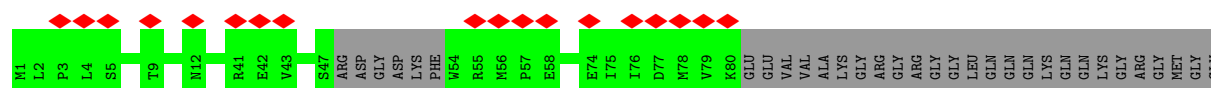
- Molecule 27: U6 snRNA-associated Sm-like protein LSm2



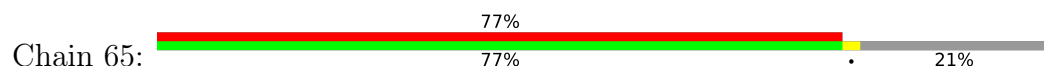
- Molecule 28: U6 snRNA-associated Sm-like protein LSm3

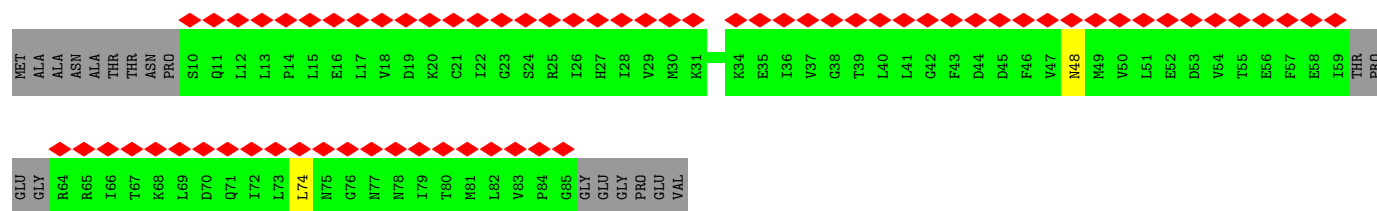


- Molecule 29: U6 snRNA-associated Sm-like protein LSm4

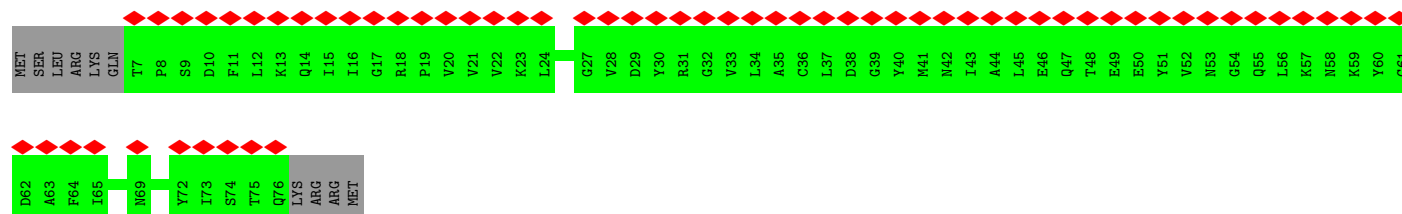
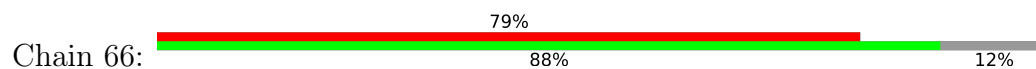


- Molecule 30: U6 snRNA-associated Sm-like protein LSm5

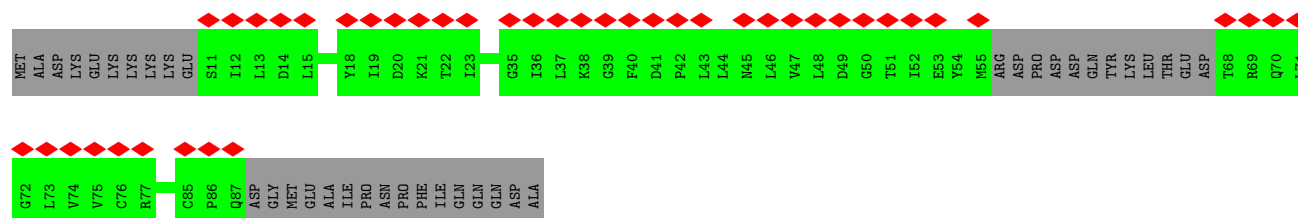
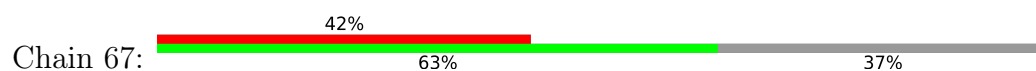




• Molecule 31: U6 snRNA-associated Sm-like protein LSm6



• Molecule 32: U6 snRNA-associated Sm-like protein LSm7



• Molecule 33: U6 snRNA-associated Sm-like protein LSm8



• Molecule 34: Small nuclear ribonucleoprotein Sm D2

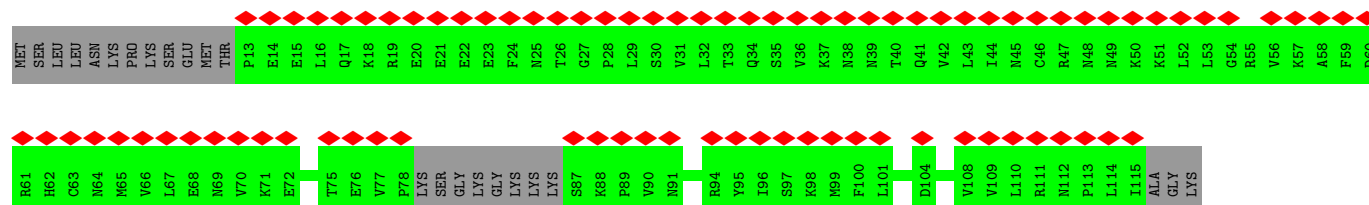
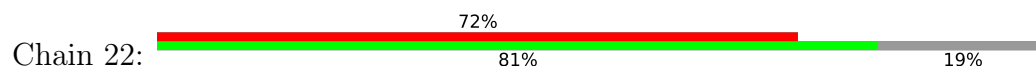


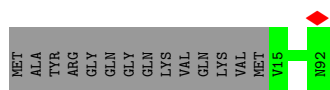
• Molecule 34: Small nuclear ribonucleoprotein Sm D2



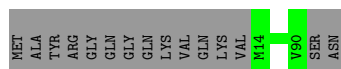
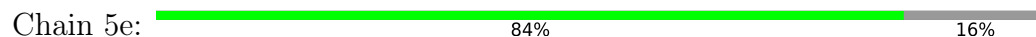


- Molecule 34: Small nuclear ribonucleoprotein Sm D2

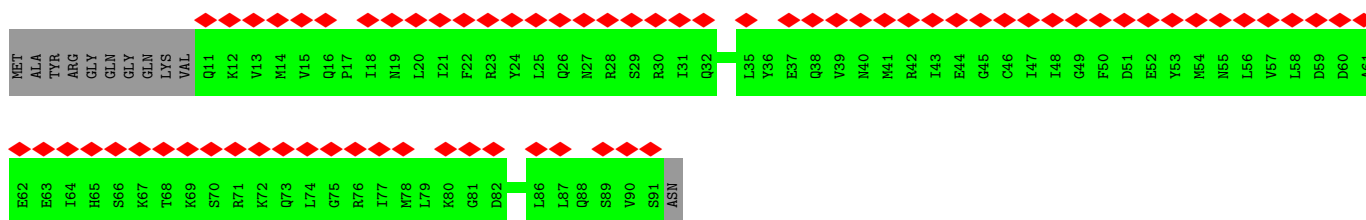
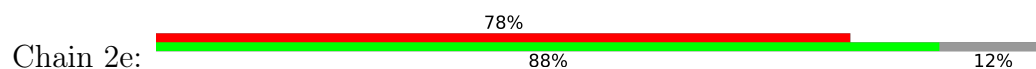




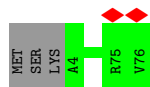
- Molecule 36: Small nuclear ribonucleoprotein E



- Molecule 36: Small nuclear ribonucleoprotein E



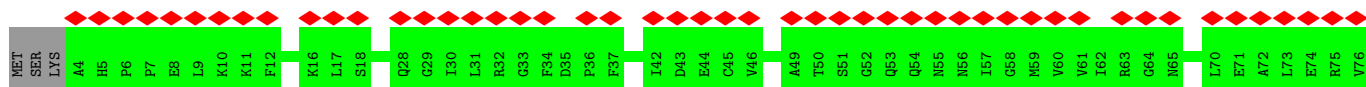
- Molecule 37: Small nuclear ribonucleoprotein G



- Molecule 37: Small nuclear ribonucleoprotein G

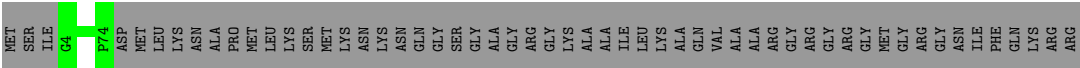


- Molecule 37: Small nuclear ribonucleoprotein G



- Molecule 38: Small nuclear ribonucleoprotein Sm D3

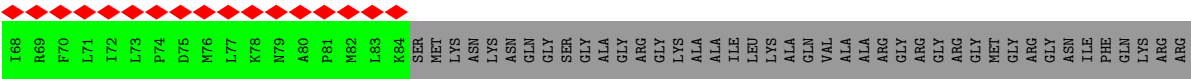
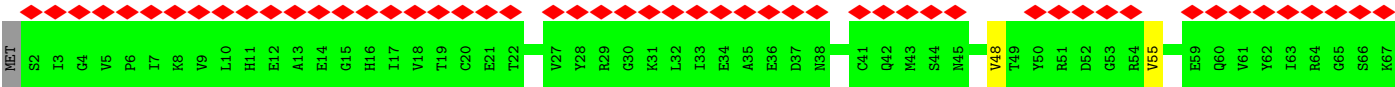




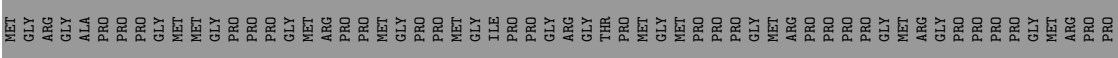
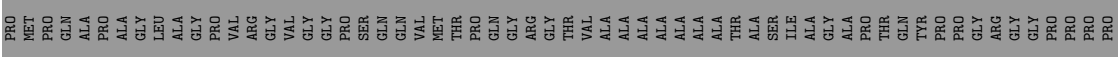
• Molecule 38: Small nuclear ribonucleoprotein Sm D3



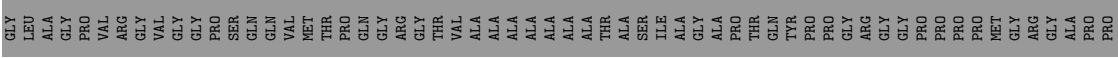
• Molecule 38: Small nuclear ribonucleoprotein Sm D3



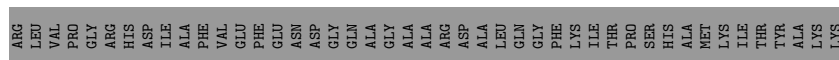
• Molecule 39: Small nuclear ribonucleoprotein-associated proteins B and B'



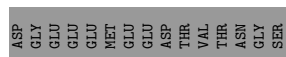
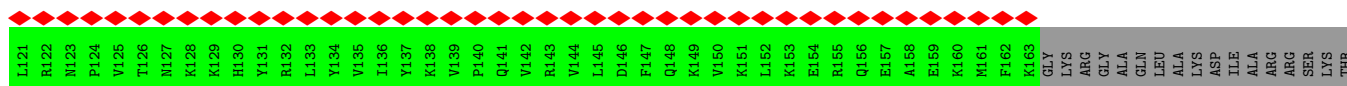
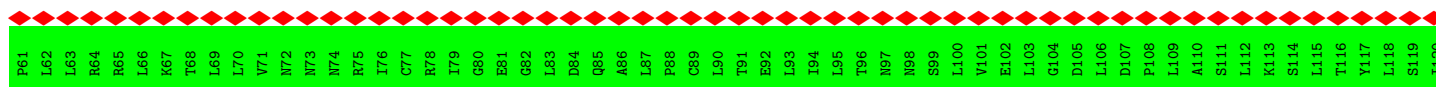
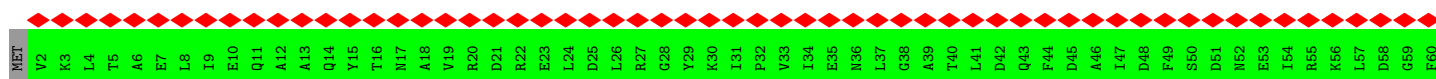
• Molecule 39: Small nuclear ribonucleoprotein-associated proteins B and B'



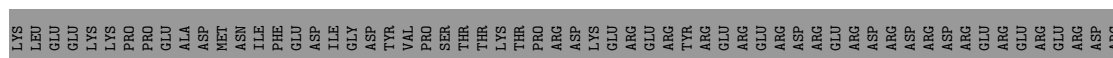
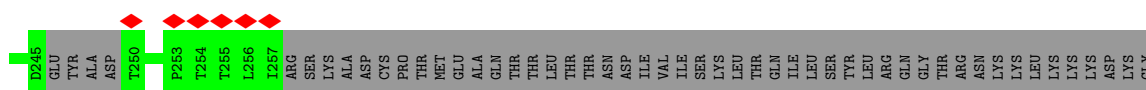
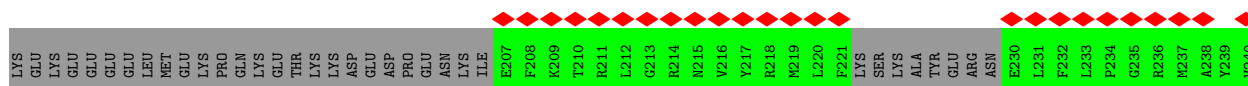
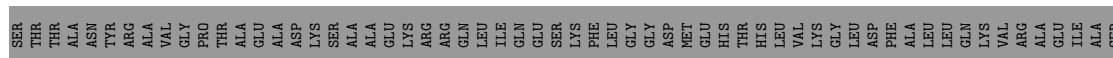
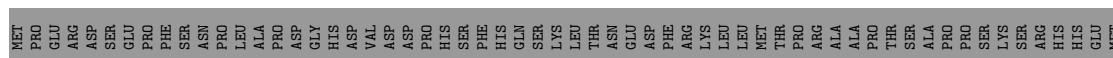
- Chain 2B:
-
- | Category | Percentage |
|----------|------------|
| Red | 41% |
| Green | 40% |
| Grey | 59% |

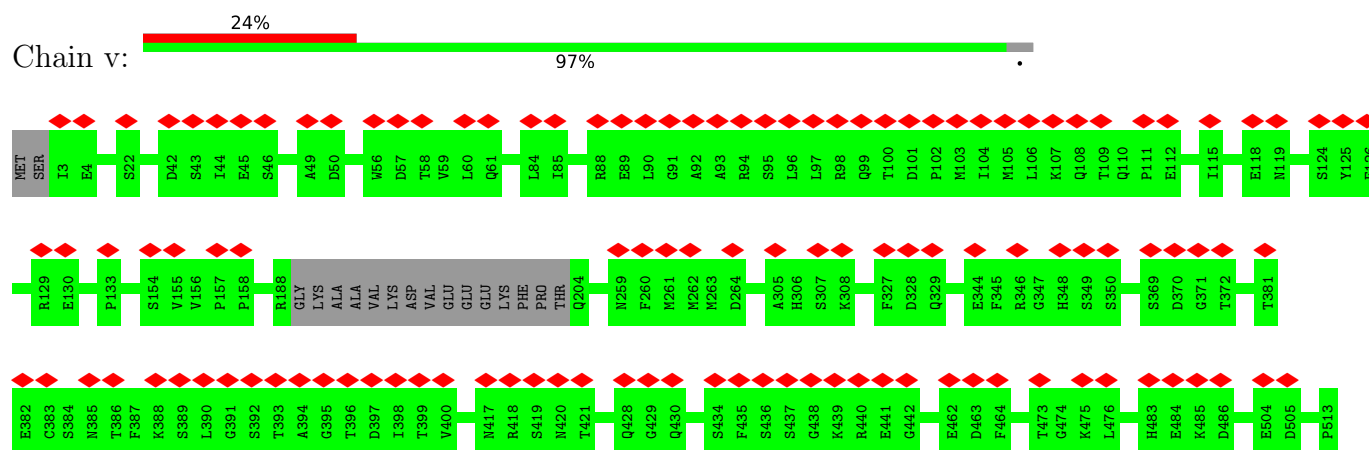


- Molecule 42: U2 small nuclear ribonucleoprotein A'

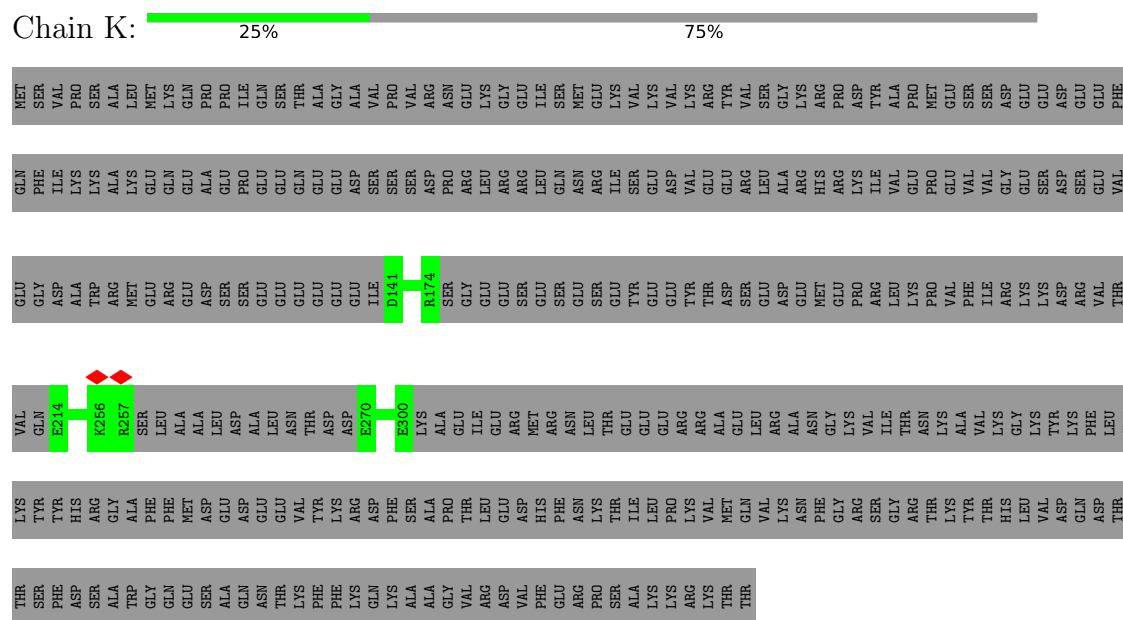


- Molecule 43: Protein Red





- Molecule 45: Microfibrillar-associated protein 1



- Molecule 46: Oligo 1



- Molecule 47: Oligo 2



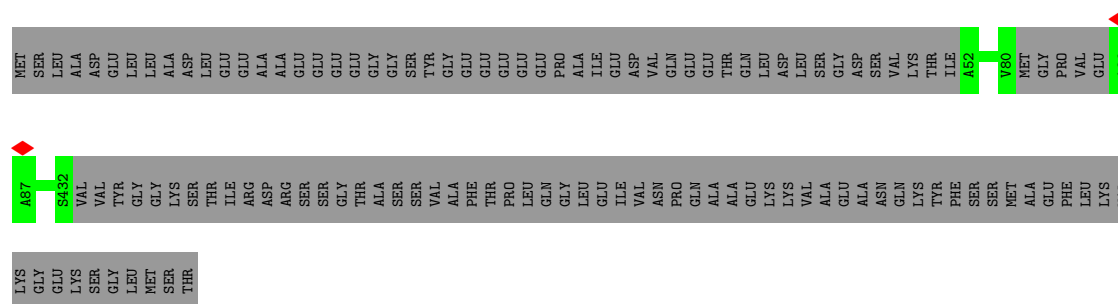
There are no outlier residues recorded for this chain.

- Molecule 48: U4/U6 small nuclear ribonucleoprotein Prp3



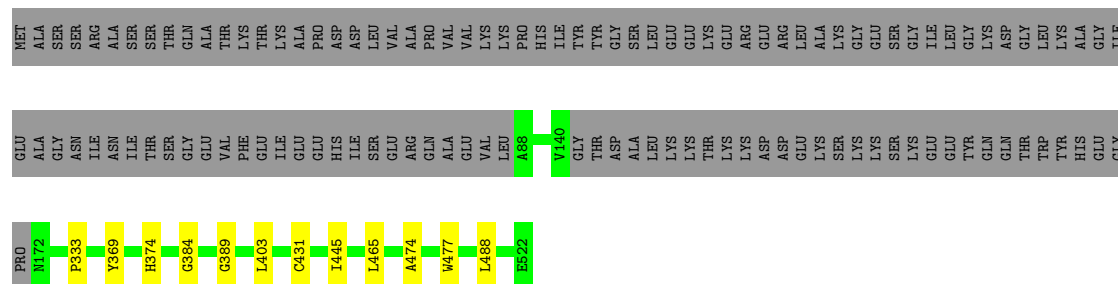
- Molecule 49: U4/U6 small nuclear ribonucleoprotein Prp31

Chain L:  75% 25%

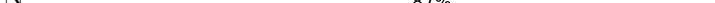


- Molecule 50: U4/U6 small nuclear ribonucleoprotein Prp4

Chain F:  75% • 23%



- Molecule 51: Pre-mRNA-processing factor 6

Chain N:  87% • 12%

4 Experimental information

| Property | Value | Source |
|--------------------------------------|---|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 334084 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 45 | Depositor |
| Minimum defocus (nm) | 1500 | Depositor |
| Maximum defocus (nm) | 5000 | Depositor |
| Magnification | Not provided | |
| Image detector | FEI FALCON III (4k x 4k) | Depositor |
| Maximum map value | 0.088 | Depositor |
| Minimum map value | -0.026 | Depositor |
| Average map value | 0.000 | Depositor |
| Map value standard deviation | 0.004 | Depositor |
| Recommended contour level | 0.011 | Depositor |
| Map size (\AA) | 540.0, 540.0, 540.0 | wwPDB |
| Map dimensions | 400, 400, 400 | wwPDB |
| Map angles ($^\circ$) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (\AA) | 1.35, 1.35, 1.35 | Depositor |

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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 | 0.25 | 0/11512 | 0.42 | 0/16156 |
| 2 | B | 0.25 | 0/8614 | 0.43 | 0/12072 |
| 3 | 5 | 0.35 | 0/2559 | 1.02 | 22/3977 (0.6%) |
| 4 | 2 | 0.32 | 0/2307 | 1.05 | 12/3582 (0.3%) |
| 5 | 6 | 0.31 | 0/1398 | 0.90 | 6/2172 (0.3%) |
| 6 | 4 | 0.25 | 0/3214 | 0.87 | 4/4998 (0.1%) |
| 7 | C | 0.26 | 0/4270 | 0.44 | 0/5983 |
| 8 | D | 0.25 | 0/712 | 0.43 | 0/995 |
| 9 | E | 0.24 | 0/1195 | 0.50 | 0/1492 |
| 10 | I | 0.23 | 0/926 | 0.41 | 0/1295 |
| 11 | M | 0.24 | 0/632 | 0.41 | 0/885 |
| 12 | U | 0.24 | 0/2330 | 0.43 | 0/3268 |
| 13 | W | 0.25 | 0/853 | 0.47 | 0/1188 |
| 14 | X | 0.24 | 0/404 | 0.36 | 0/565 |
| 15 | Z | 0.28 | 0/349 | 1.03 | 0/540 |
| 16 | 7 | 0.24 | 0/1034 | 0.39 | 0/1446 |
| 17 | r | 0.23 | 0/568 | 0.39 | 0/790 |
| 18 | B4 | 0.26 | 0/394 | 0.44 | 0/549 |
| 19 | 8 | 0.24 | 0/734 | 0.46 | 0/1025 |
| 20 | 9 | 0.24 | 0/1762 | 0.38 | 0/2460 |
| 21 | B2 | 0.25 | 0/1092 | 0.43 | 0/1536 |
| 22 | B5 | 0.24 | 0/349 | 0.36 | 0/487 |
| 23 | B3 | 0.26 | 0/6024 | 0.48 | 0/8425 |
| 24 | BP | 0.25 | 0/501 | 0.45 | 0/697 |
| 25 | B1 | 0.25 | 0/4421 | 0.43 | 0/6190 |
| 26 | B6 | 0.31 | 0/459 | 0.43 | 0/642 |
| 27 | 62 | 0.23 | 0/359 | 0.44 | 0/447 |
| 28 | 63 | 0.23 | 0/294 | 0.49 | 0/364 |
| 29 | 64 | 0.23 | 0/294 | 0.45 | 0/364 |
| 30 | 65 | 0.23 | 0/286 | 0.49 | 0/354 |
| 31 | 66 | 0.24 | 0/279 | 0.49 | 0/347 |
| 32 | 67 | 0.24 | 0/258 | 0.51 | 0/319 |
| 33 | 68 | 0.22 | 0/242 | 0.49 | 0/299 |
| 34 | 22 | 0.24 | 0/485 | 0.44 | 0/677 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|---------|-------------|------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 34 | 42 | 0.23 | 0/298 | 0.48 | 0/370 |
| 34 | 52 | 0.43 | 0/805 | 0.71 | 1/1081 (0.1%) |
| 35 | 2f | 0.26 | 0/362 | 0.48 | 0/502 |
| 35 | 4f | 0.24 | 0/291 | 0.52 | 0/363 |
| 35 | 5f | 0.44 | 0/579 | 0.79 | 0/783 |
| 36 | 2e | 0.24 | 0/403 | 0.45 | 0/561 |
| 36 | 4e | 0.22 | 0/313 | 0.51 | 0/390 |
| 36 | 5e | 0.37 | 0/646 | 0.70 | 0/867 |
| 37 | 2g | 0.24 | 0/366 | 0.49 | 0/509 |
| 37 | 4g | 0.25 | 0/297 | 0.53 | 0/371 |
| 37 | 5g | 0.41 | 0/584 | 0.72 | 1/779 (0.1%) |
| 38 | 23 | 0.26 | 0/417 | 0.48 | 0/581 |
| 38 | 43 | 0.24 | 0/287 | 0.51 | 0/358 |
| 38 | 53 | 0.44 | 0/665 | 0.56 | 0/896 |
| 39 | 2b | 0.25 | 0/416 | 0.47 | 0/581 |
| 39 | 4b | 0.22 | 0/254 | 0.50 | 0/314 |
| 39 | 5b | 0.42 | 0/602 | 0.59 | 0/801 |
| 40 | 21 | 0.23 | 0/404 | 0.48 | 0/564 |
| 40 | 41 | 0.22 | 0/333 | 0.48 | 0/416 |
| 40 | 51 | 0.40 | 0/649 | 0.73 | 1/878 (0.1%) |
| 41 | 2B | 0.24 | 0/463 | 0.41 | 0/646 |
| 42 | 2A | 0.24 | 0/821 | 0.46 | 0/1149 |
| 43 | x | 0.43 | 0/196 | 0.47 | 0/270 |
| 43 | y | 0.37 | 0/186 | 0.44 | 0/256 |
| 44 | v | 0.25 | 0/2491 | 0.45 | 0/3477 |
| 44 | w | 0.29 | 0/2486 | 0.46 | 0/3469 |
| 45 | K | 0.22 | 0/540 | 0.28 | 0/750 |
| 46 | z1 | 0.25 | 0/268 | 0.77 | 0/416 |
| 47 | z2 | 0.20 | 0/101 | 0.79 | 0/156 |
| 48 | J | 0.24 | 0/1131 | 0.39 | 0/1580 |
| 49 | L | 0.24 | 0/1899 | 0.38 | 0/2654 |
| 50 | F | 0.24 | 0/2034 | 0.45 | 0/2838 |
| 51 | N | 0.23 | 0/4224 | 0.39 | 0/5915 |
| 52 | S | 0.40 | 0/858 | 0.46 | 0/1191 |
| All | All | 0.27 | 0/87779 | 0.54 | 47/123318 (0.0%) |

There are no bond length outliers.

The worst 5 of 47 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-----------|--------|-------------|----------|
| 5 | 6 | 66 | C | P-O3'-C3' | -10.19 | 107.47 | 119.70 |
| 5 | 6 | 67 | G | P-O3'-C3' | -9.98 | 107.72 | 119.70 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-----------|-------|-------------|----------|
| 3 | 5 | 75 | G | P-O3'-C3' | -9.83 | 107.90 | 119.70 |
| 3 | 5 | 76 | A | P-O3'-C3' | -9.79 | 107.95 | 119.70 |
| 3 | 5 | 115 | C | C2-N1-C1' | 9.67 | 129.44 | 118.80 |

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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 | 11389 | 0 | 5553 | 17 | 0 |
| 2 | B | 8538 | 0 | 4146 | 7 | 0 |
| 3 | 5 | 2296 | 0 | 1163 | 29 | 0 |
| 4 | 2 | 2071 | 0 | 1049 | 11 | 0 |
| 5 | 6 | 1251 | 0 | 630 | 16 | 0 |
| 6 | 4 | 2881 | 0 | 1461 | 15 | 0 |
| 7 | C | 4223 | 0 | 2099 | 9 | 0 |
| 8 | D | 708 | 0 | 328 | 0 | 0 |
| 9 | E | 1196 | 0 | 337 | 0 | 0 |
| 10 | I | 920 | 0 | 433 | 1 | 0 |
| 11 | M | 627 | 0 | 315 | 1 | 0 |
| 12 | U | 2308 | 0 | 1104 | 3 | 0 |
| 13 | W | 844 | 0 | 426 | 9 | 0 |
| 14 | X | 403 | 0 | 200 | 6 | 0 |
| 15 | Z | 314 | 0 | 160 | 1 | 0 |
| 16 | 7 | 1028 | 0 | 487 | 0 | 0 |
| 17 | r | 568 | 0 | 245 | 0 | 0 |
| 18 | B4 | 391 | 0 | 197 | 0 | 0 |
| 19 | 8 | 729 | 0 | 356 | 4 | 0 |
| 20 | 9 | 1755 | 0 | 823 | 1 | 0 |
| 21 | B2 | 1072 | 0 | 563 | 1 | 0 |
| 22 | B5 | 347 | 0 | 171 | 0 | 0 |
| 23 | B3 | 5969 | 0 | 2985 | 14 | 0 |
| 24 | BP | 498 | 0 | 241 | 2 | 0 |
| 25 | B1 | 4383 | 0 | 2195 | 2 | 0 |
| 26 | B6 | 455 | 0 | 227 | 4 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 27 | 62 | 360 | 0 | 95 | 0 | 0 |
| 28 | 63 | 296 | 0 | 76 | 0 | 0 |
| 29 | 64 | 296 | 0 | 77 | 0 | 0 |
| 30 | 65 | 288 | 0 | 78 | 1 | 0 |
| 31 | 66 | 280 | 0 | 81 | 0 | 0 |
| 32 | 67 | 260 | 0 | 75 | 0 | 0 |
| 33 | 68 | 244 | 0 | 71 | 1 | 0 |
| 34 | 22 | 482 | 0 | 220 | 0 | 0 |
| 34 | 42 | 300 | 0 | 80 | 2 | 0 |
| 34 | 52 | 796 | 0 | 821 | 38 | 0 |
| 35 | 2f | 359 | 0 | 179 | 0 | 0 |
| 35 | 4f | 292 | 0 | 93 | 0 | 0 |
| 35 | 5f | 567 | 0 | 575 | 0 | 0 |
| 36 | 2e | 403 | 0 | 173 | 0 | 0 |
| 36 | 4e | 314 | 0 | 86 | 0 | 0 |
| 36 | 5e | 638 | 0 | 657 | 0 | 0 |
| 37 | 2g | 364 | 0 | 176 | 0 | 0 |
| 37 | 4g | 298 | 0 | 89 | 0 | 0 |
| 37 | 5g | 577 | 0 | 603 | 0 | 0 |
| 38 | 23 | 415 | 0 | 198 | 1 | 0 |
| 38 | 43 | 288 | 0 | 84 | 0 | 0 |
| 38 | 53 | 657 | 0 | 675 | 10 | 0 |
| 39 | 2b | 413 | 0 | 194 | 0 | 0 |
| 39 | 4b | 256 | 0 | 70 | 0 | 0 |
| 39 | 5b | 594 | 0 | 615 | 0 | 0 |
| 40 | 21 | 402 | 0 | 184 | 0 | 0 |
| 40 | 41 | 334 | 0 | 92 | 0 | 0 |
| 40 | 51 | 641 | 0 | 681 | 15 | 0 |
| 41 | 2B | 461 | 0 | 218 | 1 | 0 |
| 42 | 2A | 816 | 0 | 386 | 0 | 0 |
| 43 | x | 197 | 0 | 90 | 0 | 0 |
| 43 | y | 187 | 0 | 86 | 0 | 0 |
| 44 | v | 2478 | 0 | 1181 | 0 | 0 |
| 44 | w | 2474 | 0 | 1177 | 0 | 0 |
| 45 | K | 543 | 0 | 238 | 0 | 0 |
| 46 | z1 | 239 | 0 | 119 | 0 | 0 |
| 47 | z2 | 90 | 0 | 45 | 0 | 0 |
| 48 | J | 1125 | 0 | 551 | 1 | 0 |
| 49 | L | 1887 | 0 | 934 | 0 | 0 |
| 50 | F | 2020 | 0 | 1002 | 6 | 0 |
| 51 | N | 4192 | 0 | 2152 | 7 | 0 |
| 52 | S | 858 | 0 | 408 | 2 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| All | All | 86145 | 0 | 43579 | 202 | 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 2.

The worst 5 of 202 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) |
|------------------|-----------------|--------------------------|-------------------|
| 13:W:153:LYS:HA | 14:X:72:ALA:HB2 | 1.20 | 1.10 |
| 7:C:191:PRO:HA | 7:C:197:SER:HA | 1.45 | 0.97 |
| 13:W:153:LYS:CA | 14:X:72:ALA:HB2 | 2.00 | 0.92 |
| 13:W:153:LYS:HA | 14:X:72:ALA:CB | 2.03 | 0.89 |
| 23:B3:886:GLU:HA | 23:B3:910:ALA:O | 1.73 | 0.88 |

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-----------------|------------|---------|----------|-------------|-----|
| 1 | A | 2243/2335 (96%) | 2208 (98%) | 35 (2%) | 0 | 100 | 100 |
| 2 | B | 1691/2136 (79%) | 1643 (97%) | 47 (3%) | 1 (0%) | 51 | 84 |
| 7 | C | 834/972 (86%) | 815 (98%) | 18 (2%) | 1 (0%) | 51 | 84 |
| 8 | D | 139/142 (98%) | 138 (99%) | 1 (1%) | 0 | 100 | 100 |
| 9 | E | 297/357 (83%) | 283 (95%) | 14 (5%) | 0 | 100 | 100 |
| 10 | I | 181/312 (58%) | 176 (97%) | 5 (3%) | 0 | 100 | 100 |
| 11 | M | 122/128 (95%) | 122 (100%) | 0 | 0 | 100 | 100 |
| 12 | U | 454/565 (80%) | 447 (98%) | 7 (2%) | 0 | 100 | 100 |
| 13 | W | 167/177 (94%) | 163 (98%) | 4 (2%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-----------------|------------|---------|----------|-------------|-----|
| 14 | X | 78/376 (21%) | 78 (100%) | 0 | 0 | 100 | 100 |
| 16 | 7 | 200/793 (25%) | 197 (98%) | 3 (2%) | 0 | 100 | 100 |
| 17 | r | 110/199 (55%) | 109 (99%) | 1 (1%) | 0 | 100 | 100 |
| 18 | B4 | 76/424 (18%) | 76 (100%) | 0 | 0 | 100 | 100 |
| 19 | 8 | 138/464 (30%) | 136 (99%) | 2 (1%) | 0 | 100 | 100 |
| 20 | 9 | 344/501 (69%) | 336 (98%) | 8 (2%) | 0 | 100 | 100 |
| 21 | B2 | 204/895 (23%) | 200 (98%) | 4 (2%) | 0 | 100 | 100 |
| 22 | B5 | 67/86 (78%) | 66 (98%) | 1 (2%) | 0 | 100 | 100 |
| 23 | B3 | 1176/1217 (97%) | 1131 (96%) | 45 (4%) | 0 | 100 | 100 |
| 24 | BP | 98/110 (89%) | 96 (98%) | 2 (2%) | 0 | 100 | 100 |
| 25 | B1 | 866/1304 (66%) | 840 (97%) | 26 (3%) | 0 | 100 | 100 |
| 26 | B6 | 88/125 (70%) | 86 (98%) | 1 (1%) | 1 (1%) | 14 | 50 |
| 27 | 62 | 88/95 (93%) | 84 (96%) | 4 (4%) | 0 | 100 | 100 |
| 28 | 63 | 70/102 (69%) | 66 (94%) | 4 (6%) | 0 | 100 | 100 |
| 29 | 64 | 70/139 (50%) | 66 (94%) | 4 (6%) | 0 | 100 | 100 |
| 30 | 65 | 68/91 (75%) | 64 (94%) | 4 (6%) | 0 | 100 | 100 |
| 31 | 66 | 68/80 (85%) | 63 (93%) | 5 (7%) | 0 | 100 | 100 |
| 32 | 67 | 61/103 (59%) | 59 (97%) | 2 (3%) | 0 | 100 | 100 |
| 33 | 68 | 57/96 (59%) | 55 (96%) | 2 (4%) | 0 | 100 | 100 |
| 34 | 22 | 91/118 (77%) | 90 (99%) | 1 (1%) | 0 | 100 | 100 |
| 34 | 42 | 70/118 (59%) | 67 (96%) | 3 (4%) | 0 | 100 | 100 |
| 34 | 52 | 94/118 (80%) | 86 (92%) | 6 (6%) | 2 (2%) | 7 | 38 |
| 35 | 2f | 70/86 (81%) | 68 (97%) | 2 (3%) | 0 | 100 | 100 |
| 35 | 4f | 69/86 (80%) | 66 (96%) | 3 (4%) | 0 | 100 | 100 |
| 35 | 5f | 71/86 (83%) | 64 (90%) | 7 (10%) | 0 | 100 | 100 |
| 36 | 2e | 79/92 (86%) | 79 (100%) | 0 | 0 | 100 | 100 |
| 36 | 4e | 76/92 (83%) | 75 (99%) | 1 (1%) | 0 | 100 | 100 |
| 36 | 5e | 75/92 (82%) | 72 (96%) | 3 (4%) | 0 | 100 | 100 |
| 37 | 2g | 71/76 (93%) | 70 (99%) | 1 (1%) | 0 | 100 | 100 |
| 37 | 4g | 71/76 (93%) | 65 (92%) | 6 (8%) | 0 | 100 | 100 |
| 37 | 5g | 72/76 (95%) | 66 (92%) | 6 (8%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-------------------|-------------|----------|----------|-------------|-----|
| 38 | 23 | 81/126 (64%) | 79 (98%) | 2 (2%) | 0 | 100 | 100 |
| 38 | 43 | 69/126 (55%) | 68 (99%) | 1 (1%) | 0 | 100 | 100 |
| 38 | 53 | 82/126 (65%) | 77 (94%) | 5 (6%) | 0 | 100 | 100 |
| 39 | 2b | 80/240 (33%) | 80 (100%) | 0 | 0 | 100 | 100 |
| 39 | 4b | 60/240 (25%) | 58 (97%) | 2 (3%) | 0 | 100 | 100 |
| 39 | 5b | 69/240 (29%) | 67 (97%) | 2 (3%) | 0 | 100 | 100 |
| 40 | 21 | 78/119 (66%) | 76 (97%) | 2 (3%) | 0 | 100 | 100 |
| 40 | 41 | 80/119 (67%) | 78 (98%) | 2 (2%) | 0 | 100 | 100 |
| 40 | 51 | 79/119 (66%) | 75 (95%) | 4 (5%) | 0 | 100 | 100 |
| 41 | 2B | 90/225 (40%) | 90 (100%) | 0 | 0 | 100 | 100 |
| 42 | 2A | 160/255 (63%) | 157 (98%) | 3 (2%) | 0 | 100 | 100 |
| 43 | x | 33/557 (6%) | 29 (88%) | 4 (12%) | 0 | 100 | 100 |
| 43 | y | 31/557 (6%) | 28 (90%) | 3 (10%) | 0 | 100 | 100 |
| 44 | v | 492/513 (96%) | 484 (98%) | 8 (2%) | 0 | 100 | 100 |
| 44 | w | 489/513 (95%) | 478 (98%) | 10 (2%) | 1 (0%) | 47 | 80 |
| 45 | K | 103/439 (24%) | 103 (100%) | 0 | 0 | 100 | 100 |
| 48 | J | 220/683 (32%) | 217 (99%) | 3 (1%) | 0 | 100 | 100 |
| 49 | L | 372/499 (74%) | 364 (98%) | 8 (2%) | 0 | 100 | 100 |
| 50 | F | 400/522 (77%) | 386 (96%) | 14 (4%) | 0 | 100 | 100 |
| 51 | N | 823/941 (88%) | 799 (97%) | 24 (3%) | 0 | 100 | 100 |
| 52 | S | 161/800 (20%) | 160 (99%) | 1 (1%) | 0 | 100 | 100 |
| All | All | 15016/23399 (64%) | 14624 (97%) | 386 (3%) | 6 (0%) | 100 | 100 |

5 of 6 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 34 | 52 | 49 | ASN |
| 34 | 52 | 91 | ASN |
| 44 | w | 177 | LEU |
| 2 | B | 1292 | PRO |
| 7 | C | 199 | LEU |

5.3.2 Protein sidechains ⓘ

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

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|---------------|------------|----------|-------------|-----|
| 1 | A | 125/2108 (6%) | 125 (100%) | 0 | 100 | 100 |
| 2 | B | 77/1908 (4%) | 77 (100%) | 0 | 100 | 100 |
| 7 | C | 48/866 (6%) | 48 (100%) | 0 | 100 | 100 |
| 8 | D | 5/130 (4%) | 5 (100%) | 0 | 100 | 100 |
| 10 | I | 7/293 (2%) | 7 (100%) | 0 | 100 | 100 |
| 11 | M | 6/111 (5%) | 6 (100%) | 0 | 100 | 100 |
| 12 | U | 23/511 (4%) | 23 (100%) | 0 | 100 | 100 |
| 13 | W | 10/148 (7%) | 10 (100%) | 0 | 100 | 100 |
| 14 | X | 2/333 (1%) | 2 (100%) | 0 | 100 | 100 |
| 16 | 7 | 8/709 (1%) | 8 (100%) | 0 | 100 | 100 |
| 17 | r | 2/181 (1%) | 2 (100%) | 0 | 100 | 100 |
| 18 | B4 | 4/336 (1%) | 4 (100%) | 0 | 100 | 100 |
| 19 | 8 | 8/382 (2%) | 8 (100%) | 0 | 100 | 100 |
| 20 | 9 | 10/446 (2%) | 10 (100%) | 0 | 100 | 100 |
| 21 | B2 | 22/776 (3%) | 22 (100%) | 0 | 100 | 100 |
| 22 | B5 | 3/77 (4%) | 3 (100%) | 0 | 100 | 100 |
| 23 | B3 | 60/1051 (6%) | 60 (100%) | 0 | 100 | 100 |
| 24 | BP | 4/95 (4%) | 4 (100%) | 0 | 100 | 100 |
| 25 | B1 | 40/1104 (4%) | 40 (100%) | 0 | 100 | 100 |
| 26 | B6 | 5/109 (5%) | 5 (100%) | 0 | 100 | 100 |
| 34 | 22 | 5/110 (4%) | 5 (100%) | 0 | 100 | 100 |
| 34 | 52 | 93/110 (84%) | 91 (98%) | 2 (2%) | 52 | 71 |
| 35 | 2f | 4/74 (5%) | 4 (100%) | 0 | 100 | 100 |
| 35 | 5f | 61/74 (82%) | 59 (97%) | 2 (3%) | 38 | 62 |
| 36 | 2e | 1/84 (1%) | 1 (100%) | 0 | 100 | 100 |
| 36 | 5e | 72/84 (86%) | 72 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-----------------|------------|----------|-------------|-----|
| 37 | 2g | 3/66 (4%) | 3 (100%) | 0 | 100 | 100 |
| 37 | 5g | 64/66 (97%) | 46 (72%) | 18 (28%) | 0 | 3 |
| 38 | 23 | 3/101 (3%) | 3 (100%) | 0 | 100 | 100 |
| 38 | 53 | 73/101 (72%) | 73 (100%) | 0 | 100 | 100 |
| 39 | 2b | 4/177 (2%) | 4 (100%) | 0 | 100 | 100 |
| 39 | 5b | 67/177 (38%) | 65 (97%) | 2 (3%) | 41 | 64 |
| 40 | 21 | 3/101 (3%) | 3 (100%) | 0 | 100 | 100 |
| 40 | 51 | 76/101 (75%) | 55 (72%) | 21 (28%) | 0 | 3 |
| 41 | 2B | 3/195 (2%) | 3 (100%) | 0 | 100 | 100 |
| 42 | 2A | 6/218 (3%) | 6 (100%) | 0 | 100 | 100 |
| 43 | x | 2/498 (0%) | 2 (100%) | 0 | 100 | 100 |
| 43 | y | 2/498 (0%) | 2 (100%) | 0 | 100 | 100 |
| 44 | v | 15/450 (3%) | 15 (100%) | 0 | 100 | 100 |
| 44 | w | 15/450 (3%) | 15 (100%) | 0 | 100 | 100 |
| 48 | J | 8/599 (1%) | 8 (100%) | 0 | 100 | 100 |
| 49 | L | 14/424 (3%) | 14 (100%) | 0 | 100 | 100 |
| 50 | F | 16/442 (4%) | 16 (100%) | 0 | 100 | 100 |
| 51 | N | 36/792 (4%) | 36 (100%) | 0 | 100 | 100 |
| 52 | S | 5/681 (1%) | 5 (100%) | 0 | 100 | 100 |
| All | All | 1120/18347 (6%) | 1075 (96%) | 45 (4%) | 35 | 57 |

5 of 45 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 37 | 5g | 10 | LYS |
| 37 | 5g | 46 | VAL |
| 37 | 5g | 11 | LYS |
| 37 | 5g | 35 | ASP |
| 37 | 5g | 50 | THR |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 40 | 51 | 64 | ASN |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 39 | 5b | 22 | GLN |
| 37 | 5g | 55 | ASN |
| 37 | 5g | 5 | HIS |
| 37 | 5g | 26 | HIS |

5.3.3 RNA ⓘ

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|---------------|-------------------|-----------------|
| 15 | Z | 14/15 (93%) | 1 (7%) | 0 |
| 3 | 5 | 107/117 (91%) | 34 (31%) | 3 (2%) |
| 4 | 2 | 94/188 (50%) | 18 (19%) | 4 (4%) |
| 46 | z1 | 10/11 (90%) | 5 (50%) | 0 |
| 47 | z2 | 3/4 (75%) | 0 | 0 |
| 5 | 6 | 55/106 (51%) | 11 (20%) | 3 (5%) |
| 6 | 4 | 133/144 (92%) | 39 (29%) | 0 |
| All | All | 416/585 (71%) | 108 (25%) | 10 (2%) |

5 of 108 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 3 | 5 | 8 | G |
| 3 | 5 | 9 | G |
| 3 | 5 | 10 | U |
| 3 | 5 | 20 | G |
| 3 | 5 | 21 | A |

5 of 10 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 5 | 6 | 45 | A |
| 5 | 6 | 51 | U |
| 5 | 6 | 77 | C |
| 4 | 2 | 37 | U |
| 4 | 2 | 46 | U |

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides 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.

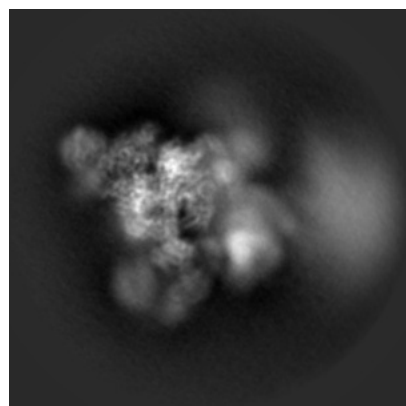
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18781. These allow visual inspection of the internal detail of the map and identification of artifacts.

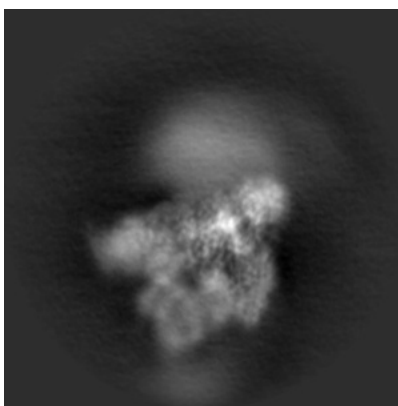
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

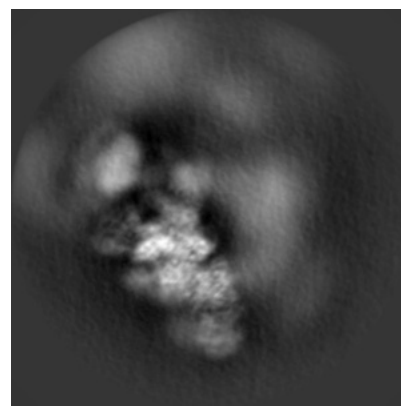
6.1.1 Primary map



X

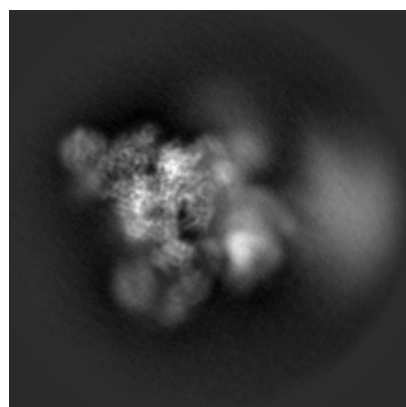


Y

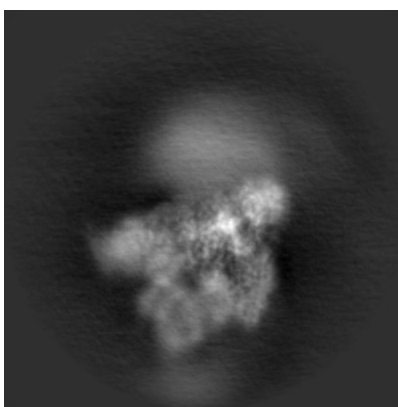


Z

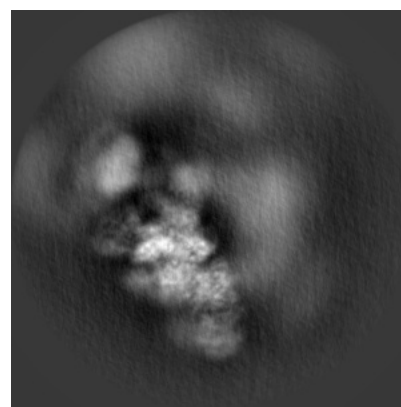
6.1.2 Raw map



X



Y

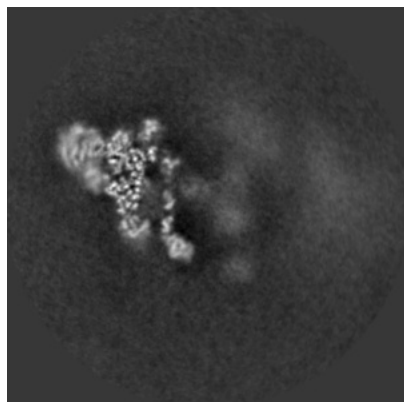


Z

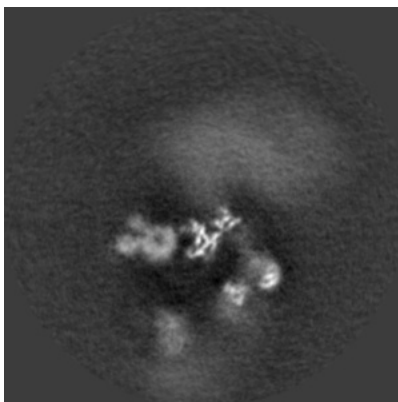
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

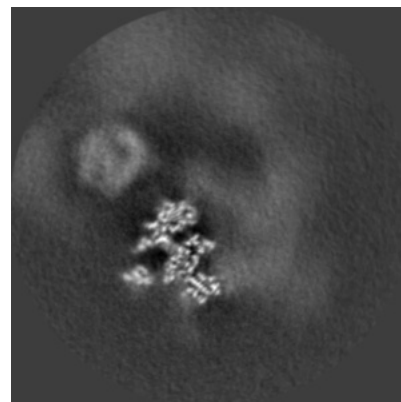
6.2.1 Primary map



X Index: 200

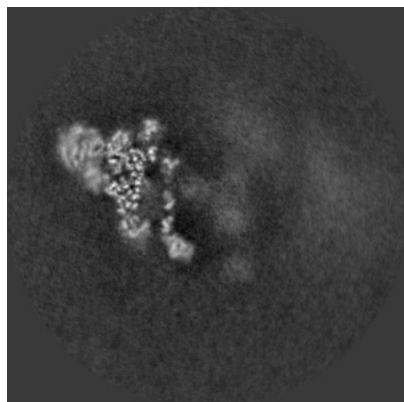


Y Index: 200

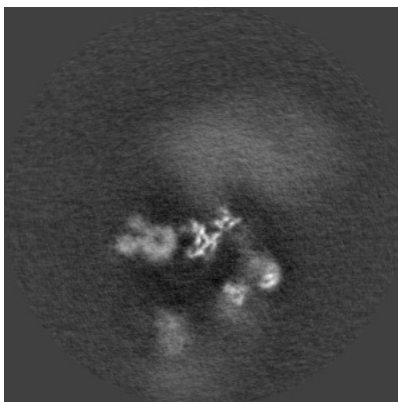


Z Index: 200

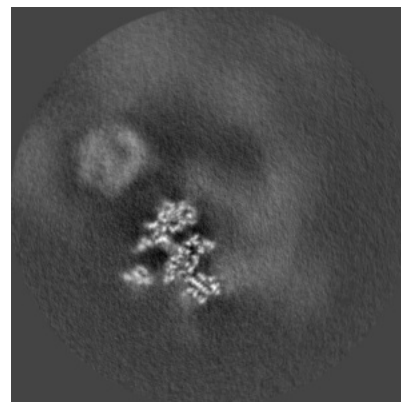
6.2.2 Raw map



X Index: 200



Y Index: 200

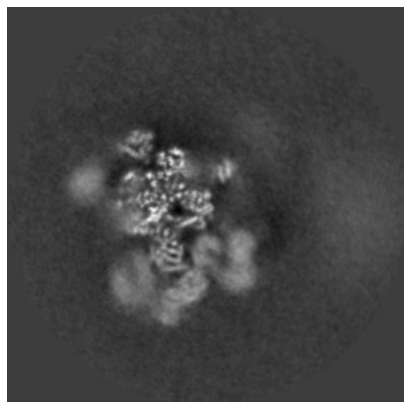


Z Index: 200

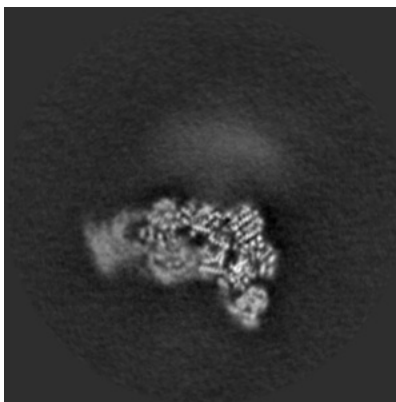
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

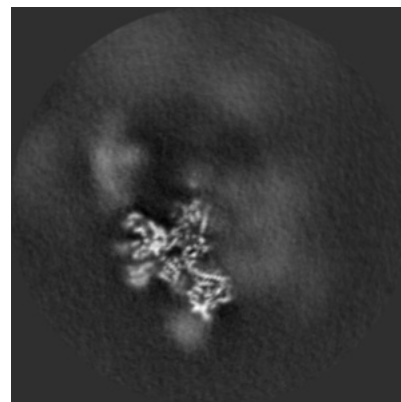
6.3.1 Primary map



X Index: 171

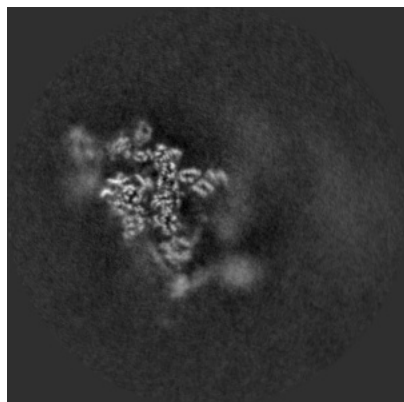


Y Index: 164

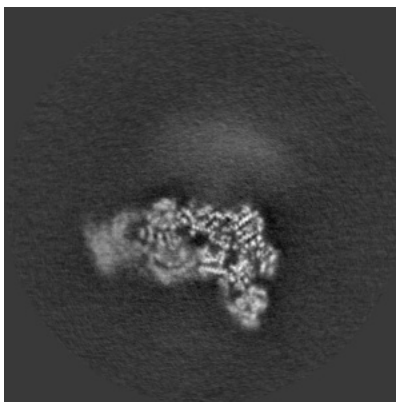


Z Index: 216

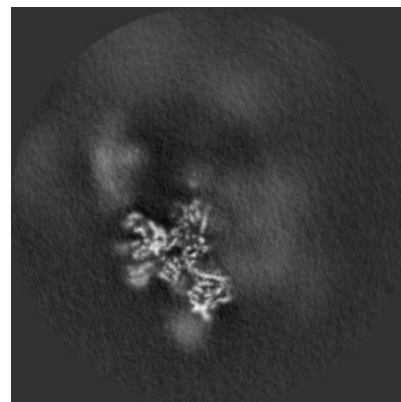
6.3.2 Raw map



X Index: 187



Y Index: 165

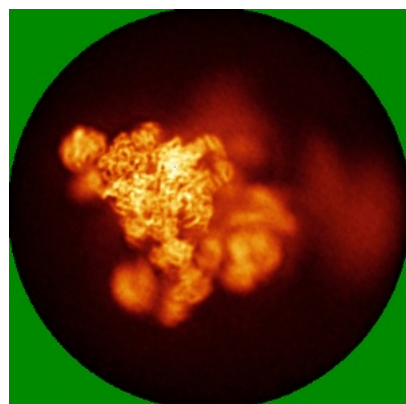


Z Index: 216

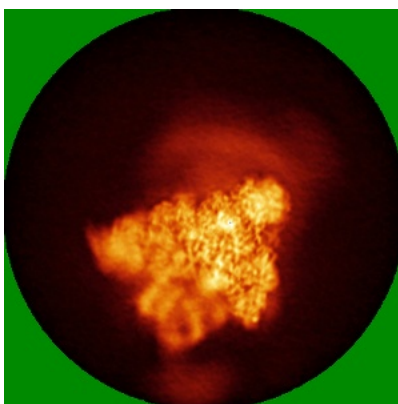
The images above show the largest variance slices of the map in three orthogonal directions.

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

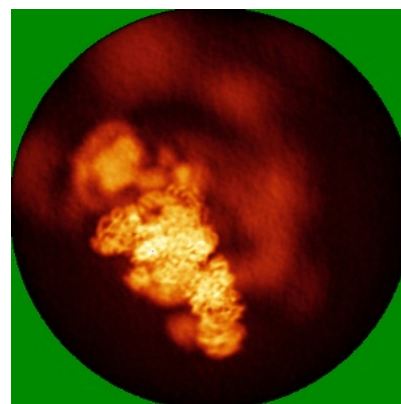
6.4.1 Primary map



X

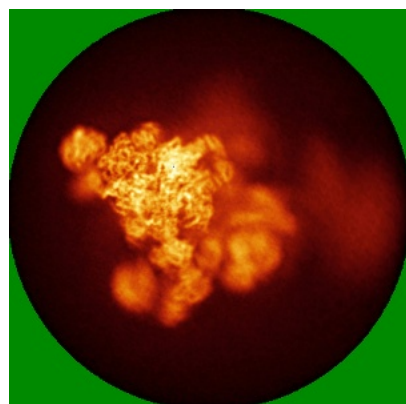


Y

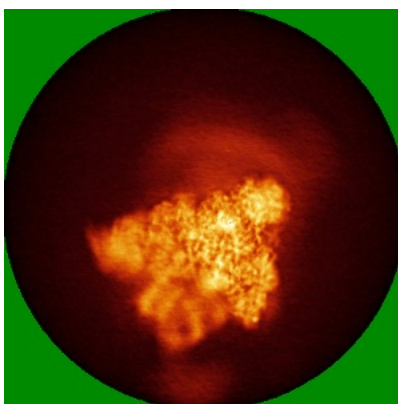


Z

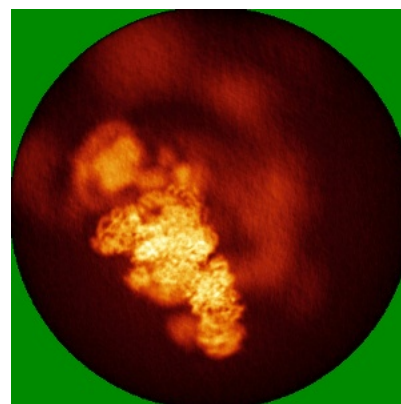
6.4.2 Raw map



X



Y

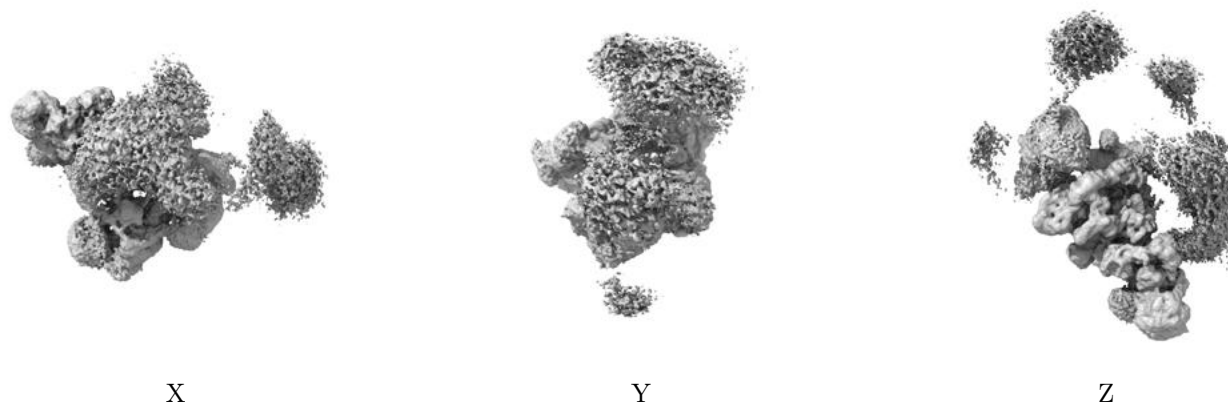


Z

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.

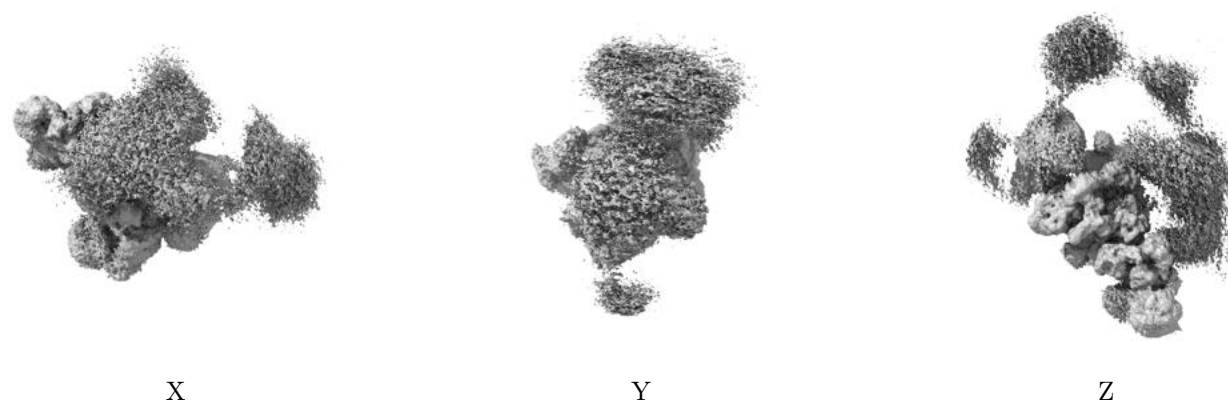
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.011. 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.

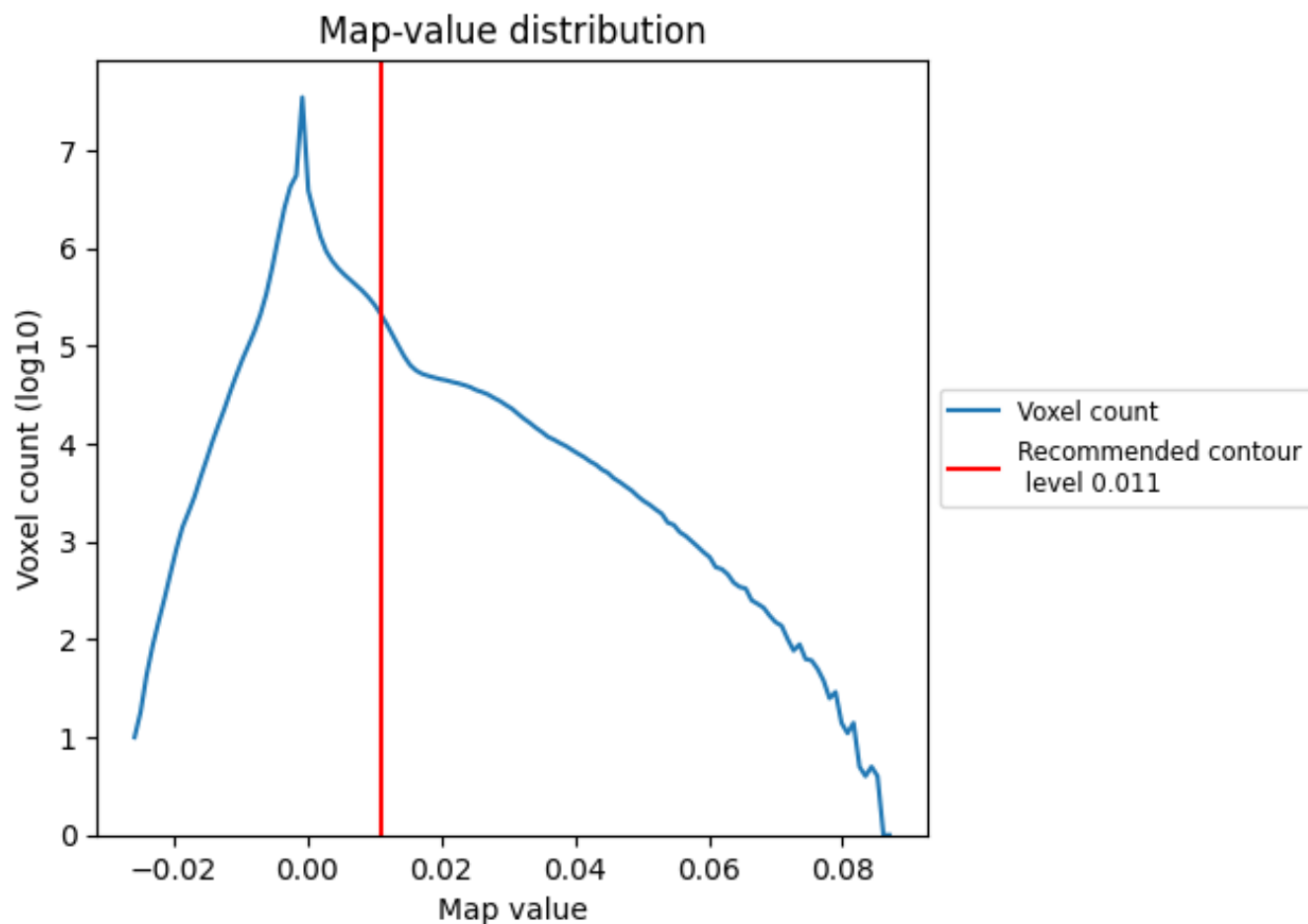
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

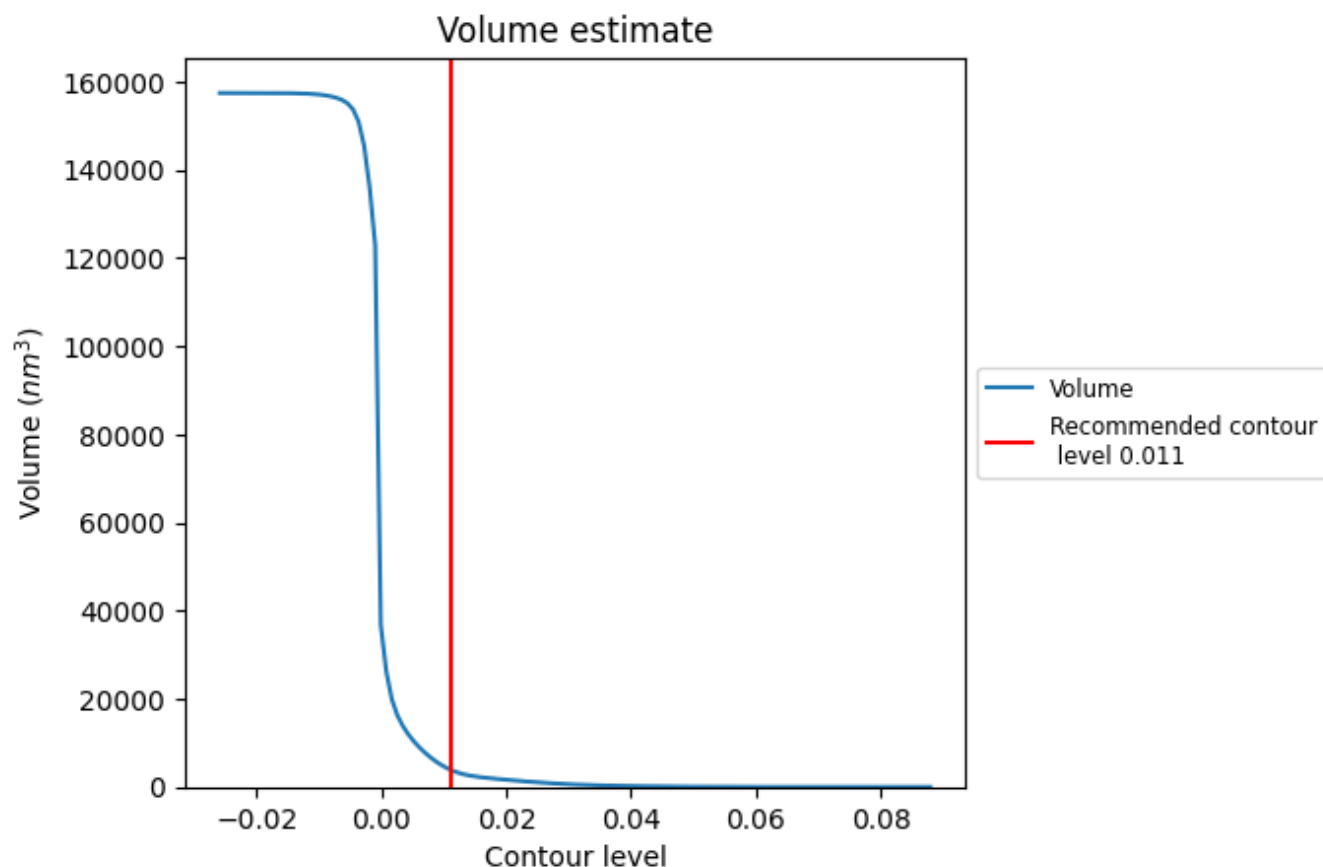
This section contains the results of statistical analysis of the map.

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.

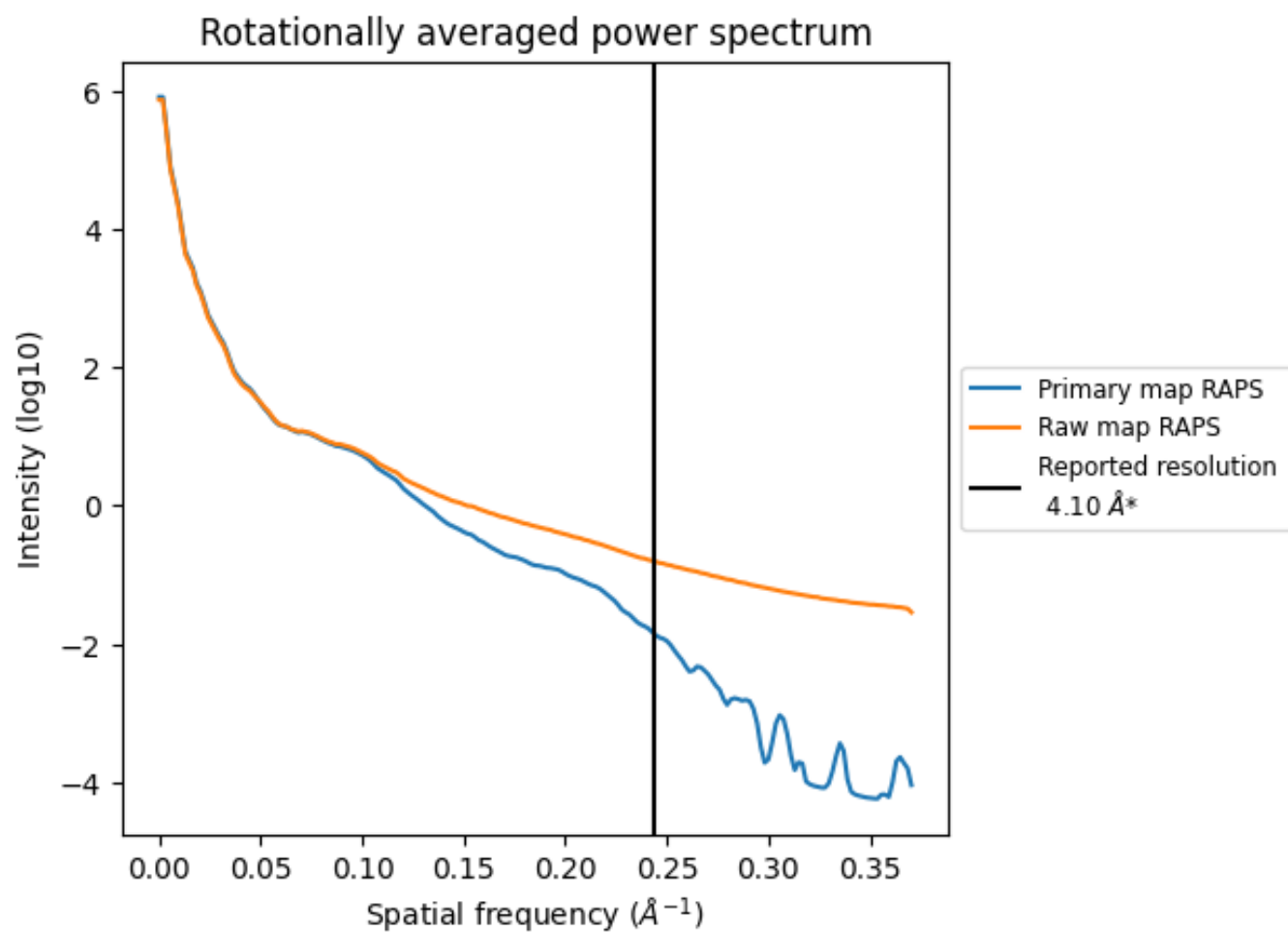
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3969 nm^3 ; this corresponds to an approximate mass of 3585 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 ⓘ

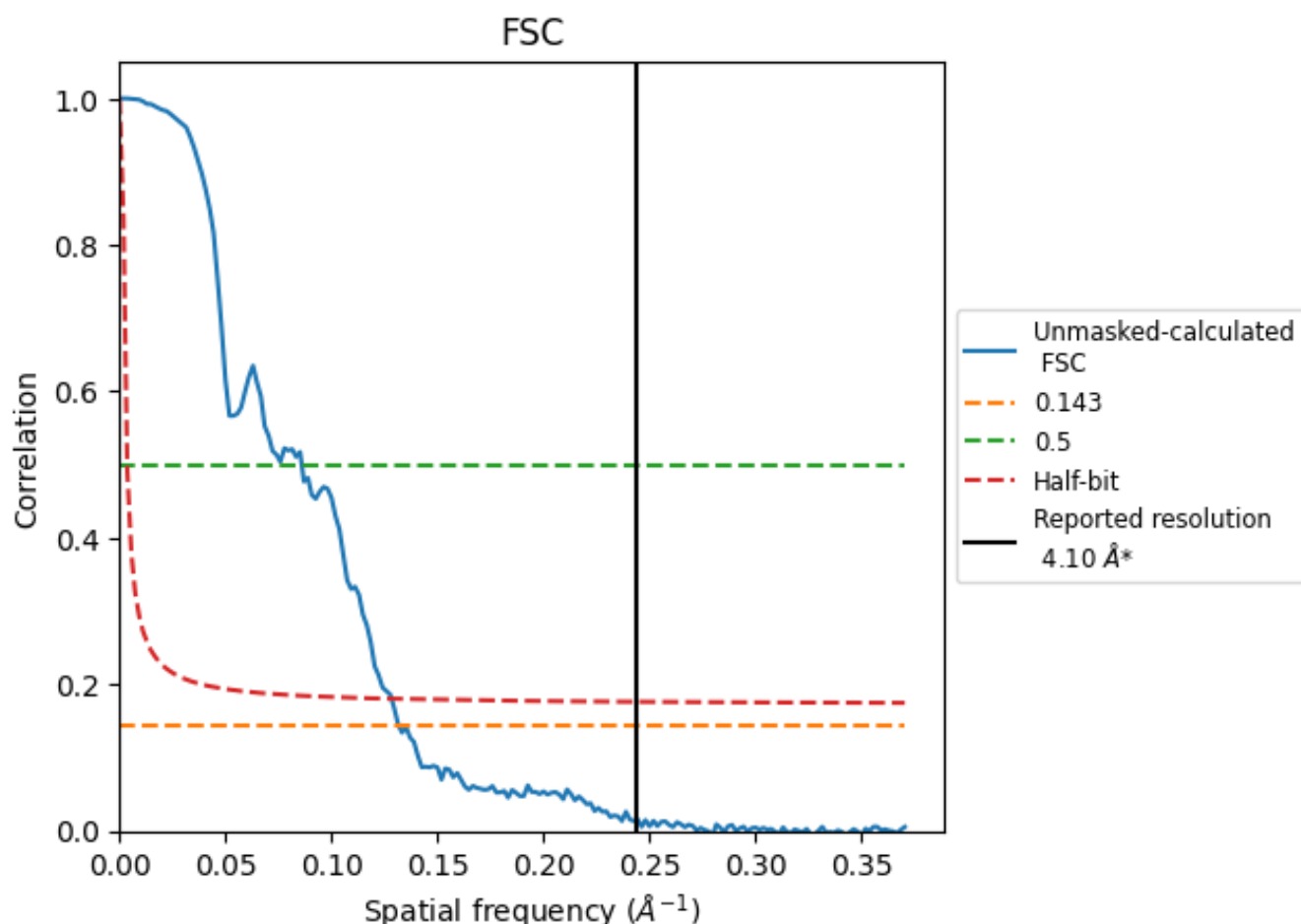


*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

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 0.244 Å⁻¹

8.2 Resolution estimates [i](#)

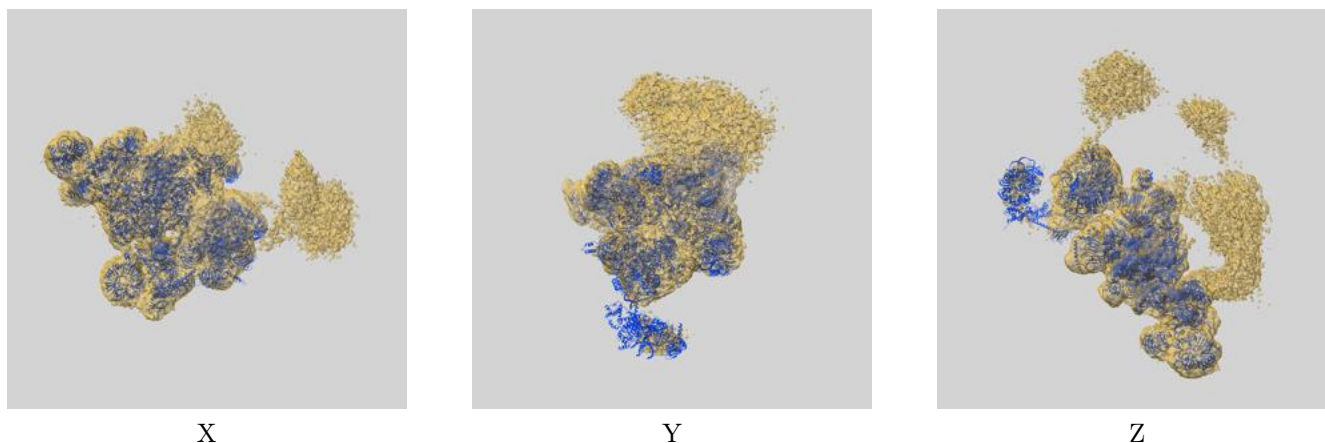
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---------------------------|------------------------------------|-------|----------|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 4.10 | - | - |
| Author-provided FSC curve | - | - | - |
| Unmasked-calculated* | 7.59 | 11.63 | 7.79 |

*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 7.59 differs from the reported value 4.1 by more than 10 %

9 Map-model fit [i](#)

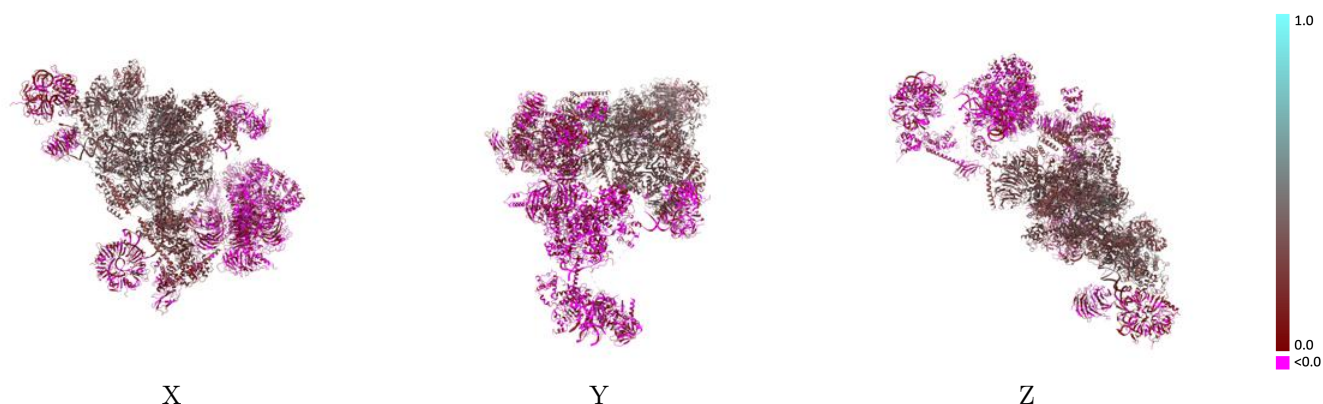
This section contains information regarding the fit between EMDB map EMD-18781 and PDB model 8QZS. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



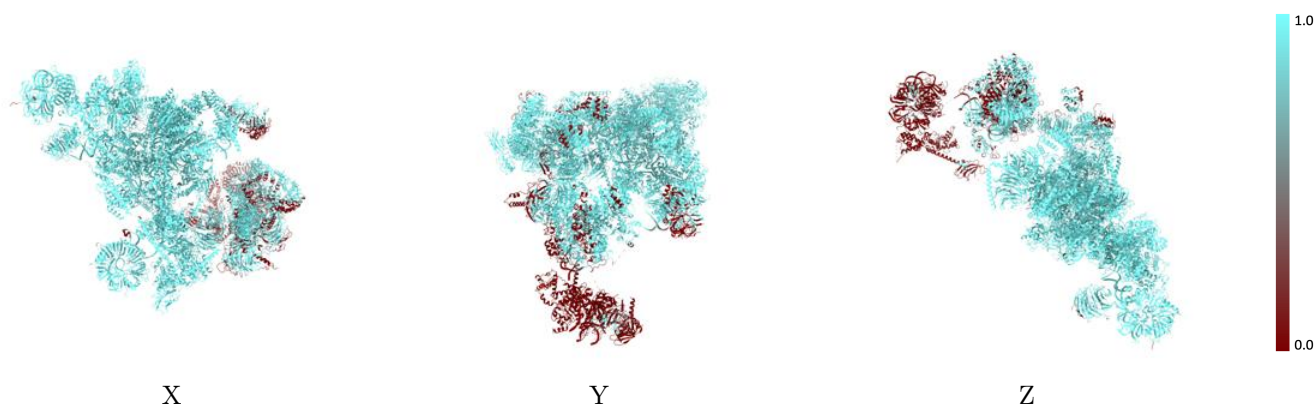
The images above show the 3D surface view of the map at the recommended contour level 0.011 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



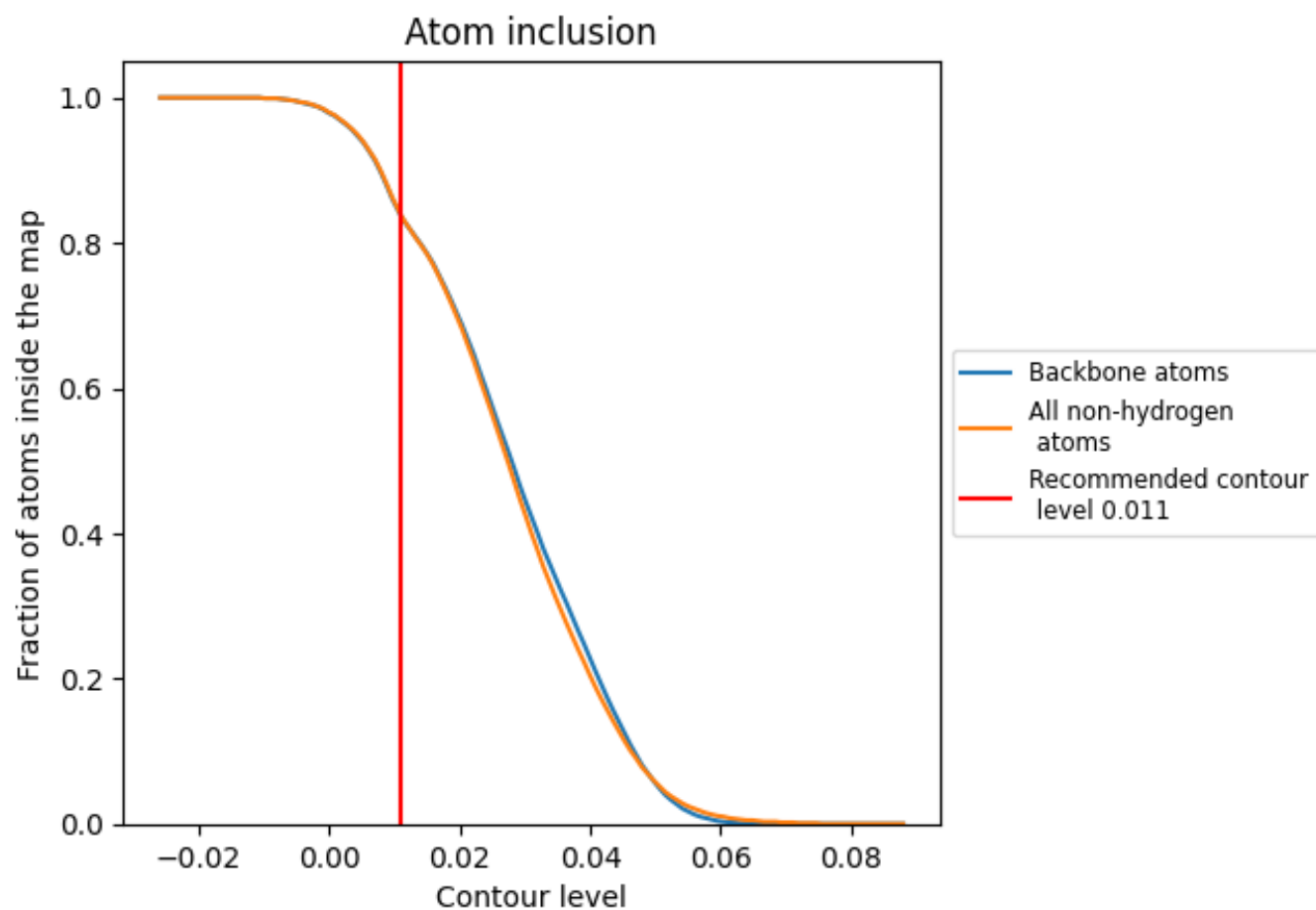
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.011).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





































































The table lists the average atom inclusion at the recommended contour level (0.011) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|--|---|
| All |  0.8380 |  0.1680 |
| 2 |  0.3540 |  -0.0190 |
| 21 |  0.0900 |  0.0130 |
| 22 |  0.0980 |  0.0220 |
| 23 |  0.1730 |  0.0220 |
| 2A |  0.0040 |  -0.0060 |
| 2B |  0.0090 |  0.0360 |
| 2b |  0.1190 |  -0.0180 |
| 2e |  0.1090 |  -0.0070 |
| 2f |  0.0470 |  0.0470 |
| 2g |  0.3430 |  0.0280 |
| 4 |  0.9500 |  0.1680 |
| 41 |  1.0000 |  0.0610 |
| 42 |  1.0000 |  0.0610 |
| 43 |  0.9970 |  0.0530 |
| 4b |  0.9920 |  0.0540 |
| 4e |  0.9840 |  0.0580 |
| 4f |  0.9830 |  0.0330 |
| 4g |  0.9730 |  0.0790 |
| 5 |  0.9980 |  0.2060 |
| 51 |  1.0000 |  0.0990 |
| 52 |  0.9230 |  0.0950 |
| 53 |  0.9810 |  0.0860 |
| 5b |  0.9930 |  0.0910 |
| 5e |  0.9700 |  0.0730 |
| 5f |  0.9610 |  0.0810 |
| 5g |  0.9820 |  0.0570 |
| 6 |  0.9190 |  0.2200 |
| 62 |  0.7610 |  0.0080 |
| 63 |  0.5340 |  0.0060 |
| 64 |  0.6930 |  0.0110 |
| 65 |  0.0210 |  -0.0540 |
| 66 |  0.0790 |  -0.0320 |
| 67 |  0.3000 |  0.0020 |
| 68 |  0.9550 |  -0.0080 |



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| Chain | Atom inclusion | Q-score |
|-------|--|---|
| 7 |  0.4520 |  0.1340 |
| 8 |  0.3060 |  0.0100 |
| 9 |  0.1180 |  0.0150 |
| A |  0.9970 |  0.3450 |
| B |  0.9950 |  0.2040 |
| B1 |  0.7250 |  -0.0010 |
| B2 |  0.6230 |  -0.0080 |
| B3 |  0.7530 |  0.0100 |
| B4 |  0.7750 |  0.0500 |
| B5 |  0.8700 |  0.0380 |
| B6 |  0.9870 |  0.0020 |
| BP |  0.9020 |  -0.0080 |
| C |  1.0000 |  0.3320 |
| D |  1.0000 |  0.3700 |
| E |  0.9580 |  0.0470 |
| F |  1.0000 |  0.2960 |
| I |  0.9990 |  0.3150 |
| J |  1.0000 |  0.3140 |
| K |  0.9820 |  0.2080 |
| L |  0.9940 |  0.3270 |
| M |  1.0000 |  0.3490 |
| N |  0.9990 |  0.2840 |
| S |  0.9710 |  0.2950 |
| U |  0.9580 |  0.3090 |
| W |  1.0000 |  0.2400 |
| X |  1.0000 |  0.3080 |
| Z |  0.9780 |  -0.0170 |
| r |  0.9790 |  0.3070 |
| v |  0.7610 |  0.0240 |
| w |  0.8150 |  0.0420 |
| x |  0.1880 |  -0.0090 |
| y |  0.8400 |  -0.0060 |
| z1 |  1.0000 |  0.3250 |
| z2 |  1.0000 |  0.2400 |