



## wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 01:30 AM UTC

PDB ID : 8H6K / pdb\_00008h6k  
EMDB ID : EMD-34507  
Title : Cryo-EM structure of human exon-defined spliceosome in the mature B state.  
Authors : Zhang, W.; Zhan, X.; Zhang, X.; Bai, R.; Lei, J.; Yan, C.; Shi, Y.  
Deposited on : 2022-10-18  
Resolution : 2.70 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

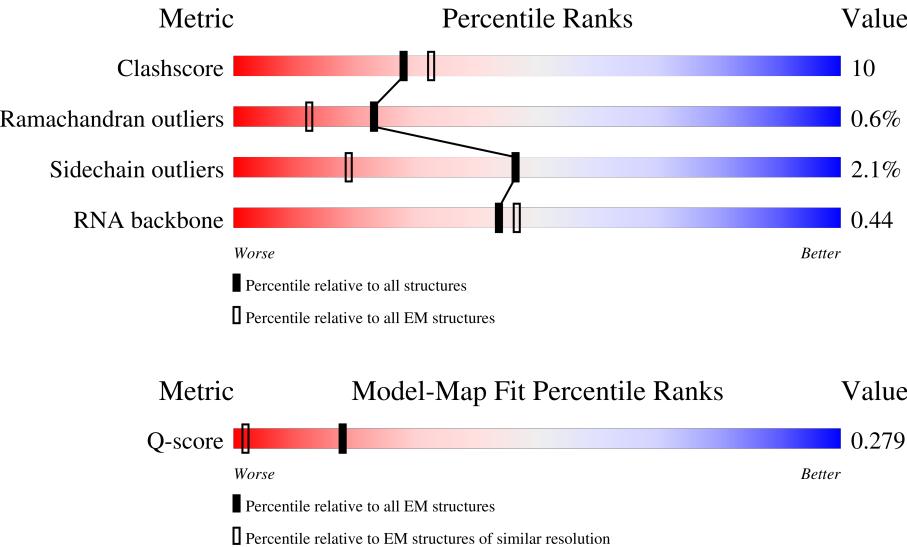
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 2.70 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.



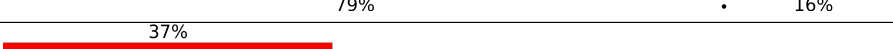
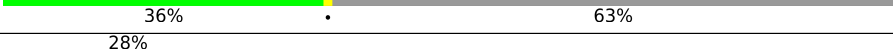
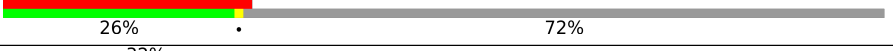
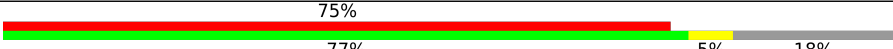
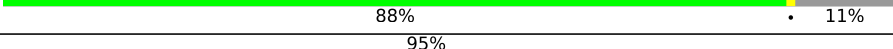
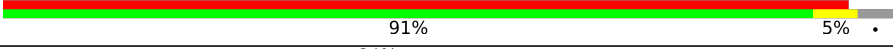
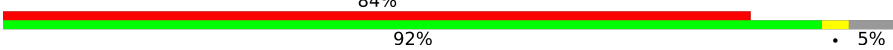
| Metric                | Whole archive<br>(#Entries) | EM structures<br>(#Entries) | Similar EM resolution<br>(#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|-----------------------------|----------------------------------------------------------|
| Clashscore            | 229148                      | 23984                       | -                                                        |
| Ramachandran outliers | 224038                      | 23583                       | -                                                        |
| Sidechain outliers    | 223484                      | 23102                       | -                                                        |
| RNA backbone          | 8273                        | 3508                        | -                                                        |
| Q-score               | -                           | 25397                       | 10327 ( 2.20 - 3.20 )                                    |

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     | 144    | <div> <div>29%</div> <div>8% 12% 21% . 56%</div> </div> |
| 2   | 5A    | 117    | <div> <div>40%</div> <div>46% 38% 15% .</div> </div>    |
| 3   | 5B    | 2335   | <div> <div>6%</div> <div>84% 12% . .</div> </div>       |

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| Mol | Chain | Length | Quality of chain                                                                     |
|-----|-------|--------|--------------------------------------------------------------------------------------|
| 4   | 5C    | 972    |    |
| 5   | 5D    | 2136   |    |
| 6   | 5E    | 357    |    |
| 7   | 2a    | 231    |    |
| 7   | 4a    | 231    |    |
| 7   | 5a    | 231    |    |
| 8   | 2b    | 119    |    |
| 8   | 4b    | 119    |    |
| 8   | 5b    | 119    |    |
| 9   | 2c    | 118    |    |
| 9   | 4c    | 118    |    |
| 9   | 5c    | 118    |    |
| 10  | 2d    | 86     |    |
| 10  | 4d    | 86     |   |
| 10  | 5d    | 86     |  |
| 11  | 2e    | 92     |  |
| 11  | 4e    | 92     |  |
| 11  | 5e    | 92     |  |
| 12  | 2f    | 76     |  |
| 12  | 4f    | 76     |  |
| 12  | 5f    | 76     |  |
| 13  | 2g    | 126    |  |
| 13  | 4g    | 126    |  |
| 13  | 5g    | 126    |  |
| 14  | 6A    | 107    |  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 15  | 6a    | 95     |                  |
| 16  | 6b    | 102    |                  |
| 17  | 6c    | 139    |                  |
| 18  | 6d    | 91     |                  |
| 19  | 6e    | 80     |                  |
| 20  | 6f    | 103    |                  |
| 21  | 6g    | 96     |                  |
| 22  | 4A    | 145    |                  |
| 23  | 4B    | 683    |                  |
| 24  | 4C    | 522    |                  |
| 25  | 4D    | 499    |                  |
| 26  | 4E    | 128    |                  |
| 27  | 4F    | 142    |                  |
| 28  | 4G    | 941    |                  |
| 29  | 4H    | 177    |                  |
| 30  | 4I    | 376    |                  |
| 31  | 4J    | 800    |                  |
| 32  | 4K    | 439    |                  |
| 33  | 4L    | 312    |                  |
| 34  | 4M    | 73     |                  |
| 35  | 4N    | 199    |                  |
| 36  | 4Z    | 513    |                  |
| 37  | 2A    | 188    |                  |
| 38  | 2B    | 255    |                  |
| 39  | 2C    | 225    |                  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 40  | 2D    | 793    |                  |
| 41  | 2E    | 464    |                  |
| 42  | 2F    | 501    |                  |
| 43  | 2G    | 1304   |                  |
| 44  | 2H    | 895    |                  |
| 45  | 2I    | 1217   |                  |
| 46  | 2J    | 424    |                  |
| 47  | 2K    | 125    |                  |
| 48  | 2L    | 110    |                  |
| 49  | 2M    | 86     |                  |

## 2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 98459 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 pre-mRNA.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 1   | A     | 64       | Total | C   | N   | O   | P  | 0       | 0     |
|     |       |          | 1334  | 597 | 209 | 464 | 64 |         |       |

- Molecule 2 is a RNA chain called U5 snRNA.

| Mol | Chain | Residues | Atoms |      |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 2   | 5A    | 115      | Total | C    | N   | O   | P   | 0       | 0     |
|     |       |          | 2420  | 1084 | 403 | 818 | 115 |         |       |

- Molecule 3 is a protein called Pre-mRNA-processing-splicing factor 8.

| Mol | Chain | Residues | Atoms |       |      |      |    | AltConf | Trace |
|-----|-------|----------|-------|-------|------|------|----|---------|-------|
| 3   | 5B    | 2253     | Total | C     | N    | O    | S  | 0       | 0     |
|     |       |          | 18639 | 11991 | 3249 | 3318 | 81 |         |       |

- Molecule 4 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

| Mol | Chain | Residues | Atoms |      |      |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| 4   | 5C    | 818      | Total | C    | N    | O    | S  | 0       | 0     |
|     |       |          | 6430  | 4108 | 1085 | 1205 | 32 |         |       |

- Molecule 5 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

| Mol | Chain | Residues | Atoms |      |      |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| 5   | 5D    | 1696     | Total | C    | N    | O    | S  | 0       | 0     |
|     |       |          | 13633 | 8715 | 2329 | 2519 | 70 |         |       |

- Molecule 6 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 6   | 5E    | 299      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 1196  | 598 | 299 | 299 |         |       |

- Molecule 7 is a protein called Isoform SM-B of Small nuclear ribonucleoprotein-associated proteins B and B'.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 7   | 5a    | 84       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 336   | 168 | 84 | 84 |         |       |
| 7   | 4a    | 64       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 256   | 128 | 64 | 64 |         |       |
| 7   | 2a    | 86       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 344   | 172 | 86 | 86 |         |       |

- Molecule 8 is a protein called Small nuclear ribonucleoprotein Sm D1.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 8   | 5b    | 82       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 328   | 164 | 82 | 82 |         |       |
| 8   | 4b    | 82       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 334   | 170 | 82 | 82 |         |       |
| 8   | 2b    | 82       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 328   | 164 | 82 | 82 |         |       |

- Molecule 9 is a protein called Small nuclear ribonucleoprotein Sm D2.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 9   | 5c    | 97       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 388   | 194 | 97 | 97 |         |       |
| 9   | 4c    | 74       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 300   | 152 | 74 | 74 |         |       |
| 9   | 2c    | 85       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 340   | 170 | 85 | 85 |         |       |

- Molecule 10 is a protein called Small nuclear ribonucleoprotein F.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 10  | 5d    | 74       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 296   | 148 | 74 | 74 |         |       |
| 10  | 4d    | 71       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 292   | 150 | 71 | 71 |         |       |
| 10  | 2d    | 74       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 296   | 148 | 74 | 74 |         |       |

- Molecule 11 is a protein called Small nuclear ribonucleoprotein E.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 11  | 5e    | 79       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 316   | 158 | 79 | 79 |         |       |
| 11  | 4e    | 78       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 314   | 158 | 78 | 78 |         |       |
| 11  | 2e    | 79       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 316   | 158 | 79 | 79 |         |       |

- Molecule 12 is a protein called Small nuclear ribonucleoprotein G.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 12  | 5f    | 72       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 288   | 144 | 72 | 72 |         |       |
| 12  | 4f    | 73       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 298   | 152 | 73 | 73 |         |       |
| 12  | 2f    | 68       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 272   | 136 | 68 | 68 |         |       |

- Molecule 13 is a protein called Small nuclear ribonucleoprotein Sm D3.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 13  | 5g    | 77       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 308   | 154 | 77 | 77 |         |       |
| 13  | 4g    | 71       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 288   | 146 | 71 | 71 |         |       |
| 13  | 2g    | 80       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 320   | 160 | 80 | 80 |         |       |

- Molecule 14 is a RNA chain called U6 snRNA.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 14  | 6A    | 60       | Total | C   | N   | O   | P  | 0       | 0     |
|     |       |          | 1273  | 568 | 235 | 410 | 60 |         |       |

- Molecule 15 is a protein called U6 snRNA-associated Sm-like protein LSm2.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 15  | 6a    | 90       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 360   | 180 | 90 | 90 |         |       |

- Molecule 16 is a protein called U6 snRNA-associated Sm-like protein LSm3.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 16  | 6b    | 74       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 296   | 148 | 74 | 74 |         |       |

- Molecule 17 is a protein called U6 snRNA-associated Sm-like protein LSm4.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 17  | 6c    | 74       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 296   | 148 | 74 | 74 |         |       |

- Molecule 18 is a protein called U6 snRNA-associated Sm-like protein LSm5.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 18  | 6d    | 72       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 288   | 144 | 72 | 72 |         |       |

- Molecule 19 is a protein called U6 snRNA-associated Sm-like protein LSm6.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 19  | 6e    | 70       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 280   | 140 | 70 | 70 |         |       |

- Molecule 20 is a protein called U6 snRNA-associated Sm-like protein LSm7.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 20  | 6f    | 65       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 260   | 130 | 65 | 65 |         |       |

- Molecule 21 is a protein called U6 snRNA-associated Sm-like protein LSm8.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 21  | 6g    | 61       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 244   | 122 | 61 | 61 |         |       |

- Molecule 22 is a RNA chain called U4 snRNA.

| Mol | Chain | Residues | Atoms |      |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 22  | 4A    | 129      | Total | C    | N   | O   | P   | 0       | 0     |
|     |       |          | 2744  | 1225 | 472 | 917 | 130 |         |       |

- Molecule 23 is a protein called U4/U6 small nuclear ribonucleoprotein Prp3.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 23  | 4B    | 256      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 2076  | 1316 | 385 | 367 | 8 |         |       |

- Molecule 24 is a protein called U4/U6 small nuclear ribonucleoprotein Prp4.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 24  | 4C    | 426      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 3370  | 2118 | 612 | 620 | 20 |         |       |

- Molecule 25 is a protein called U4/U6 small nuclear ribonucleoprotein Prp31.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 25  | 4D    | 376      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2874  | 1788 | 524 | 550 | 12 |         |       |

- Molecule 26 is a protein called NHP2-like protein 1.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 26  | 4E    | 124      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 962   | 608 | 171 | 178 | 5 |         |       |

- Molecule 27 is a protein called Thioredoxin-like protein 4A.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 27  | 4F    | 141      | Total | C   | N   | O   | S  | 0       | 0     |
|     |       |          | 1169  | 751 | 194 | 214 | 10 |         |       |

- Molecule 28 is a protein called Pre-mRNA-processing factor 6.

| Mol | Chain | Residues | Atoms |      |      |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| 28  | 4G    | 801      | Total | C    | N    | O    | S  | 0       | 0     |
|     |       |          | 5504  | 3419 | 1043 | 1026 | 16 |         |       |

- Molecule 29 is a protein called Peptidyl-prolyl cis-trans isomerase H.

| Mol | Chain | Residues | Atoms |     |     |     |  | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|-------|
| 29  | 4H    | 169      | Total | C   | N   | O   |  | 0       | 0     |
|     |       |          | 844   | 506 | 169 | 169 |  |         |       |

- Molecule 30 is a protein called WW domain-binding protein 4.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 30  | 4I    | 75       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 494   | 304 | 96 | 91 | 3 |         |       |

- Molecule 31 is a protein called U4/U6.U5 tri-snRNP-associated protein 1.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 31  | 4J    | 152      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1144  | 709 | 204 | 229 | 2 |         |       |

- Molecule 32 is a protein called Microfibrillar-associated protein 1.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 32  | 4K    | 188      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1192  | 741 | 219 | 230 | 2 |         |       |

- Molecule 33 is a protein called Pre-mRNA-splicing factor 38A.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 33  | 4L    | 175      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1452  | 934 | 244 | 265 | 9 |         |       |

- Molecule 34 is a protein called Ubiquitin-like protein 5.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 34  | 4M    | 73       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 599   | 383 | 103 | 109 | 4 |         |       |

- Molecule 35 is a protein called Zinc finger matrin-type protein 2.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 35  | 4N    | 80       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 640   | 397 | 116 | 120 | 7 |         |       |

- Molecule 36 is a protein called WD40 repeat-containing protein SMU1.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 36  | 4Z    | 420      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 2092  | 1252 | 420 | 420 |   |         |       |

- Molecule 37 is a RNA chain called U2 snRNA.

| Mol | Chain | Residues | Atoms |      |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 37  | 2A    | 109      | Total | C    | N   | O   | P   | 0       | 0     |
|     |       |          | 2311  | 1032 | 396 | 774 | 109 |         |       |

- Molecule 38 is a protein called U2 small nuclear ribonucleoprotein A'.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 38  | 2B    | 162      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 648   | 324 | 162 | 162 |         |       |

- Molecule 39 is a protein called U2 small nuclear ribonucleoprotein B'.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 39  | 2C    | 94       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 376   | 188 | 94 | 94 |         |       |

- Molecule 40 is a protein called Splicing factor 3A subunit 1.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 40  | 2D    | 204      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1134  | 644 | 238 | 250 | 2 |         |       |

- Molecule 41 is a protein called Splicing factor 3A subunit 2.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 41  | 2E    | 94       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 376   | 188 | 94 | 94 |         |       |

- Molecule 42 is a protein called Splicing factor 3A subunit 3.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 42  | 2F    | 423      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 1693  | 847 | 423 | 423 |         |       |

- Molecule 43 is a protein called Splicing factor 3B subunit 1.

| Mol | Chain | Residues | Atoms |      |      |      | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|---------|-------|
| 43  | 2G    | 1048     | Total | C    | N    | O    | 0       | 0     |
|     |       |          | 4192  | 2096 | 1048 | 1048 |         |       |

- Molecule 44 is a protein called Splicing factor 3B subunit 2.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 44  | 2H    | 213      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 959   | 510 | 220 | 226 | 3 |         |       |

- Molecule 45 is a protein called Splicing factor 3B subunit 3.

| Mol | Chain | Residues | Atoms |      |      |      |  | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|--|---------|-------|
| 45  | 2I    | 1168     | Total | C    | N    | O    |  | 0       | 0     |
|     |       |          | 4672  | 2336 | 1168 | 1168 |  |         |       |

- Molecule 46 is a protein called Splicing factor 3B subunit 4.

| Mol | Chain | Residues | Atoms |     |    |    |  | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|--|---------|-------|
| 46  | 2J    | 78       | Total | C   | N  | O  |  | 0       | 0     |
|     |       |          | 312   | 156 | 78 | 78 |  |         |       |

- Molecule 47 is a protein called Splicing factor 3B subunit 6.

| Mol | Chain | Residues | Atoms |     |     |     |  | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|-------|
| 47  | 2K    | 108      | Total | C   | N   | O   |  | 0       | 0     |
|     |       |          | 432   | 216 | 108 | 108 |  |         |       |

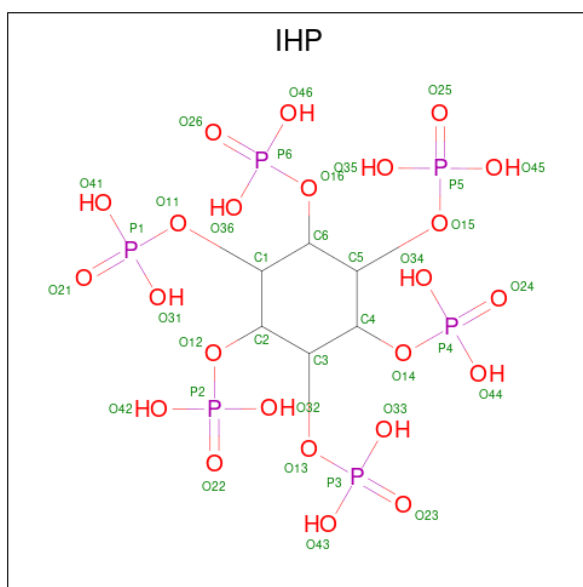
- Molecule 48 is a protein called PHD finger-like domain-containing protein 5A.

| Mol | Chain | Residues | Atoms |     |    |    |  | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|--|---------|-------|
| 48  | 2L    | 89       | Total | C   | N  | O  |  | 0       | 0     |
|     |       |          | 356   | 178 | 89 | 89 |  |         |       |

- Molecule 49 is a protein called Splicing factor 3B subunit 5.

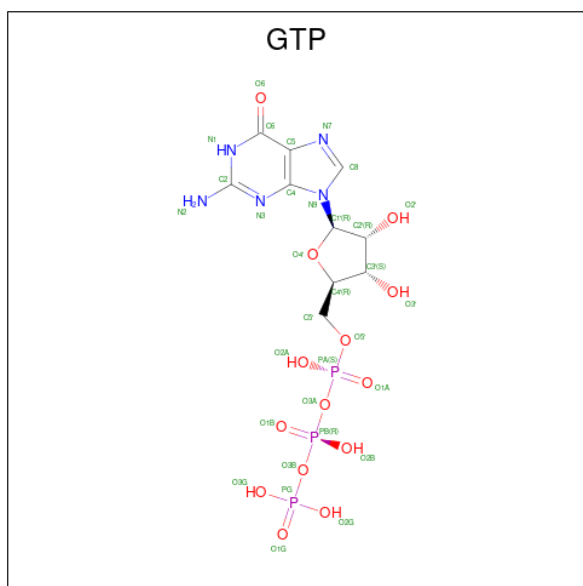
| Mol | Chain | Residues | Atoms |     |    |    |  | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|--|---------|-------|
| 49  | 2M    | 66       | Total | C   | N  | O  |  | 0       | 0     |
|     |       |          | 264   | 132 | 66 | 66 |  |         |       |

- Molecule 50 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: C<sub>6</sub>H<sub>18</sub>O<sub>24</sub>P<sub>6</sub>).



| Mol | Chain | Residues | Atoms |   |    |   | AltConf |
|-----|-------|----------|-------|---|----|---|---------|
| 50  | 5B    | 1        | Total | C | O  | P | 0       |
|     |       |          | 36    | 6 | 24 | 6 |         |

- Molecule 51 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula:  $C_{10}H_{16}N_5O_{14}P_3$ ).



| Mol | Chain | Residues | Atoms |    |   |    |   | AltConf |
|-----|-------|----------|-------|----|---|----|---|---------|
| 51  | 5C    | 1        | Total | C  | N | O  | P | 0       |
|     |       |          | 32    | 10 | 5 | 14 | 3 |         |

- Molecule 52 is MAGNESIUM ION (CCD ID: MG) (formula:  $Mg$ ).

| Mol | Chain | Residues | Atoms |    | AltConf |
|-----|-------|----------|-------|----|---------|
| 52  | 5C    | 1        | Total | Mg | 0       |
|     |       |          | 1     | 1  |         |

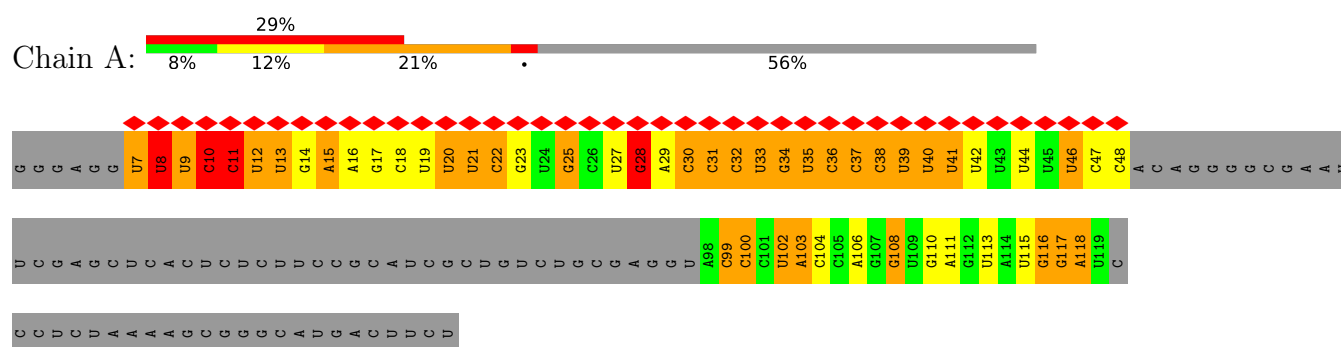
- Molecule 53 is ZINC ION (CCD ID: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms |    | AltConf |
|-----|-------|----------|-------|----|---------|
| 53  | 4I    | 1        | Total | Zn | 0       |
|     |       |          | 1     | 1  |         |
| 53  | 4N    | 1        | Total | Zn | 0       |
|     |       |          | 1     | 1  |         |

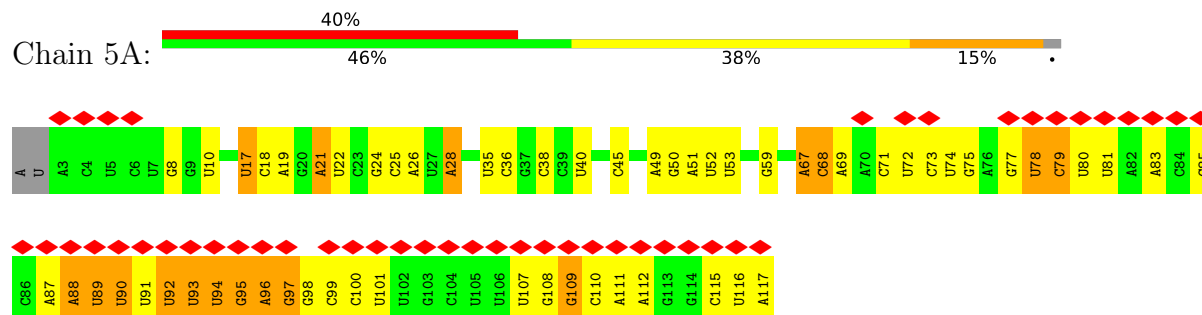
### 3 Residue-property plots

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.

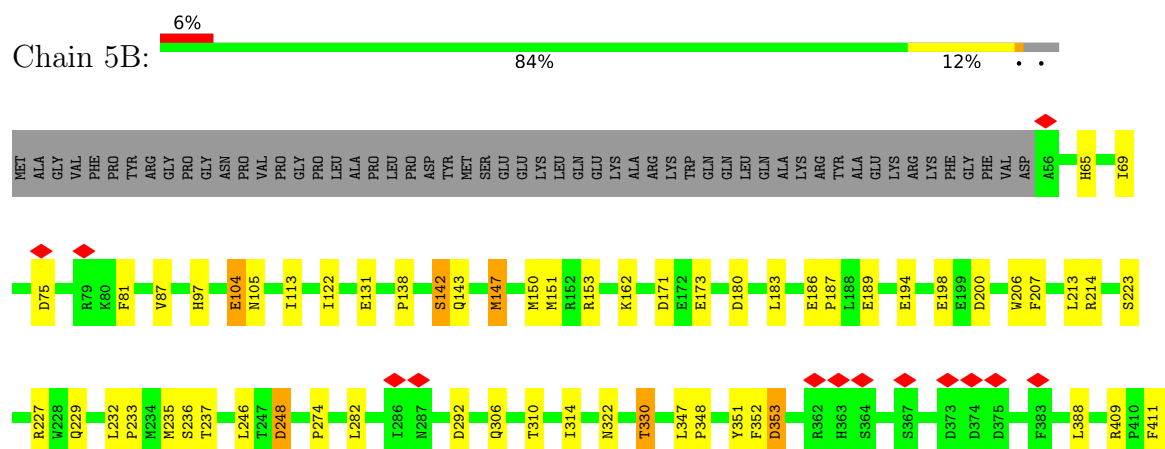
#### • Molecule 1: pre-mRNA



#### • Molecule 2: U5 snRNA



#### • Molecule 3: Pre-mRNA-processing-splicing factor 8





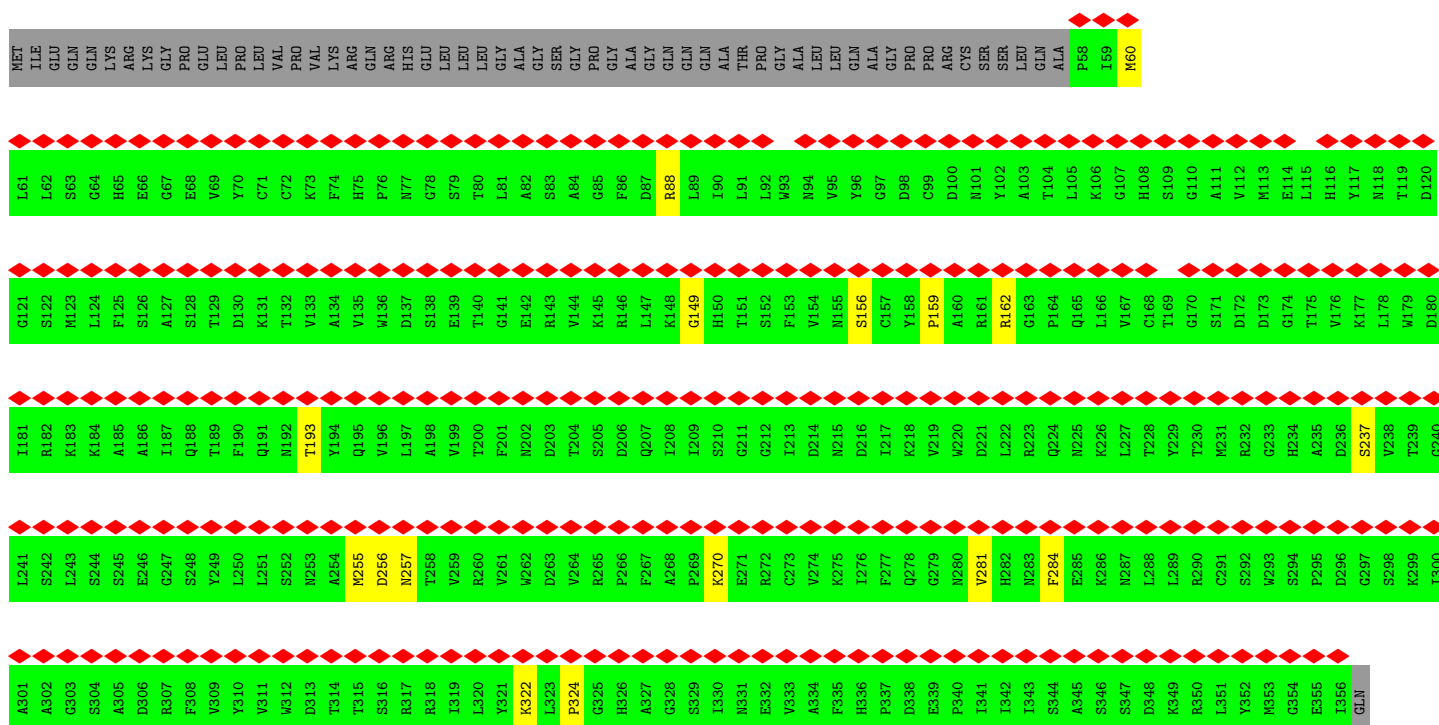


|       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| D1344 | M1345 | F1347 | V1348 | G1349 | A1350 | P1351 | T1352 | G1353 | S1354 | G1355 | K1356 | T1357 | I1358 | G1359 | A1360 | E1361 | F1362 | A1363 | I1364 | I1365 | R1366 | M1367 | L1368 | L1369 | Q1370 | S1371 | S1372 | S1373 | G1374 | R1375 | C1376 | I1377 | Y1378 | I1379 | T1380 | M1381 | M1382 | A1384 | L1385 | A1386 | E1387 | Q1388 | F1389 | Y1390 | M1391 | L1392 | W1393 | Y1394 | E1395 | K1396 | F1397 | Q1398 | L1399 | R1400 | N1401 | N1402 | K1403 |       |
| V1284 | S1285 | F1286 | R1287 | H1288 | L1289 | I1290 | L1291 | P1292 | E1293 | K1294 | Y1295 | P1296 | P1297 | P1298 | T1299 | E1300 | L1301 | L1302 | D1303 | L1304 | Q1305 | P1306 | L1307 | P1308 | S1309 | S1310 | A1311 | L1312 | R1313 | N1314 | S1315 | A1316 | F1317 | F1318 | S1319 | L1320 | Y1321 | Q1322 | D1323 | K1324 | P1326 | F1327 | I1328 | F1329 | P1330 | I1331 | Q1332 | T1333 | Q1334 | V1335 | F1336 | F1337 | T1338 | V1339 | Y1340 | N1341 | S1342 | D1343 |
| W1222 | I1223 | E1226 | D1227 | V1228 | D1229 | S1230 | E1231 | K1232 | V1233 | I1233 | L1234 | H1235 | H1236 | E1237 | Y1238 | F1239 | L1240 | L1241 | K1242 | A1243 | K1244 | Y1245 | A1246 | Q1247 | D1248 | E1249 | H1250 | L1251 | I1252 | T1253 | F1254 | V1255 | V1256 | P1257 | V1258 | F1259 | E1260 | P1261 | L1262 | P1263 | F1264 | Q1265 | F1266 | P1267 | I1268 | R1269 | V1270 | V1271 | S1272 | D1273 | R1274 | W1275 | L1276 | S1277 | C1278 | E1279 | L1282 | P1283 |
| V1284 | S1285 | F1286 | R1287 | H1288 | L1289 | I1290 | L1291 | P1292 | E1293 | K1294 | Y1295 | P1296 | P1297 | P1298 | T1299 | E1300 | L1301 | L1302 | D1303 | L1304 | Q1305 | P1306 | L1307 | P1308 | S1309 | S1310 | A1311 | L1312 | R1313 | N1314 | S1315 | A1316 | F1317 | F1318 | S1319 | L1320 | Y1321 | Q1322 | D1323 | K1324 | P1326 | F1327 | I1328 | F1329 | P1330 | I1331 | Q1332 | T1333 | Q1334 | V1335 | F1336 | F1337 | T1338 | V1339 | Y1340 | N1341 | S1342 | D1343 |
| A1094 | I1095 | F1096 | E1097 | I1098 | V1099 | L1100 | M1101 | R1102 | G1103 | W1104 | L1107 | T1108 | L1112 | I1118 | D1119 | K1120 | R1121 | M1122 | W1123 | Q1124 | S1125 | M1126 | C1127 | P1128 | L1129 | R1130 | Q1131 | F1132 | R1133 | K1134 | L1135 | P1136 | E1137 | E1138 | V1139 | K1141 | L1143 | E1144 | K1145 | K1146 | N1147 | F1148 | P1149 | F1150 | E1151 | R1152 | L1153 | Y1154 | D1155 | L1156 | N1157 | H1158 | N1159 | E1160 |       |       |       |       |
| I1161 | G1162 | E1163 | L1164 | I1165 | R1166 | M1167 | P1168 | K1169 | M1170 | G1171 | T1172 | T1173 | I1174 | K1175 | K1176 | H1179 | L1180 | F1181 | P1182 | K1183 | L1184 | E1185 | L1186 | S1187 | H1188 | H1189 | L1190 | Q1191 | P1192 | I1193 | F1194 | L1195 | S1196 | T1197 | L1198 | K1199 | V1200 | E1201 | L1202 | T1203 | I1204 | T1205 | P1206 | D1207 | F1208 | Q1209 | W1210 | D1211 | E1212 | K1213 | V1214 | H1215 | G1216 | S1217 | S1218 | E1219 | A1220 | F1221 |
| W1222 | I1223 | E1226 | D1227 | V1228 | D1229 | S1230 | E1231 | K1232 | V1233 | I1233 | L1234 | H1235 | H1236 | E1237 | Y1238 | F1239 | L1240 | L1241 | K1242 | A1243 | K1244 | Y1245 | A1246 | Q1247 | D1248 | E1249 | H1250 | L1251 | I1252 | T1253 | F1254 | V1255 | V1256 | P1257 | V1258 | F1259 | E1260 | P1261 | L1262 | P1263 | F1264 | Q1265 | F1266 | P1267 | I1268 | R1269 | V1270 | V1271 | S1272 | D1273 | R1274 | W1275 | L1276 | S1277 | C1278 | E1279 | L1282 | P1283 |
| V1284 | S1285 | F1286 | R1287 | H1288 | L1289 | I1290 | L1291 | P1292 | E1293 | K1294 | Y1295 | P1296 | P1297 | P1298 | T1299 | E1300 | L1301 | L1302 | D1303 | L1304 | Q1305 | P1306 | L1307 | P1308 | S1309 | S1310 | A1311 | L1312 | R1313 | N1314 | S1315 | A1316 | F1317 | F1318 | S1319 | L1320 | Y1321 | Q1322 | D1323 | K1324 | P1326 | F1327 | I1328 | F1329 | P1330 | I1331 | Q1332 | T1333 | Q1334 | V1335 | F1336 | F1337 | T1338 | V1339 | Y1340 | N1341 | S1342 | D1343 |
| D1344 | M1345 | F1347 | V1348 | G1349 | A1350 | P1351 | T1352 | G1353 | S1354 | G1355 | K1356 | T1357 | I1358 | G1359 | A1360 | E1361 | F1362 | A1363 | I1364 | I1365 | R1366 | M1367 | L1368 | L1369 | Q1370 | S1371 | S1372 | S1373 | G1374 | R1375 | C1376 | I1377 | Y1378 | I1379 | T1380 | M1381 | M1382 | A1384 | L1385 | A1386 | E1387 | Q1388 | F1389 | Y1390 | M1391 | L1392 | W1393 | Y1394 | E1395 | K1396 | F1397 | Q1398 | L1399 | R1400 | N1401 | N1402 | K1403 |       |
| R545  | S546  | L547  | V548  | Q549  | E550  | M551  | V552  | G553  | S554  | F555  | G556  | K557  | R558  | L559  | A560  | T561  | Y562  | G563  | I564  | T565  | V566  | A567  | E568  | L569  | T570  | G571  | D572  | H573  | Q574  | L575  | C576  | K577  | E578  | E579  | I580  | S581  | A582  | T583  | Q584  | I585  | I586  | V587  | C588  | T589  | E590  | E591  | K592  | V593  | D594  | I595  | I596  | T597  | R598  | K599  | G600  | E602  | R603  | T604  |
| Y605  | T606  | Q607  | L608  | V609  | R610  | L611  | I612  | I613  | L614  | D615  | E616  | I617  | H618  | L619  | A620  | H621  | D622  | D623  | R624  | G625  | P626  | V627  | L628  | E629  | A630  | L631  | V632  | A633  | R634  | A635  | I636  | R637  | N638  | I639  | E640  | E641  | T642  | Q643  | E644  | D645  | V646  | R647  | L648  | I649  | G650  | L651  | S652  | P656  | N657  | Y658  | E659  | D660  | V661  | A662  | T663  | F664  | L665  | R666  |
| V667  | D668  | P669  | A670  | K671  | G672  | L673  | F674  | Y675  | F676  | D677  | F680  | E686  | Q687  | T688  | Y689  | V690  | G691  | I692  | T693  | E694  | P695  | V697  | K698  | E699  | R700  | I703  | M704  | N705  | E706  | I707  | F708  | Y709  | I712  | A713  | E714  | H715  | A716  | G717  | V721  | L722  | V723  | K729  | E730  | T731  | T734  | R739  | D740  | L743  | E744  | K745  |       |       |       |       |       |       |       |       |
| D746  | T747  | L748  | F751  | L752  | R753  | E754  | G755  | S756  | A757  | E760  | V761  | L762  | R763  | T764  | E765  | A766  | E767  | Q768  | C769  | K770  | N771  | L772  | E773  | L774  | K775  | D776  | L777  | L778  | G781  | F782  | A783  | I784  | H785  | H786  | A787  | G788  | M789  | T790  | V792  | D793  | R794  | T795  | L796  | V797  | F801  | A802  | I806  | L809  | V810  | L815  | A816  |       |       |       |       |       |       |       |
| W817  | G818  | V819  | H820  | L821  | H824  | I827  | I828  | K829  | G830  | T831  | Q832  | V833  | E837  | K838  | G839  | R840  | W841  | T842  | E843  | L844  | G845  | A846  | L847  | D848  | H852  | L853  | G854  | R855  | P859  | Q860  | Y861  | D862  | G865  | E866  | G867  | I868  | L869  | T870  | S872  | T871  | H873  | G874  | E875  | L876  | Q877  | Y878  | Y879  | L880  | S881  | L882  | L883  | N884  | Q885  |       |       |       |       |       |
| Q886  | L887  | P888  | L889  | E890  | S891  | Q892  | M893  | V894  | S895  | K896  | L897  | P898  | D899  | N900  | L901  | N902  | A903  | E904  | I905  | V906  | L907  | G908  | N909  | V910  | Q911  | K914  | L913  | A923  | Y924  | L925  | Y926  | I927  | R928  | G929  | L930  | R931  | S932  | P933  | T934  | L935  | Y936  | Q937  | I938  | S939  | H940  | D941  | D942  | L943  | K944  | G945  | D946  | P947  | L948  | L949  | D950  | Q951  |       |       |
| R952  | L953  | D954  | D955  | V957  | H958  | V959  | A960  | A961  | L962  | M963  | L964  | D965  | K966  | N967  | N968  | L969  | V970  | K971  | Y972  | D973  | K974  | K975  | T976  | F979  | Q980  | V981  | R982  | E983  | L984  | G985  | R986  | L987  | H990  | Y991  | Y992  | I993  | T994  | N995  | D996  | T997  | V998  | Q999  | T1000 | Y1001 | N1002 | Q1003 | L1004 | L1005 | K1006 | T1008 | L1009 | S1010 | E1011 | L1014 |       |       |       |       |
| F1015 | R1016 | V1017 | L1020 | S1021 | S1022 | E1023 | H1026 | I1027 | T1028 | V1029 | E1032 | L1035 | E1036 | L1037 | Q1038 | K1039 | L1040 | L1041 | E1042 | R1043 | V1044 | K1049 | E1050 | S1051 | I1052 | K1058 | I1059 | L1063 | Q1064 | A1065 | F1066 | Q1069 | L1070 | K1071 | L1072 | E1073 | G1074 | F1075 | M1078 | A1079 | W1080 | W1081 | V1082 | Q1086 | R1090 | L1091 | M1092 | R1093 |       |       |       |       |       |       |       |       |       |       |
| A1094 | I1095 | F1096 | E1097 | I1098 | V1099 | L1100 | M1101 | R1102 | G1103 | W1104 | L1107 | T1108 | L1112 | I1118 | D1119 | K1120 | R1121 | M1122 | W1123 | Q1124 | S1125 | M1126 | C1127 | P1128 | L1129 | R1130 | Q1131 | F1132 | R1133 | K1134 | L1135 | P1136 | E1137 | E1138 | V1139 | K1141 | L1143 | E1144 | K1145 | K1146 | N1147 | F1148 | P1149 | F1150 | E1151 | R1152 | L1153 | Y1154 | D1155 | L1156 | N1157 | H1158 | N1159 | E1160 |       |       |       |       |
| I1161 | G1162 | E1163 | L1164 | I1165 | R1166 | M1167 | P1168 | K1169 | M1170 | G1171 | T1172 | T1173 | I1174 | K1175 | K1176 | H1179 | L1180 | F1181 | P1182 | K1183 | L1184 | E1185 | L1186 | S1187 | H1188 | H1189 | L1190 | Q1191 | P1192 | I1193 | F1194 | L1195 | S1196 | T1197 | L1198 | K1199 | V1200 | E1201 | L1202 | T1203 | I1204 | T1205 | P1206 | D1207 | F1208 | Q1209 | W1210 | D1211 | E1212 | K1213 | V1214 | H1215 | G1216 | S1217 | S1218 | E1219 | A1220 | F1221 |
| W1222 | I1223 | E1226 | D1227 | V1228 | D1229 | S1230 | E1231 | K1232 | V1233 | I1233 | L1234 | H1235 | H1236 | E1237 | Y1238 | F1239 | L1240 | L1241 | K1242 | A1243 | K1244 | Y1245 | A1246 | Q1247 | D1248 | E1249 | H1250 | L1251 | I1252 | T1253 | F1254 | V1255 | V1256 | P1257 | V1258 | F1259 | E1260 | P1261 | L1262 | P1263 | F1264 | Q1265 | F1266 | P1267 | I1268 | R1269 | V1270 | V1271 | S1272 | D1273 | R1274 | W1275 | L1276 | S1277 | C1278 | E1279 | L1282 | P1283 |
| V1284 | S1285 | F1286 | R1287 | H1288 | L1289 | I1290 | L1291 | P1292 | E1293 | K1294 | Y1295 | P1296 | P1297 | P1298 | T1299 | E1300 | L1301 | L1302 | D1303 | L1304 | Q1305 | P1306 | L1307 | P1308 | S1309 | S1310 | A1311 | L1312 | R1313 | N1314 | S1315 | A1316 | F1317 | F1318 | S1319 | L1320 | Y1321 | Q1322 | D1323 | K1324 | P1326 | F1327 | I1328 | F1329 | P1330 | I1331 | Q1332 | T1333 | Q1334 | V1335 | F1336 | F1337 | T1338 | V1339 | Y1340 | N1341 | S1342 | D1343 |
| D1344 | M1345 | F1347 | V1348 | G1349 | A1350 | P1351 | T1352 | G1353 | S1354 | G1355 | K1356 | T1357 | I1358 | G1359 | A1360 | E1361 | F1362 | A1363 | I1364 | I1365 | R1366 | M1367 | L1368 | L1369 | Q1370 | S1371 | S1372 | S1373 | G1374 | R1375 | C1376 | I1377 | Y1378 | I1379 | T1380 | M1381 | M1382 | A1384 | L1385 | A1386 | E1387 | Q1388 | F1389 | Y1390 | M1391 | L1392 | W1393 | Y1394 | E1395 | K1396 | F13   |       |       |       |       |       |       |       |

|       |     |
|-------|-----|
| V2124 | VAL |
| D2125 | LYS |
|       | GLU |
|       | ALA |
|       | GLU |
|       | THR |
|       | ASP |
|       | SER |
|       | ASP |
|       | SER |
|       | ASP |

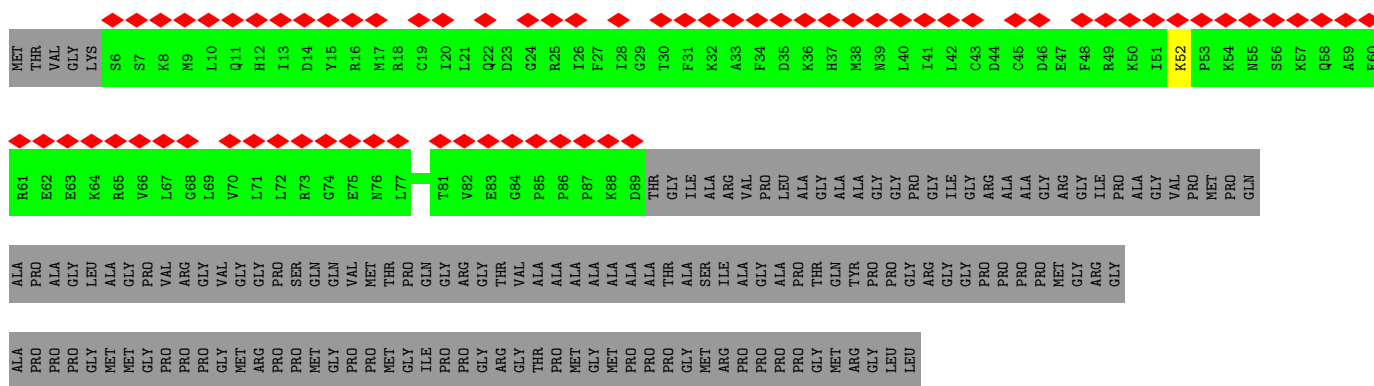
- Molecule 6: U5 small nuclear ribonucleoprotein 40 kDa protein

Chain 5E: 



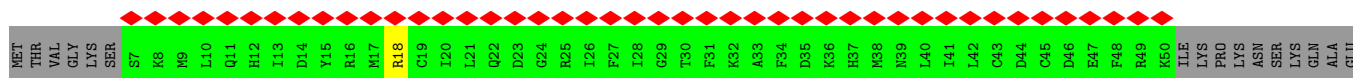
- Molecule 7: Isoform SM-B of Small nuclear ribonucleoprotein-associated proteins B and B'

Chain 5a: 

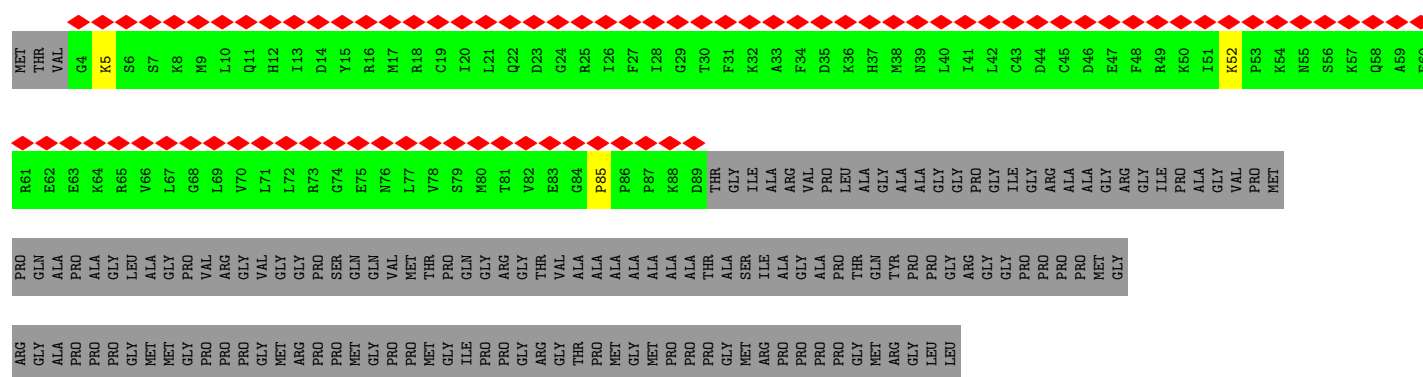


- Molecule 7: Isoform SM-B of Small nuclear ribonucleoprotein-associated proteins B and B'

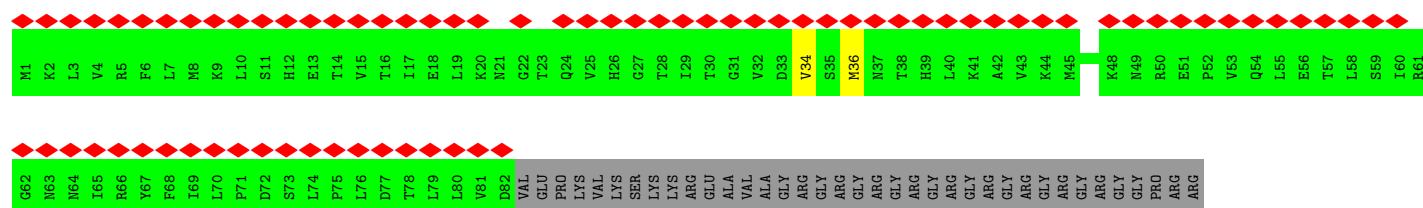
Chain 4a: 



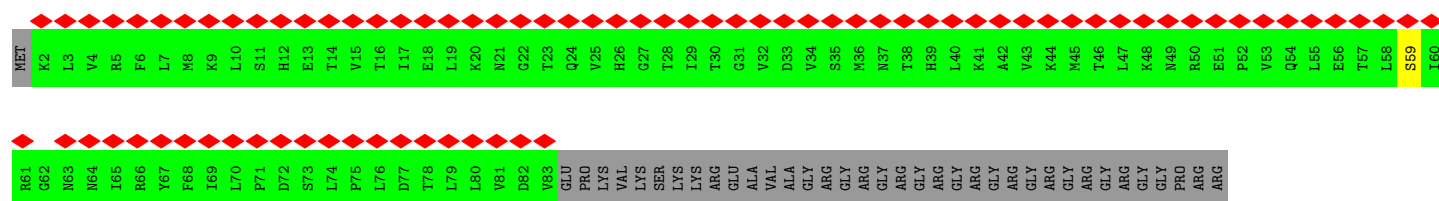
- Molecule 7: Isoform SM-B of Small nuclear ribonucleoprotein-associated proteins B and B'



- Molecule 8: Small nuclear ribonucleoprotein Sm D1

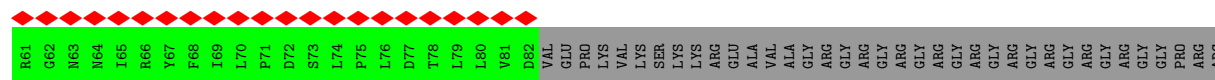


- Molecule 8: Small nuclear ribonucleoprotein Sm D1

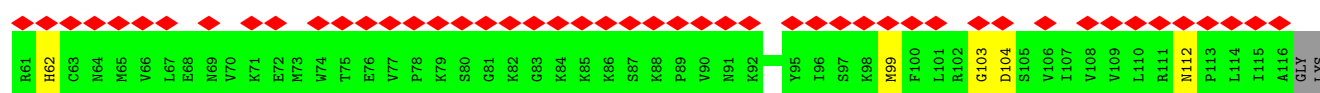
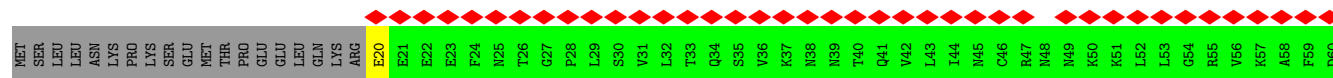
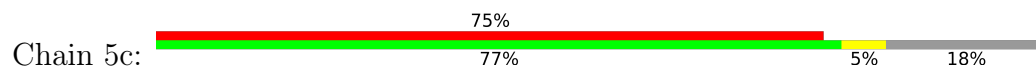


- Molecule 8: Small nuclear ribonucleoprotein Sm D1

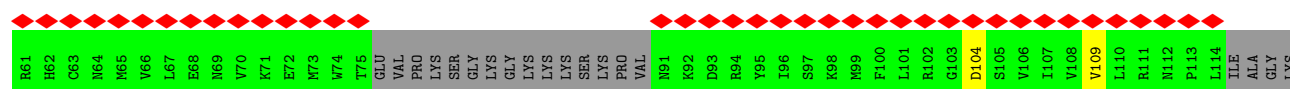




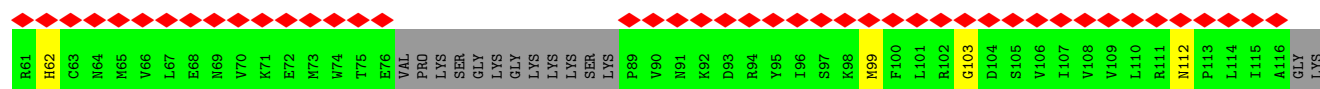
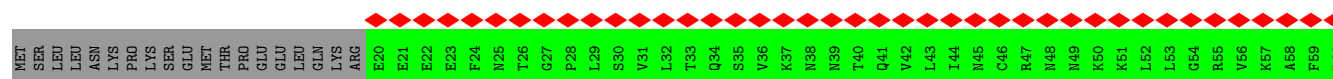
• Molecule 9: Small nuclear ribonucleoprotein Sm D2



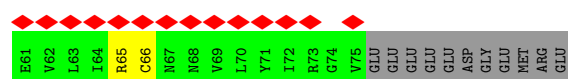
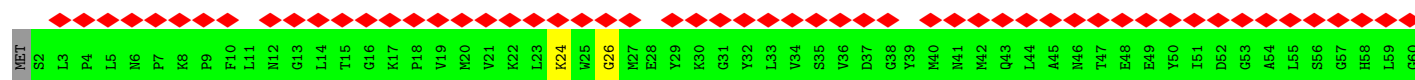
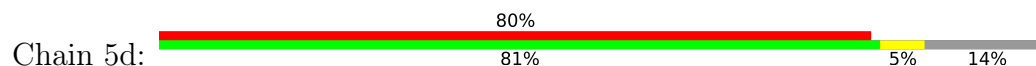
• Molecule 9: Small nuclear ribonucleoprotein Sm D2



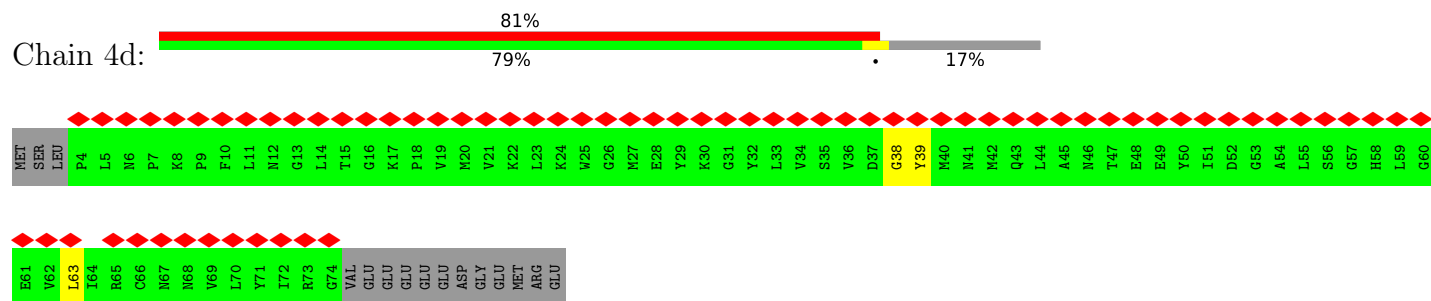
• Molecule 9: Small nuclear ribonucleoprotein Sm D2



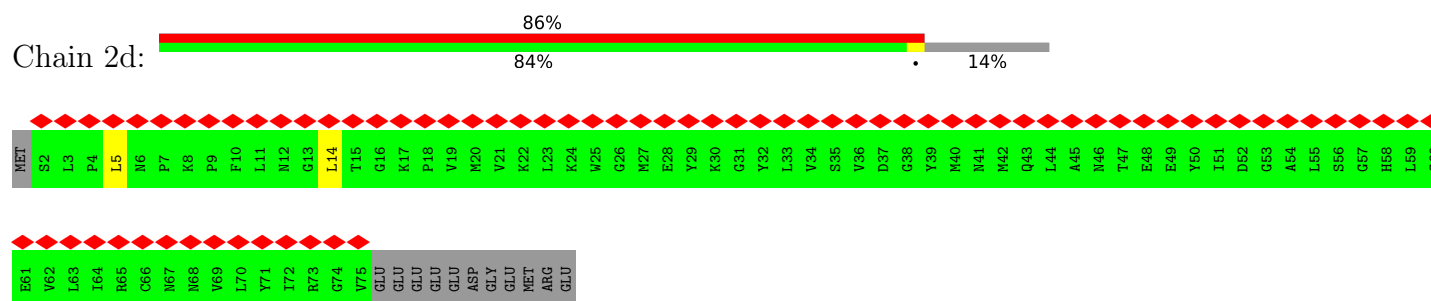
• Molecule 10: Small nuclear ribonucleoprotein F



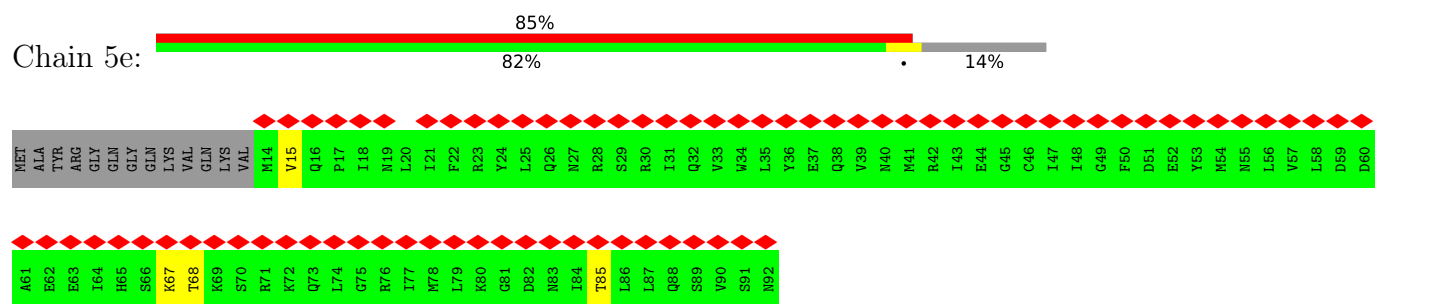
- Molecule 10: Small nuclear ribonucleoprotein F



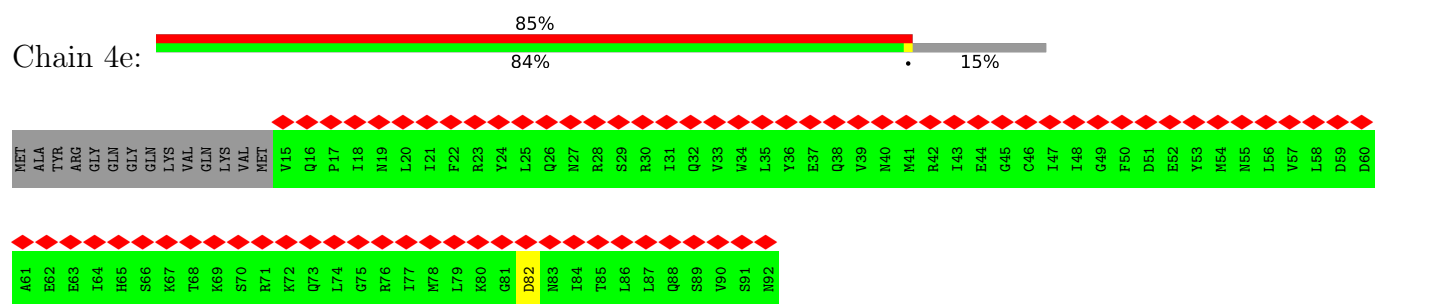
- Molecule 10: Small nuclear ribonucleoprotein F



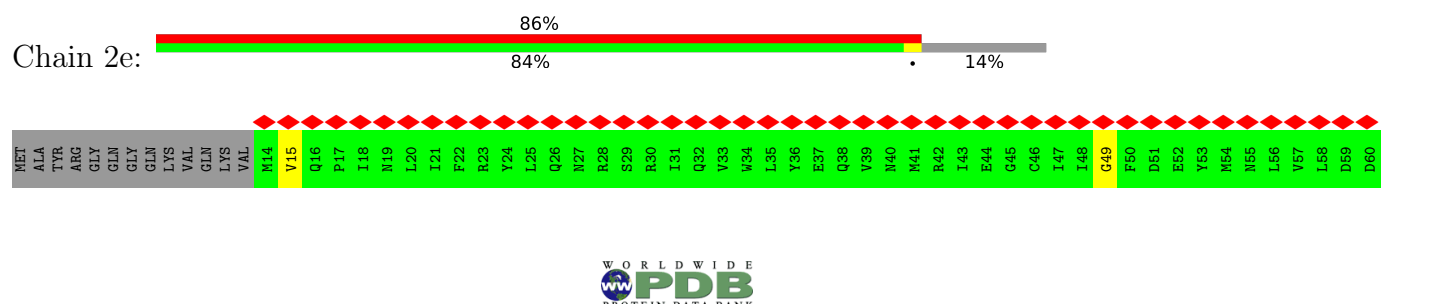
- Molecule 11: Small nuclear ribonucleoprotein E



- Molecule 11: Small nuclear ribonucleoprotein E

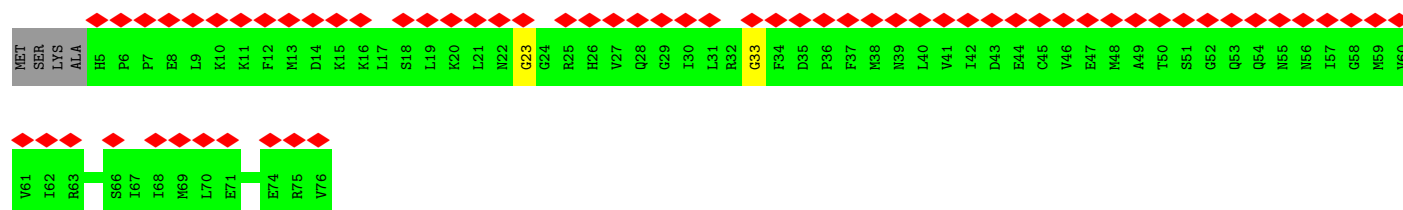
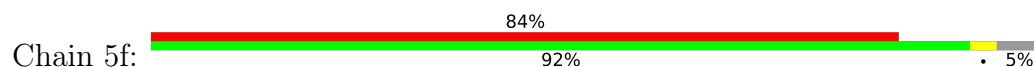


- Molecule 11: Small nuclear ribonucleoprotein E

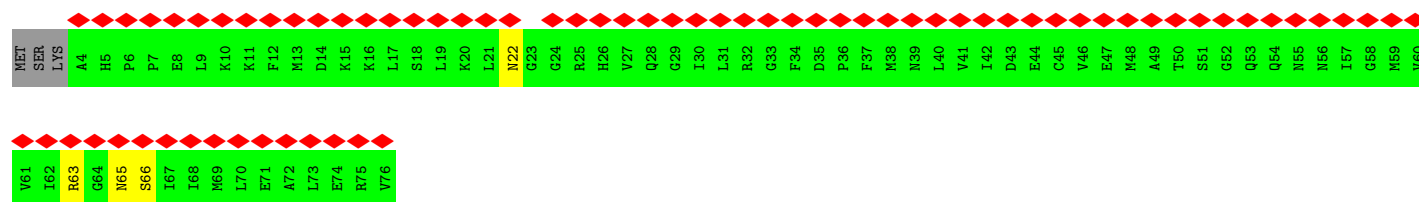
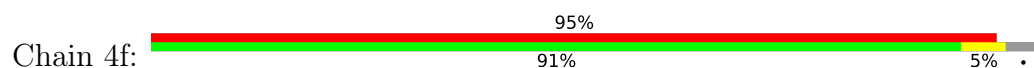




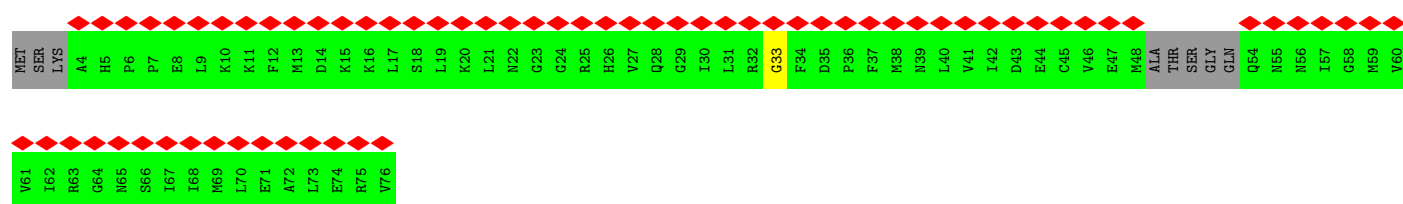
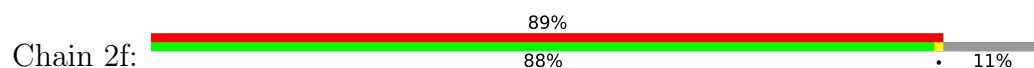
• Molecule 12: Small nuclear ribonucleoprotein G



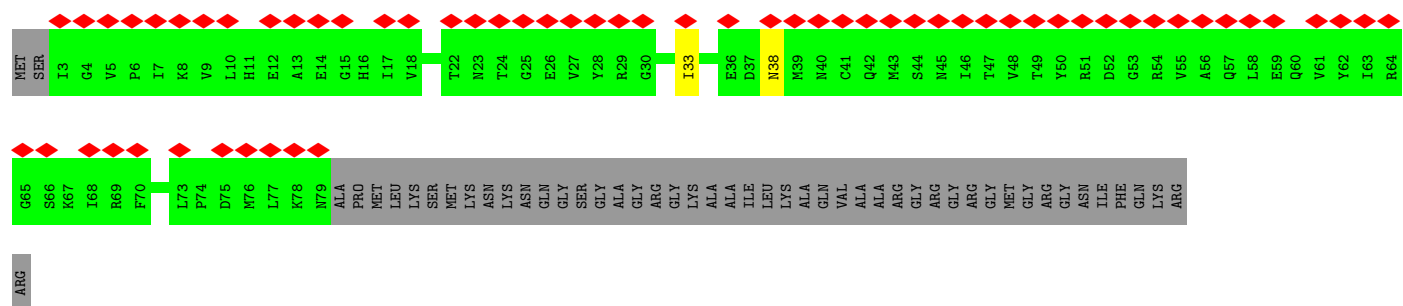
• Molecule 12: Small nuclear ribonucleoprotein G



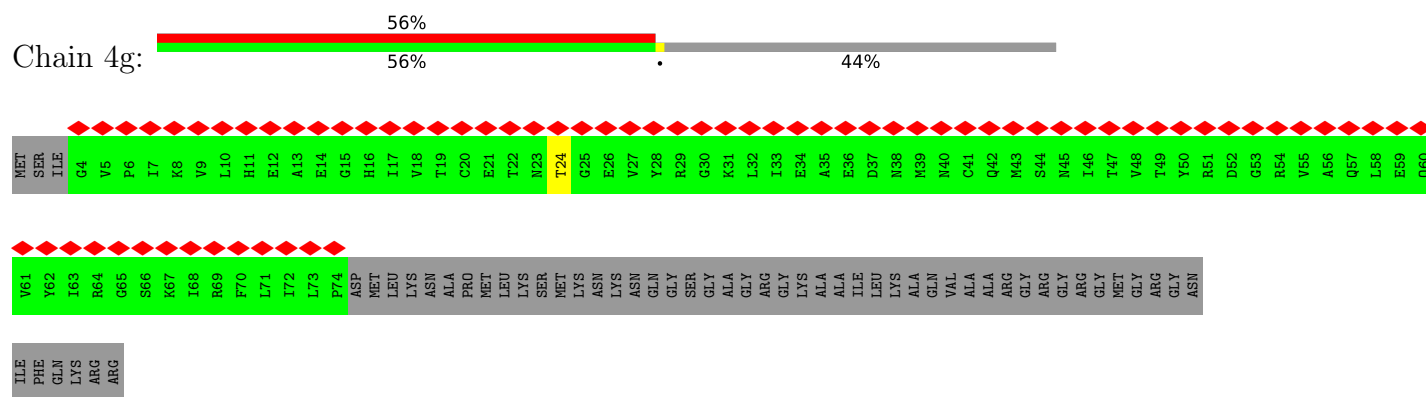
• Molecule 12: Small nuclear ribonucleoprotein G



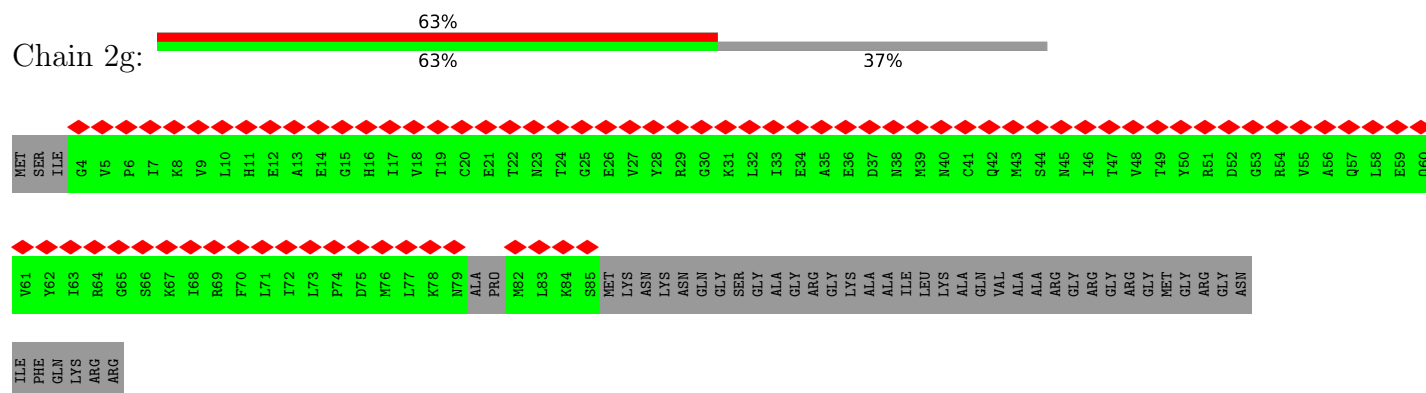
• Molecule 13: Small nuclear ribonucleoprotein Sm D3



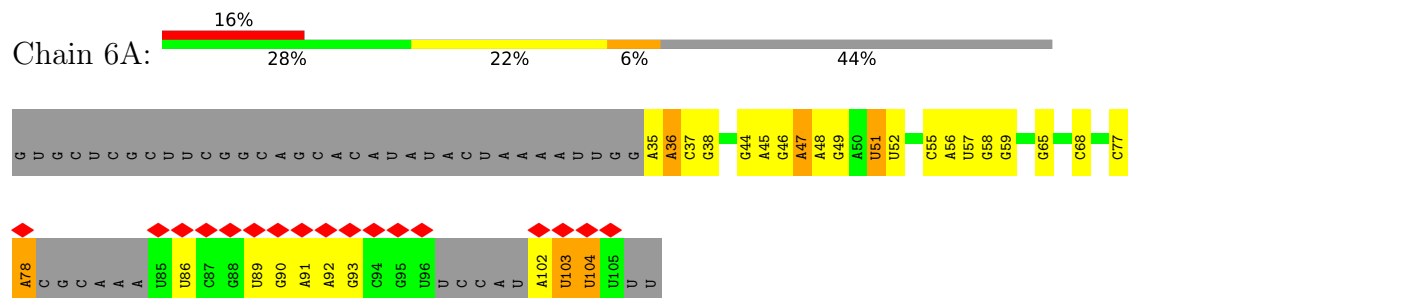
• Molecule 13: Small nuclear ribonucleoprotein Sm D3



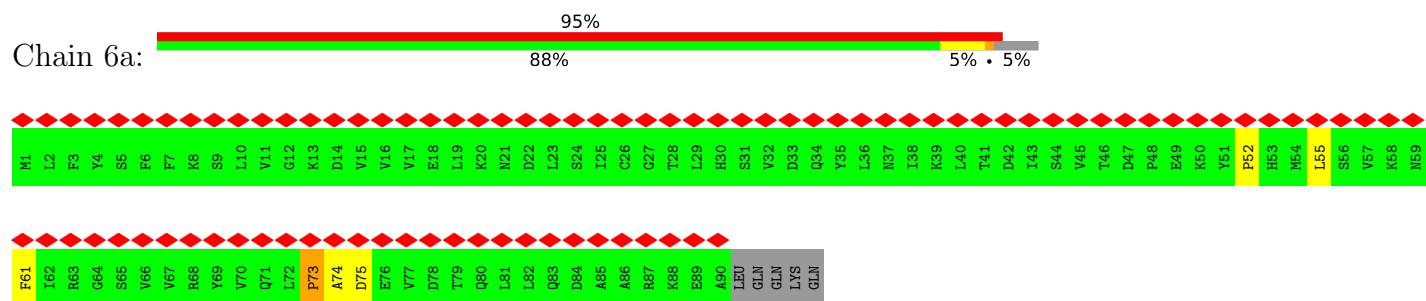
- Molecule 13: Small nuclear ribonucleoprotein Sm D3



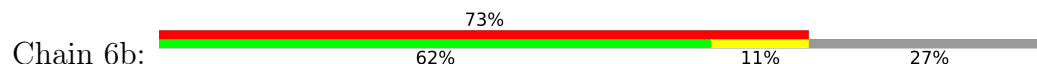
- Molecule 14: U6 snRNA



- Molecule 15: U6 snRNA-associated Sm-like protein LSm2

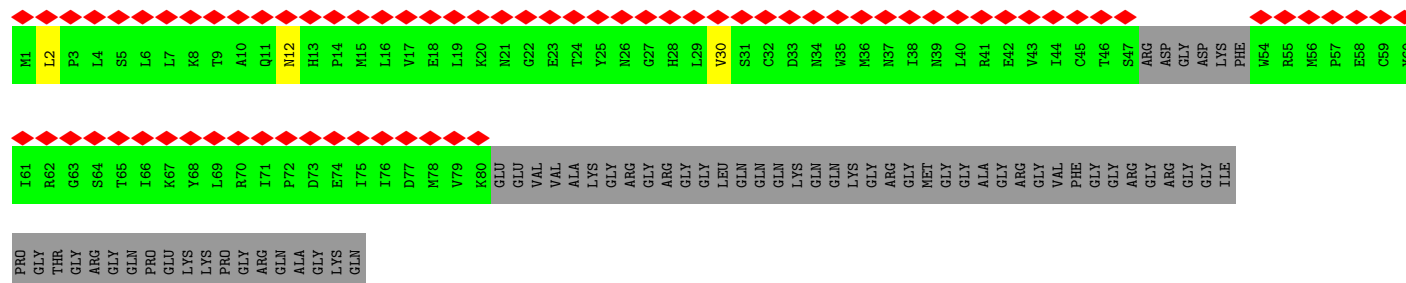


- Molecule 16: U6 snRNA-associated Sm-like protein LSm3

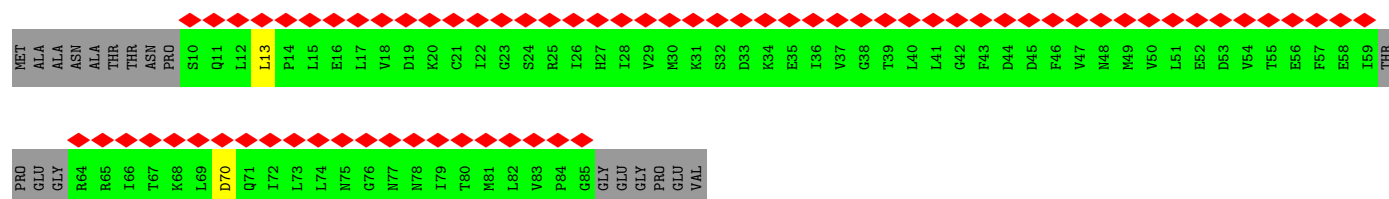
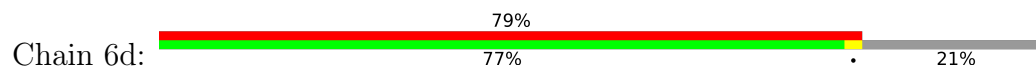




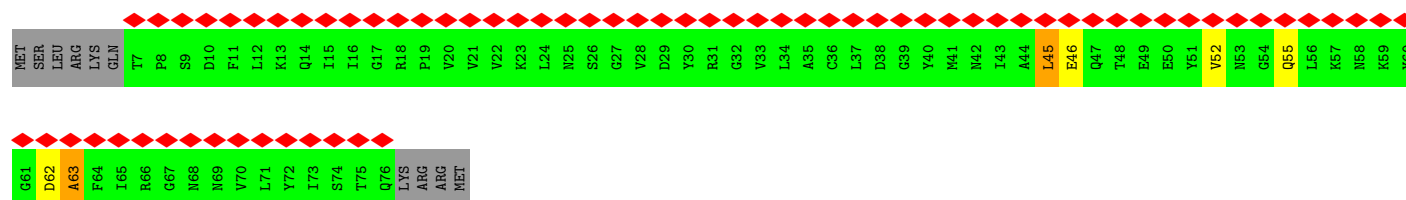
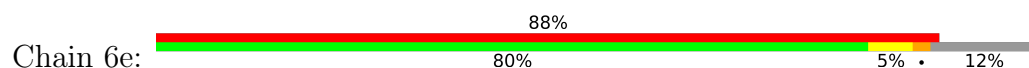
• Molecule 17: U6 snRNA-associated Sm-like protein LSm4



• Molecule 18: U6 snRNA-associated Sm-like protein LSm5

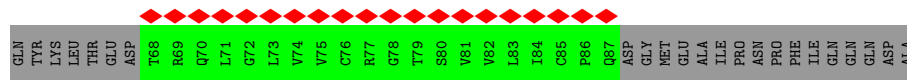


• Molecule 19: U6 snRNA-associated Sm-like protein LSm6

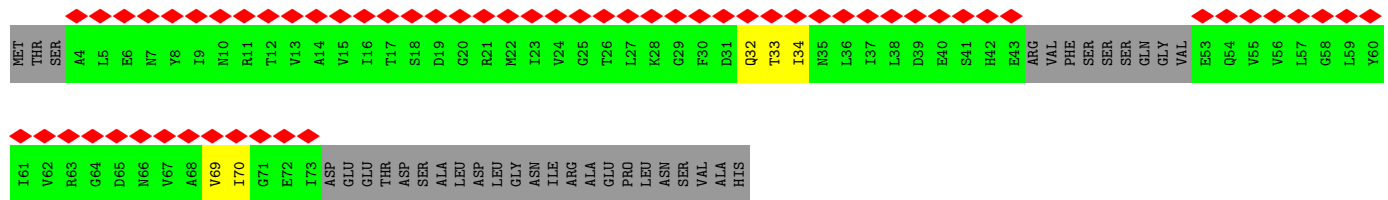


• Molecule 20: U6 snRNA-associated Sm-like protein LSm7

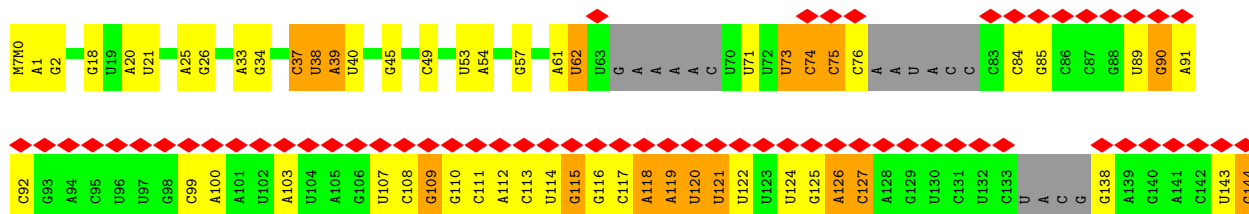
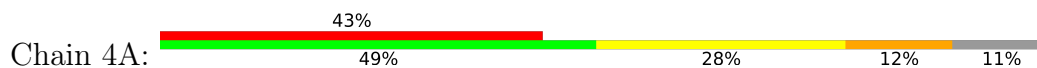




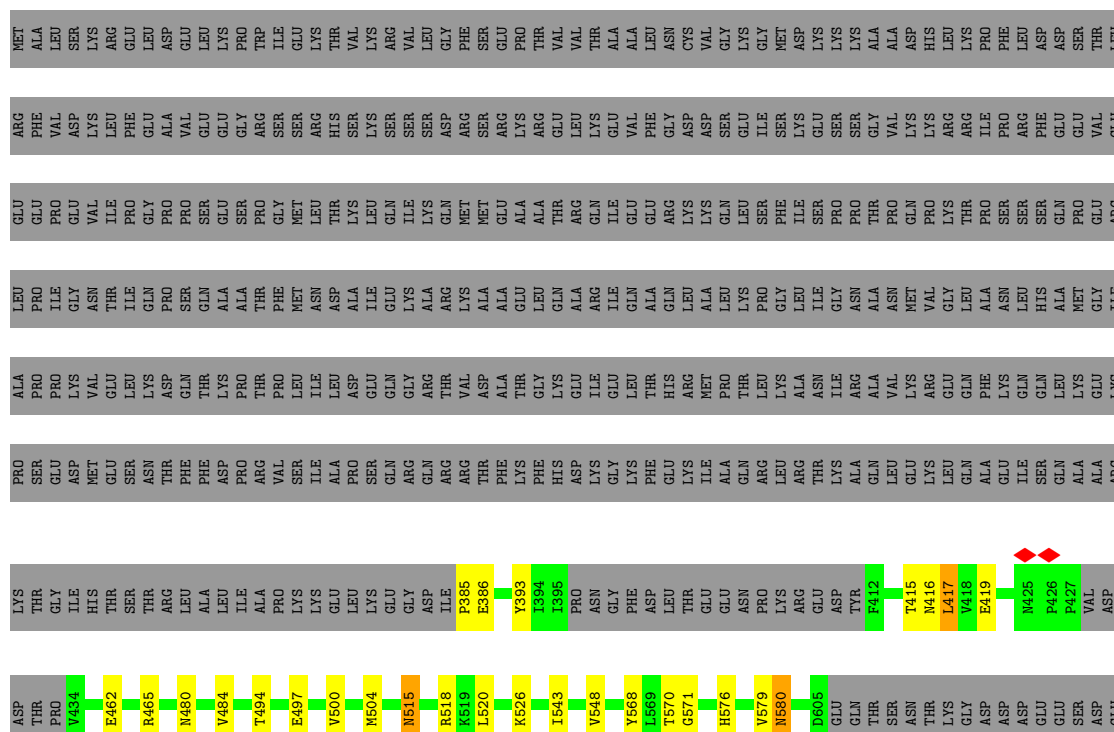
• Molecule 21: U6 snRNA-associated Sm-like protein LSm8



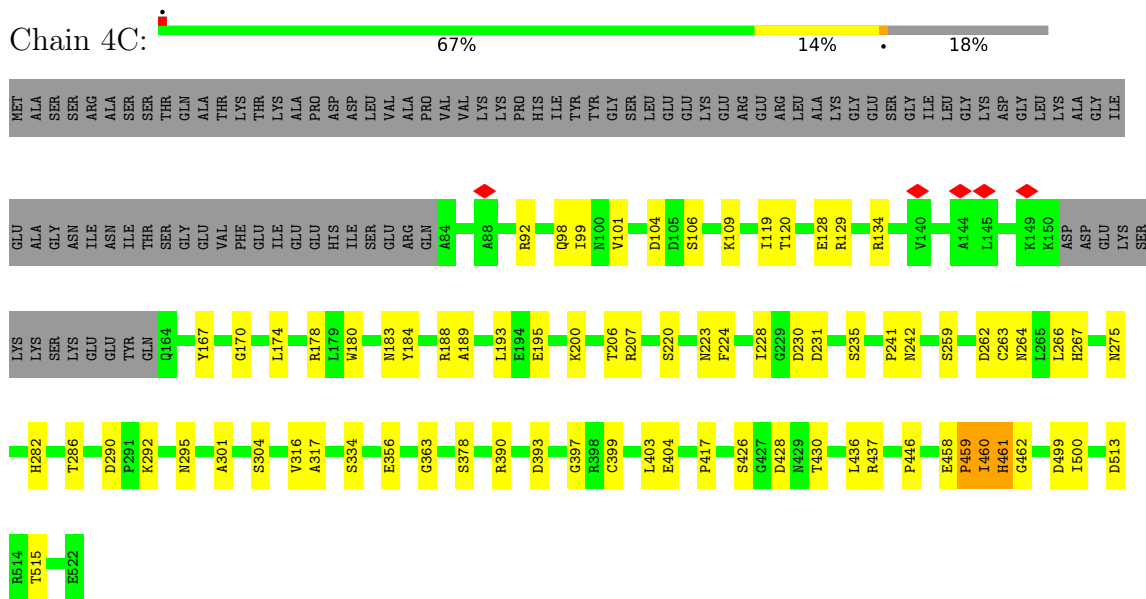
• Molecule 22: U4 snRNA



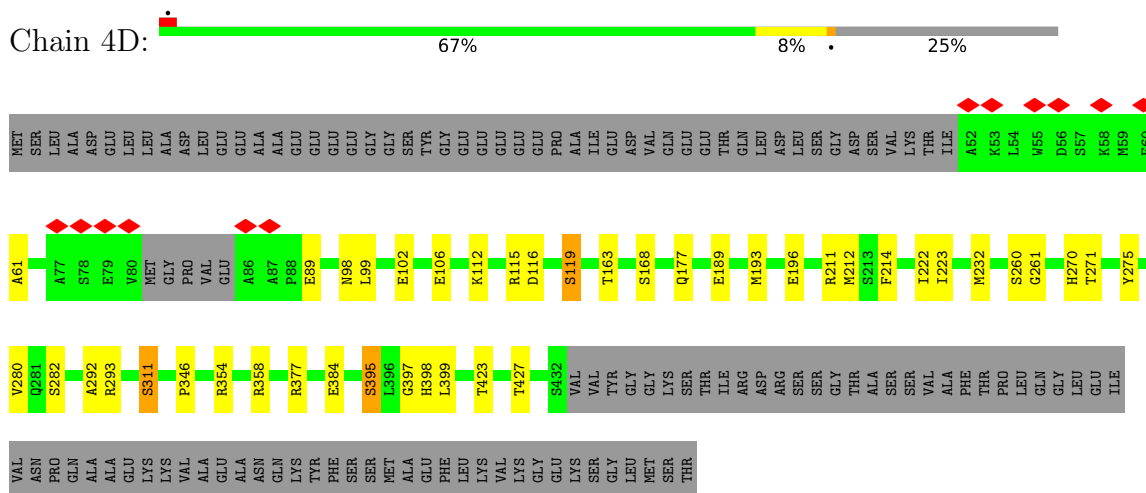
• Molecule 23: U4/U6 small nuclear ribonucleoprotein Prp3



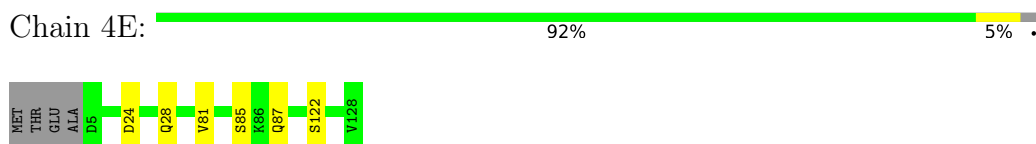
- Molecule 24: U4/U6 small nuclear ribonucleoprotein Prp4



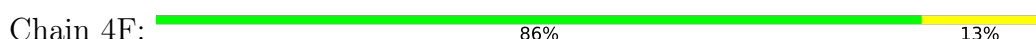
- Molecule 25: U4/U6 small nuclear ribonucleoprotein Prp31

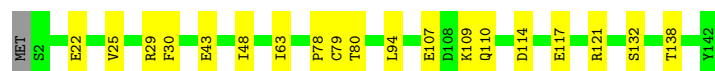


- Molecule 26: NHP2-like protein 1

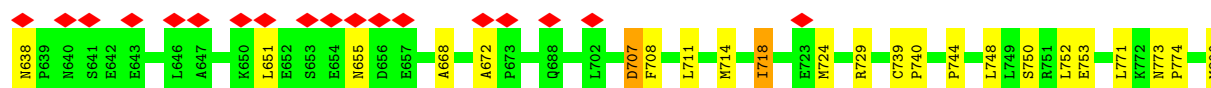
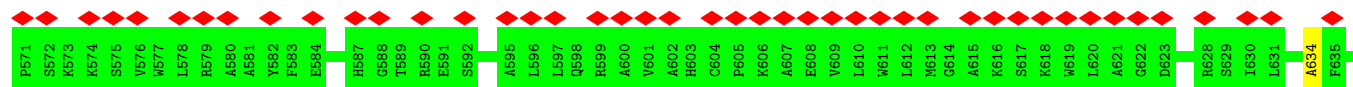
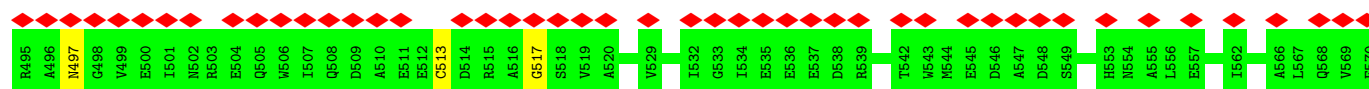
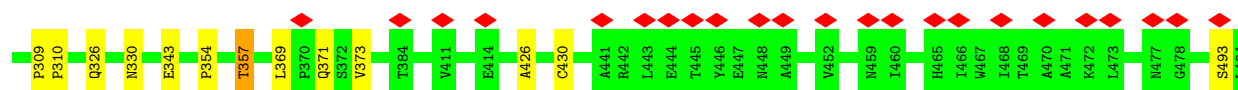
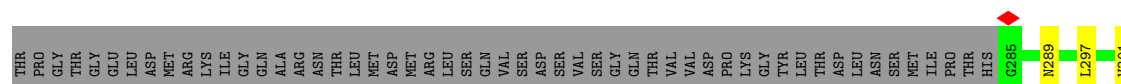
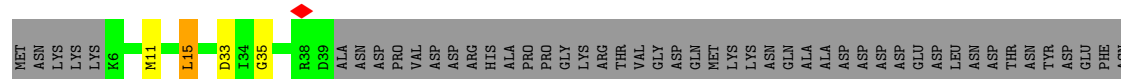
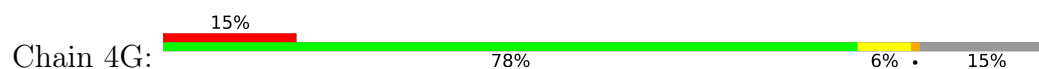


- Molecule 27: Thioredoxin-like protein 4A

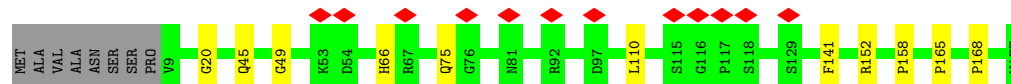
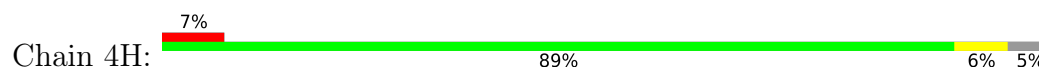




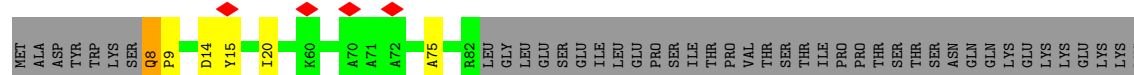
• Molecule 28: Pre-mRNA-processing factor 6



• Molecule 29: Peptidyl-prolyl cis-trans isomerase H

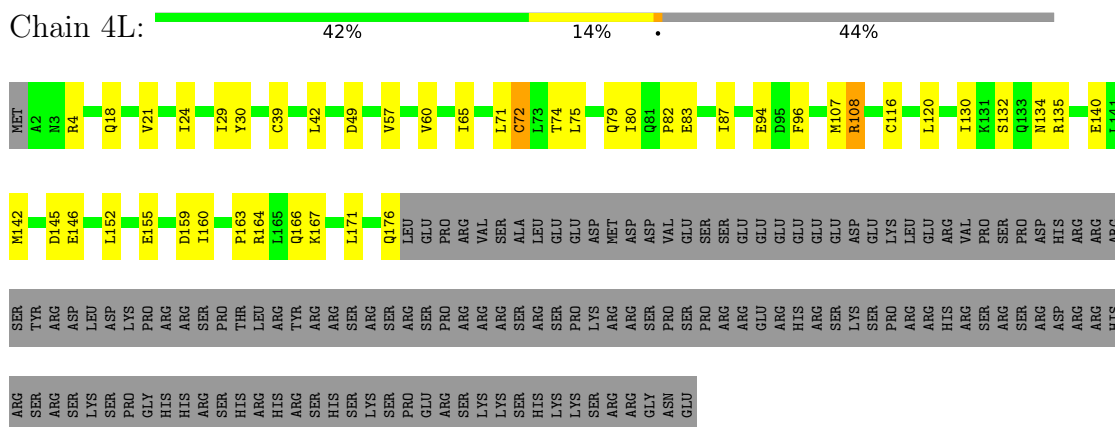


• Molecule 30: WW domain-binding protein 4

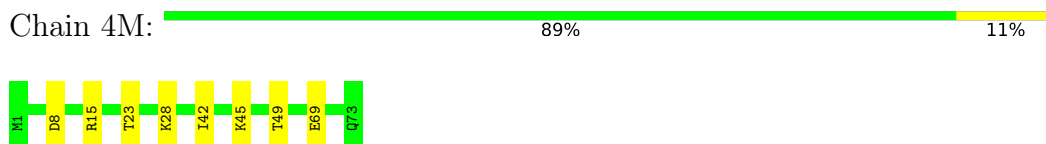




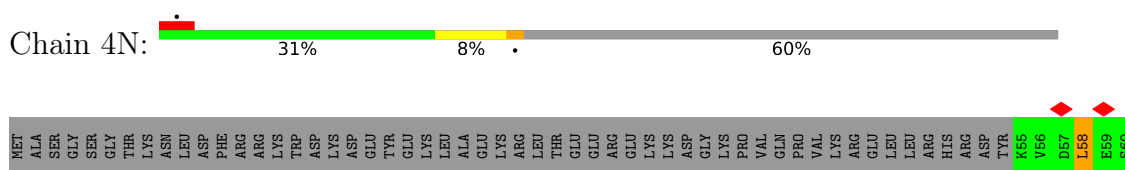
- Molecule 33: Pre-mRNA-splicing factor 38A



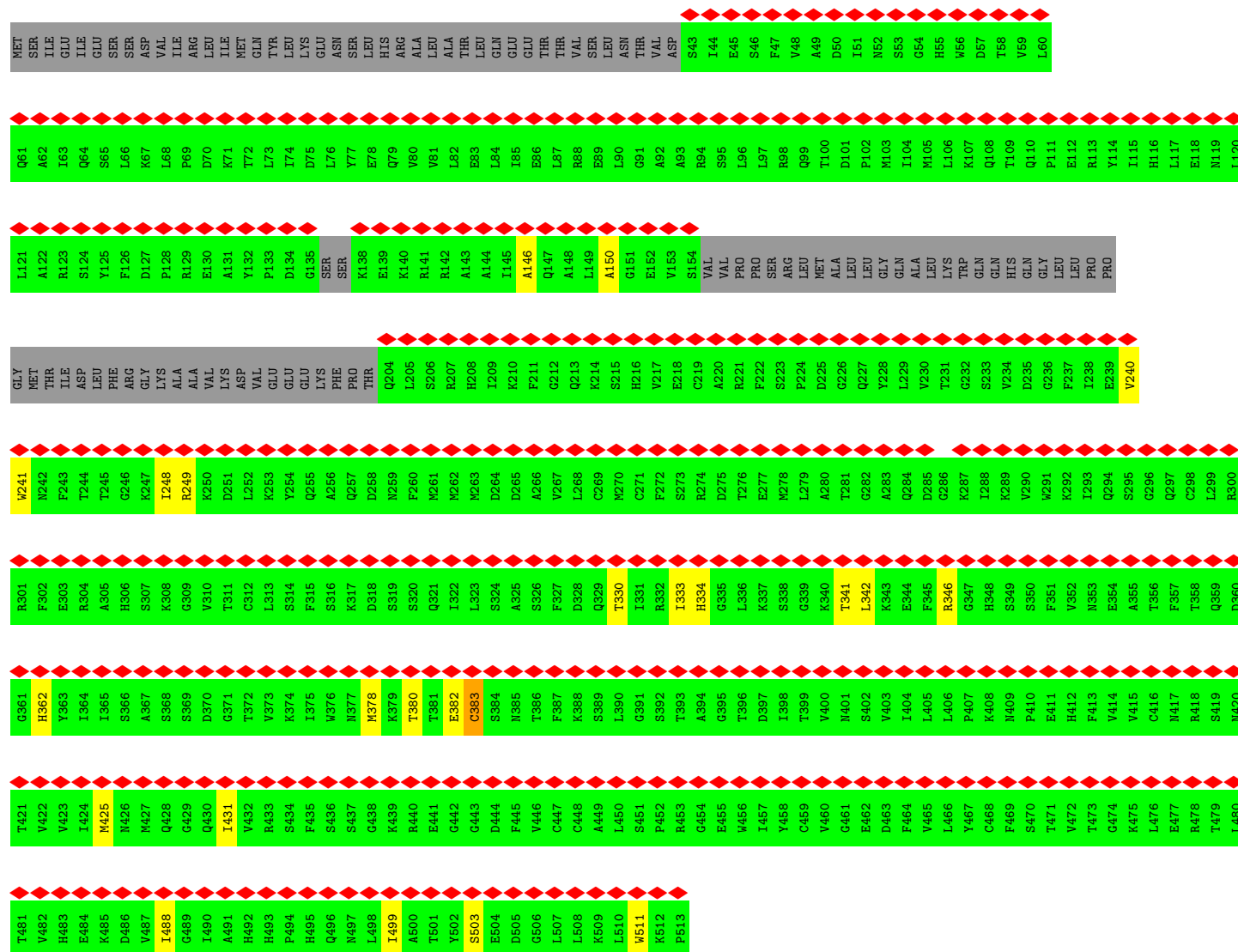
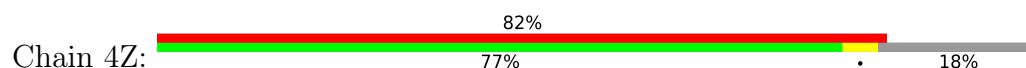
- Molecule 34: Ubiquitin-like protein 5



- Molecule 35: Zinc finger matrin-type protein 2

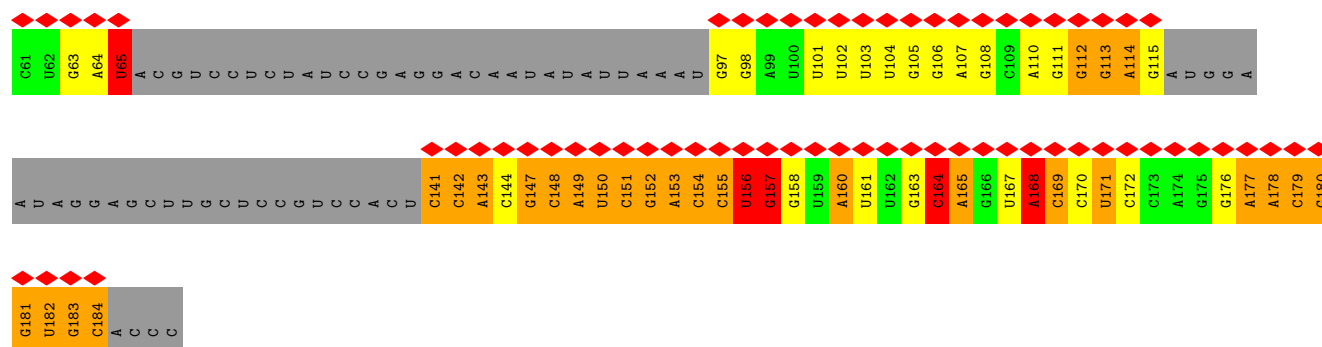


- Molecule 36: WD40 repeat-containing protein SMU1

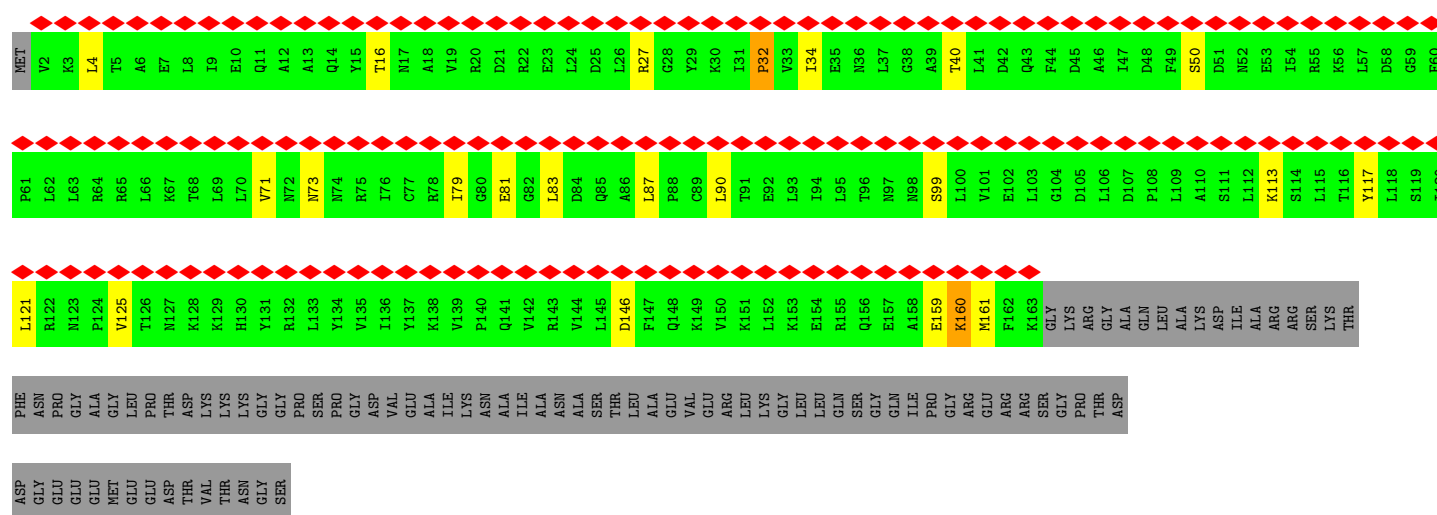


- Molecule 37: U2 snRNA

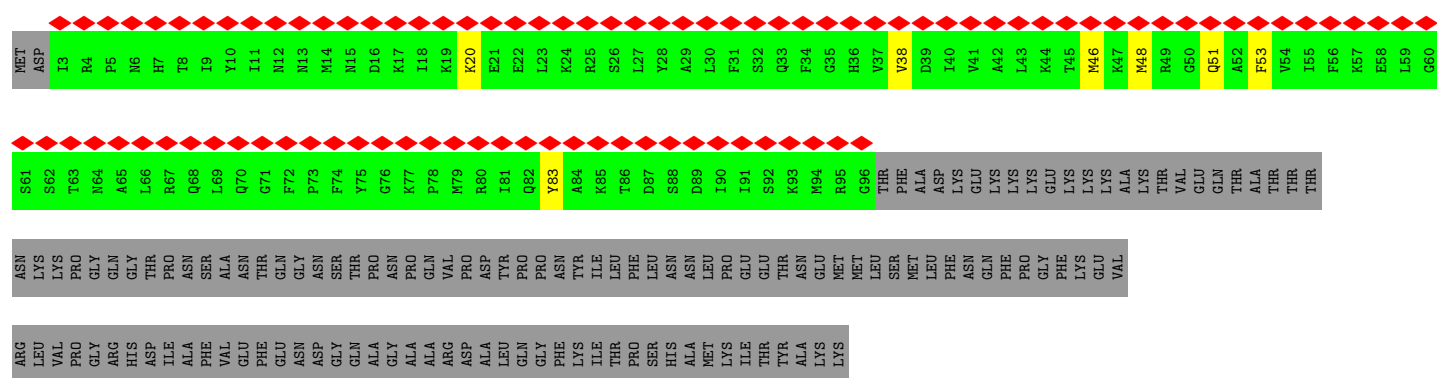




• Molecule 38: U2 small nuclear ribonucleoprotein A'



• Molecule 39: U2 small nuclear ribonucleoprotein B''



• Molecule 40: Splicing factor 3A subunit 1







ASP  
SER  
SER  
GLY  
ASN  
VAL  
VAL  
ASN  
ASN  
LYS  
LYS  
THR  
THR  
TYR  
GLU  
ASP  
LEU  
LEU

## ● Molecule 43: Splicing factor 3B subunit 1

Chain 2G: 

MET  
ALA  
LYS  
ILE  
ALA  
LYS  
THR  
HIS  
GLU  
ASP  
ILE  
GLU  
ALA  
GLN  
ILE  
ARG  
GLU  
LEU  
GLN  
GLY  
GLN  
VAL  
GLY  
LEU  
ASP  
SER  
THR  
GLY  
LYS  
ASP  
SER  
ARG  
PHE  
ALA  
GLY  
TYR  
VAL  
THR  
SER  
ILE  
ALA

THR  
GLU  
LEU  
GLU  
ASP  
ASP  
ASP  
TYR  
SER  
SER  
SER  
THR  
GLN  
SER  
ILE  
GLU  
ARG  
GLN  
GLY  
LYS  
LYS  
P82  
G83  
Y84  
H85  
A86  
P87  
V88  
A89  
L90  
L91  
N92  
D93  
I94  
P95  
Q96  
S97  
T98  
GLU  
GLN  
TYR  
ASP  
P103  
F104  
A105  
E106  
H107  
R108  
P109  
P110  
K111  
I112  
A113  
D114  
R115  
E116  
D117  
E118  
Y119  
K120

K121  
H122  
R123  
R124  
T125  
M126  
I127  
I128  
S129  
PRO  
GLU  
ARG  
LEU  
ASP  
PRO  
PHE  
ALA  
ASP  
GLY  
GLY  
LYS  
LYS  
G83  
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H85  
A86  
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A89  
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D93  
I94  
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Q96  
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GLU  
GLN  
TYR  
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E118  
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ARG  
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ARG  
TRP  
ASP  
GLN  
THR  
A204  
D205  
M206  
MET  
ASN  
ALA  
A208  
G209  
A210  
T211  
P212  
K213  
K214  
L215  
S216  
S217  
W218  
D219  
Q220  
A221  
E222  
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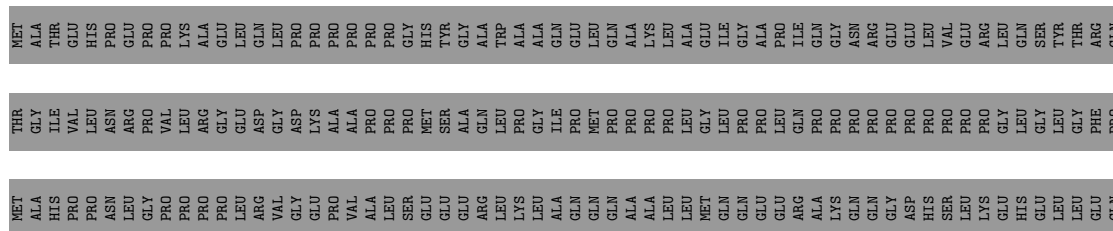
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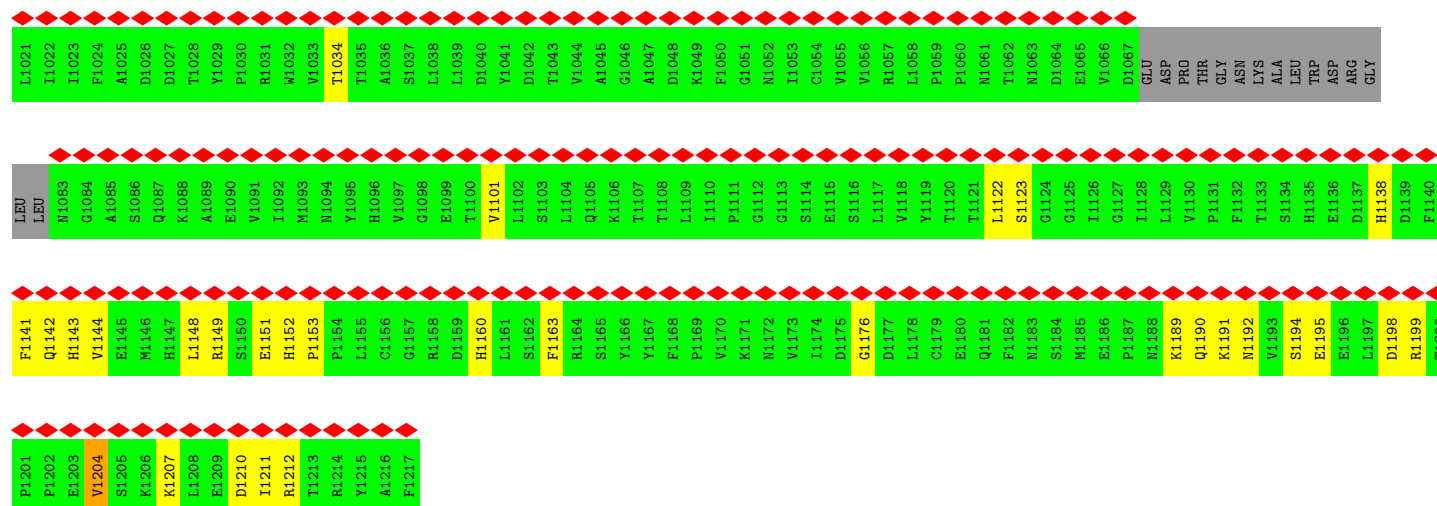
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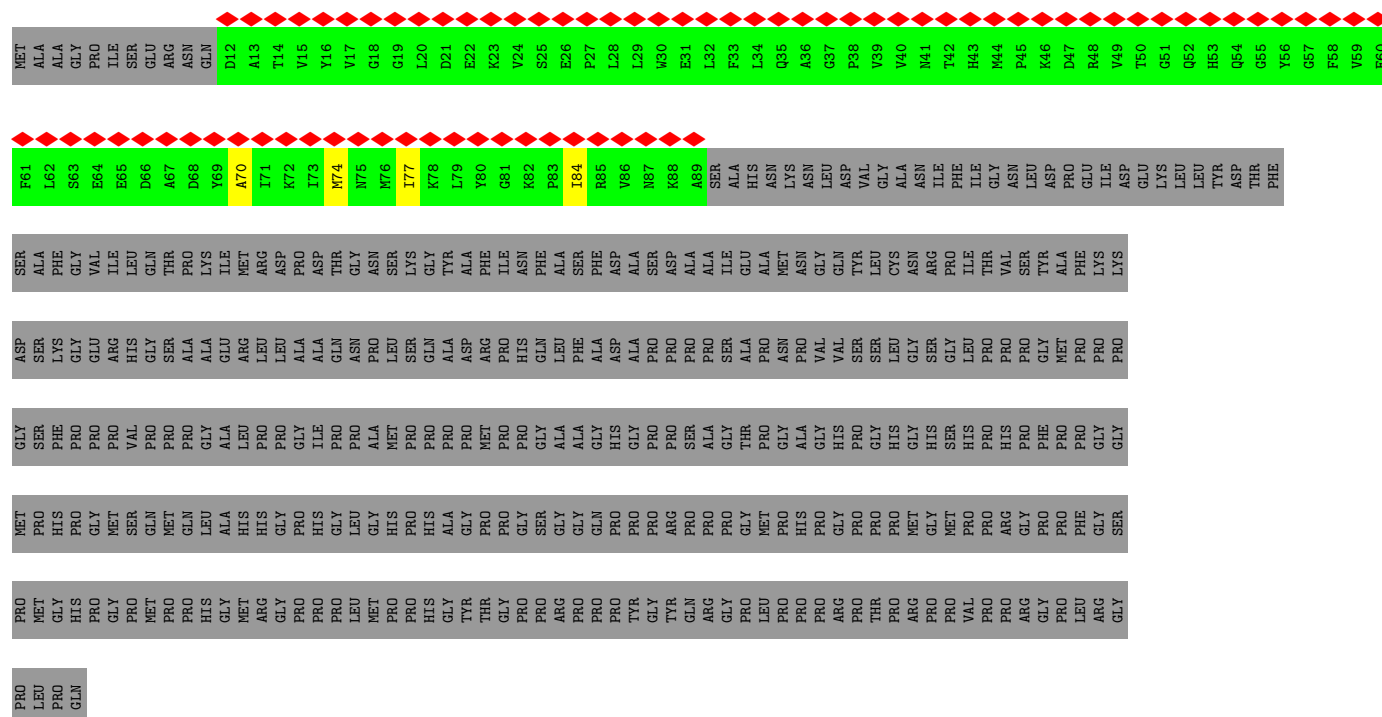




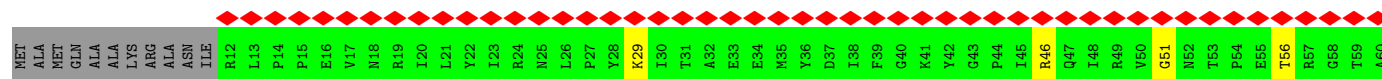
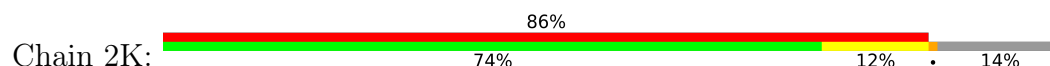
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| D902  | F842 | Q782 | S722 | F662 | S602 | K542 | T482 | Q422 | A362 | L302 | S242 | F182 |
| W903  | L843 | Q783 | Y723 | L663 | R603 | K543 | T483 | Q423 | H363 | A303 | S243 | A183 |
| Y904  | N844 | T784 | S724 | Y664 | F604 | I544 | V484 | Y424 | L364 | Q304 | G244 | C184 |
| V905  | E845 | P785 | Y725 | L665 | L605 | V545 | L485 | V425 | G365 | T305 | P245 | L185 |
| L906  | N846 | R786 | Q726 | N666 | A606 | K546 | S486 | A426 | D366 | E306 | S246 | E186 |
| Y907  | L847 | K787 | S727 | I667 | V607 | C547 | T487 | A427 | D367 | Q307 | G247 | M187 |
| G908  | P848 | F788 | R728 | G668 | G608 | A548 | Q488 | G428 | D368 | G308 | V248 | D188 |
| V909  | E849 | V789 | F729 | L669 | L609 | V549 | E489 | R429 | E369 | D309 | L249 | Y189 |
| A910  | S850 | T790 | H730 | Q670 | V610 | N550 | T490 | G430 | E370 | I310 | I250 | E190 |
| K911  | I851 | H791 | L731 | M671 | D611 | Q551 | V491 | P431 | P371 | F311 | C251 | E191 |
| D912  | F852 | P792 | T732 | G672 | N612 | R552 | E492 | R432 | E372 | K312 | S252 | A192 |
| L913  | G853 | T793 | P733 | V673 | T613 | Q553 | E493 | S433 | F373 | E253 | S253 | D193 |
| I914  | A854 | S794 | L734 | L674 | V614 | V554 | V494 | S434 | S374 | T314 | N254 | N194 |
| L915  | P855 | N795 | S735 | L675 | R615 | V555 | T495 | L435 | S375 | L315 | Y255 | D195 |
| N916  | K856 | N796 | V736 | R676 | I616 | I556 | D496 | R436 | A376 | E316 | I256 | P196 |
| P917  | A857 | T797 | E737 | T677 | I617 | A557 | S497 | V437 | M377 | T317 | T257 | T197 |
| R918  | G858 | I798 | T738 | V678 | S618 | L558 | Q498 | L438 | PR0  | D318 | Y258 | G198 |
| S919  | N859 | I799 | L739 | L679 | L619 | T559 | Q499 | R439 | GLU  | E319 | Y259 | E199 |
| V920  | G860 | I800 | E740 | D680 | D620 | G560 | L500 | HIS  | GLU  | D320 | N260 | A200 |
| A921  | Q861 | E801 | F741 | P681 | P621 | G561 | G501 | G441 | ASP  | M321 | F261 | A201 |
| Q922  | W862 | T802 | A742 | V682 | S622 | E562 | T502 | L442 | T384 | V322 | G262 | A202 |
| G923  | N863 | D803 | T743 | T683 | D623 | L563 | T503 | E443 | F384 | T263 | G263 | A202 |
| F924  | A864 | H804 | G744 | G684 | C624 | V564 | P504 | V444 | F385 | E324 | Q264 | T204 |
| V925  | V865 | N805 | F745 | D685 | L625 | Y565 | T505 | S445 | F386 | I325 | P265 | Q205 |
| Y926  | I866 | A806 | A746 | L686 | Q626 | F566 | L506 | E446 | F387 | R326 | D266 | Q206 |
| T927  | R867 | Y807 | S747 | S687 | P627 | E567 | S507 | M447 | Q388 | L327 | I267 | T207 |
| Y928  | V868 | T808 | E748 | D688 | L628 | M568 | C508 | A448 | P389 | K328 | R268 | L208 |
| K929  | N869 | E809 | Q749 | T689 | S629 | D569 | S509 | V449 | R390 | Y329 | C269 | T209 |
| L930  | N870 | A810 | C750 | R690 | M630 | P570 | L510 | S450 | P391 | F330 | P270 | F210 |
| S931  | P871 | T811 | P751 | T691 | Q631 | S571 | L511 | E451 | L392 | F331 | I271 | F211 |
| G932  | I872 | K812 | E752 | ARG  | A632 | G572 | G512 | L452 | K393 | T332 | P272 | E212 |
| N933  | Q873 | A813 | G753 | LEU  | L633 | Q573 | D513 | P453 | N394 | V333 | R273 | L213 |
| Q934  | G874 | Q814 | I754 | G695 | P634 | L574 | D514 | G454 | L395 | P334 | R274 | D214 |
| E935  | N875 | R815 | V755 | S696 | A635 | N575 | A515 | M455 | V396 | V335 | R275 | L215 |
| K936  | T876 | K816 | A756 | R697 | Q636 | E576 | L516 | P456 | L397 | A336 | N276 | G216 |
| L937  | L877 | Q817 | I757 | P698 | P637 | Y577 | V517 | M457 | V398 | A337 | D277 | L217 |
| E938  | D878 | Q818 | S758 | V699 | E638 | T578 | Q518 | A458 | D399 | A338 | L278 | N218 |
| F939  | L879 | M819 | T759 | R700 | S639 | E579 | V519 | V459 | E400 | M339 | D279 | H219 |
| L940  | V880 | A820 | N760 | L701 | L640 | R580 | Y520 | M460 | L401 | C340 | D280 | V220 |
| H941  | Q881 | E821 | T761 | F702 | C641 | K581 | P521 | T461 | D402 | V341 | V221 | V221 |
| K942  | L882 | E822 | L762 | R703 | I642 | E582 | D522 | V462 | S403 | L342 | E282 | R222 |
| T943  | S883 | M823 | R763 | V704 | E643 | M583 | G523 | R463 | L404 | K223 | G284 | K223 |
| D1004 | Q884 | V824 | I764 | R705 | E644 | S584 | I524 | R464 | S405 | T344 | G284 | Y224 |
| V945  | N885 | E825 | L765 | M706 | M645 | A585 | R525 | H465 | P406 | G345 | M285 | Z224 |
| E946  | E886 | A826 | A766 | Q707 | GLY  | D586 | H526 | I466 | I407 | F346 | E226 | E226 |
| E947  | A887 | A827 | L767 | Q708 | GLY  | V587 | I527 | E467 | L408 | P227 | L286 | E227 |
| V948  | L888 | GLY  | E768 | T709 | THR  | V588 | R528 | D468 | F409 | F227 | I288 | L228 |
| P949  | F889 | ASP  | K769 | Q709 | GLU  | V589 | A529 | E469 | C410 | V288 | C289 | E229 |
| A950  | S890 | GLU  | L770 | LYS  | GLN  | C589 | R529 | F470 | Q411 | V349 | S290 | E230 |
| W1011 | V891 | ARG  | L771 | A711 | ASP  | M590 | D530 | D471 | I412 | A350 | S290 | E230 |
| L952  | A892 | GLU  | G771 | V712 | GLU  | L592 | R532 | A472 | E352 | A413 | T292 | G232 |
| A953  | R893 | LEU  | V773 | L713 | LEU  | A593 | V533 | Y473 | D414 | F353 | H293 | G233 |
| P954  | C894 | A835 | F774 | A714 | GLY  | N594 | N534 | I474 | L415 | G354 | K294 | F234 |
| F955  | R895 | A836 | N775 | ARG  | GLU  | V595 | E535 | I475 | A416 | N355 | T295 | L235 |
| Q956  | F896 | E837 | Q776 | T716 | GLY  | V596 | E536 | V476 | N417 | H356 | K296 | I236 |
| R1016 | K957 | M838 | V777 | S717 | SER  | P596 | M536 | S477 | E418 | Y357 | T297 | L237 |
| N1017 | S897 | T718 | V778 | T718 | ILE  | P597 | K537 | V478 | T297 | L358 | M298 | V238 |
| E1018 | N898 | A839 | A778 | S719 |      | G598 | T538 | F479 | D419 | F239 | M299 | V239 |
| N1019 | V899 | A840 | F779 | S719 |      | E599 | P539 | V479 | T420 | Y359 | F299 | G240 |
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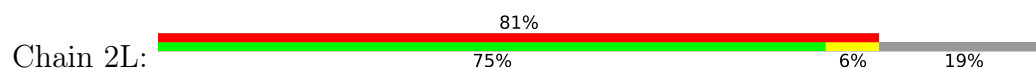
• Molecule 46: Splicing factor 3B subunit 4



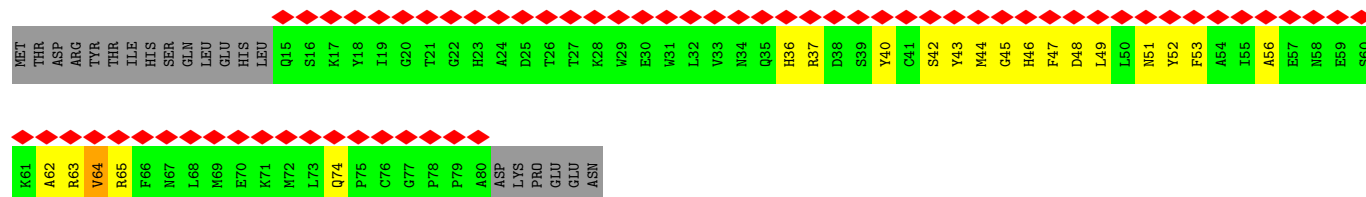
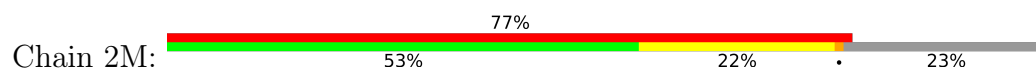
• Molecule 47: Splicing factor 3B subunit 6



- Molecule 48: PHD finger-like domain-containing protein 5A



- Molecule 49: Splicing factor 3B subunit 5



## 4 Experimental information

| Property                             | Value               | Source    |
|--------------------------------------|---------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE     | Depositor |
| Imposed symmetry                     | POINT, Not provided |           |
| Number of particles used             | 414060              | Depositor |
| Resolution determination method      | FSC 0.143 CUT-OFF   | Depositor |
| CTF correction method                | NONE                | Depositor |
| Microscope                           | FEI TITAN KRIOS     | Depositor |
| Voltage (kV)                         | 300                 | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 50                  | Depositor |
| Minimum defocus (nm)                 | 1000                | Depositor |
| Maximum defocus (nm)                 | 2500                | Depositor |
| Magnification                        | Not provided        |           |
| Image detector                       | GATAN K3 (6k x 4k)  | Depositor |
| Maximum map value                    | 0.173               | Depositor |
| Minimum map value                    | -0.110              | Depositor |
| Average map value                    | -0.000              | Depositor |
| Map value standard deviation         | 0.003               | Depositor |
| Recommended contour level            | 0.01                | Depositor |
| Map size ( $\text{\AA}$ )            | 563.2, 563.2, 563.2 | wwPDB     |
| Map dimensions                       | 512, 512, 512       | wwPDB     |
| Map angles ( $^\circ$ )              | 90.0, 90.0, 90.0    | wwPDB     |
| Pixel spacing ( $\text{\AA}$ )       | 1.1, 1.1, 1.1       | Depositor |

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, IHP, MG, GTP, M7M

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

| Mol | Chain | Bond lengths |               | Bond angles |                |
|-----|-------|--------------|---------------|-------------|----------------|
|     |       | RMSZ         | # Z  >5       | RMSZ        | # Z  >5        |
| 1   | A     | 0.62         | 6/1481 (0.4%) | 0.71        | 2/2297 (0.1%)  |
| 2   | 5A    | 0.24         | 0/2698        | 0.43        | 1/4195 (0.0%)  |
| 3   | 5B    | 0.14         | 0/19154       | 0.32        | 1/26000 (0.0%) |
| 4   | 5C    | 0.14         | 0/6573        | 0.36        | 0/8929         |
| 5   | 5D    | 0.15         | 0/13923       | 0.32        | 2/18868 (0.0%) |
| 6   | 5E    | 1.08         | 0/1195        | 1.21        | 5/1492 (0.3%)  |
| 7   | 2a    | 0.86         | 0/343         | 1.21        | 3/427 (0.7%)   |
| 7   | 4a    | 0.13         | 0/254         | 0.39        | 0/314          |
| 7   | 5a    | 0.85         | 0/335         | 1.18        | 2/417 (0.5%)   |
| 8   | 2b    | 0.89         | 0/327         | 1.11        | 0/407          |
| 8   | 4b    | 0.15         | 0/333         | 0.46        | 0/416          |
| 8   | 5b    | 0.89         | 0/327         | 1.11        | 0/407          |
| 9   | 2c    | 1.18         | 0/338         | 1.20        | 1/419 (0.2%)   |
| 9   | 4c    | 0.16         | 0/298         | 0.49        | 0/370          |
| 9   | 5c    | 1.14         | 0/387         | 1.21        | 1/482 (0.2%)   |
| 10  | 2d    | 1.24         | 1/295 (0.3%)  | 1.26        | 0/367          |
| 10  | 4d    | 0.21         | 0/291         | 0.47        | 0/363          |
| 10  | 5d    | 1.23         | 0/295         | 1.26        | 0/367          |
| 11  | 2e    | 1.02         | 0/315         | 1.26        | 0/392          |
| 11  | 4e    | 0.17         | 0/313         | 0.47        | 0/390          |
| 11  | 5e    | 1.03         | 0/315         | 1.27        | 1/392 (0.3%)   |
| 12  | 2f    | 0.86         | 0/270         | 1.05        | 0/334          |
| 12  | 4f    | 0.24         | 0/297         | 0.59        | 0/371          |
| 12  | 5f    | 0.85         | 0/287         | 1.03        | 0/357          |
| 13  | 2g    | 0.81         | 0/318         | 1.01        | 0/394          |
| 13  | 4g    | 0.14         | 0/287         | 0.35        | 0/358          |
| 13  | 5g    | 0.78         | 0/307         | 1.01        | 0/382          |
| 14  | 6A    | 0.14         | 0/1423        | 0.29        | 0/2211         |
| 15  | 6a    | 0.69         | 0/359         | 1.28        | 0/447          |
| 16  | 6b    | 0.75         | 0/294         | 1.37        | 3/364 (0.8%)   |
| 17  | 6c    | 0.58         | 0/294         | 1.32        | 3/364 (0.8%)   |
| 18  | 6d    | 0.71         | 0/286         | 1.28        | 2/354 (0.6%)   |

| Mol | Chain | Bond lengths |                  | Bond angles |                   |
|-----|-------|--------------|------------------|-------------|-------------------|
|     |       | RMSZ         | # Z  >5          | RMSZ        | # Z  >5           |
| 19  | 6e    | 0.71         | 0/279            | 1.40        | 2/347 (0.6%)      |
| 20  | 6f    | 0.60         | 0/258            | 1.14        | 0/319             |
| 21  | 6g    | 0.67         | 0/242            | 1.21        | 1/299 (0.3%)      |
| 22  | 4A    | 0.19         | 0/3025           | 0.36        | 0/4702            |
| 23  | 4B    | 0.12         | 0/2114           | 0.32        | 0/2836            |
| 24  | 4C    | 0.14         | 0/3452           | 0.33        | 0/4675            |
| 25  | 4D    | 0.12         | 0/2912           | 0.29        | 0/3924            |
| 26  | 4E    | 0.10         | 0/974            | 0.27        | 0/1316            |
| 27  | 4F    | 0.24         | 0/1198           | 0.47        | 2/1620 (0.1%)     |
| 28  | 4G    | 0.11         | 0/5592           | 0.33        | 2/7615 (0.0%)     |
| 29  | 4H    | 0.17         | 0/853            | 0.33        | 0/1188            |
| 30  | 4I    | 0.13         | 0/502            | 0.27        | 0/683             |
| 31  | 4J    | 0.11         | 0/1149           | 0.29        | 0/1542            |
| 32  | 4K    | 0.13         | 0/1209           | 0.30        | 0/1655            |
| 33  | 4L    | 0.14         | 0/1481           | 0.39        | 0/1995            |
| 34  | 4M    | 0.10         | 0/609            | 0.30        | 0/819             |
| 35  | 4N    | 0.17         | 0/646            | 0.37        | 0/859             |
| 36  | 4Z    | 0.17         | 0/2100           | 0.48        | 1/2926 (0.0%)     |
| 37  | 2A    | 0.71         | 12/2576 (0.5%)   | 1.11        | 27/4003 (0.7%)    |
| 38  | 2B    | 0.99         | 0/647            | 2.34        | 33/807 (4.1%)     |
| 39  | 2C    | 0.97         | 0/375            | 1.97        | 7/467 (1.5%)      |
| 40  | 2D    | 0.26         | 0/1139           | 0.68        | 2/1477 (0.1%)     |
| 41  | 2E    | 0.38         | 0/373            | 1.77        | 4/461 (0.9%)      |
| 42  | 2F    | 0.38         | 0/1688           | 0.92        | 3/2102 (0.1%)     |
| 43  | 2G    | 1.72         | 38/4184 (0.9%)   | 1.43        | 27/5216 (0.5%)    |
| 44  | 2H    | 1.02         | 0/957            | 1.08        | 2/1209 (0.2%)     |
| 45  | 2I    | 1.39         | 25/4664 (0.5%)   | 1.20        | 9/5816 (0.2%)     |
| 46  | 2J    | 1.02         | 0/311            | 0.99        | 0/387             |
| 47  | 2K    | 1.27         | 2/431 (0.5%)     | 1.27        | 1/537 (0.2%)      |
| 48  | 2L    | 1.16         | 0/355            | 1.11        | 0/442             |
| 49  | 2M    | 1.59         | 1/263 (0.4%)     | 1.23        | 0/327             |
| All | All   | 0.60         | 85/100770 (0.1%) | 0.69        | 150/136218 (0.1%) |

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

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 3   | 5B    | 0                   | 1                   |
| 9   | 2c    | 0                   | 1                   |
| 9   | 5c    | 0                   | 1                   |

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| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 42  | 2F    | 0                   | 1                   |
| 43  | 2G    | 0                   | 11                  |
| 44  | 2H    | 0                   | 3                   |
| 45  | 2I    | 0                   | 11                  |
| 47  | 2K    | 0                   | 1                   |
| 49  | 2M    | 0                   | 1                   |
| All | All   | 0                   | 31                  |

The worst 5 of 85 bond length outliers are listed below:

| Mol | Chain | Res  | Type | Atoms | Z     | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|-------|-------|-------------|----------|
| 43  | 2G    | 407  | MET  | N-CA  | 22.52 | 1.71        | 1.46     |
| 43  | 2G    | 406  | ALA  | C-N   | 14.95 | 1.52        | 1.33     |
| 43  | 2G    | 1243 | PRO  | N-CA  | -9.49 | 1.35        | 1.47     |
| 43  | 2G    | 944  | SER  | N-CA  | -8.41 | 1.34        | 1.46     |
| 45  | 2I    | 84   | SER  | CA-C  | -7.80 | 1.42        | 1.53     |

The worst 5 of 150 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms  | Z      | Observed(°) | Ideal(°) |
|-----|-------|-----|------|--------|--------|-------------|----------|
| 41  | 2E    | 146 | MET  | CA-C-N | 21.07  | 146.17      | 119.84   |
| 41  | 2E    | 146 | MET  | C-N-CA | 21.07  | 146.17      | 119.84   |
| 43  | 2G    | 406 | ALA  | CA-C-N | 17.67  | 147.39      | 120.89   |
| 43  | 2G    | 406 | ALA  | C-N-CA | 17.67  | 147.39      | 120.89   |
| 43  | 2G    | 406 | ALA  | CA-C-O | -13.04 | 105.77      | 120.24   |

There are no chirality outliers.

5 of 31 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group     |
|-----|-------|-----|------|-----------|
| 42  | 2F    | 443 | THR  | Peptide   |
| 43  | 2G    | 220 | GLN  | Peptide   |
| 43  | 2G    | 415 | LEU  | Mainchain |
| 3   | 5B    | 941 | LYS  | Peptide   |
| 9   | 5c    | 112 | ASN  | Peptide   |

## 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     | 1334  | 0        | 681      | 160     | 0            |
| 2   | 5A    | 2420  | 0        | 1226     | 82      | 0            |
| 3   | 5B    | 18639 | 0        | 18495    | 192     | 0            |
| 4   | 5C    | 6430  | 0        | 6446     | 114     | 0            |
| 5   | 5D    | 13633 | 0        | 13769    | 315     | 0            |
| 6   | 5E    | 1196  | 0        | 337      | 2       | 0            |
| 7   | 2a    | 344   | 0        | 93       | 4       | 0            |
| 7   | 4a    | 256   | 0        | 70       | 2       | 0            |
| 7   | 5a    | 336   | 0        | 89       | 0       | 0            |
| 8   | 2b    | 328   | 0        | 89       | 0       | 0            |
| 8   | 4b    | 334   | 0        | 92       | 1       | 0            |
| 8   | 5b    | 328   | 0        | 89       | 5       | 0            |
| 9   | 2c    | 340   | 0        | 87       | 1       | 0            |
| 9   | 4c    | 300   | 0        | 80       | 5       | 0            |
| 9   | 5c    | 388   | 0        | 102      | 7       | 0            |
| 10  | 2d    | 296   | 0        | 87       | 1       | 0            |
| 10  | 4d    | 292   | 0        | 93       | 7       | 0            |
| 10  | 5d    | 296   | 0        | 87       | 10      | 0            |
| 11  | 2e    | 316   | 0        | 85       | 2       | 0            |
| 11  | 4e    | 314   | 0        | 86       | 3       | 0            |
| 11  | 5e    | 316   | 0        | 85       | 4       | 0            |
| 12  | 2f    | 272   | 0        | 75       | 1       | 0            |
| 12  | 4f    | 298   | 0        | 89       | 5       | 0            |
| 12  | 5f    | 288   | 0        | 82       | 5       | 0            |
| 13  | 2g    | 320   | 0        | 88       | 0       | 0            |
| 13  | 4g    | 288   | 0        | 84       | 1       | 0            |
| 13  | 5g    | 308   | 0        | 86       | 5       | 0            |
| 14  | 6A    | 1273  | 0        | 641      | 31      | 0            |
| 15  | 6a    | 360   | 0        | 95       | 2       | 0            |
| 16  | 6b    | 296   | 0        | 76       | 5       | 0            |
| 17  | 6c    | 296   | 0        | 77       | 0       | 0            |
| 18  | 6d    | 288   | 0        | 78       | 0       | 0            |
| 19  | 6e    | 280   | 0        | 81       | 8       | 0            |
| 20  | 6f    | 260   | 0        | 75       | 0       | 0            |
| 21  | 6g    | 244   | 0        | 71       | 3       | 0            |
| 22  | 4A    | 2744  | 0        | 1395     | 65      | 0            |
| 23  | 4B    | 2076  | 0        | 2148     | 29      | 0            |
| 24  | 4C    | 3370  | 0        | 3300     | 46      | 0            |
| 25  | 4D    | 2874  | 0        | 2856     | 25      | 0            |
| 26  | 4E    | 962   | 0        | 1012     | 2       | 0            |
| 27  | 4F    | 1169  | 0        | 1139     | 9       | 0            |
| 28  | 4G    | 5504  | 0        | 4772     | 47      | 0            |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 29  | 4H    | 844   | 0        | 426      | 6       | 0            |
| 30  | 4I    | 494   | 0        | 384      | 8       | 0            |
| 31  | 4J    | 1144  | 0        | 1094     | 10      | 0            |
| 32  | 4K    | 1192  | 0        | 841      | 9       | 0            |
| 33  | 4L    | 1452  | 0        | 1465     | 31      | 0            |
| 34  | 4M    | 599   | 0        | 613      | 5       | 0            |
| 35  | 4N    | 640   | 0        | 664      | 16      | 0            |
| 36  | 4Z    | 2092  | 0        | 992      | 15      | 0            |
| 37  | 2A    | 2311  | 0        | 1170     | 144     | 0            |
| 38  | 2B    | 648   | 0        | 167      | 1       | 0            |
| 39  | 2C    | 376   | 0        | 102      | 0       | 0            |
| 40  | 2D    | 1134  | 0        | 764      | 8       | 0            |
| 41  | 2E    | 376   | 0        | 85       | 0       | 0            |
| 42  | 2F    | 1693  | 0        | 454      | 22      | 0            |
| 43  | 2G    | 4192  | 0        | 1110     | 234     | 0            |
| 44  | 2H    | 959   | 0        | 417      | 11      | 0            |
| 45  | 2I    | 4672  | 0        | 1260     | 71      | 0            |
| 46  | 2J    | 312   | 0        | 87       | 3       | 0            |
| 47  | 2K    | 432   | 0        | 114      | 6       | 0            |
| 48  | 2L    | 356   | 0        | 105      | 4       | 0            |
| 49  | 2M    | 264   | 0        | 70       | 11      | 0            |
| 50  | 5B    | 36    | 0        | 6        | 0       | 0            |
| 51  | 5C    | 32    | 0        | 12       | 2       | 0            |
| 52  | 5C    | 1     | 0        | 0        | 0       | 0            |
| 53  | 4I    | 1     | 0        | 0        | 0       | 0            |
| 53  | 4N    | 1     | 0        | 0        | 0       | 0            |
| All | All   | 98459 | 0        | 72990    | 1644    | 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 10.

The worst 5 of 1644 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) |
|------------------|------------------|--------------------------|-------------------|
| 43:2G:407:MET:N  | 43:2G:407:MET:CA | 1.71                     | 1.53              |
| 1:A:30:C:C2'     | 1:A:31:C:H5''    | 1.54                     | 1.35              |
| 30:4I:8:GLN:HE21 | 30:4I:8:GLN:N    | 1.33                     | 1.24              |
| 1:A:30:C:N4      | 1:A:31:C:C4      | 2.10                     | 1.18              |
| 1:A:38:C:H4'     | 1:A:39:U:OP1     | 1.42                     | 1.18              |

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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 |     |
|-----|-------|-----------------|------------|---------|----------|-------------|-----|
| 3   | 5B    | 2249/2335 (96%) | 2156 (96%) | 93 (4%) | 0        | 100         | 100 |
| 4   | 5C    | 814/972 (84%)   | 755 (93%)  | 58 (7%) | 1 (0%)   | 48          | 73  |
| 5   | 5D    | 1694/2136 (79%) | 1618 (96%) | 75 (4%) | 1 (0%)   | 48          | 73  |
| 6   | 5E    | 297/357 (83%)   | 272 (92%)  | 16 (5%) | 9 (3%)   | 3           | 8   |
| 7   | 2a    | 84/231 (36%)    | 82 (98%)   | 2 (2%)  | 0        | 100         | 100 |
| 7   | 4a    | 60/231 (26%)    | 57 (95%)   | 3 (5%)  | 0        | 100         | 100 |
| 7   | 5a    | 82/231 (36%)    | 80 (98%)   | 2 (2%)  | 0        | 100         | 100 |
| 8   | 2b    | 80/119 (67%)    | 77 (96%)   | 3 (4%)  | 0        | 100         | 100 |
| 8   | 4b    | 80/119 (67%)    | 76 (95%)   | 4 (5%)  | 0        | 100         | 100 |
| 8   | 5b    | 80/119 (67%)    | 77 (96%)   | 3 (4%)  | 0        | 100         | 100 |
| 9   | 2c    | 81/118 (69%)    | 78 (96%)   | 3 (4%)  | 0        | 100         | 100 |
| 9   | 4c    | 70/118 (59%)    | 68 (97%)   | 2 (3%)  | 0        | 100         | 100 |
| 9   | 5c    | 95/118 (80%)    | 91 (96%)   | 4 (4%)  | 0        | 100         | 100 |
| 10  | 2d    | 72/86 (84%)     | 68 (94%)   | 4 (6%)  | 0        | 100         | 100 |
| 10  | 4d    | 69/86 (80%)     | 67 (97%)   | 2 (3%)  | 0        | 100         | 100 |
| 10  | 5d    | 72/86 (84%)     | 69 (96%)   | 3 (4%)  | 0        | 100         | 100 |
| 11  | 2e    | 77/92 (84%)     | 76 (99%)   | 1 (1%)  | 0        | 100         | 100 |
| 11  | 4e    | 76/92 (83%)     | 70 (92%)   | 6 (8%)  | 0        | 100         | 100 |
| 11  | 5e    | 77/92 (84%)     | 76 (99%)   | 1 (1%)  | 0        | 100         | 100 |
| 12  | 2f    | 64/76 (84%)     | 62 (97%)   | 2 (3%)  | 0        | 100         | 100 |
| 12  | 4f    | 71/76 (93%)     | 67 (94%)   | 4 (6%)  | 0        | 100         | 100 |
| 12  | 5f    | 70/76 (92%)     | 68 (97%)   | 2 (3%)  | 0        | 100         | 100 |
| 13  | 2g    | 76/126 (60%)    | 75 (99%)   | 1 (1%)  | 0        | 100         | 100 |
| 13  | 4g    | 69/126 (55%)    | 69 (100%)  | 0       | 0        | 100         | 100 |
| 13  | 5g    | 75/126 (60%)    | 73 (97%)   | 2 (3%)  | 0        | 100         | 100 |

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| Mol | Chain | Analysed        | Favoured   | Allowed   | Outliers | Percentiles |     |
|-----|-------|-----------------|------------|-----------|----------|-------------|-----|
| 15  | 6a    | 88/95 (93%)     | 77 (88%)   | 7 (8%)    | 4 (4%)   | 2           | 4   |
| 16  | 6b    | 70/102 (69%)    | 64 (91%)   | 3 (4%)    | 3 (4%)   | 2           | 4   |
| 17  | 6c    | 70/139 (50%)    | 63 (90%)   | 6 (9%)    | 1 (1%)   | 9           | 23  |
| 18  | 6d    | 68/91 (75%)     | 63 (93%)   | 4 (6%)    | 1 (2%)   | 8           | 22  |
| 19  | 6e    | 68/80 (85%)     | 64 (94%)   | 2 (3%)    | 2 (3%)   | 3           | 9   |
| 20  | 6f    | 61/103 (59%)    | 56 (92%)   | 5 (8%)    | 0        | 100         | 100 |
| 21  | 6g    | 57/96 (59%)     | 52 (91%)   | 4 (7%)    | 1 (2%)   | 6           | 18  |
| 23  | 4B    | 248/683 (36%)   | 235 (95%)  | 13 (5%)   | 0        | 100         | 100 |
| 24  | 4C    | 422/522 (81%)   | 393 (93%)  | 28 (7%)   | 1 (0%)   | 43          | 68  |
| 25  | 4D    | 372/499 (74%)   | 353 (95%)  | 19 (5%)   | 0        | 100         | 100 |
| 26  | 4E    | 122/128 (95%)   | 115 (94%)  | 7 (6%)    | 0        | 100         | 100 |
| 27  | 4F    | 139/142 (98%)   | 134 (96%)  | 5 (4%)    | 0        | 100         | 100 |
| 28  | 4G    | 795/941 (84%)   | 747 (94%)  | 48 (6%)   | 0        | 100         | 100 |
| 29  | 4H    | 167/177 (94%)   | 158 (95%)  | 9 (5%)    | 0        | 100         | 100 |
| 30  | 4I    | 73/376 (19%)    | 73 (100%)  | 0         | 0        | 100         | 100 |
| 31  | 4J    | 142/800 (18%)   | 136 (96%)  | 6 (4%)    | 0        | 100         | 100 |
| 32  | 4K    | 184/439 (42%)   | 174 (95%)  | 10 (5%)   | 0        | 100         | 100 |
| 33  | 4L    | 173/312 (55%)   | 165 (95%)  | 6 (4%)    | 2 (1%)   | 10          | 27  |
| 34  | 4M    | 71/73 (97%)     | 66 (93%)   | 5 (7%)    | 0        | 100         | 100 |
| 35  | 4N    | 78/199 (39%)    | 77 (99%)   | 0         | 1 (1%)   | 9           | 25  |
| 36  | 4Z    | 414/513 (81%)   | 401 (97%)  | 12 (3%)   | 1 (0%)   | 43          | 68  |
| 38  | 2B    | 160/255 (63%)   | 146 (91%)  | 12 (8%)   | 2 (1%)   | 9           | 25  |
| 39  | 2C    | 92/225 (41%)    | 90 (98%)   | 2 (2%)    | 0        | 100         | 100 |
| 40  | 2D    | 196/793 (25%)   | 180 (92%)  | 10 (5%)   | 6 (3%)   | 3           | 8   |
| 41  | 2E    | 88/464 (19%)    | 63 (72%)   | 16 (18%)  | 9 (10%)  | 0           | 0   |
| 42  | 2F    | 413/501 (82%)   | 367 (89%)  | 41 (10%)  | 5 (1%)   | 10          | 27  |
| 43  | 2G    | 1032/1304 (79%) | 844 (82%)  | 166 (16%) | 22 (2%)  | 5           | 15  |
| 44  | 2H    | 199/895 (22%)   | 179 (90%)  | 16 (8%)   | 4 (2%)   | 6           | 16  |
| 45  | 2I    | 1152/1217 (95%) | 1053 (91%) | 89 (8%)   | 10 (1%)  | 14          | 35  |
| 46  | 2J    | 76/424 (18%)    | 75 (99%)   | 1 (1%)    | 0        | 100         | 100 |
| 47  | 2K    | 106/125 (85%)   | 85 (80%)   | 18 (17%)  | 3 (3%)   | 4           | 9   |

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| Mol | Chain | Analysed          | Favoured    | Allowed  | Outliers | Percentiles |     |
|-----|-------|-------------------|-------------|----------|----------|-------------|-----|
| 48  | 2L    | 87/110 (79%)      | 74 (85%)    | 13 (15%) | 0        | 100         | 100 |
| 49  | 2M    | 64/86 (74%)       | 55 (86%)    | 7 (11%)  | 2 (3%)   | 3           | 8   |
| All | All   | 14181/21253 (67%) | 13204 (93%) | 886 (6%) | 91 (1%)  | 23          | 44  |

5 of 91 Ramachandran outliers are listed below:

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 5   | 5D    | 1086 | GLN  |
| 6   | 5E    | 193  | THR  |
| 15  | 6a    | 55   | LEU  |
| 16  | 6b    | 84   | MET  |
| 18  | 6d    | 70   | ASP  |

### 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 |     |
|-----|-------|-----------------|-------------|----------|-------------|-----|
| 3   | 5B    | 2033/2108 (96%) | 1986 (98%)  | 47 (2%)  | 44          | 73  |
| 4   | 5C    | 717/866 (83%)   | 698 (97%)   | 19 (3%)  | 40          | 70  |
| 5   | 5D    | 1517/1908 (80%) | 1513 (100%) | 4 (0%)   | 86          | 94  |
| 23  | 4B    | 225/599 (38%)   | 220 (98%)   | 5 (2%)   | 45          | 74  |
| 24  | 4C    | 362/442 (82%)   | 350 (97%)   | 12 (3%)  | 33          | 63  |
| 25  | 4D    | 299/424 (70%)   | 290 (97%)   | 9 (3%)   | 36          | 66  |
| 26  | 4E    | 108/111 (97%)   | 105 (97%)   | 3 (3%)   | 38          | 68  |
| 27  | 4F    | 129/130 (99%)   | 124 (96%)   | 5 (4%)   | 28          | 57  |
| 28  | 4G    | 417/792 (53%)   | 405 (97%)   | 12 (3%)  | 37          | 67  |
| 29  | 4H    | 10/148 (7%)     | 10 (100%)   | 0        | 100         | 100 |
| 30  | 4I    | 32/333 (10%)    | 31 (97%)    | 1 (3%)   | 35          | 65  |
| 31  | 4J    | 112/681 (16%)   | 110 (98%)   | 2 (2%)   | 51          | 78  |
| 32  | 4K    | 66/395 (17%)    | 63 (96%)    | 3 (4%)   | 24          | 52  |
| 33  | 4L    | 159/293 (54%)   | 153 (96%)   | 6 (4%)   | 29          | 58  |

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| Mol | Chain | Analysed         | Rotameric  | Outliers | Percentiles |
|-----|-------|------------------|------------|----------|-------------|
| 34  | 4M    | 66/66 (100%)     | 64 (97%)   | 2 (3%)   | 36 66       |
| 35  | 4N    | 75/181 (41%)     | 70 (93%)   | 5 (7%)   | 15 36       |
| 36  | 4Z    | 11/450 (2%)      | 11 (100%)  | 0        | 100 100     |
| 40  | 2D    | 70/709 (10%)     | 69 (99%)   | 1 (1%)   | 59 82       |
| 44  | 2H    | 26/776 (3%)      | 25 (96%)   | 1 (4%)   | 29 58       |
| All | All   | 6434/11412 (56%) | 6297 (98%) | 137 (2%) | 46 75       |

5 of 137 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 28  | 4G    | 921 | ASN  |
| 32  | 4K    | 358 | ARG  |
| 35  | 4N    | 58  | LEU  |
| 4   | 5C    | 202 | ILE  |
| 4   | 5C    | 150 | ILE  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 79 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 23  | 4B    | 423 | GLN  |
| 28  | 4G    | 308 | HIS  |
| 24  | 4C    | 282 | HIS  |
| 25  | 4D    | 376 | ASN  |
| 28  | 4G    | 805 | GLN  |

### 5.3.3 RNA ⓘ

| Mol | Chain | Analysed      | Backbone Outliers | Pucker Outliers |
|-----|-------|---------------|-------------------|-----------------|
| 1   | A     | 62/144 (43%)  | 37 (59%)          | 12 (19%)        |
| 14  | 6A    | 56/107 (52%)  | 10 (17%)          | 1 (1%)          |
| 2   | 5A    | 114/117 (97%) | 30 (26%)          | 5 (4%)          |
| 22  | 4A    | 124/145 (85%) | 33 (26%)          | 2 (1%)          |
| 37  | 2A    | 105/188 (55%) | 22 (20%)          | 3 (2%)          |
| All | All   | 461/701 (65%) | 132 (28%)         | 23 (4%)         |

5 of 132 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | A     | 8   | U    |
| 1   | A     | 9   | U    |
| 1   | A     | 10  | C    |
| 1   | A     | 11  | C    |
| 1   | A     | 12  | U    |

5 of 23 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2   | 5A    | 79  | C    |
| 14  | 6A    | 77  | C    |
| 2   | 5A    | 96  | A    |
| 22  | 4A    | 99  | C    |
| 1   | A     | 38  | C    |

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 for Mogul analysis.

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

| Mol | Type | Chain | Res  | Link | Bond lengths |      |             | Bond angles |      |             |
|-----|------|-------|------|------|--------------|------|-------------|-------------|------|-------------|
|     |      |       |      |      | Counts       | RMSZ | $\# Z  > 2$ | Counts      | RMSZ | $\# Z  > 2$ |
| 51  | GTP  | 5C    | 1500 | 52   | 33,34,34     | 0.94 | 1 (3%)      | 50,54,54    | 1.57 | 8 (16%)     |
| 50  | IHP  | 5B    | 3000 | -    | 36,36,36     | 0.76 | 0           | 60,60,60    | 1.20 | 3 (5%)      |

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

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

| Mol | Type | Chain | Res  | Link | Chirals | Torsions   | Rings   |
|-----|------|-------|------|------|---------|------------|---------|
| 51  | GTP  | 5C    | 1500 | 52   | -       | 8/22/38/38 | 0/3/3/3 |
| 50  | IHP  | 5B    | 3000 | -    | -       | 2/30/54/54 | 0/1/1/1 |

All (1) bond length outliers are listed below:

| Mol | Chain | Res  | Type | Atoms | Z    | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|-------|------|-------------|----------|
| 51  | 5C    | 1500 | GTP  | C2-N3 | 2.19 | 1.38        | 1.33     |

The worst 5 of 11 bond angle outliers are listed below:

| Mol | Chain | Res  | Type | Atoms    | Z     | Observed(°) | Ideal(°) |
|-----|-------|------|------|----------|-------|-------------|----------|
| 51  | 5C    | 1500 | GTP  | C5-C4-N3 | -5.07 | 120.32      | 128.39   |
| 51  | 5C    | 1500 | GTP  | C2-N3-C4 | 4.69  | 120.38      | 112.30   |
| 51  | 5C    | 1500 | GTP  | N9-C4-N3 | 3.13  | 132.22      | 125.95   |
| 51  | 5C    | 1500 | GTP  | C2-N1-C6 | -2.97 | 119.73      | 125.11   |
| 51  | 5C    | 1500 | GTP  | N9-C8-N7 | -2.67 | 108.45      | 113.40   |

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

| Mol | Chain | Res  | Type | Atoms          |
|-----|-------|------|------|----------------|
| 51  | 5C    | 1500 | GTP  | C5'-O5'-PA-O3A |
| 51  | 5C    | 1500 | GTP  | C5'-O5'-PA-O1A |
| 51  | 5C    | 1500 | GTP  | C5'-O5'-PA-O2A |
| 51  | 5C    | 1500 | GTP  | PB-O3A-PA-O5'  |
| 50  | 5B    | 3000 | IHP  | C4-O14-P4-O44  |

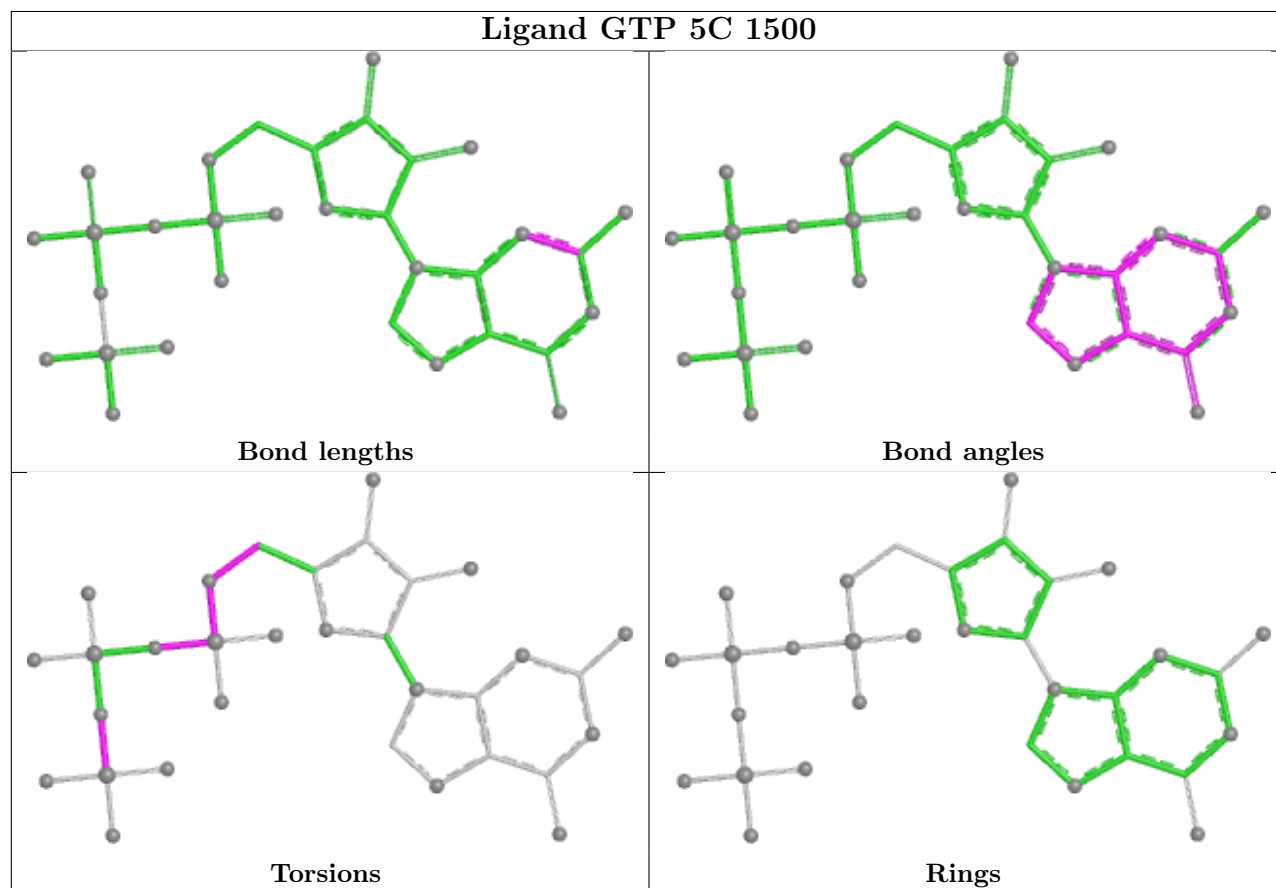
There are no ring outliers.

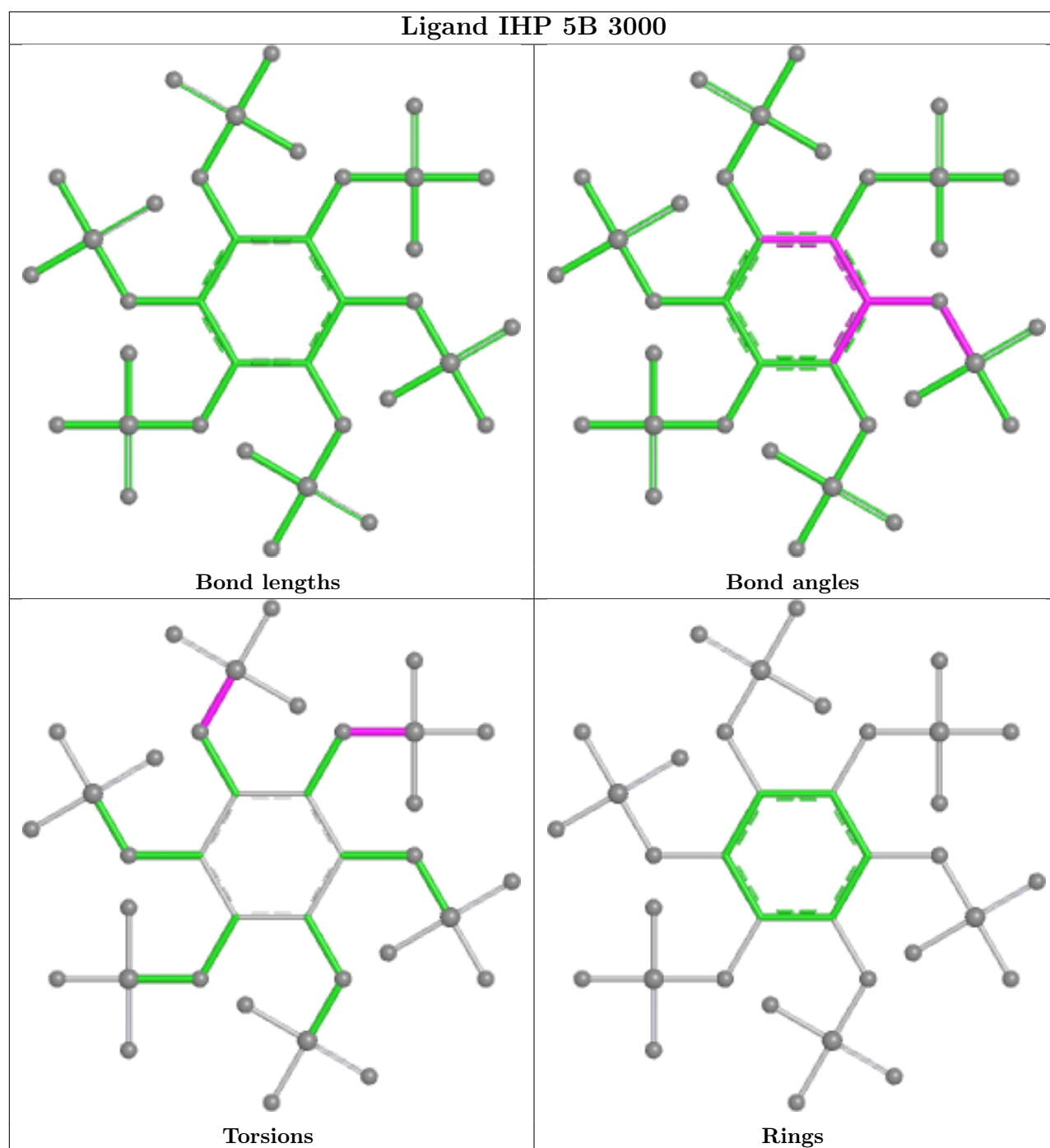
1 monomer is involved in 2 short contacts:

| Mol | Chain | Res  | Type | Clashes | Symm-Clashes |
|-----|-------|------|------|---------|--------------|
| 51  | 5C    | 1500 | GTP  | 2       | 0            |

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

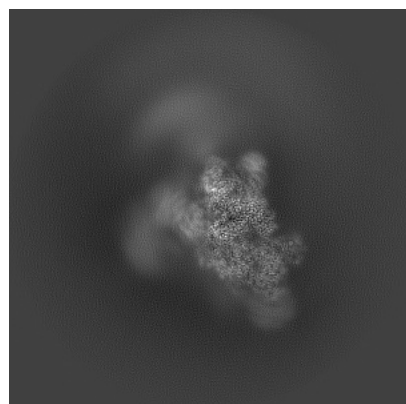
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34507. These allow visual inspection of the internal detail of the map and identification of artifacts.

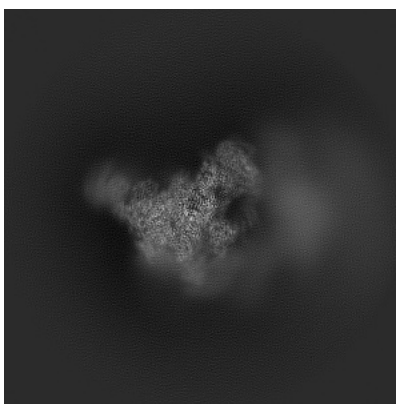
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

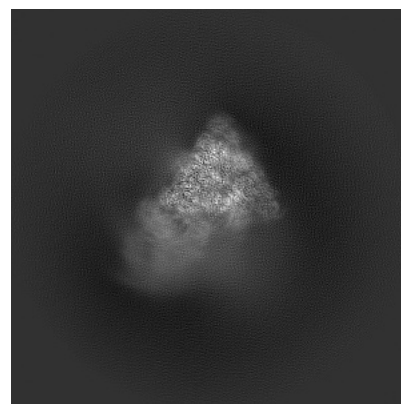
#### 6.1.1 Primary map



X

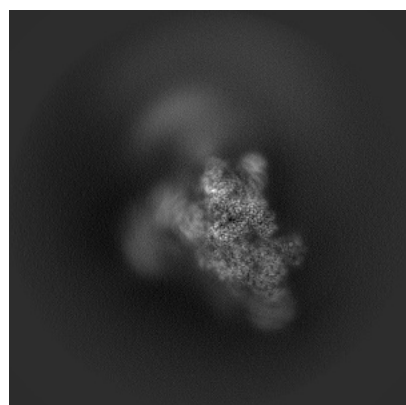


Y

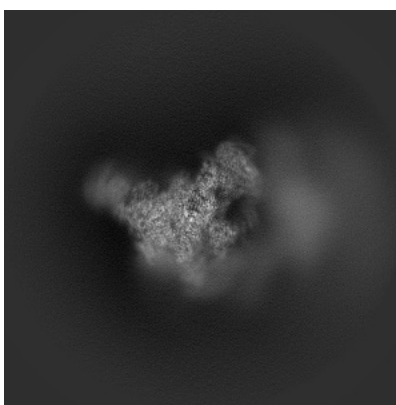


Z

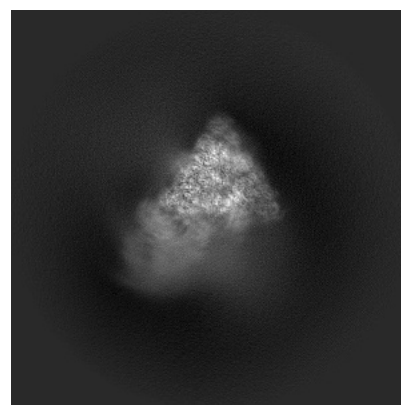
#### 6.1.2 Raw map



X



Y

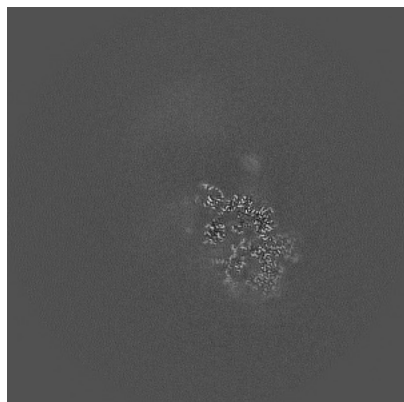


Z

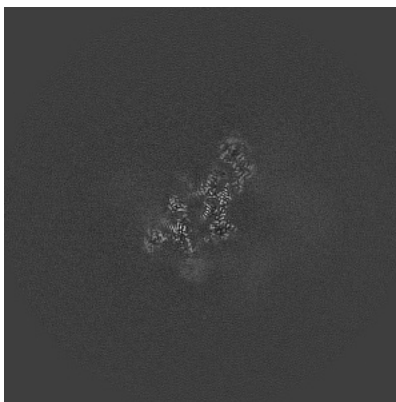
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

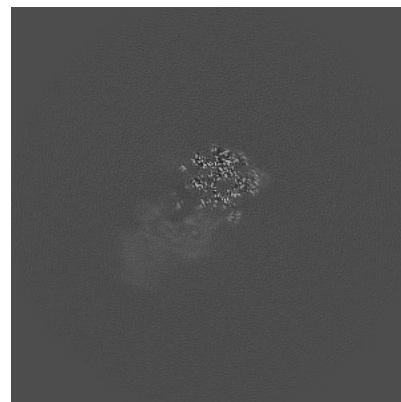
### 6.2.1 Primary map



X Index: 256

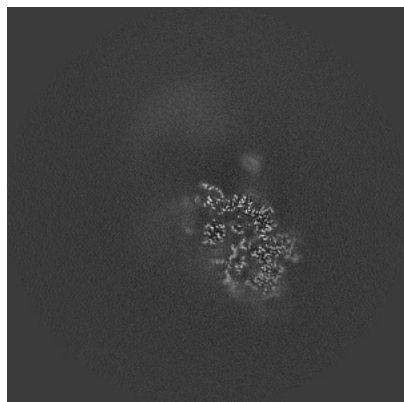


Y Index: 256

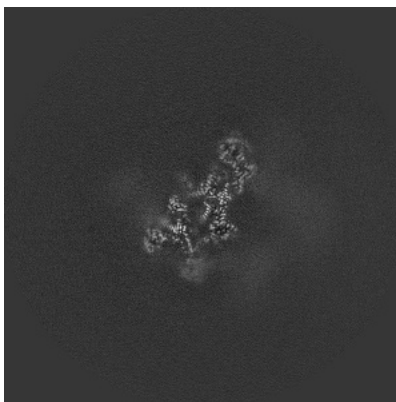


Z Index: 256

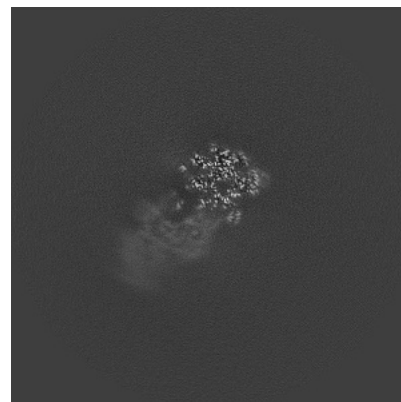
### 6.2.2 Raw map



X Index: 256



Y Index: 256

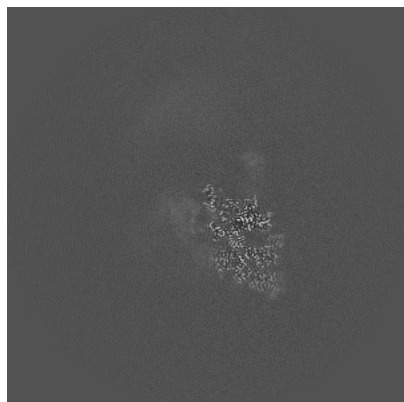


Z Index: 256

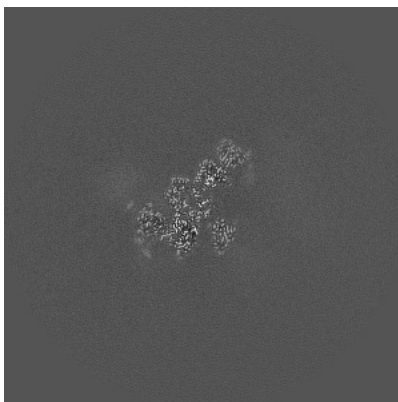
The images above show central slices of the map in three orthogonal directions.

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

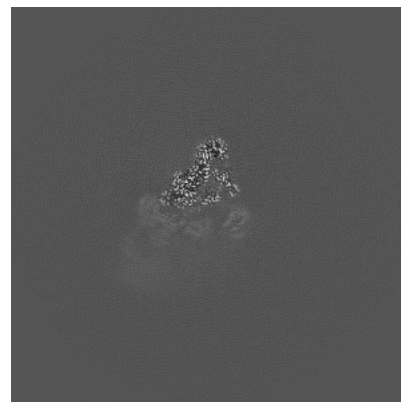
### 6.3.1 Primary map



X Index: 245

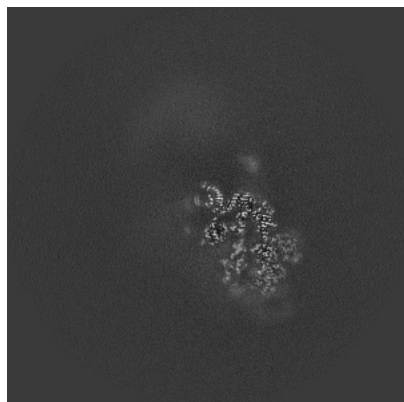


Y Index: 277

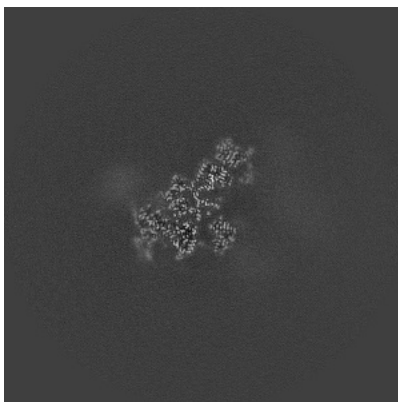


Z Index: 234

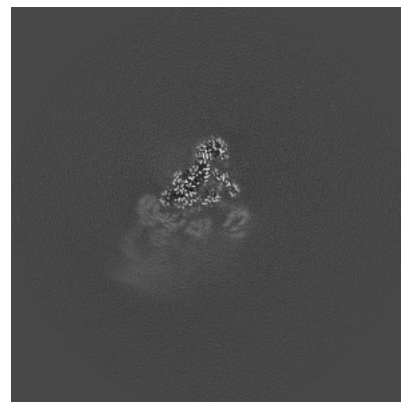
### 6.3.2 Raw map



X Index: 259



Y Index: 274

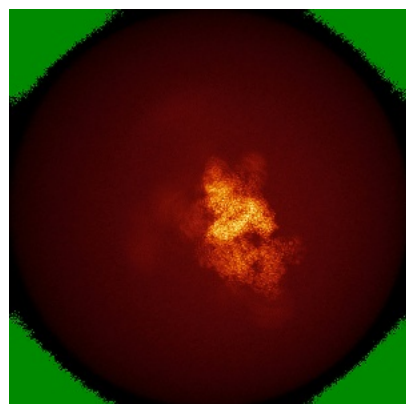


Z Index: 234

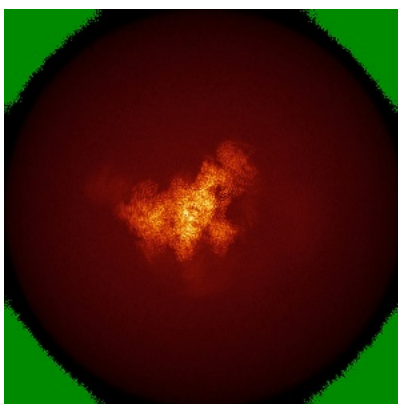
The images above show the largest variance slices of the map in three orthogonal directions.

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

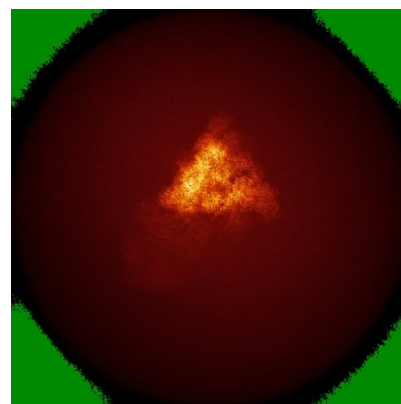
### 6.4.1 Primary map



X

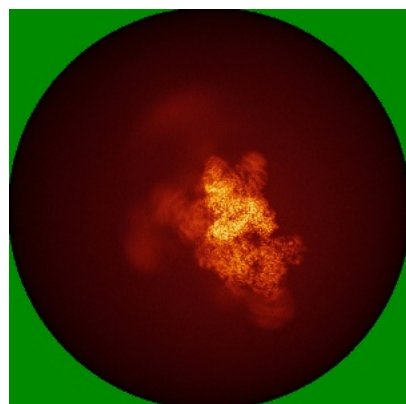


Y

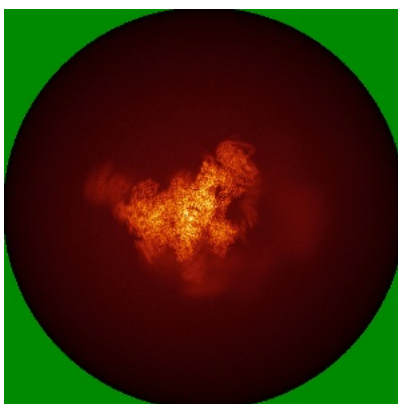


Z

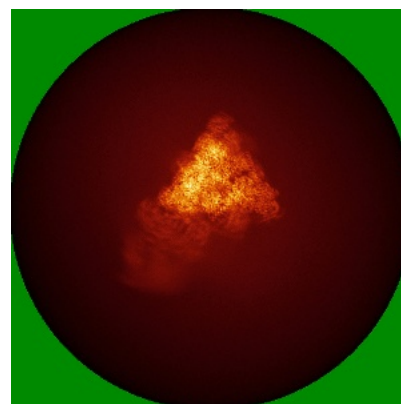
### 6.4.2 Raw map



X



Y

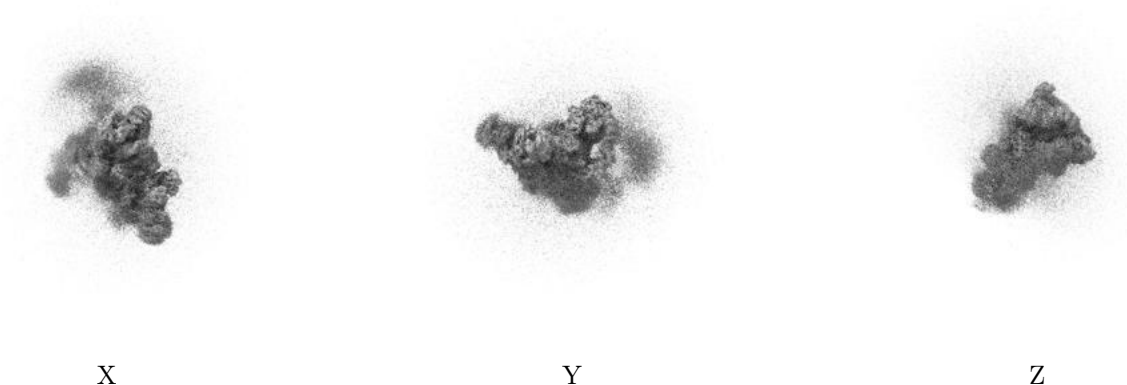


Z

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.

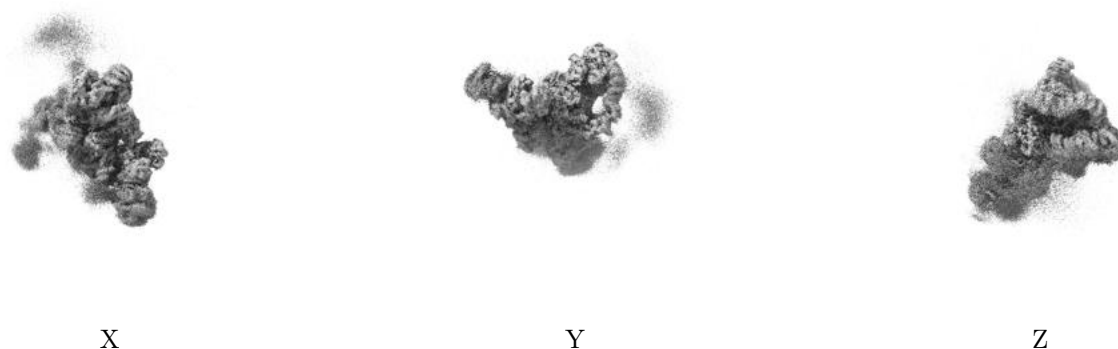
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. 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.

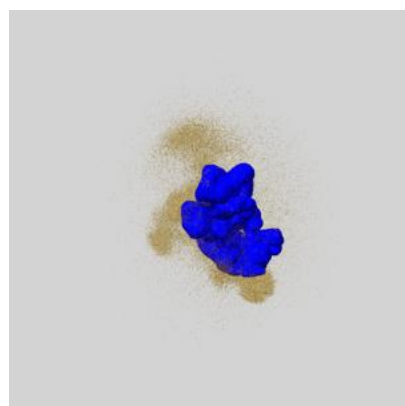
## 6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

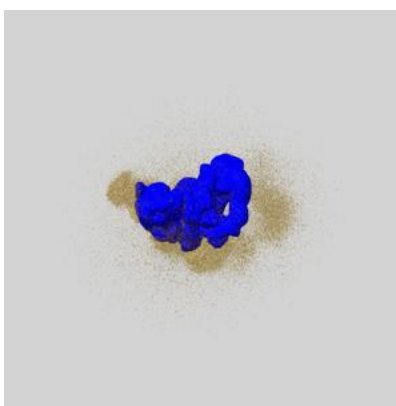
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

### 6.6.1 emd\_34507\_msk\_1.map [i](#)



X



Y

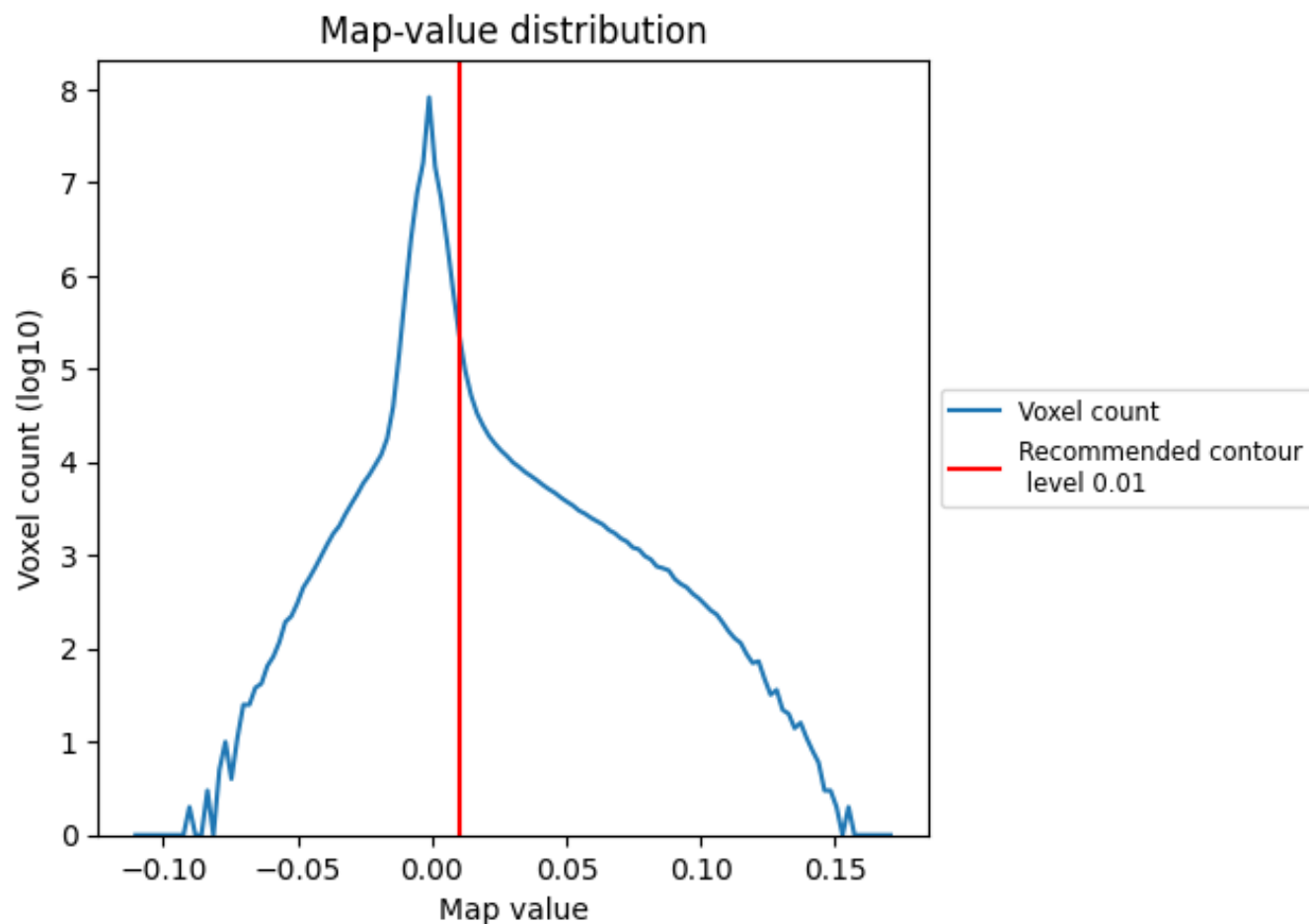


Z

## 7 Map analysis [i](#)

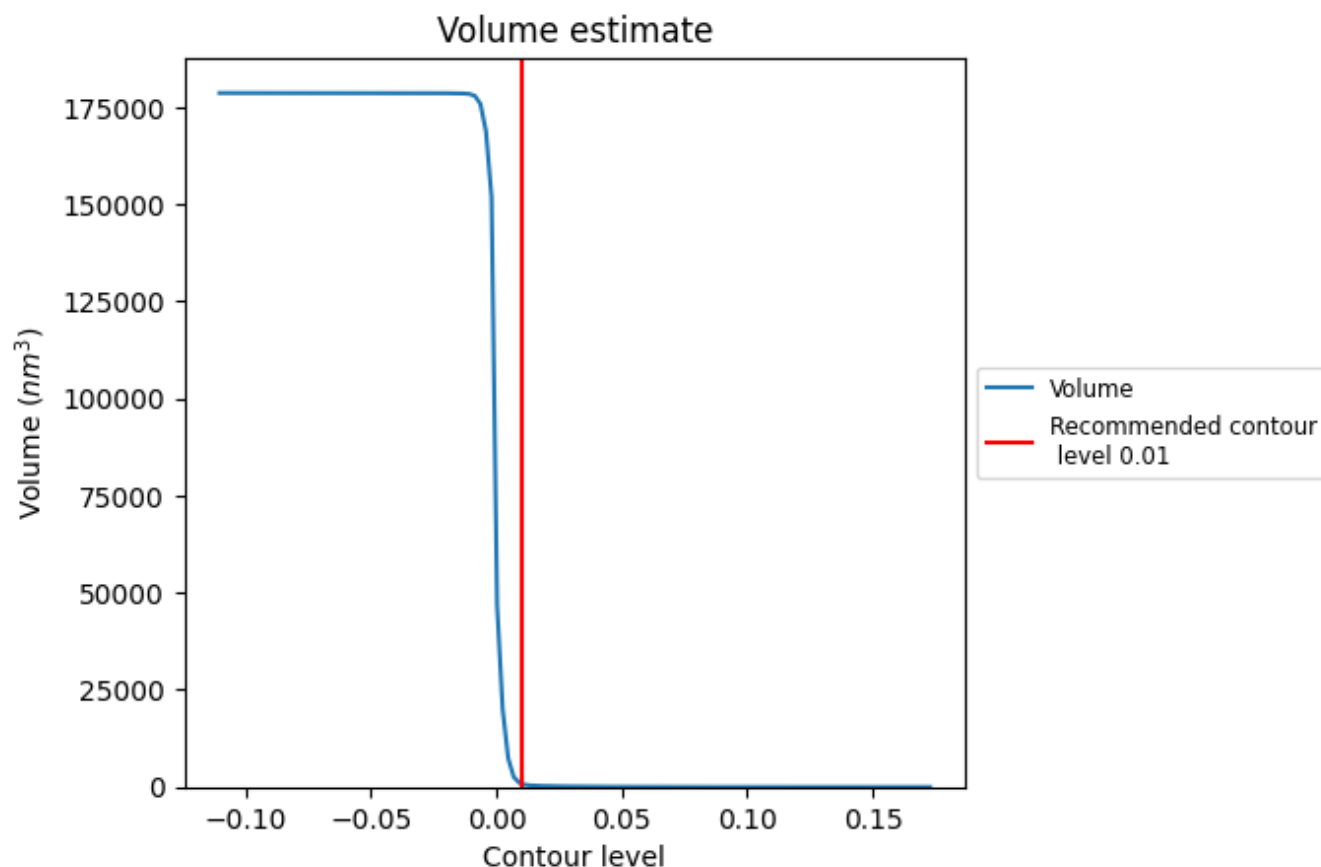
This section contains the results of statistical analysis of the map.

### 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.

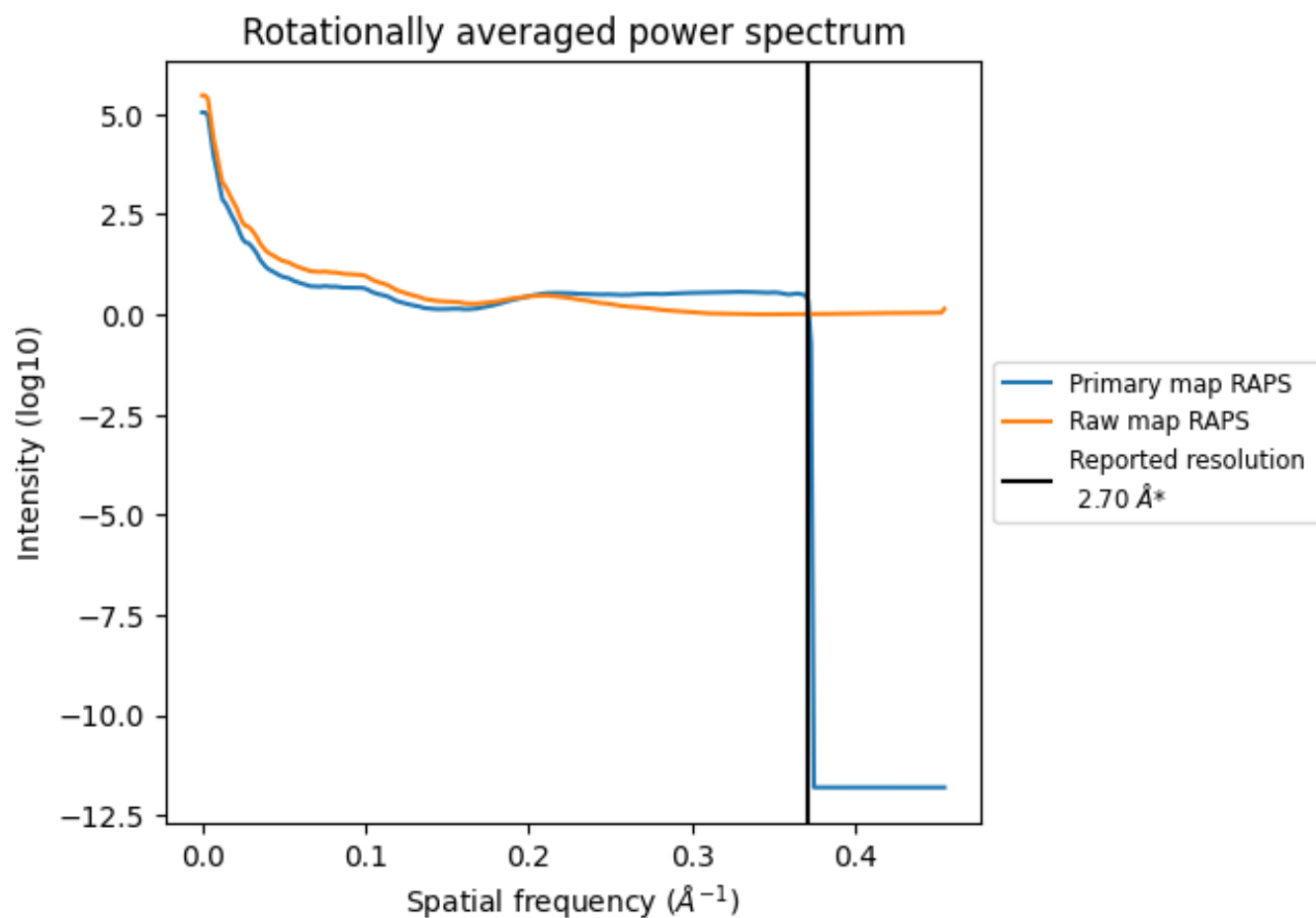
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 875  $\text{nm}^3$ ; this corresponds to an approximate mass of 791 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 ⓘ

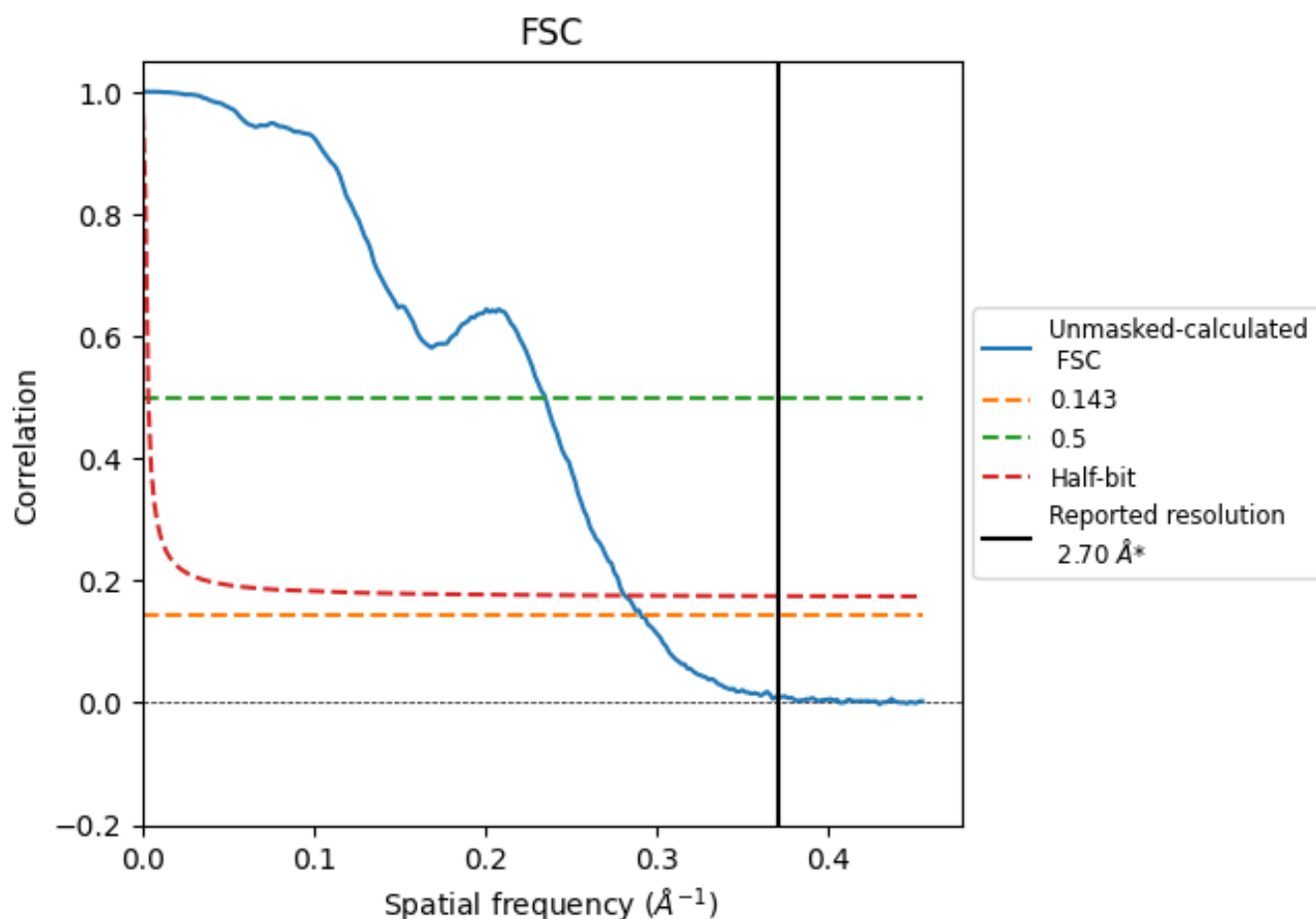


\*Reported resolution corresponds to spatial frequency of 0.370  $\text{\AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.370 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

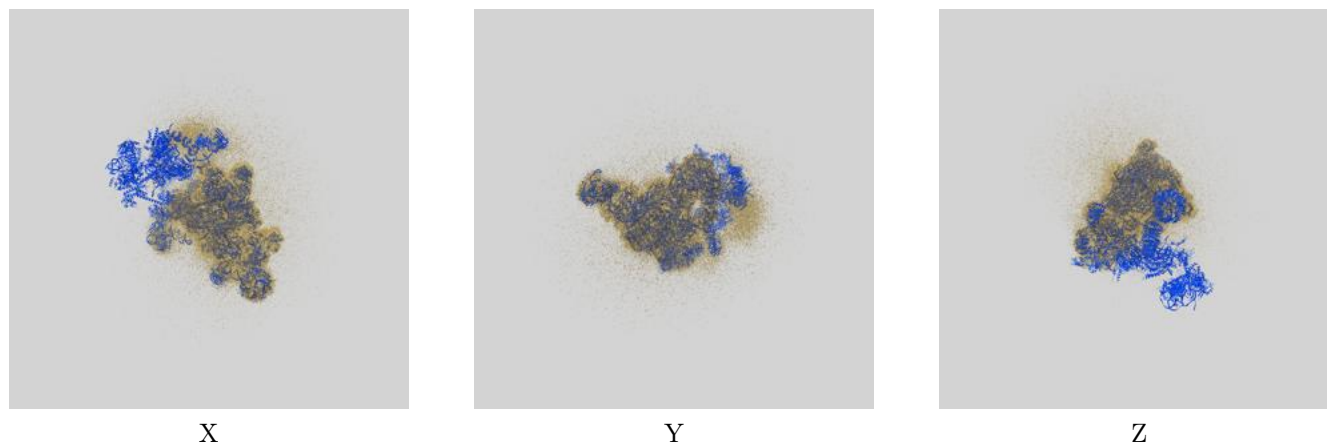
| Resolution estimate (Å)   | Estimation criterion (FSC cut-off) |      |          |
|---------------------------|------------------------------------|------|----------|
|                           | 0.143                              | 0.5  | Half-bit |
| Reported by author        | 2.70                               | -    | -        |
| Author-provided FSC curve | -                                  | -    | -        |
| Unmasked-calculated*      | 3.44                               | 4.26 | 3.55     |

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.44 differs from the reported value 2.7 by more than 10 %

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

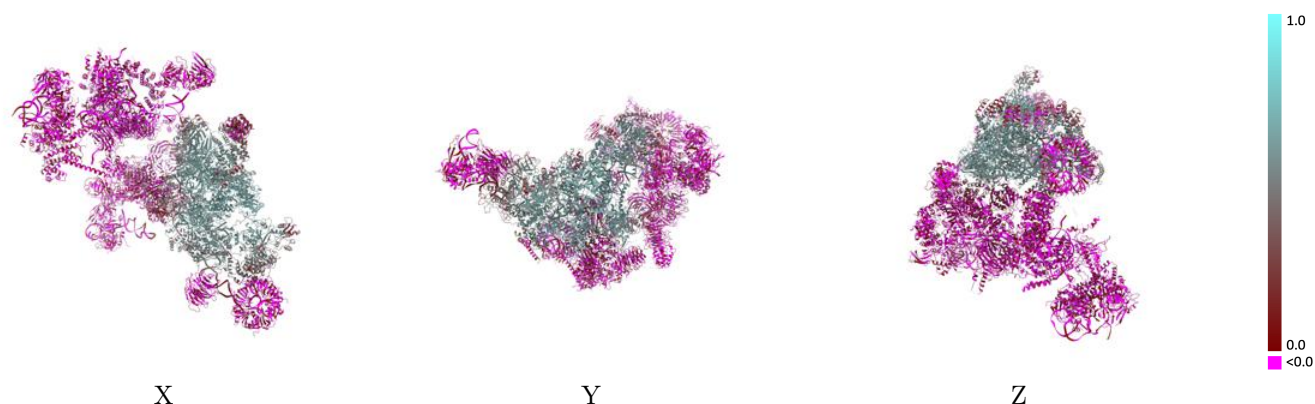
This section contains information regarding the fit between EMDB map EMD-34507 and PDB model 8H6K. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

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



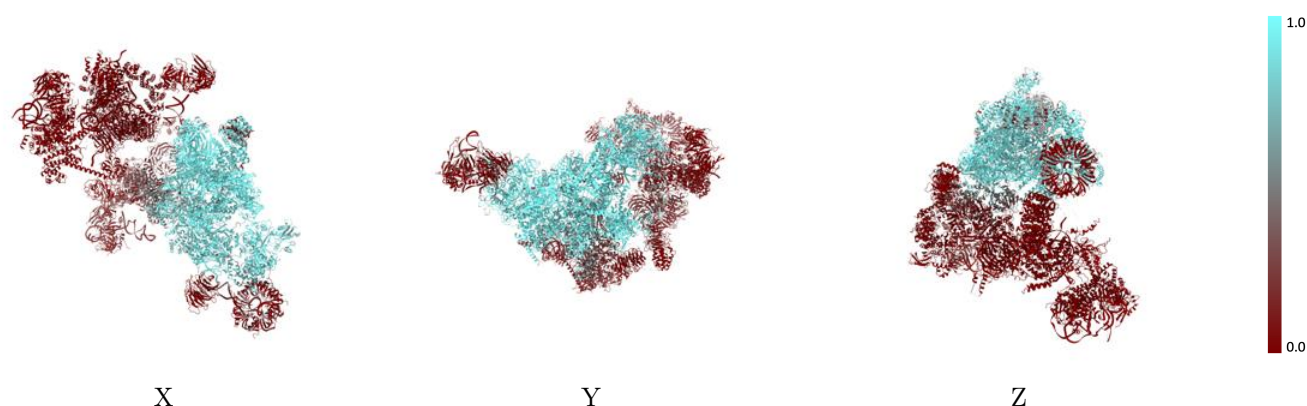
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



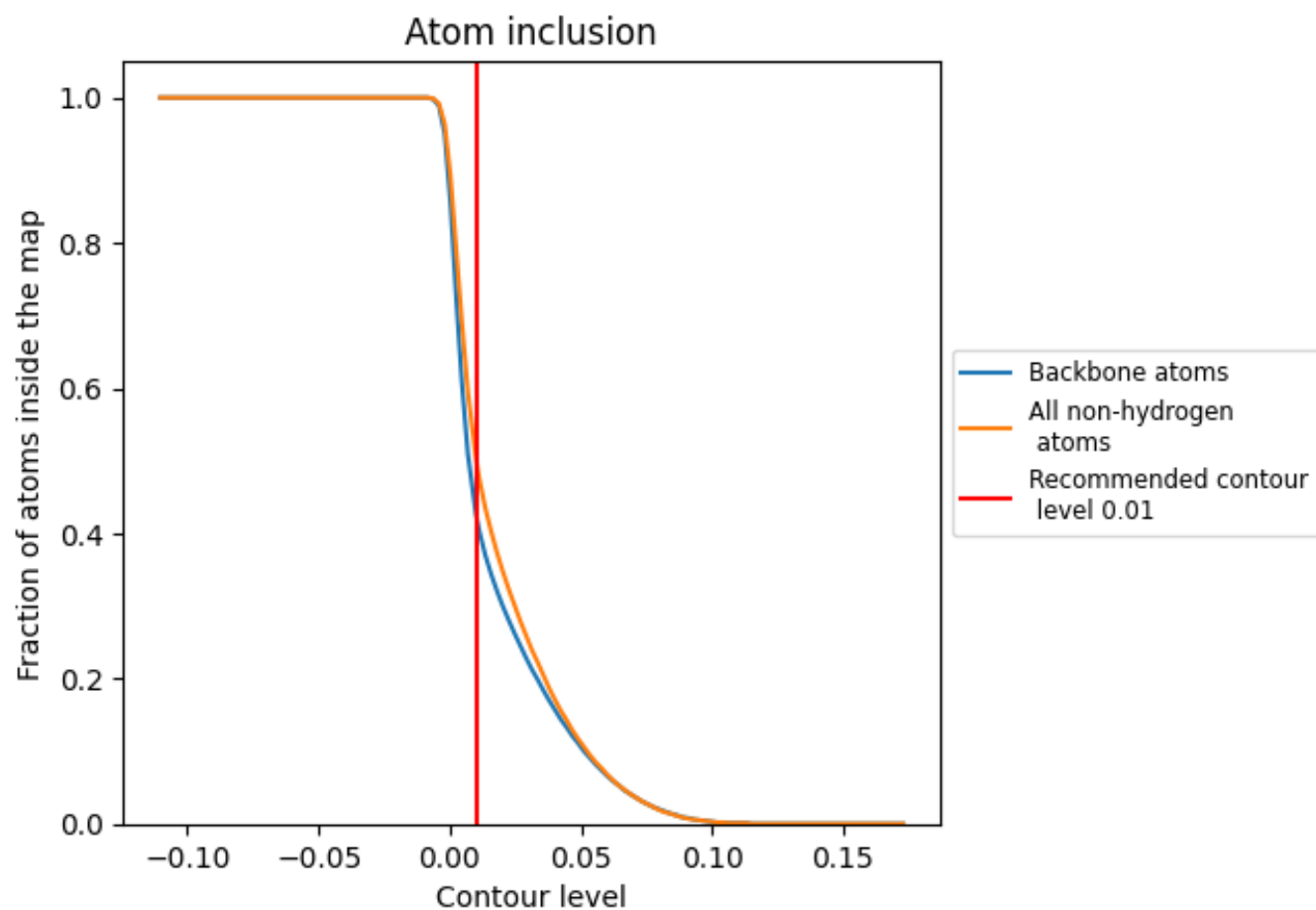
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 43% of all backbone atoms, 50% 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 (0.01) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion                                                                             | Q-score                                                                                     |
|-------|--------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------|
| All   |  0.5030   |  0.2790    |
| 2A    |  0.0020   |  -0.0150   |
| 2B    |  0.0000   |  0.0460    |
| 2C    |  0.0000   |  0.0250    |
| 2D    |  0.4950   |  0.2890    |
| 2E    |  0.0000   |  0.0250    |
| 2F    |  0.0000   |  0.0160    |
| 2G    |  0.0020   |  0.0060    |
| 2H    |  0.2270   |  0.1180    |
| 2I    |  0.0000   |  0.0020    |
| 2J    |  0.0030   |  0.0230    |
| 2K    |  0.0000   |  -0.0020   |
| 2L    |  0.0000   |  -0.0190   |
| 2M    |  0.0000   |  -0.0220   |
| 2a    |  0.0000  |  -0.0370  |
| 2b    |  0.0000 |  -0.0030 |
| 2c    |  0.0000 |  -0.0640 |
| 2d    |  0.0000 |  0.0100  |
| 2e    |  0.0000 |  -0.0200 |
| 2f    |  0.0000 |  0.0370  |
| 2g    |  0.0000 |  0.0170  |
| 4A    |  0.5220 |  0.3060  |
| 4B    |  0.9070 |  0.5190  |
| 4C    |  0.9190 |  0.5180  |
| 4D    |  0.9380 |  0.5700  |
| 4E    |  0.9780 |  0.6280  |
| 4F    |  0.9790 |  0.6330  |
| 4G    |  0.8120 |  0.4270  |
| 4H    |  0.8040 |  0.2910  |
| 4I    |  0.7400 |  0.3700  |
| 4J    |  0.8570 |  0.5110  |
| 4K    |  0.6850 |  0.3810  |
| 4L    |  0.9440 |  0.5510  |
| 4M    |  0.9900 |  0.6420  |
| 4N    |  0.7960 |  0.4350  |



*Continued on next page...*

*Continued from previous page...*

| Chain | Atom inclusion                                                                             | Q-score                                                                                     |
|-------|--------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------|
| 4Z    |  0.0240   |  0.0010    |
| 4a    |  0.0120   |  -0.0050   |
| 4b    |  0.0180   |  -0.0060   |
| 4c    |  0.0130   |  -0.0090   |
| 4d    |  0.0410   |  0.0560    |
| 4e    |  0.0480   |  0.0060    |
| 4f    |  0.0270   |  -0.0200   |
| 4g    |  0.0380   |  -0.0290   |
| 5A    |  0.5990   |  0.3000    |
| 5B    |  0.8960   |  0.5420    |
| 5C    |  0.8770   |  0.4650    |
| 5D    |  0.1830   |  0.0350    |
| 5E    |  0.0320   |  -0.0090   |
| 5a    |  0.1370   |  0.0100    |
| 5b    |  0.0730   |  0.0010    |
| 5c    |  0.1080   |  0.0050    |
| 5d    |  0.1010   |  0.0190    |
| 5e    |  0.0730  |  -0.0220  |
| 5f    |  0.1250 |  0.0070  |
| 5g    |  0.1720 |  -0.0110 |
| 6A    |  0.7020 |  0.4220  |
| 6a    |  0.0080 |  0.0260  |
| 6b    |  0.0000 |  -0.0270 |
| 6c    |  0.0000 |  -0.0050 |
| 6d    |  0.0000 |  -0.0560 |
| 6e    |  0.0110 |  0.0270  |
| 6f    |  0.0000 |  0.0110  |
| 6g    |  0.0000 |  -0.0170 |
| A     |  0.3350 |  0.1550  |