



wwPDB EM Validation Summary Report ⓘ

Apr 22, 2024 – 02:39 PM JST

PDB ID : 8XXM
EMDB ID : EMD-38753
Title : Cryo-EM structure of the human 40S ribosome with PDCD4 and eIF3G
Authors : Ye, X.; Huang, Z.; Li, Y.; Wang, M.; Cheng, J.
Deposited on : 2024-01-18
Resolution : 3.20 Å (reported)
Based on initial model : 6ZVJ

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

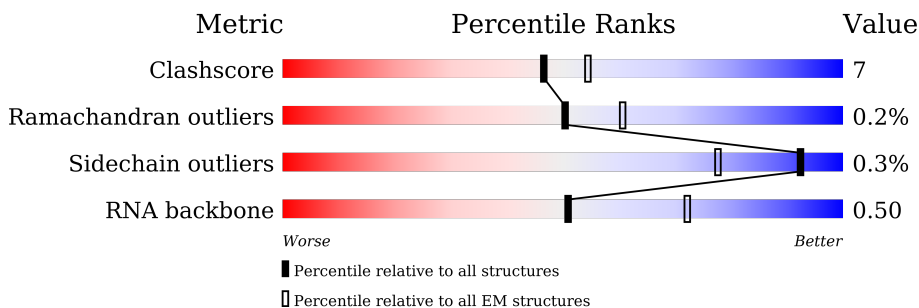
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 Å.

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





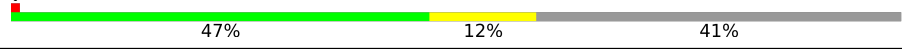









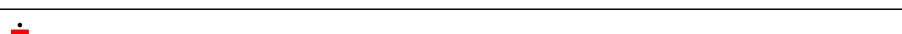
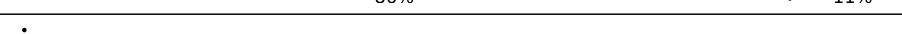
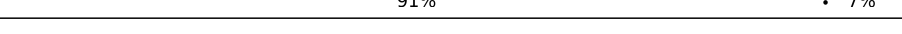
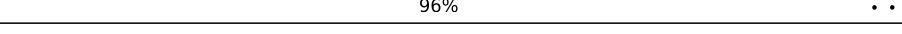
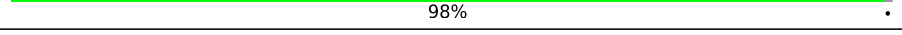








| Metric | Whole archive (#Entries) | EM structures (#Entries) |
|-----------------------|--------------------------|--------------------------|
| Clashscore | 158937 | 4297 |
| Ramachandran outliers | 154571 | 4023 |
| Sidechain outliers | 154315 | 3826 |
| RNA backbone | 4643 | 859 |

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

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1 | Ln | 25 | |
| 2 | S2 | 1869 | |
| 3 | SA | 295 | |
| 4 | SB | 264 | |
| 5 | SD | 243 | |
| 6 | SE | 263 | |
| 7 | SF | 204 | |

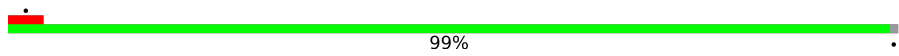
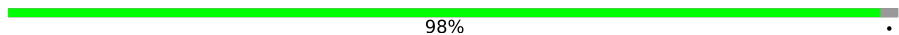



Continued on next page...

Continued from previous page...

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|---|
| 8 | SH | 194 |  79% 17% |
| 9 | SI | 208 |  76% 22% |
| 10 | SK | 165 |  47% 12% 41% |
| 11 | SL | 158 |  84% 13% |
| 12 | SP | 145 |  71% 12% 17% |
| 13 | SQ | 146 |  82% 16% |
| 14 | SR | 135 |  79% 20% |
| 15 | SS | 152 |  73% 22% 5% |
| 16 | ST | 145 |  78% 21% |
| 17 | SU | 119 |  77% 10% 13% |
| 18 | SV | 83 |  80% 20% |
| 19 | SX | 143 |  82% 17% |
| 20 | Sa | 115 |  86% 11% |
| 21 | Sc | 69 |  91% 7% |
| 22 | Sd | 56 |  96% |
| 23 | Sg | 317 |  98% |
| 24 | SC | 293 |  61% 15% 24% |
| 25 | SG | 249 |  71% 23% 6% |
| 26 | SJ | 194 |  81% 14% 5% |
| 27 | SM | 132 |  30% 67% 23% 8% |
| 28 | SN | 151 |  86% 13% |
| 29 | SO | 151 |  75% 18% 7% |
| 30 | SW | 130 |  87% 12% |
| 31 | SY | 133 |  77% 21% |
| 32 | SZ | 125 |  48% 11% 40% |

Continued on next page...

Continued from previous page...

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 33 | Sb | 84 |  99% |
| 34 | Se | 59 |  98% |
| 35 | Sf | 156 |  24% 43% 57% |
| 36 | CD | 469 |  10% 90% |
| 37 | 3G | 320 |  22% 74% |

2 Entry composition [i](#)

There are 39 unique types of molecules in this entry. The entry contains 76934 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L41.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 1 | Ln | 24 | 230 | 139 | 62 | 26 | 3 | 0 | 0 |

- Molecule 2 is a RNA chain called 18S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|-------|
| | | | Total | C | N | O | P | | |
| 2 | S2 | 1723 | 36538 | 16298 | 6533 | 11984 | 1723 | 0 | 0 |

- Molecule 3 is a protein called 40S ribosomal protein SA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 3 | SA | 221 | 1741 | 1106 | 305 | 322 | 8 | 0 | 0 |

- Molecule 4 is a protein called 40S ribosomal protein S3a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| | | | Total | C | N | O | S | | |
| 4 | SB | 214 | 1738 | 1103 | 310 | 311 | 14 | 0 | 0 |

- Molecule 5 is a protein called 40S ribosomal protein S3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 5 | SD | 227 | 1765 | 1125 | 317 | 315 | 8 | 0 | 0 |

- Molecule 6 is a protein called 40S ribosomal protein S4, X isoform.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 6 | SE | 262 | 2076 | 1324 | 386 | 358 | 8 | 0 | 0 |

- Molecule 7 is a protein called 40S ribosomal protein S5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 7 | SF | 189 | 1495 | 934 | 284 | 270 | 7 | 0 | 0 |

- Molecule 8 is a protein called 40S ribosomal protein S7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 8 | SH | 186 | 1497 | 956 | 274 | 266 | 1 | 0 | 0 |

- Molecule 9 is a protein called 40S ribosomal protein S8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 9 | SI | 206 | 1686 | 1058 | 332 | 291 | 5 | 0 | 0 |

- Molecule 10 is a protein called 40S ribosomal protein S10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 10 | SK | 98 | 827 | 539 | 148 | 134 | 6 | 0 | 0 |

- Molecule 11 is a protein called 40S ribosomal protein S11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 11 | SL | 153 | 1247 | 793 | 234 | 214 | 6 | 0 | 0 |

- Molecule 12 is a protein called 40S ribosomal protein S15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 12 | SP | 121 | 985 | 623 | 185 | 170 | 7 | 0 | 0 |

- Molecule 13 is a protein called 40S ribosomal protein S16.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 13 | SQ | 144 | 1142 | 726 | 216 | 197 | 3 | 0 | 0 |

- Molecule 14 is a protein called 40S ribosomal protein S17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 14 | SR | 135 | 1090 | 685 | 202 | 198 | 5 | 0 | 0 |

- Molecule 15 is a protein called 40S ribosomal protein S18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 15 | SS | 145 | 1198 | 751 | 242 | 203 | 2 | 0 | 0 |

- Molecule 16 is a protein called 40S ribosomal protein S19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 16 | ST | 143 | 1112 | 697 | 214 | 198 | 3 | 0 | 0 |

- Molecule 17 is a protein called 40S ribosomal protein S20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 17 | SU | 104 | 821 | 514 | 155 | 148 | 4 | 0 | 0 |

- Molecule 18 is a protein called 40S ribosomal protein S21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 18 | SV | 83 | 636 | 393 | 117 | 121 | 5 | 0 | 0 |

- Molecule 19 is a protein called 40S ribosomal protein S23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 19 | SX | 141 | 1098 | 693 | 219 | 183 | 3 | 0 | 0 |

- Molecule 20 is a protein called 40S ribosomal protein S26.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 20 | Sa | 102 | 821 | 512 | 171 | 133 | 5 | 0 | 0 |

- Molecule 21 is a protein called 40S ribosomal protein S28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 21 | Sc | 64 | Total | C | N | O | S | 0 | 0 |
| | | | 506 | 308 | 102 | 94 | 2 | | |

- Molecule 22 is a protein called 40S ribosomal protein S29.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 22 | Sd | 55 | Total | C | N | O | S | 0 | 0 |
| | | | 459 | 286 | 94 | 74 | 5 | | |

- Molecule 23 is a protein called Receptor of activated protein C kinase 1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 23 | Sg | 313 | Total | C | N | O | S | 0 | 0 |
| | | | 2436 | 1535 | 424 | 465 | 12 | | |

- Molecule 24 is a protein called 40S ribosomal protein S2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 24 | SC | 222 | Total | C | N | O | S | 0 | 0 |
| | | | 1725 | 1115 | 298 | 302 | 10 | | |

- Molecule 25 is a protein called 40S ribosomal protein S6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 25 | SG | 237 | Total | C | N | O | S | 0 | 0 |
| | | | 1923 | 1200 | 387 | 329 | 7 | | |

- Molecule 26 is a protein called 40S ribosomal protein S9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 26 | SJ | 185 | Total | C | N | O | S | 0 | 0 |
| | | | 1525 | 969 | 306 | 248 | 2 | | |

- Molecule 27 is a protein called 40S ribosomal protein S12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 27 | SM | 122 | Total | C | N | O | S | 0 | 0 |
| | | | 940 | 590 | 164 | 177 | 9 | | |

- Molecule 28 is a protein called 40S ribosomal protein S13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 28 | SN | 150 | 1208 | 773 | 229 | 205 | 1 | 0 | 0 |

- Molecule 29 is a protein called 40S ribosomal protein S14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 29 | SO | 140 | 1049 | 642 | 204 | 197 | 6 | 0 | 0 |

- Molecule 30 is a protein called 40S ribosomal protein S15a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 30 | SW | 129 | 1034 | 659 | 193 | 176 | 6 | 0 | 0 |

- Molecule 31 is a protein called 40S ribosomal protein S24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 31 | SY | 131 | 1065 | 673 | 209 | 178 | 5 | 0 | 0 |

- Molecule 32 is a protein called 40S ribosomal protein S25.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 32 | SZ | 75 | 598 | 382 | 111 | 104 | 1 | 0 | 0 |

- Molecule 33 is a protein called 40S ribosomal protein S27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 33 | Sb | 83 | 651 | 408 | 121 | 115 | 7 | 0 | 0 |

- Molecule 34 is a protein called 40S ribosomal protein S30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 34 | Se | 58 | 459 | 284 | 100 | 74 | 1 | 0 | 0 |

- Molecule 35 is a protein called Ubiquitin-40S ribosomal protein S27a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 35 | Sf | 67 | 548 | 346 | 102 | 93 | 7 | 0 | 0 |

- Molecule 36 is a protein called Programmed cell death protein 4.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| | | | Total | C | N | O | | |
| 36 | CD | 49 | 372 | 225 | 70 | 77 | 0 | 0 |

- Molecule 37 is a protein called Eukaryotic translation initiation factor 3 subunit G.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| | | | Total | C | N | O | | |
| 37 | 3G | 84 | 667 | 418 | 120 | 129 | 0 | 0 |

- Molecule 38 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| | | | Total | Mg | |
| 38 | S2 | 22 | 22 | 22 | 0 |
| 38 | SG | 1 | 1 | 1 | 0 |

- Molecule 39 is ZINC ION (three-letter code: ZN) (formula: Zn).

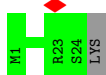
| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| | | | Total | Zn | |
| 39 | Sa | 1 | 1 | 1 | 0 |
| 39 | Sd | 1 | 1 | 1 | 0 |
| 39 | Sf | 1 | 1 | 1 | 0 |

3 Residue-property plots [i](#)

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

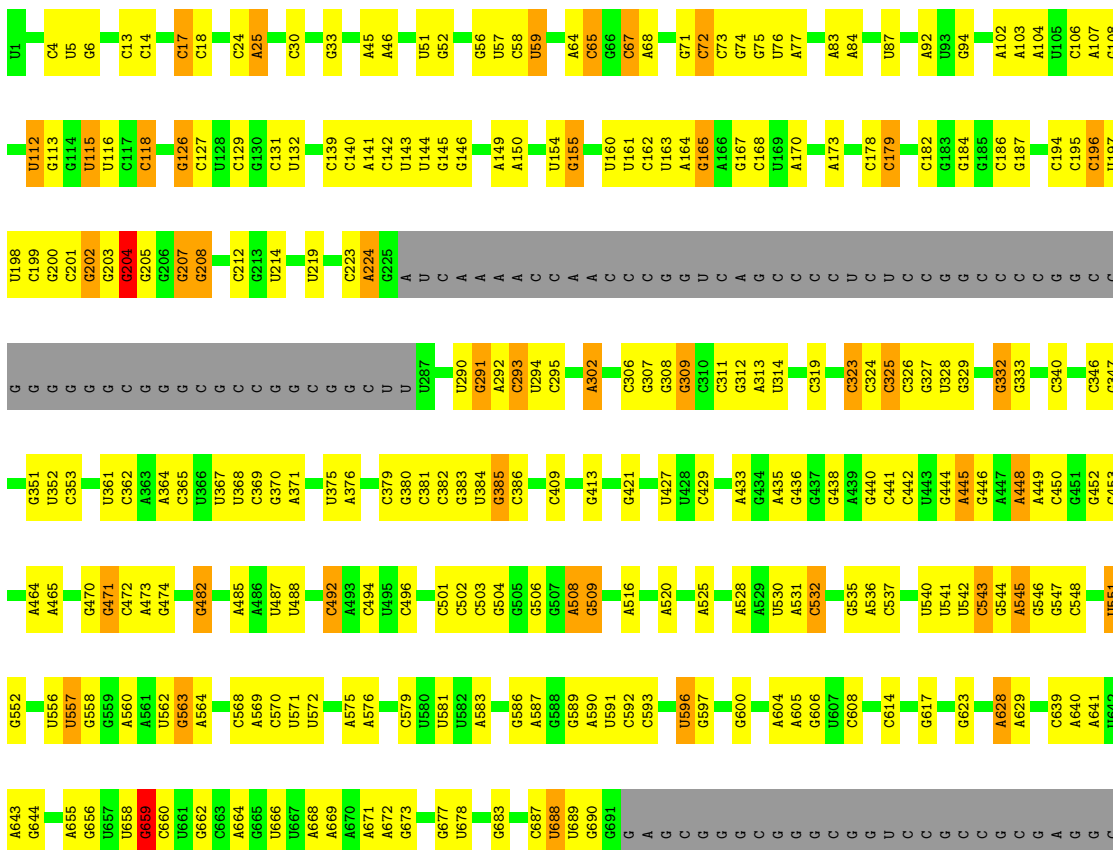
- Molecule 1: 60S ribosomal protein L41

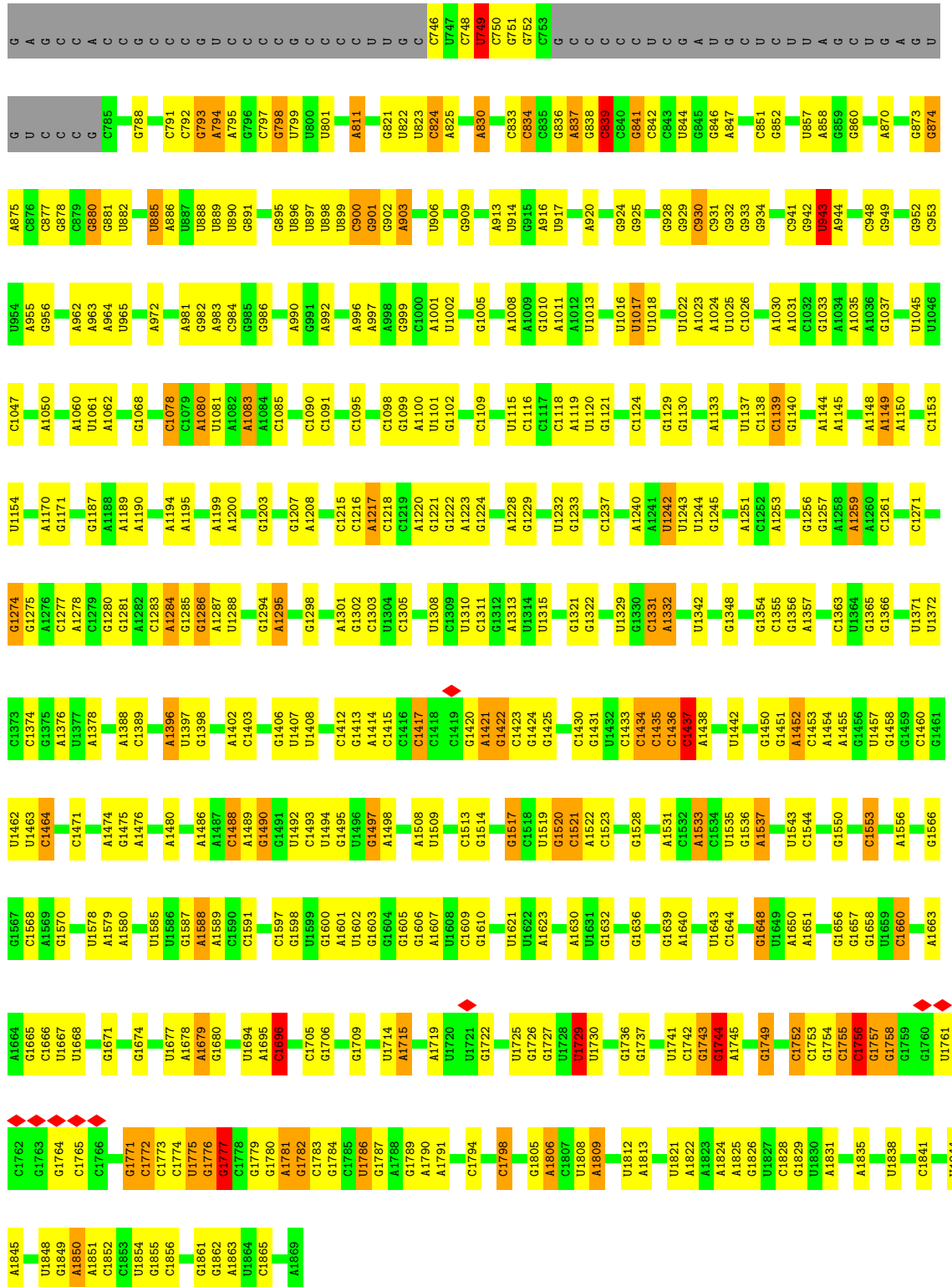
Chain Ln: 96%



- Molecule 2: 18S rRNA

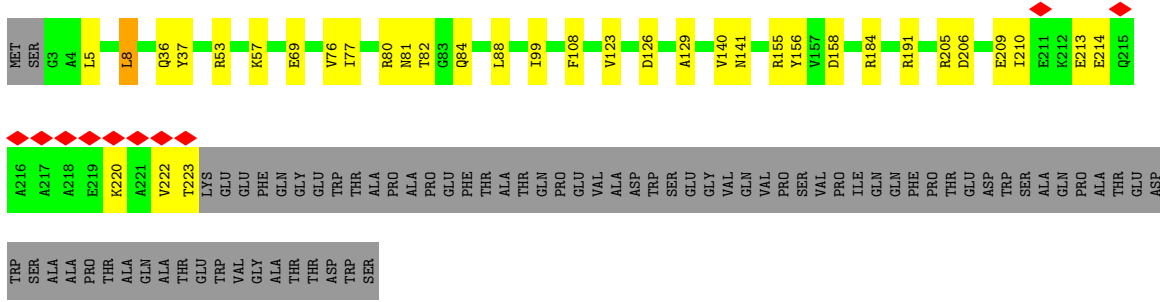
Chain S2: 53% 32% 6% 8%





• Molecule 3: 40S ribosomal protein SA





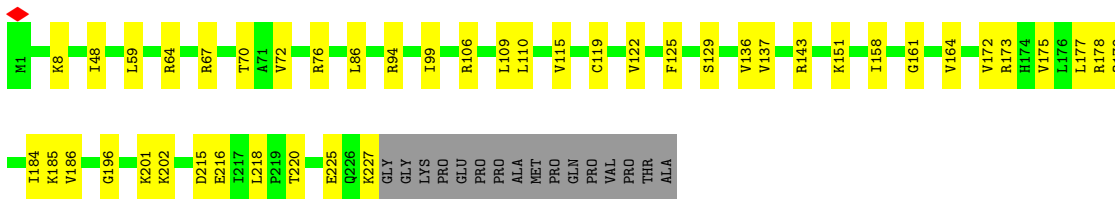
- Molecule 4: 40S ribosomal protein S3a

Chain SB:



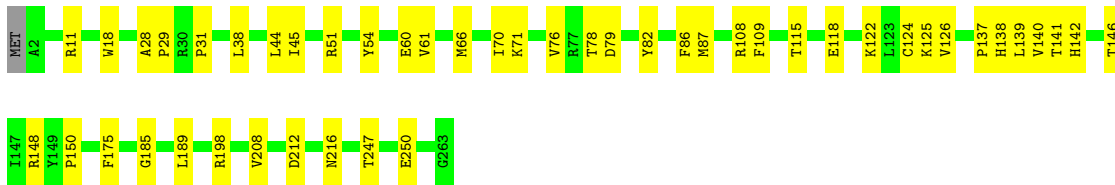
- Molecule 5: 40S ribosomal protein S3

Chain SD:



- Molecule 6: 40S ribosomal protein S4, X isoform

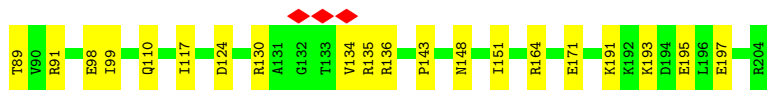
Chain SE:



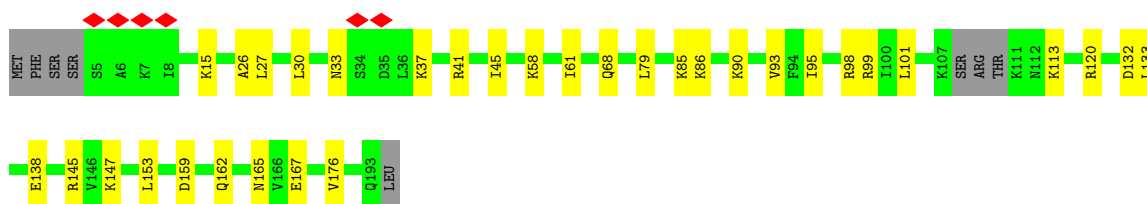
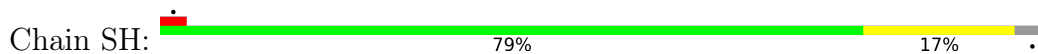
- Molecule 7: 40S ribosomal protein S5

Chain SF:

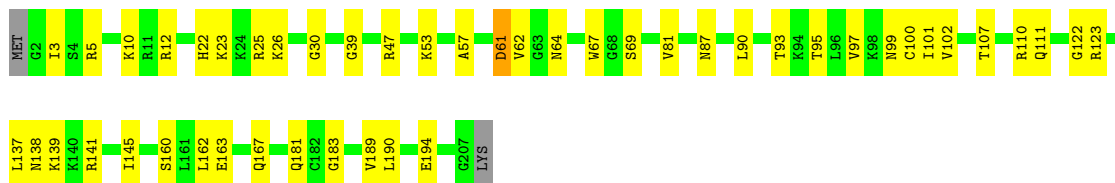
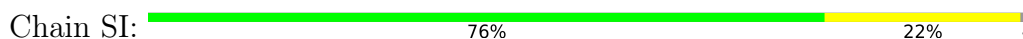




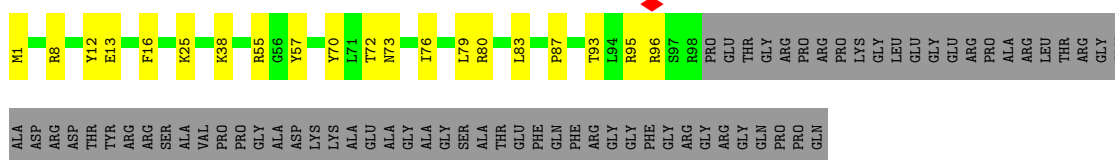
• Molecule 8: 40S ribosomal protein S7



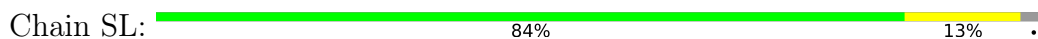
• Molecule 9: 40S ribosomal protein S8



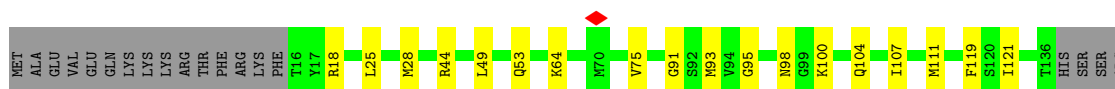
• Molecule 10: 40S ribosomal protein S10



• Molecule 11: 40S ribosomal protein S11




• Molecule 12: 40S ribosomal protein S15




PHE
ILE
PRO
LEU
LYS

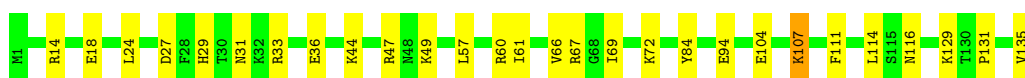
- Molecule 13: 40S ribosomal protein S16

Chain SQ:  82% 16%



- Molecule 14: 40S ribosomal protein S17

Chain SR:  79% 20%




- Molecule 15: 40S ribosomal protein S18

Chain SS:  73% 22% 5%




GLY
VAL
SER
LYS
LYS
LYS

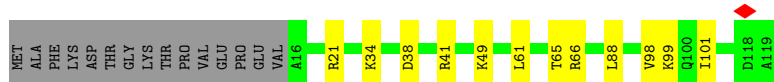
- Molecule 16: 40S ribosomal protein S19

Chain ST:  78% 21%




- Molecule 17: 40S ribosomal protein S20

Chain SU:  77% 10% 13%



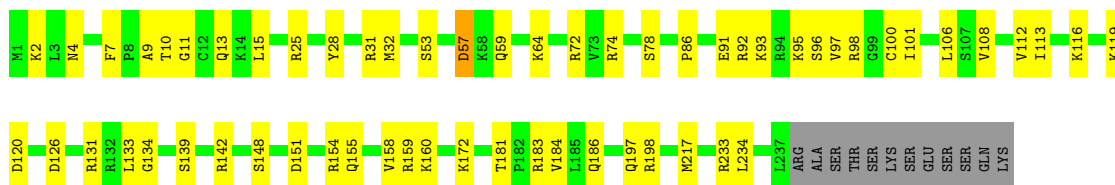
- Molecule 18: 40S ribosomal protein S21

Chain SV:  80% 20%



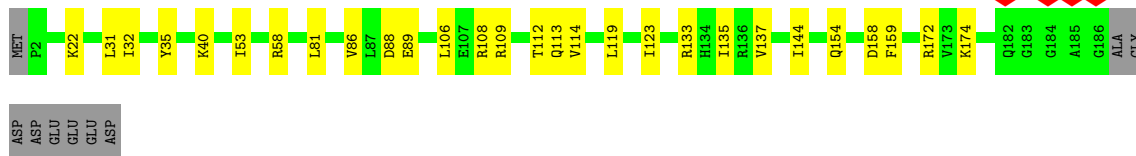
- Molecule 19: 40S ribosomal protein S23

Chain SG: 71% 23% 5%



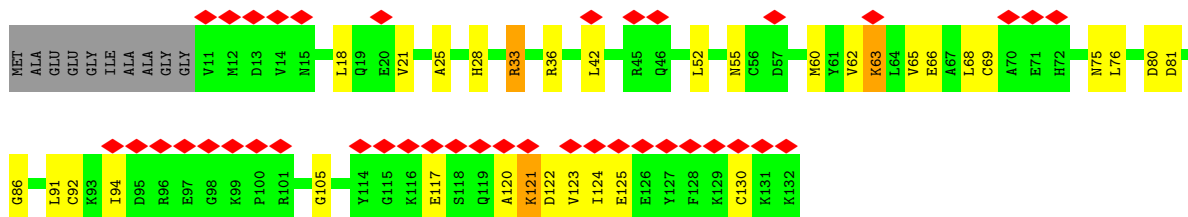
• Molecule 26: 40S ribosomal protein S9

Chain SJ: 81% 14% 5%



• Molecule 27: 40S ribosomal protein S12

Chain SM: 30% 67% 23% 8%



• Molecule 28: 40S ribosomal protein S13

Chain SN: 86% 13%



• Molecule 29: 40S ribosomal protein S14

Chain SO: 75% 18% 7%

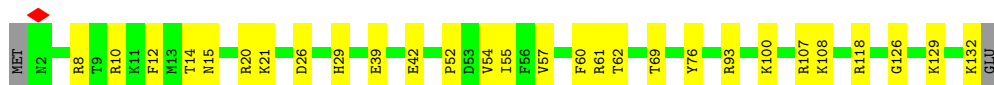
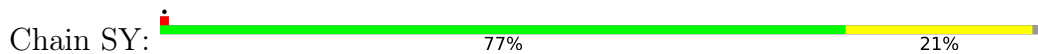


• Molecule 30: 40S ribosomal protein S15a

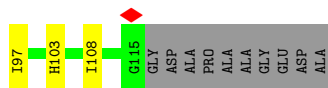
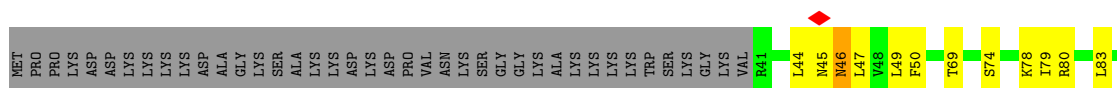
Chain SW: 87% 12%



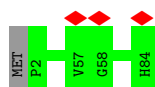
• Molecule 31: 40S ribosomal protein S24



• Molecule 32: 40S ribosomal protein S25



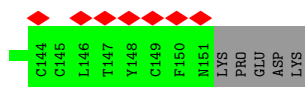
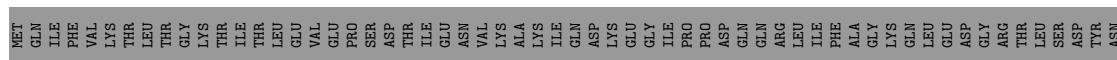
• Molecule 33: 40S ribosomal protein S27



• Molecule 34: 40S ribosomal protein S30

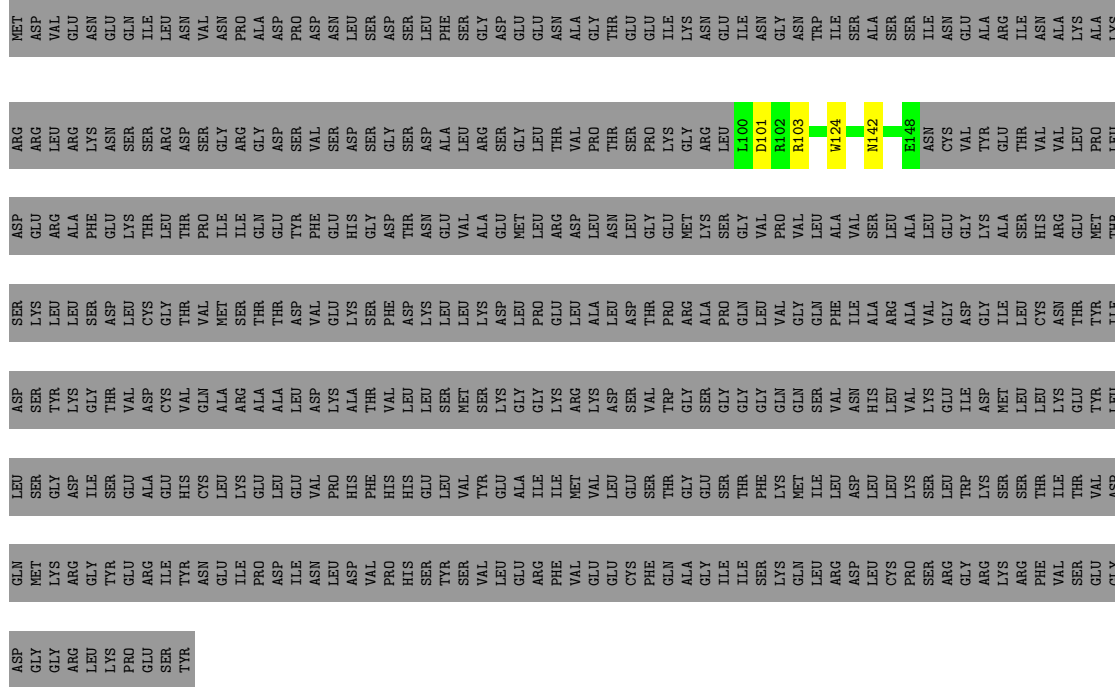


• Molecule 35: Ubiquitin-40S ribosomal protein S27a



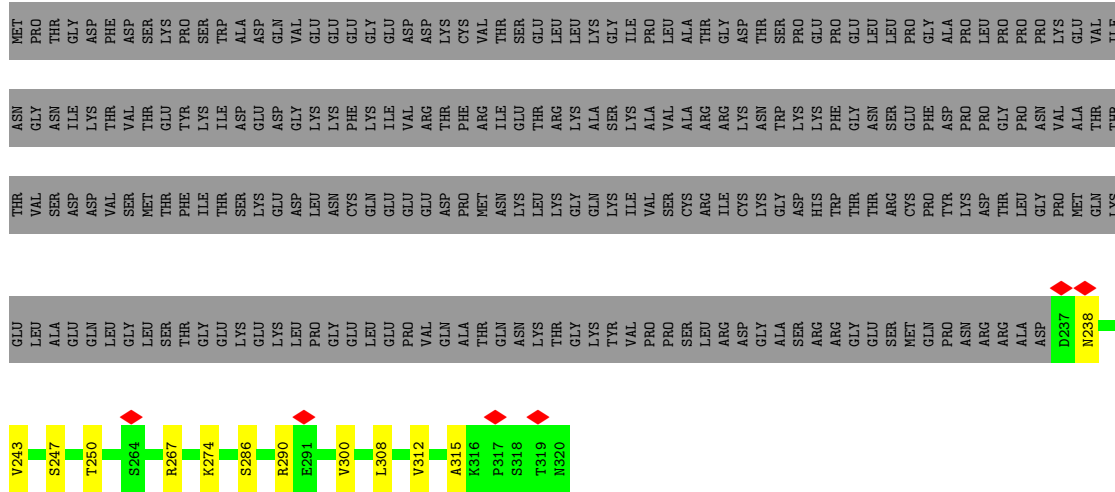
● Molecule 36: Programmed cell death protein 4

Chain CD: 10% . 90%



● Molecule 37: Eukaryotic translation initiation factor 3 subunit G

Chain 3G: 22% . 74%



4 Experimental information

| Property | Value | Source |
|--------------------------------------|---|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, C1 | Depositor |
| Number of particles used | 68929 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 58 | 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 | 0.397 | Depositor |
| Minimum map value | -0.173 | Depositor |
| Average map value | 0.000 | Depositor |
| Map value standard deviation | 0.008 | Depositor |
| Recommended contour level | 0.02 | Depositor |
| Map size (Å) | 446.88, 446.88, 446.88 | wwPDB |
| Map dimensions | 420, 420, 420 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.064, 1.064, 1.064 | Depositor |

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|---------|-------------|------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 1 | Ln | 0.28 | 0/231 | 0.74 | 0/294 |
| 2 | S2 | 0.51 | 0/40843 | 0.99 | 127/63639 (0.2%) |
| 3 | SA | 0.33 | 0/1778 | 0.62 | 2/2416 (0.1%) |
| 4 | SB | 0.32 | 0/1765 | 0.61 | 1/2362 (0.0%) |
| 5 | SD | 0.34 | 0/1793 | 0.62 | 0/2414 |
| 6 | SE | 0.33 | 0/2118 | 0.62 | 1/2849 (0.0%) |
| 7 | SF | 0.34 | 0/1516 | 0.71 | 2/2037 (0.1%) |
| 8 | SH | 0.30 | 0/1519 | 0.65 | 0/2033 |
| 9 | SI | 0.34 | 0/1715 | 0.70 | 1/2287 (0.0%) |
| 10 | SK | 0.33 | 0/851 | 0.64 | 0/1147 |
| 11 | SL | 0.35 | 0/1268 | 0.58 | 0/1696 |
| 12 | SP | 0.30 | 0/1003 | 0.68 | 0/1342 |
| 13 | SQ | 0.36 | 0/1160 | 0.73 | 1/1553 (0.1%) |
| 14 | SR | 0.29 | 0/1105 | 0.66 | 1/1484 (0.1%) |
| 15 | SS | 0.29 | 0/1216 | 0.68 | 1/1628 (0.1%) |
| 16 | ST | 0.31 | 0/1131 | 0.58 | 0/1515 |
| 17 | SU | 0.30 | 0/831 | 0.69 | 0/1115 |
| 18 | SV | 0.34 | 0/643 | 0.63 | 0/860 |
| 19 | SX | 0.38 | 0/1116 | 0.64 | 0/1490 |
| 20 | Sa | 0.36 | 0/836 | 0.70 | 2/1121 (0.2%) |
| 21 | Sc | 0.32 | 0/508 | 0.87 | 1/680 (0.1%) |
| 22 | Sd | 0.37 | 0/470 | 0.67 | 0/623 |
| 23 | Sg | 0.28 | 0/2493 | 0.67 | 1/3394 (0.0%) |
| 24 | SC | 0.38 | 0/1762 | 0.64 | 0/2381 |
| 25 | SG | 0.30 | 0/1946 | 0.70 | 2/2590 (0.1%) |
| 26 | SJ | 0.35 | 0/1550 | 0.63 | 0/2069 |
| 27 | SM | 0.29 | 0/950 | 0.63 | 0/1275 |
| 28 | SN | 0.31 | 0/1232 | 0.57 | 0/1656 |
| 29 | SO | 0.32 | 0/1062 | 0.63 | 0/1425 |
| 30 | SW | 0.35 | 0/1051 | 0.65 | 1/1406 (0.1%) |
| 31 | SY | 0.35 | 0/1083 | 0.65 | 0/1438 |
| 32 | SZ | 0.29 | 0/604 | 0.78 | 0/810 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|---------|-------------|-------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 33 | Sb | 0.30 | 0/665 | 0.62 | 0/891 |
| 34 | Se | 0.30 | 0/465 | 0.61 | 0/612 |
| 35 | Sf | 0.29 | 0/560 | 0.65 | 0/745 |
| 36 | CD | 0.28 | 0/378 | 0.60 | 0/506 |
| 37 | 3G | 0.28 | 0/680 | 0.69 | 0/916 |
| All | All | 0.43 | 0/81897 | 0.85 | 144/118699 (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 |
|-----|-------|---------------------|---------------------|
| 14 | SR | 0 | 1 |
| 19 | SX | 0 | 1 |
| 26 | SJ | 0 | 1 |
| 32 | SZ | 0 | 1 |
| All | All | 0 | 4 |

There are no bond length outliers.

The worst 5 of 144 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|-----------|--------|-------------|----------|
| 2 | S2 | 1772 | C | N1-C2-O2 | 13.51 | 127.01 | 118.90 |
| 2 | S2 | 1772 | C | N3-C2-O2 | -12.94 | 112.84 | 121.90 |
| 2 | S2 | 501 | C | N1-C2-O2 | 12.07 | 126.14 | 118.90 |
| 2 | S2 | 501 | C | C2-N1-C1' | 11.93 | 131.92 | 118.80 |
| 2 | S2 | 293 | C | N1-C2-O2 | 11.78 | 125.97 | 118.90 |

There are no chirality outliers.

All (4) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 26 | SJ | 137 | VAL | Peptide |
| 14 | SR | 67 | ARG | Peptide |
| 19 | SX | 126 | ALA | Peptide |
| 32 | SZ | 46 | ASN | Peptide |

5.2 Too-close contacts [i](#)

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

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | Ln | 230 | 0 | 276 | 0 | 0 |
| 2 | S2 | 36538 | 0 | 18415 | 329 | 0 |
| 3 | SA | 1741 | 0 | 1746 | 25 | 0 |
| 4 | SB | 1738 | 0 | 1809 | 29 | 0 |
| 5 | SD | 1765 | 0 | 1865 | 30 | 0 |
| 6 | SE | 2076 | 0 | 2177 | 27 | 0 |
| 7 | SF | 1495 | 0 | 1549 | 29 | 0 |
| 8 | SH | 1497 | 0 | 1590 | 17 | 0 |
| 9 | SI | 1686 | 0 | 1772 | 35 | 0 |
| 10 | SK | 827 | 0 | 854 | 14 | 0 |
| 11 | SL | 1247 | 0 | 1323 | 15 | 0 |
| 12 | SP | 985 | 0 | 1031 | 15 | 0 |
| 13 | SQ | 1142 | 0 | 1213 | 18 | 0 |
| 14 | SR | 1090 | 0 | 1149 | 16 | 0 |
| 15 | SS | 1198 | 0 | 1261 | 24 | 0 |
| 16 | ST | 1112 | 0 | 1146 | 20 | 0 |
| 17 | SU | 821 | 0 | 883 | 7 | 0 |
| 18 | SV | 636 | 0 | 637 | 14 | 0 |
| 19 | SX | 1098 | 0 | 1167 | 15 | 0 |
| 20 | Sa | 821 | 0 | 870 | 0 | 0 |
| 21 | Sc | 506 | 0 | 536 | 0 | 0 |
| 22 | Sd | 459 | 0 | 448 | 0 | 0 |
| 23 | Sg | 2436 | 0 | 2393 | 0 | 0 |
| 24 | SC | 1725 | 0 | 1813 | 31 | 0 |
| 25 | SG | 1923 | 0 | 2088 | 43 | 0 |
| 26 | SJ | 1525 | 0 | 1640 | 17 | 0 |
| 27 | SM | 940 | 0 | 965 | 19 | 0 |
| 28 | SN | 1208 | 0 | 1294 | 15 | 0 |
| 29 | SO | 1049 | 0 | 1073 | 24 | 0 |
| 30 | SW | 1034 | 0 | 1080 | 10 | 0 |
| 31 | SY | 1065 | 0 | 1142 | 20 | 0 |
| 32 | SZ | 598 | 0 | 656 | 11 | 0 |
| 33 | Sb | 651 | 0 | 672 | 0 | 0 |
| 34 | Se | 459 | 0 | 503 | 0 | 0 |
| 35 | Sf | 548 | 0 | 555 | 0 | 0 |
| 36 | CD | 372 | 0 | 352 | 5 | 0 |
| 37 | 3G | 667 | 0 | 647 | 13 | 0 |

Continued on next page...

Continued from previous page...

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 38 | S2 | 22 | 0 | 0 | 0 | 0 |
| 38 | SG | 1 | 0 | 0 | 0 | 0 |
| 39 | Sa | 1 | 0 | 0 | 0 | 0 |
| 39 | Sd | 1 | 0 | 0 | 0 | 0 |
| 39 | Sf | 1 | 0 | 0 | 0 | 0 |
| All | All | 76934 | 0 | 60590 | 746 | 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 7.

The worst 5 of 746 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) |
|----------------|------------------|--------------------------|-------------------|
| 2:S2:886:A:N6 | 2:S2:901:G:C4 | 2.22 | 1.08 |
| 2:S2:1756:C:N4 | 2:S2:1775:U:H3 | 1.63 | 0.96 |
| 2:S2:543:C:H1' | 37:3G:274:LYS:NZ | 1.83 | 0.93 |
| 2:S2:140:C:N4 | 2:S2:313:A:H61 | 1.66 | 0.92 |
| 2:S2:885:U:H3 | 2:S2:901:G:H1 | 1.12 | 0.92 |

There are no symmetry-related clashes.

5.3 Torsion angles [\(i\)](#)

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

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

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

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|---------|----------|-------------|-----|
| 1 | Ln | 22/25 (88%) | 22 (100%) | 0 | 0 | 100 | 100 |
| 3 | SA | 219/295 (74%) | 205 (94%) | 14 (6%) | 0 | 100 | 100 |
| 4 | SB | 212/264 (80%) | 195 (92%) | 17 (8%) | 0 | 100 | 100 |
| 5 | SD | 225/243 (93%) | 212 (94%) | 12 (5%) | 1 (0%) | 34 | 69 |
| 6 | SE | 260/263 (99%) | 250 (96%) | 10 (4%) | 0 | 100 | 100 |

Continued on next page...

Continued from previous page...

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 7 | SF | 187/204 (92%) | 169 (90%) | 17 (9%) | 1 (0%) | 29 | 67 |
| 8 | SH | 182/194 (94%) | 163 (90%) | 17 (9%) | 2 (1%) | 14 | 51 |
| 9 | SI | 204/208 (98%) | 185 (91%) | 18 (9%) | 1 (0%) | 29 | 67 |
| 10 | SK | 96/165 (58%) | 88 (92%) | 8 (8%) | 0 | 100 | 100 |
| 11 | SL | 151/158 (96%) | 141 (93%) | 10 (7%) | 0 | 100 | 100 |
| 12 | SP | 119/145 (82%) | 117 (98%) | 2 (2%) | 0 | 100 | 100 |
| 13 | SQ | 142/146 (97%) | 130 (92%) | 10 (7%) | 2 (1%) | 11 | 46 |
| 14 | SR | 133/135 (98%) | 122 (92%) | 10 (8%) | 1 (1%) | 19 | 58 |
| 15 | SS | 143/152 (94%) | 134 (94%) | 9 (6%) | 0 | 100 | 100 |
| 16 | ST | 141/145 (97%) | 134 (95%) | 7 (5%) | 0 | 100 | 100 |
| 17 | SU | 102/119 (86%) | 92 (90%) | 10 (10%) | 0 | 100 | 100 |
| 18 | SV | 81/83 (98%) | 76 (94%) | 5 (6%) | 0 | 100 | 100 |
| 19 | SX | 139/143 (97%) | 129 (93%) | 9 (6%) | 1 (1%) | 22 | 61 |
| 20 | Sa | 100/115 (87%) | 92 (92%) | 7 (7%) | 1 (1%) | 15 | 54 |
| 21 | Sc | 62/69 (90%) | 48 (77%) | 14 (23%) | 0 | 100 | 100 |
| 22 | Sd | 53/56 (95%) | 45 (85%) | 7 (13%) | 1 (2%) | 8 | 39 |
| 23 | Sg | 311/317 (98%) | 274 (88%) | 37 (12%) | 0 | 100 | 100 |
| 24 | SC | 220/293 (75%) | 208 (94%) | 11 (5%) | 1 (0%) | 29 | 67 |
| 25 | SG | 235/249 (94%) | 221 (94%) | 14 (6%) | 0 | 100 | 100 |
| 26 | SJ | 183/194 (94%) | 176 (96%) | 7 (4%) | 0 | 100 | 100 |
| 27 | SM | 120/132 (91%) | 115 (96%) | 5 (4%) | 0 | 100 | 100 |
| 28 | SN | 148/151 (98%) | 143 (97%) | 5 (3%) | 0 | 100 | 100 |
| 29 | SO | 138/151 (91%) | 131 (95%) | 7 (5%) | 0 | 100 | 100 |
| 30 | SW | 127/130 (98%) | 123 (97%) | 4 (3%) | 0 | 100 | 100 |
| 31 | SY | 129/133 (97%) | 118 (92%) | 11 (8%) | 0 | 100 | 100 |
| 32 | SZ | 73/125 (58%) | 56 (77%) | 17 (23%) | 0 | 100 | 100 |
| 33 | Sb | 81/84 (96%) | 70 (86%) | 11 (14%) | 0 | 100 | 100 |
| 34 | Se | 56/59 (95%) | 53 (95%) | 3 (5%) | 0 | 100 | 100 |
| 35 | Sf | 65/156 (42%) | 59 (91%) | 6 (9%) | 0 | 100 | 100 |
| 36 | CD | 47/469 (10%) | 41 (87%) | 6 (13%) | 0 | 100 | 100 |
| 37 | 3G | 82/320 (26%) | 81 (99%) | 1 (1%) | 0 | 100 | 100 |

Continued on next page...

Continued from previous page...

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles |
|-----|-------|-----------------|------------|----------|----------|-------------|
| All | All | 4988/6290 (79%) | 4618 (93%) | 358 (7%) | 12 (0%) | 50 79 |

5 of 12 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 5 | SD | 178 | ARG |
| 9 | SI | 160 | SER |
| 19 | SX | 127 | ASN |
| 8 | SH | 15 | LYS |
| 13 | SQ | 43 | GLU |

5.3.2 Protein sidechains [i](#)

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

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles |
|-----|-------|----------------|------------|----------|-------------|
| 1 | Ln | 23/24 (96%) | 23 (100%) | 0 | 100 100 |
| 3 | SA | 183/243 (75%) | 183 (100%) | 0 | 100 100 |
| 4 | SB | 195/231 (84%) | 195 (100%) | 0 | 100 100 |
| 5 | SD | 190/202 (94%) | 189 (100%) | 1 (0%) | 88 95 |
| 6 | SE | 224/225 (100%) | 224 (100%) | 0 | 100 100 |
| 7 | SF | 159/170 (94%) | 159 (100%) | 0 | 100 100 |
| 8 | SH | 166/174 (95%) | 164 (99%) | 2 (1%) | 71 88 |
| 9 | SI | 178/180 (99%) | 178 (100%) | 0 | 100 100 |
| 10 | SK | 89/136 (65%) | 89 (100%) | 0 | 100 100 |
| 11 | SL | 137/142 (96%) | 136 (99%) | 1 (1%) | 84 94 |
| 12 | SP | 107/130 (82%) | 107 (100%) | 0 | 100 100 |
| 13 | SQ | 119/121 (98%) | 119 (100%) | 0 | 100 100 |
| 14 | SR | 122/122 (100%) | 120 (98%) | 2 (2%) | 62 84 |
| 15 | SS | 126/132 (96%) | 126 (100%) | 0 | 100 100 |
| 16 | ST | 113/115 (98%) | 112 (99%) | 1 (1%) | 78 91 |
| 17 | SU | 94/107 (88%) | 93 (99%) | 1 (1%) | 73 88 |

Continued on next page...

Continued from previous page...

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-----------------|-------------|----------|-------------|-----|
| 18 | SV | 67/67 (100%) | 67 (100%) | 0 | 100 | 100 |
| 19 | SX | 113/115 (98%) | 113 (100%) | 0 | 100 | 100 |
| 20 | Sa | 89/98 (91%) | 89 (100%) | 0 | 100 | 100 |
| 21 | Sc | 57/62 (92%) | 57 (100%) | 0 | 100 | 100 |
| 22 | Sd | 48/49 (98%) | 48 (100%) | 0 | 100 | 100 |
| 23 | Sg | 272/275 (99%) | 272 (100%) | 0 | 100 | 100 |
| 24 | SC | 188/225 (84%) | 188 (100%) | 0 | 100 | 100 |
| 25 | SG | 207/218 (95%) | 206 (100%) | 1 (0%) | 88 | 95 |
| 26 | SJ | 161/168 (96%) | 161 (100%) | 0 | 100 | 100 |
| 27 | SM | 102/108 (94%) | 99 (97%) | 3 (3%) | 42 | 74 |
| 28 | SN | 130/131 (99%) | 130 (100%) | 0 | 100 | 100 |
| 29 | SO | 110/119 (92%) | 110 (100%) | 0 | 100 | 100 |
| 30 | SW | 112/113 (99%) | 112 (100%) | 0 | 100 | 100 |
| 31 | SY | 113/115 (98%) | 111 (98%) | 2 (2%) | 59 | 82 |
| 32 | SZ | 66/103 (64%) | 66 (100%) | 0 | 100 | 100 |
| 33 | Sb | 75/76 (99%) | 75 (100%) | 0 | 100 | 100 |
| 34 | Se | 47/48 (98%) | 47 (100%) | 0 | 100 | 100 |
| 35 | Sf | 60/140 (43%) | 60 (100%) | 0 | 100 | 100 |
| 36 | CD | 38/404 (9%) | 38 (100%) | 0 | 100 | 100 |
| 37 | 3G | 70/277 (25%) | 70 (100%) | 0 | 100 | 100 |
| All | All | 4350/5365 (81%) | 4336 (100%) | 14 (0%) | 92 | 96 |

5 of 14 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 17 | SU | 49 | LYS |
| 25 | SG | 119 | LYS |
| 31 | SY | 132 | LYS |
| 27 | SM | 121 | LYS |
| 31 | SY | 118 | ARG |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 18 | SV | 35 | ASN |
| 24 | SC | 267 | GLN |
| 25 | SG | 13 | GLN |
| 11 | SL | 19 | ASN |
| 8 | SH | 165 | ASN |

5.3.3 RNA [i](#)

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 2 | S2 | 1701/1869 (91%) | 413 (24%) | 7 (0%) |

5 of 413 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2 | S2 | 4 | C |
| 2 | S2 | 14 | C |
| 2 | S2 | 17 | C |
| 2 | S2 | 25 | A |
| 2 | S2 | 33 | G |

5 of 7 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 2 | S2 | 543 | C |
| 2 | S2 | 688 | U |
| 2 | S2 | 1781 | A |
| 2 | S2 | 1434 | C |
| 2 | S2 | 541 | U |

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 26 ligands modelled in this entry, 26 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

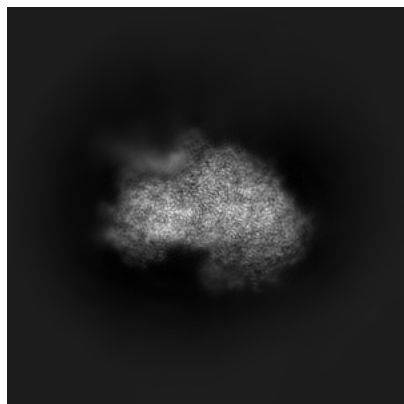
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38753. These allow visual inspection of the internal detail of the map and identification of artifacts.

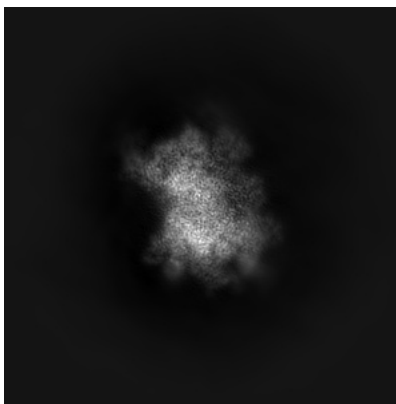
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

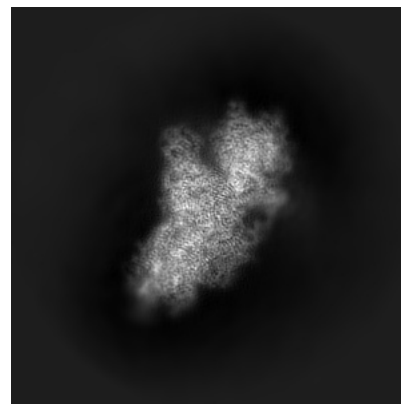
6.1.1 Primary map



X

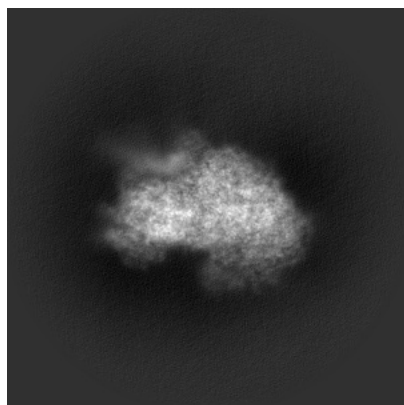


Y

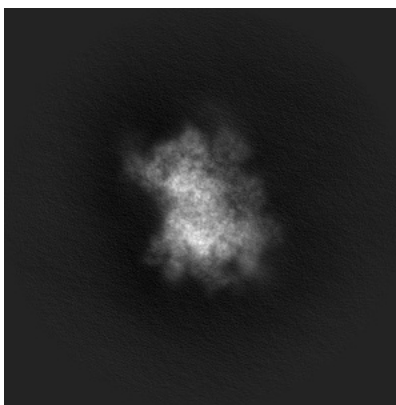


Z

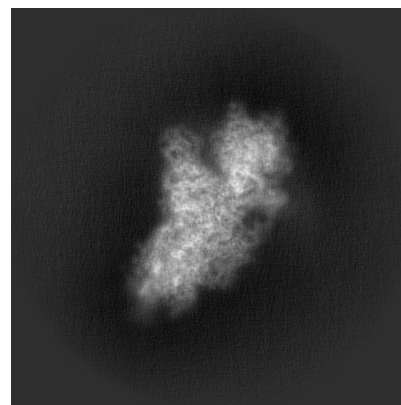
6.1.2 Raw map



X



Y

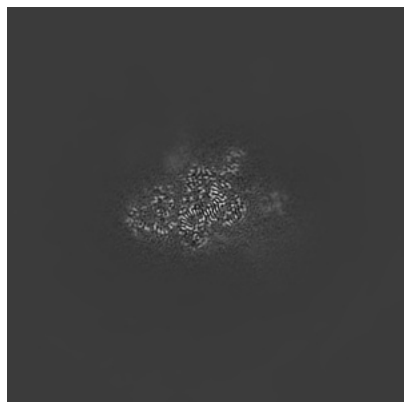


Z

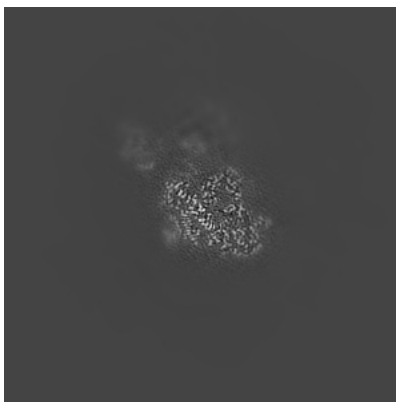
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

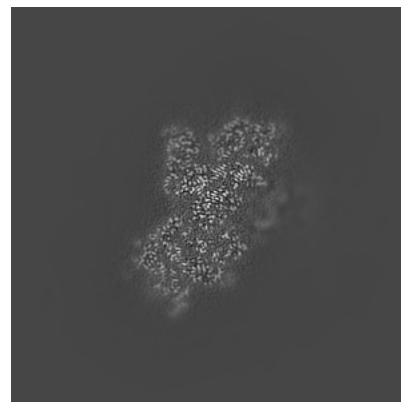
6.2.1 Primary map



X Index: 210

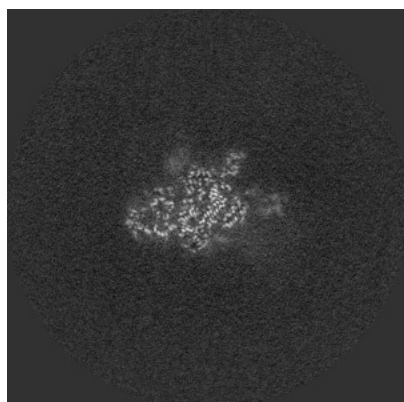


Y Index: 210

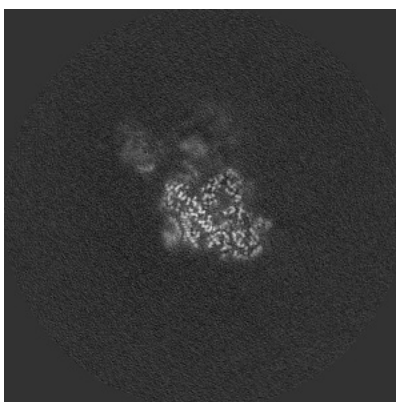


Z Index: 210

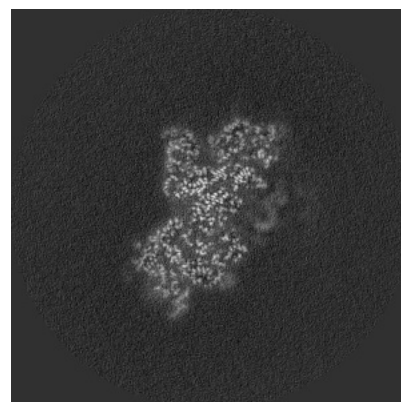
6.2.2 Raw map



X Index: 210



Y Index: 210

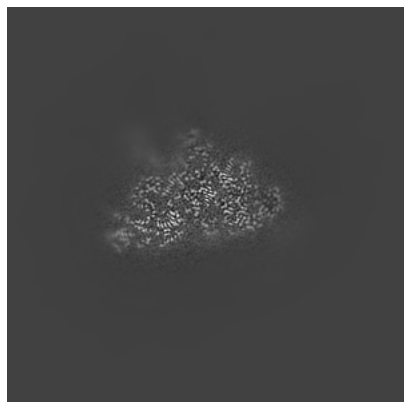


Z Index: 210

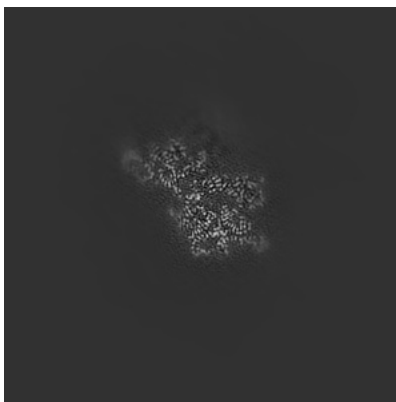
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

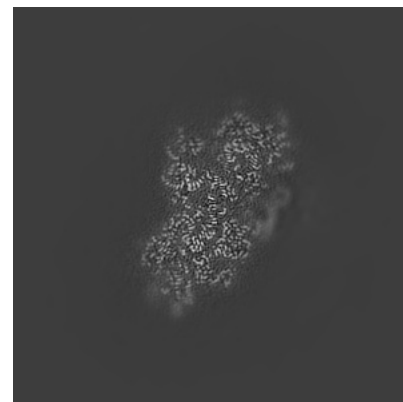
6.3.1 Primary map



X Index: 190

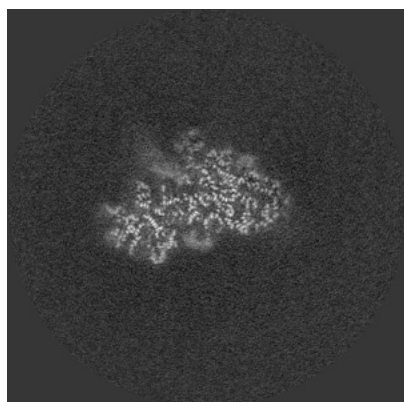


Y Index: 233

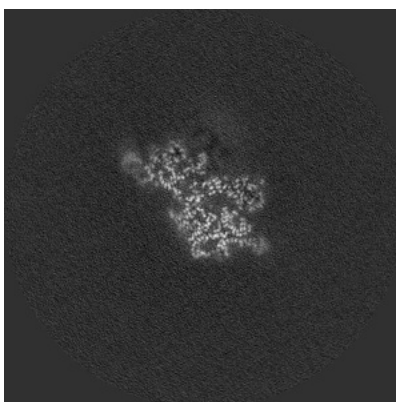


Z Index: 204

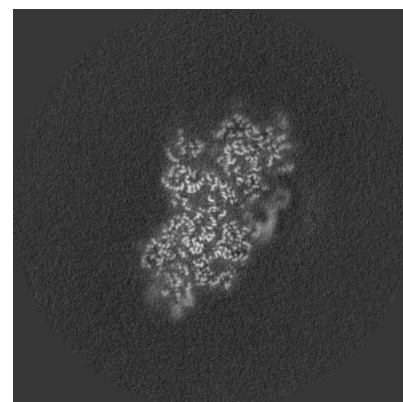
6.3.2 Raw map



X Index: 178



Y Index: 233

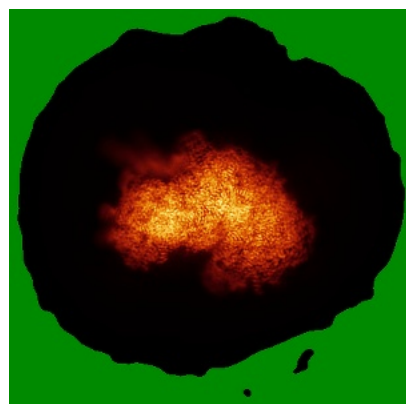


Z Index: 204

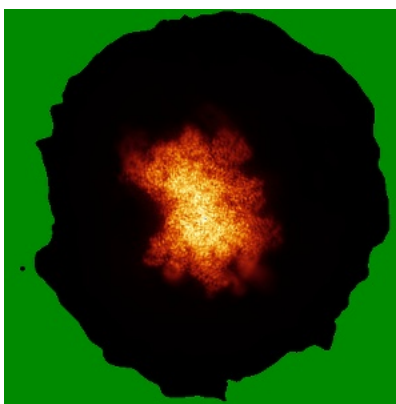
The images above show the largest variance slices of the map in three orthogonal directions.

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

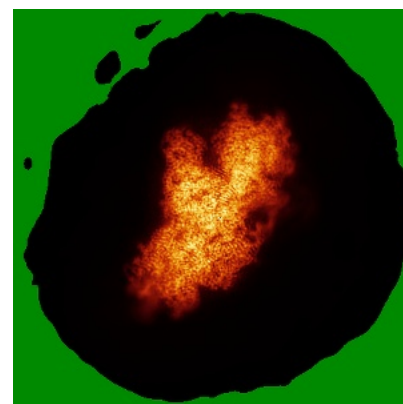
6.4.1 Primary map



X

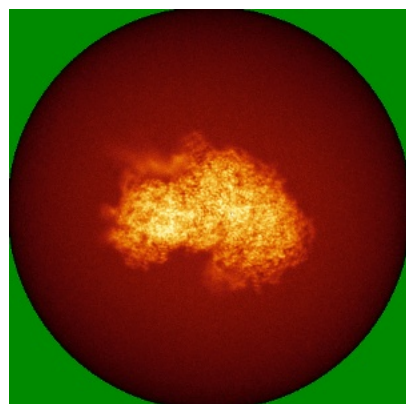


Y

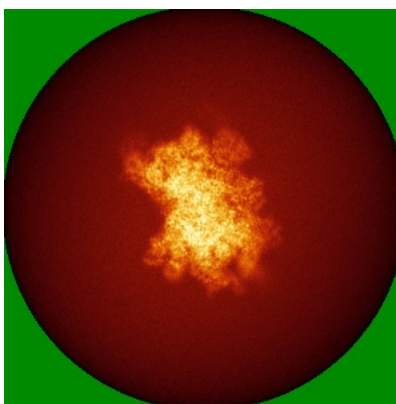


Z

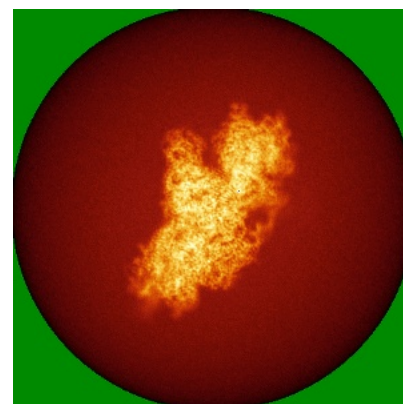
6.4.2 Raw map



X



Y

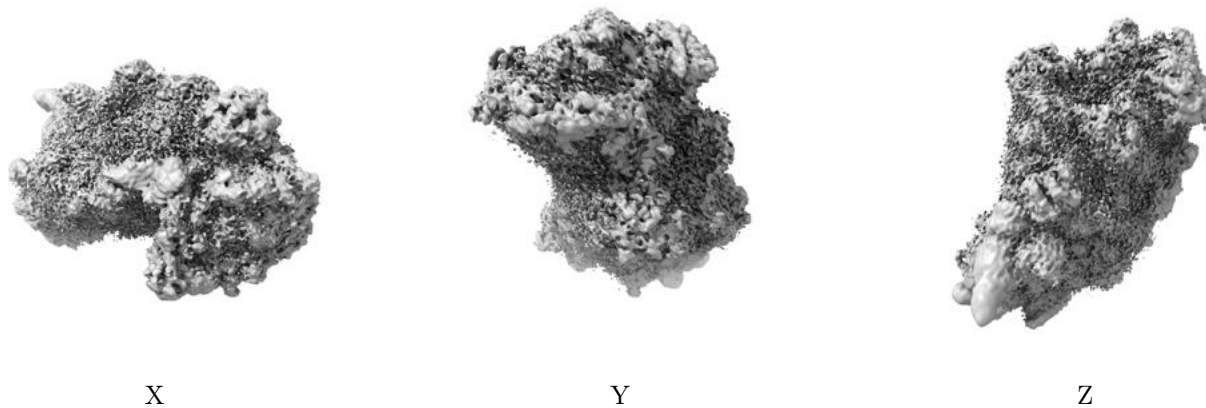


Z

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.

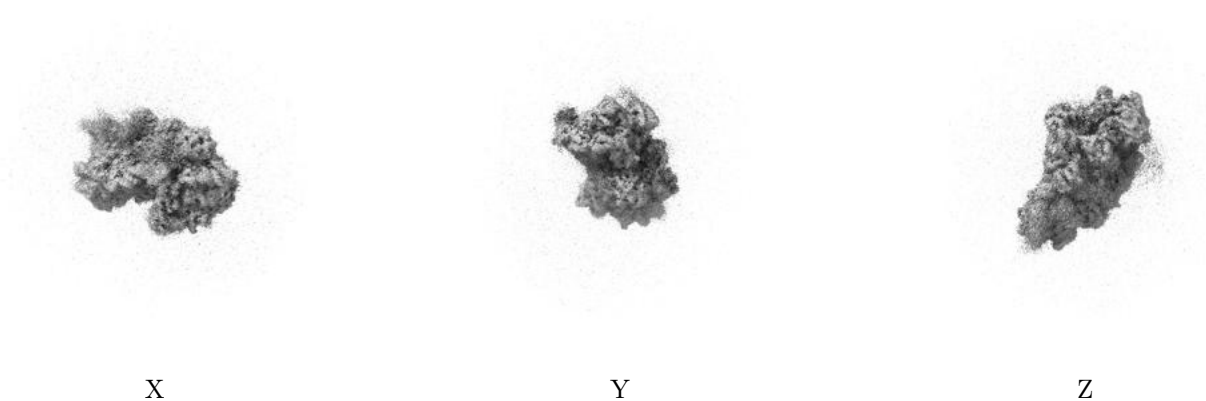
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

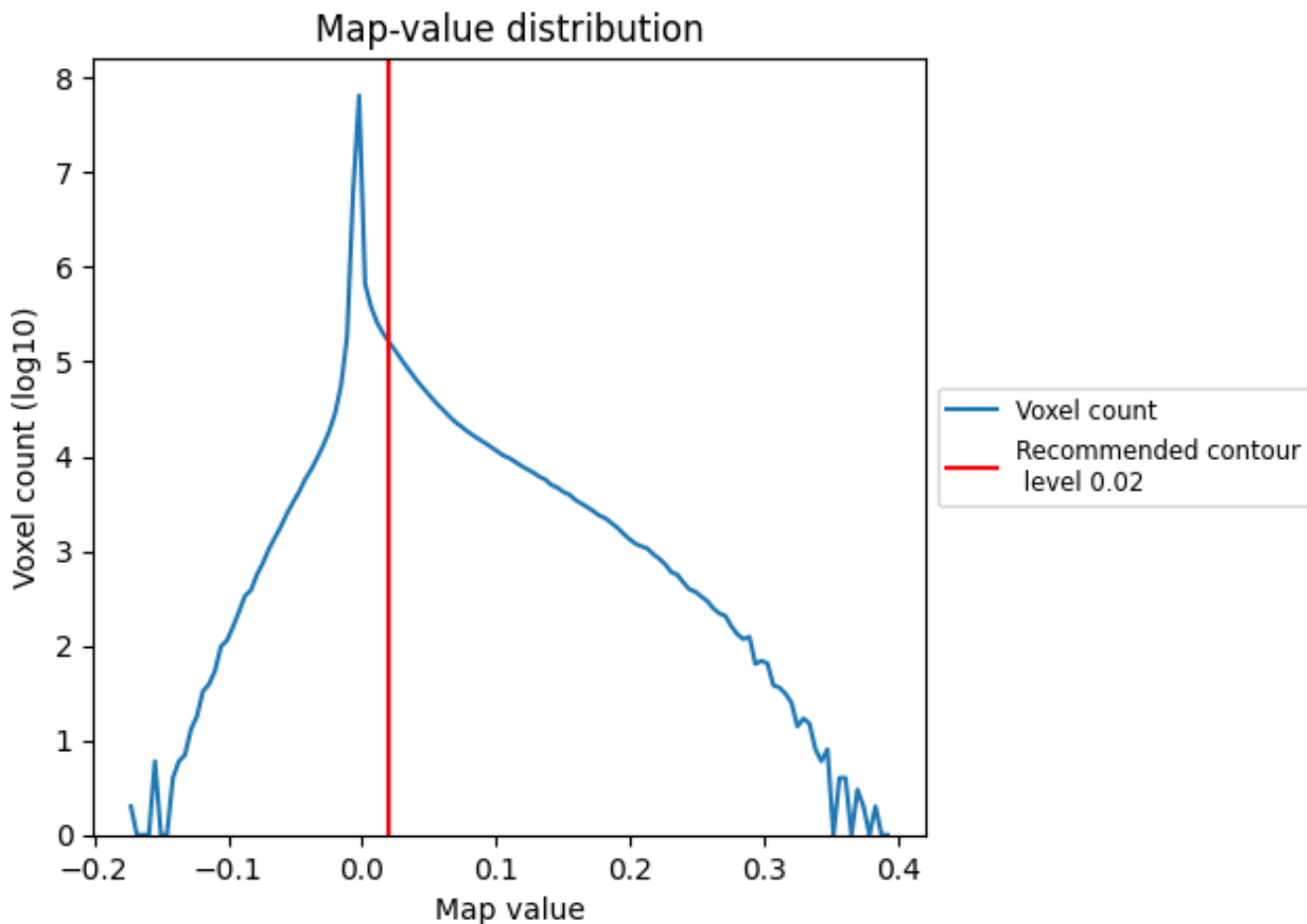
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

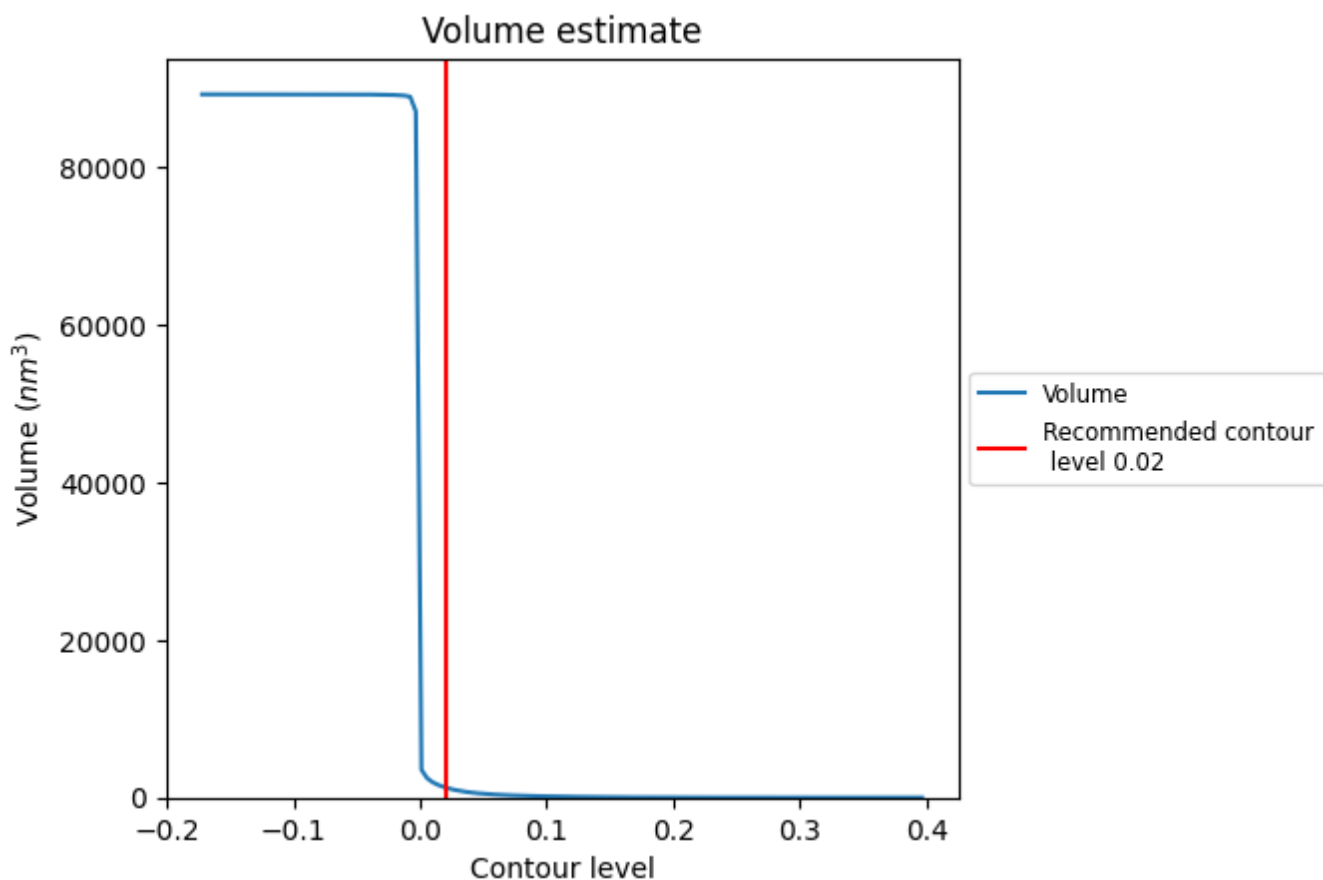
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

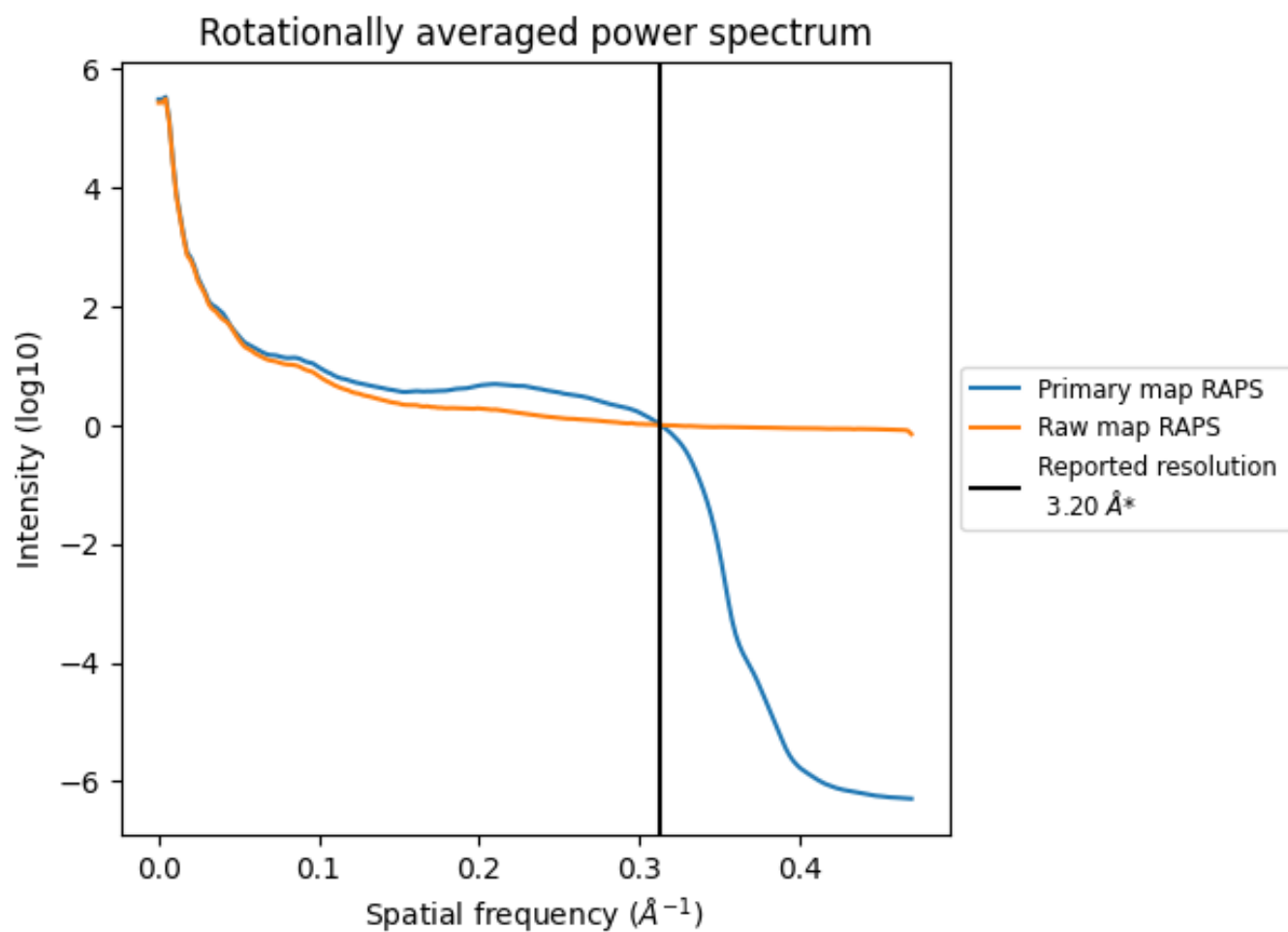
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1276 nm³; this corresponds to an approximate mass of 1153 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

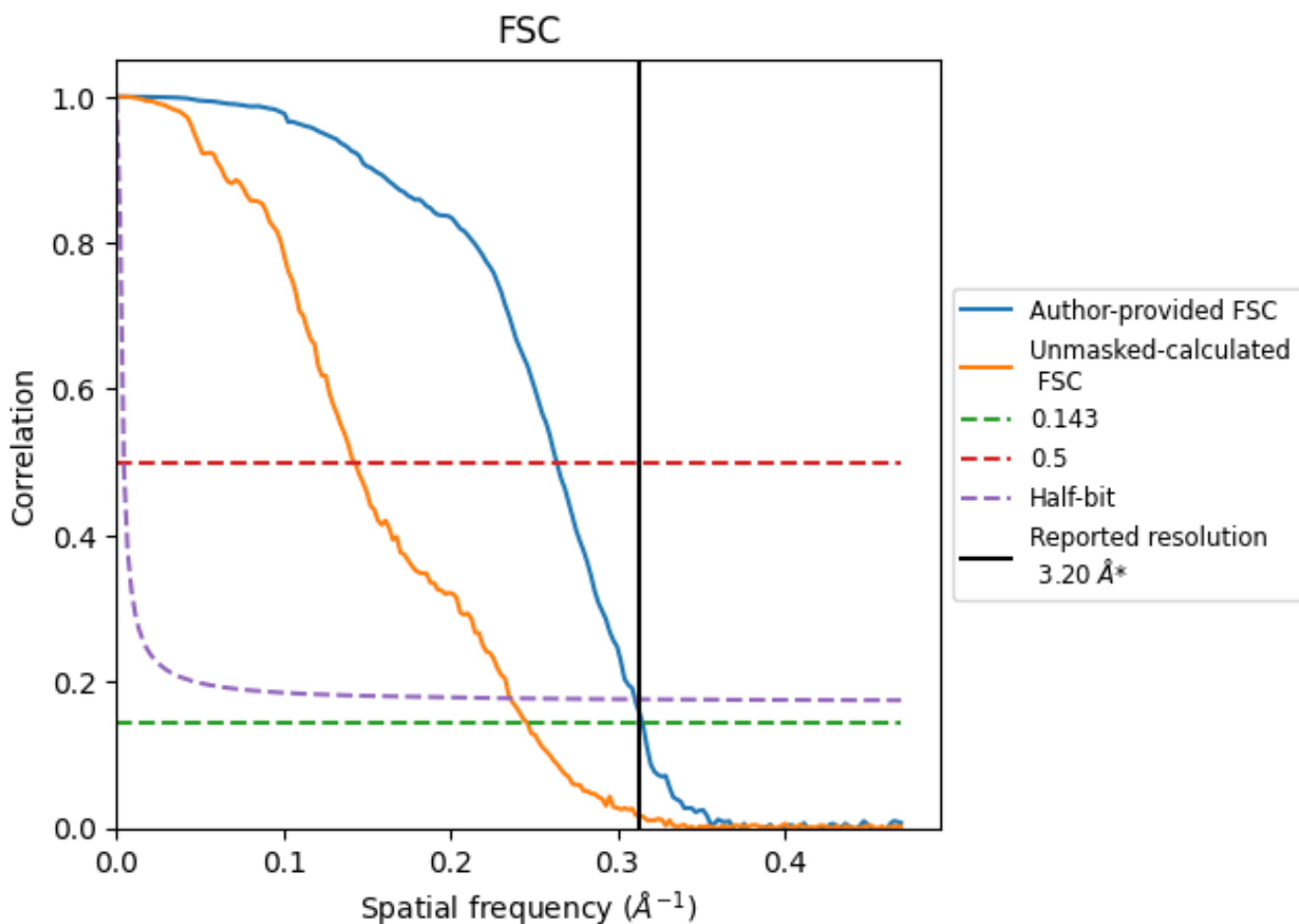


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312\AA^{-1}

8.2 Resolution estimates [i](#)

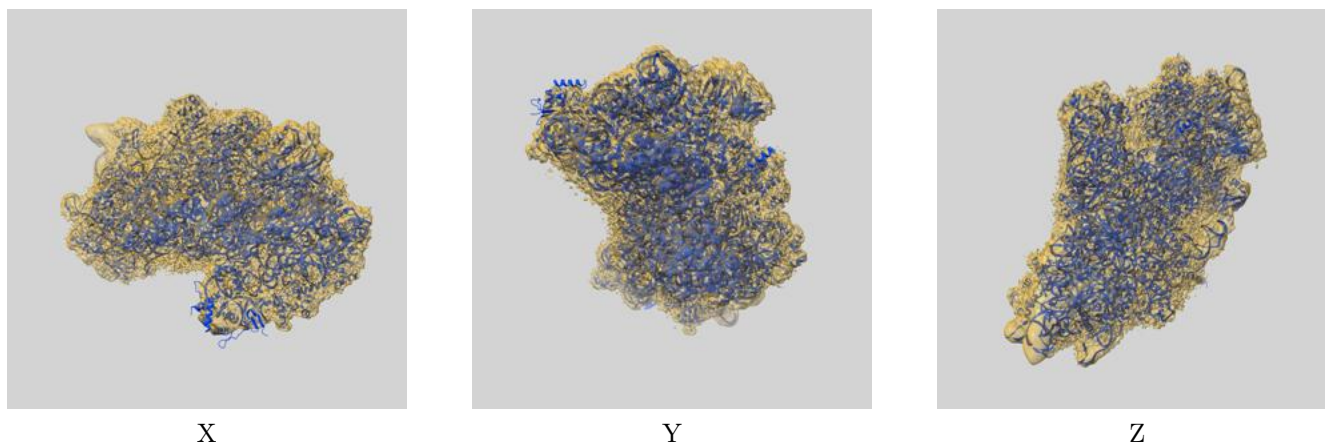
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---------------------------|------------------------------------|------|----------|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 3.20 | - | - |
| Author-provided FSC curve | 3.17 | 3.79 | 3.22 |
| Unmasked-calculated* | 4.06 | 7.01 | 4.24 |

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.06 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

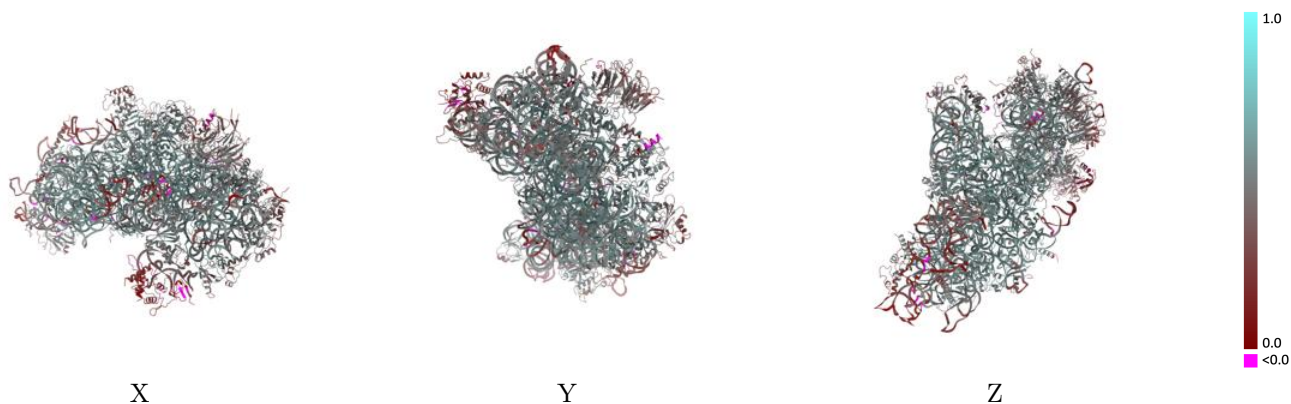
This section contains information regarding the fit between EMDB map EMD-38753 and PDB model 8XXM. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



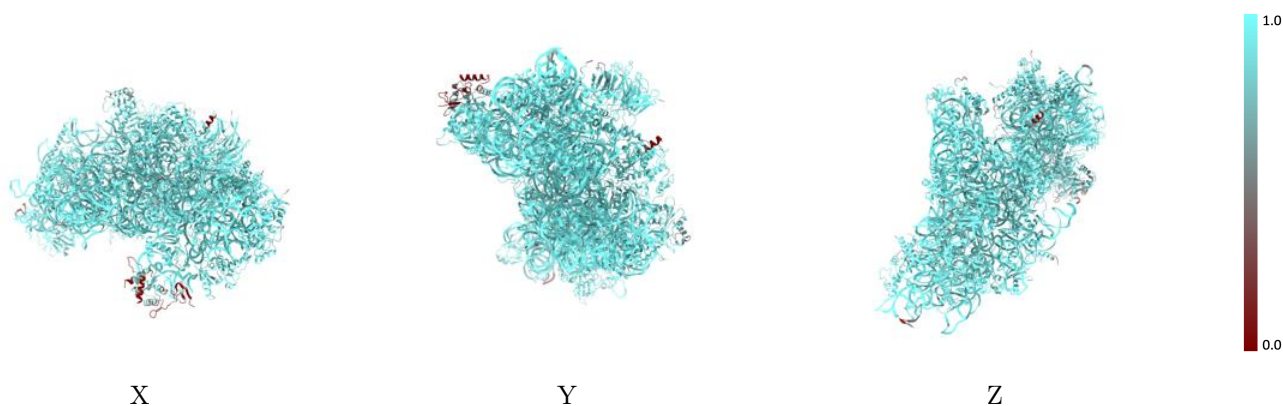
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



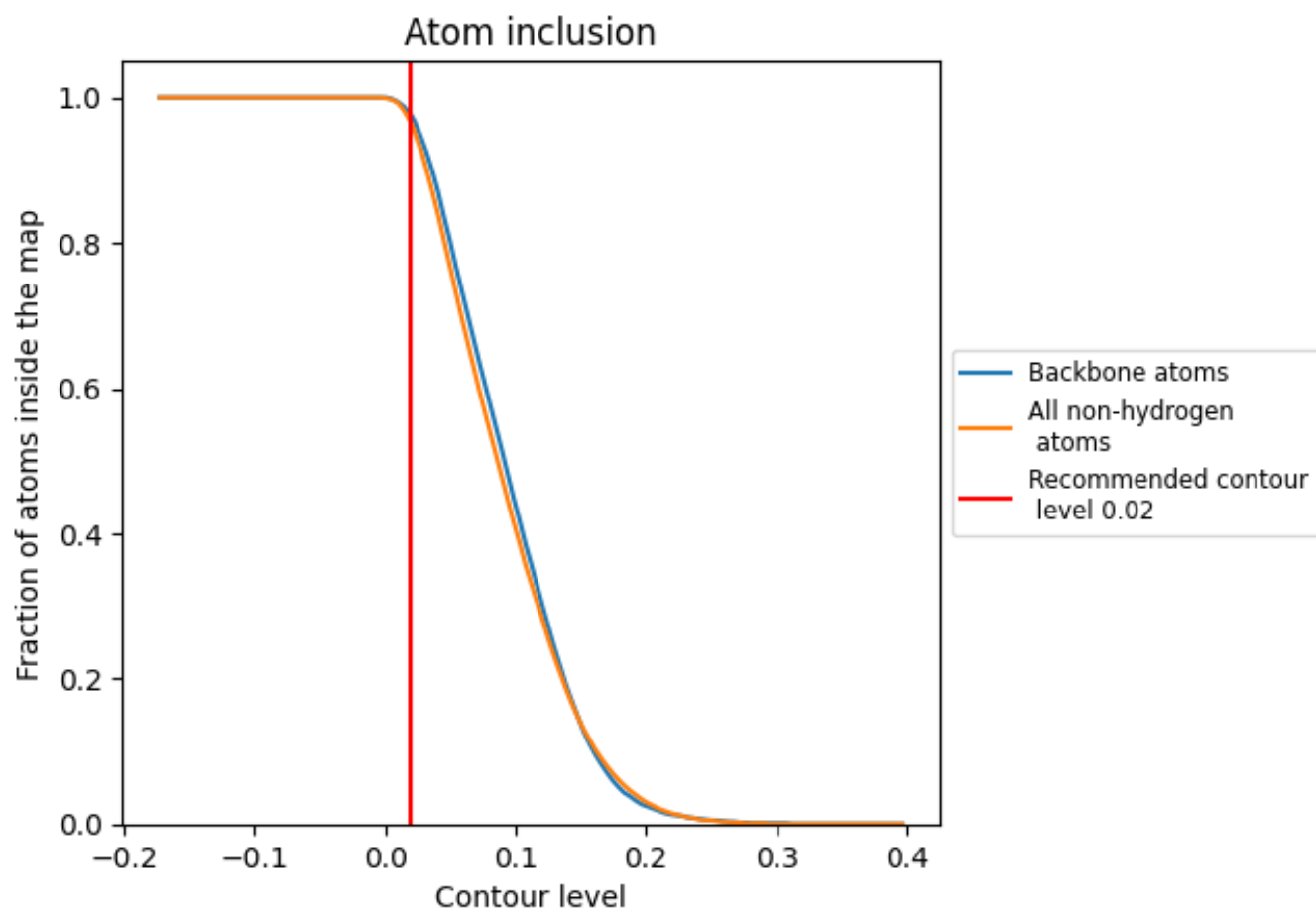
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 97% 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 (0.02) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|--|--|
| All |  0.9660 |  0.4910 |
| 3G |  0.7940 |  0.2310 |
| CD |  0.9420 |  0.4810 |
| Ln |  0.9520 |  0.4770 |
| S2 |  0.9910 |  0.5100 |
| SA |  0.9490 |  0.5170 |
| SB |  0.9530 |  0.4950 |
| SC |  0.9870 |  0.5610 |
| SD |  0.9650 |  0.5160 |
| SE |  0.9960 |  0.5570 |
| SF |  0.9610 |  0.4660 |
| SG |  0.9750 |  0.4410 |
| SH |  0.8950 |  0.3940 |
| SI |  0.9770 |  0.4810 |
| SJ |  0.9790 |  0.5500 |
| SK |  0.9710 |  0.4630 |
| SL |  0.9690 |  0.5200 |
| SM |  0.5070 |  0.1740 |
| SN |  0.9910 |  0.5300 |
| SO |  0.9390 |  0.4900 |
| SP |  0.9560 |  0.4660 |
| SQ |  0.9720 |  0.5100 |
| SR |  0.9430 |  0.4710 |
| SS |  0.9380 |  0.4320 |
| ST |  0.9860 |  0.4930 |
| SU |  0.9590 |  0.4740 |
| SV |  0.9840 |  0.5250 |
| SW |  0.9950 |  0.5840 |
| SX |  0.9960 |  0.5600 |
| SY |  0.9690 |  0.5040 |
| SZ |  0.9090 |  0.3520 |
| Sa |  0.9660 |  0.5260 |
| Sb |  0.9470 |  0.4620 |
| Sc |  0.9240 |  0.4070 |
| Sd |  0.9730 |  0.5130 |



Continued on next page...

Continued from previous page...

| Chain | Atom inclusion | Q-score |
|-------|--|--|
| Se |  0.9620 |  0.5090 |
| Sf |  0.3840 |  0.1460 |
| Sg |  0.9410 |  0.3830 |