



wwPDB EM Validation Summary Report ⓘ

Jan 1, 2025 – 10:55 AM EST

PDB ID : 8TID
EMDB ID : EMD-41284
Title : Combined linker domain of N-DRC and associated proteins Tetrahymena
Authors : Ghanaeian, A.G.; Majhi, S.M.; McCaffrey, C.M.; Nami, B.N.; Black, C.B.;
Yang, S.K.; Legal, T.L.; Papoulas, O.P.; Janowska, M.J.; Valente-Paterno,
M.V.; Marcotte, E.M.; Wloga, D.W.; Bui, K.H.
Deposited on : 2023-07-19
Resolution : 3.60 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

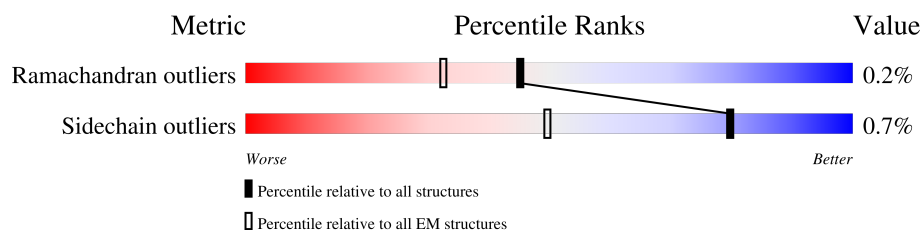
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

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 3.60 Å.

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



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

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

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|---|
| 1 | A | 826 | <div> <div>18%</div> <div>54%</div> <div>45%</div> </div> |
| 2 | B | 506 | <div> <div>32%</div> <div>89%</div> <div>9%</div> </div> |
| 3 | C | 575 | <div> <div>92%</div> <div>7%</div> </div> |
| 4 | D | 472 | <div> <div>19%</div> <div>96%</div> </div> |
| 5 | E | 468 | <div> <div>11%</div> <div>96%</div> </div> |
| 6 | F | 461 | <div> <div>72%</div> <div>100%</div> </div> |
| 7 | G | 345 | <div> <div>25%</div> <div>99%</div> </div> |
| 8 | H | 852 | <div> <div>24%</div> <div>95%</div> </div> |
| 9 | I | 185 | <div> <div>100%</div> </div> |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 9 | i | 185 | |
| 10 | J | 372 | |
| 11 | K | 434 | |
| 12 | L | 862 | |
| 13 | M | 644 | |
| 14 | N | 963 | |
| 14 | n | 963 | |
| 15 | O | 893 | |
| 15 | o | 893 | |
| 16 | P | 794 | |
| 17 | Q | 202 | |
| 17 | R | 202 | |
| 18 | S | 187 | |
| 18 | s | 187 | |
| 19 | T | 361 | |
| 20 | U | 597 | |
| 20 | V | 597 | |
| 21 | W | 1308 | |
| 22 | Z | 1079 | |
| 23 | g | 195 | |
| 24 | w | 1293 | |

2 Entry composition [i](#)

There are 24 unique types of molecules in this entry. The entry contains 123416 atoms, of which 12979 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 Dynein regulatory complex protein 1/2 N-terminal domain-containing protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 1 | A | 458 | Total | C | N | O | S | 0 | 0 |
| | | | 3929 | 2479 | 695 | 734 | 21 | | |

- Molecule 2 is a protein called Coiled-coil protein, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 2 | B | 460 | Total | C | N | O | S | 0 | 0 |
| | | | 3873 | 2427 | 697 | 733 | 16 | | |

- Molecule 3 is a protein called LRRC48 protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 3 | C | 533 | Total | C | N | O | S | 0 | 0 |
| | | | 4433 | 2771 | 760 | 890 | 12 | | |

- Molecule 4 is a protein called Growth-arrest-specific microtubule-binding protein.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 4 | D | 461 | Total | C | H | N | O | S | 0 | 0 |
| | | | 6572 | 2431 | 2704 | 672 | 756 | 9 | | |

- Molecule 5 is a protein called Growth-arrest-specific microtubule-binding protein.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 5 | E | 464 | Total | C | H | N | O | S | 0 | 0 |
| | | | 6424 | 2418 | 2565 | 678 | 754 | 9 | | |

- Molecule 6 is a protein called Flagellar associated protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 6 | F | 461 | Total | C | N | O | S | 0 | 0 |
| | | | 3714 | 2351 | 632 | 714 | 17 | | |

- Molecule 7 is a protein called Kinase domain protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 7 | G | 345 | Total | C | N | O | S | 0 | 0 |
| | | | 2780 | 1763 | 474 | 527 | 16 | | |

- Molecule 8 is a protein called Coiled-coil lobo-like protein, putative.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| 8 | H | 820 | Total | C | N | O | S | 0 | 0 |
| | | | 6857 | 4318 | 1192 | 1314 | 33 | | |

- Molecule 9 is a protein called EF-hand calcium-binding domain protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 9 | I | 185 | Total | C | N | O | S | 0 | 0 |
| | | | 1553 | 1002 | 244 | 301 | 6 | | |
| 9 | i | 185 | Total | C | N | O | S | 0 | 0 |
| | | | 1553 | 1002 | 244 | 301 | 6 | | |

- Molecule 10 is a protein called Dynein regulatory complex protein 9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 10 | J | 372 | Total | C | N | O | S | 0 | 0 |
| | | | 3151 | 1949 | 574 | 620 | 8 | | |

- Molecule 11 is a protein called Dynein regulatory complex protein 10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 11 | K | 434 | Total | C | N | O | S | 0 | 0 |
| | | | 3588 | 2229 | 647 | 699 | 13 | | |

- Molecule 12 is a protein called AAA family ATPase CDC48 subfamily protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| 12 | L | 862 | Total | C | N | O | S | 0 | 0 |
| | | | 7102 | 4513 | 1213 | 1345 | 31 | | |

- Molecule 13 is a protein called Cilia- and flagella-associated protein 91.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 13 | M | 164 | Total | C | N | O | S | 0 | 0 |
| | | | 1373 | 851 | 259 | 260 | 3 | | |

- Molecule 14 is a protein called Flagella associated protein.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|----|---------|-------|
| 14 | N | 434 | Total | C | H | N | O | S | 0 | 0 |
| | | | 5707 | 2237 | 2099 | 650 | 709 | 12 | | |
| 14 | n | 208 | Total | C | H | N | O | S | 0 | 0 |
| | | | 3483 | 1076 | 1740 | 312 | 352 | 3 | | |

- Molecule 15 is a protein called Coiled-coil protein, putative.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 15 | O | 430 | Total | C | H | N | O | S | 0 | 0 |
| | | | 5711 | 2223 | 2107 | 653 | 721 | 7 | | |
| 15 | o | 205 | Total | C | H | N | O | S | 0 | 0 |
| | | | 3470 | 1063 | 1764 | 302 | 334 | 7 | | |

- Molecule 16 is a protein called DUF4201 domain-containing protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|------|----|---------|-------|
| 16 | P | 631 | Total | C | N | O | S | 0 | 0 |
| | | | 5310 | 3305 | 956 | 1034 | 15 | | |

- Molecule 17 is a protein called Calmodulin 7-2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 17 | Q | 202 | Total | C | N | O | S | 0 | 0 |
| | | | 1679 | 1061 | 276 | 338 | 4 | | |
| 17 | R | 202 | Total | C | N | O | S | 0 | 0 |
| | | | 1679 | 1061 | 276 | 338 | 4 | | |

- Molecule 18 is a protein called Coiled-coil domain-containing protein 153.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 18 | S | 187 | Total | C | N | O | S | 0 | 0 |
| | | | 1542 | 943 | 274 | 314 | 11 | | |
| 18 | s | 187 | Total | C | N | O | S | 0 | 0 |
| | | | 1542 | 943 | 274 | 314 | 11 | | |

- Molecule 19 is a protein called Flagellar associated protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 19 | T | 335 | Total | C | N | O | S | 0 | 0 |
| | | | 2782 | 1740 | 489 | 548 | 5 | | |

- Molecule 20 is a protein called L-shape (Unknown-protein).

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 20 | U | 597 | Total | C | N | O | 0 | 0 |
| | | | 2985 | 1791 | 597 | 597 | | |
| 20 | V | 594 | Total | C | N | O | 0 | 0 |
| | | | 2970 | 1782 | 594 | 594 | | |

- Molecule 21 is a protein called WD40 domain protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| 21 | W | 1171 | Total | C | N | O | S | 0 | 0 |
| | | | 9536 | 5994 | 1665 | 1830 | 47 | | |

- Molecule 22 is a protein called EF hand protein.

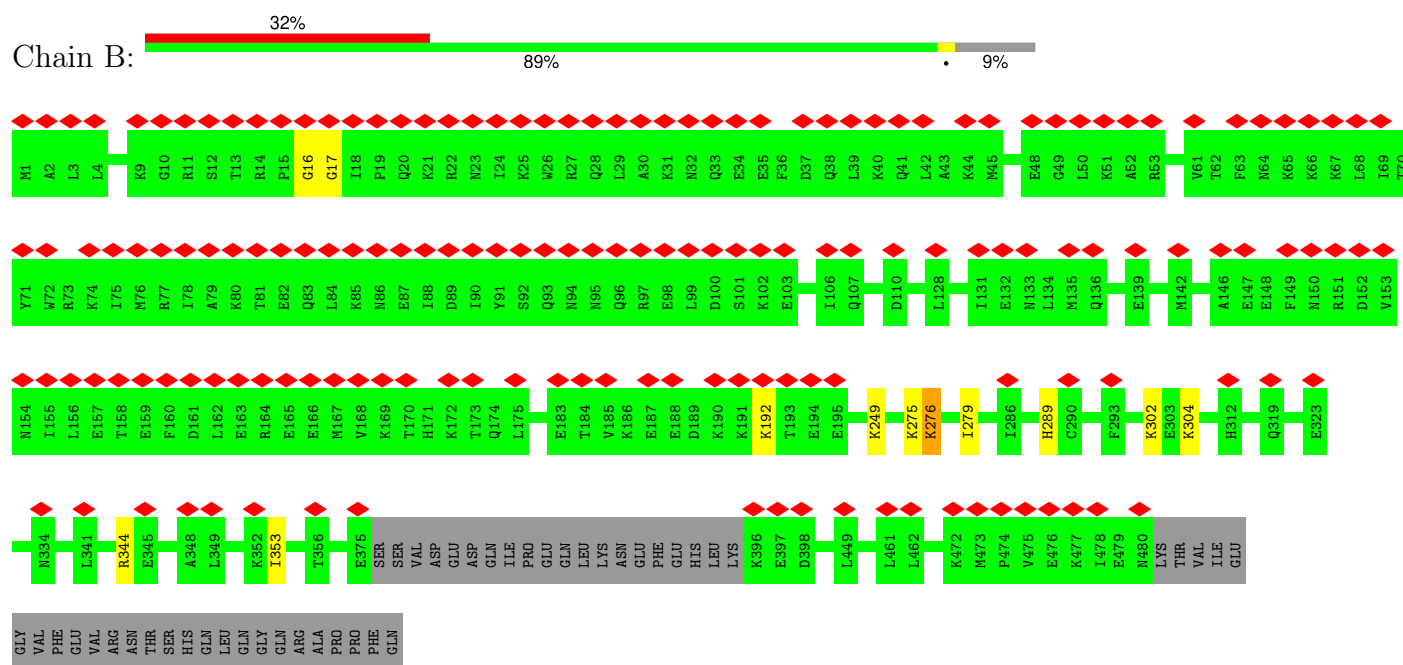
| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| 22 | Z | 830 | Total | C | N | O | S | 0 | 0 |
| | | | 6730 | 4277 | 1134 | 1286 | 33 | | |

- Molecule 23 is a protein called CFAP20.

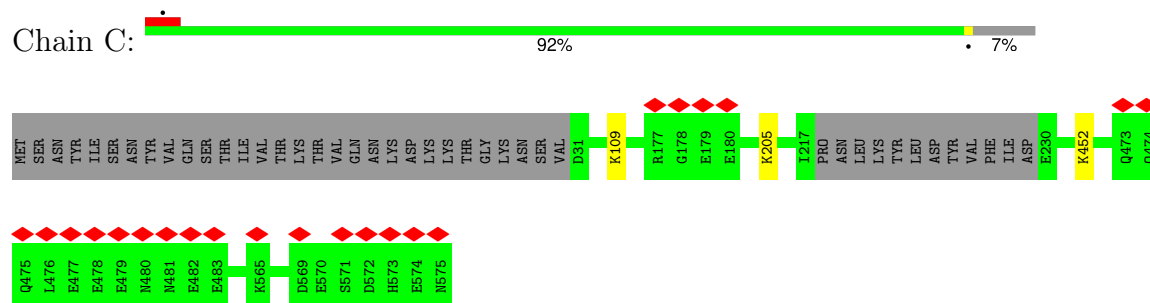
| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 23 | g | 187 | Total | C | N | O | S | 0 | 0 |
| | | | 1556 | 1003 | 269 | 277 | 7 | | |

- Molecule 24 is a protein called WD40 domain protein.

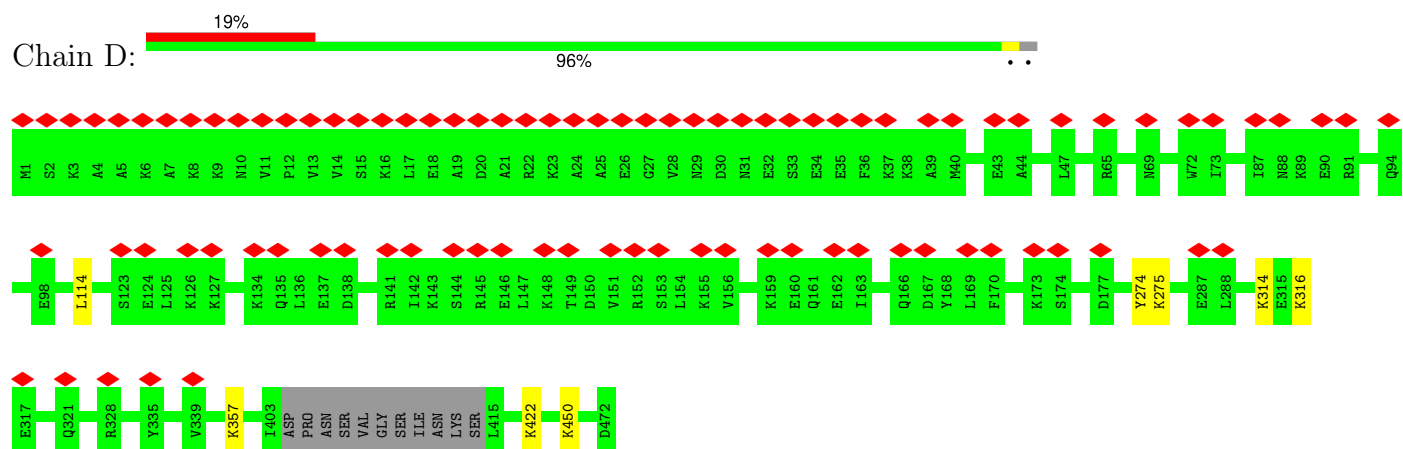
| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| 24 | w | 1192 | Total | C | N | O | S | 0 | 0 |
| | | | 9832 | 6196 | 1691 | 1893 | 52 | | |



- Molecule 3: LRRC48 protein

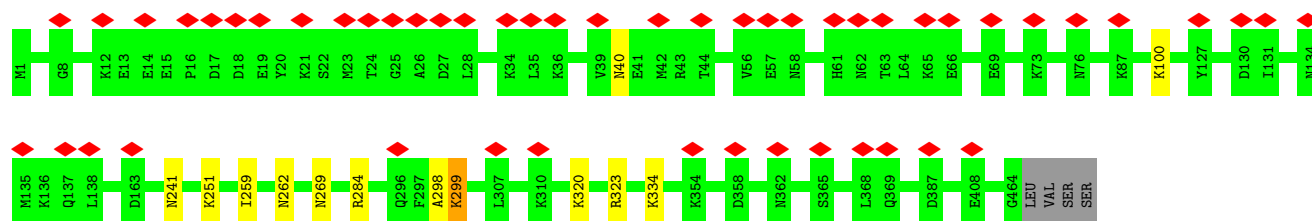


- Molecule 4: Growth-arrest-specific microtubule-binding protein

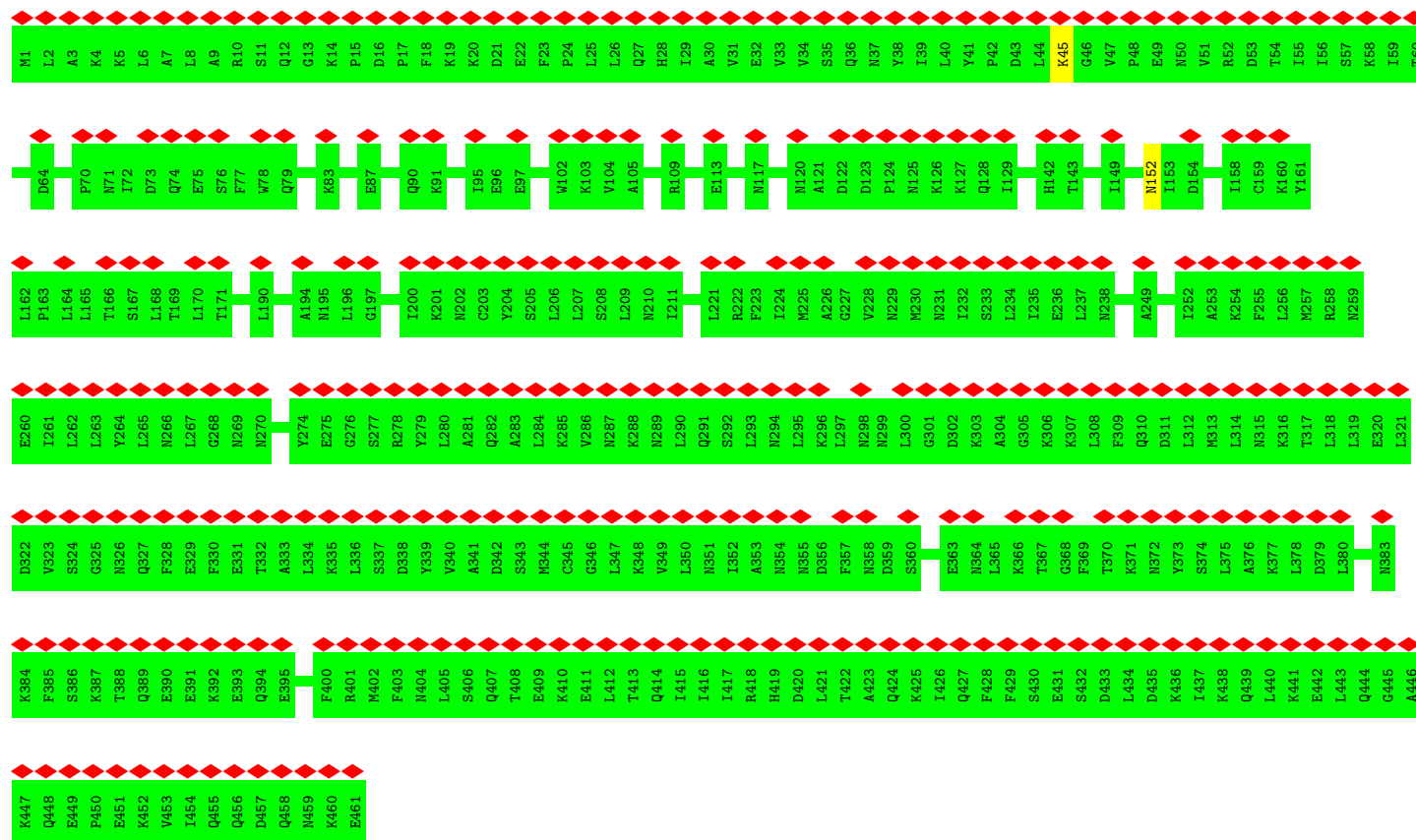


- Molecule 5: Growth-arrest-specific microtubule-binding protein

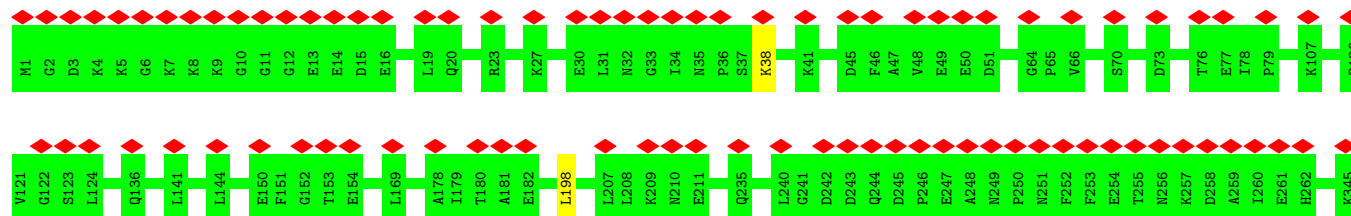




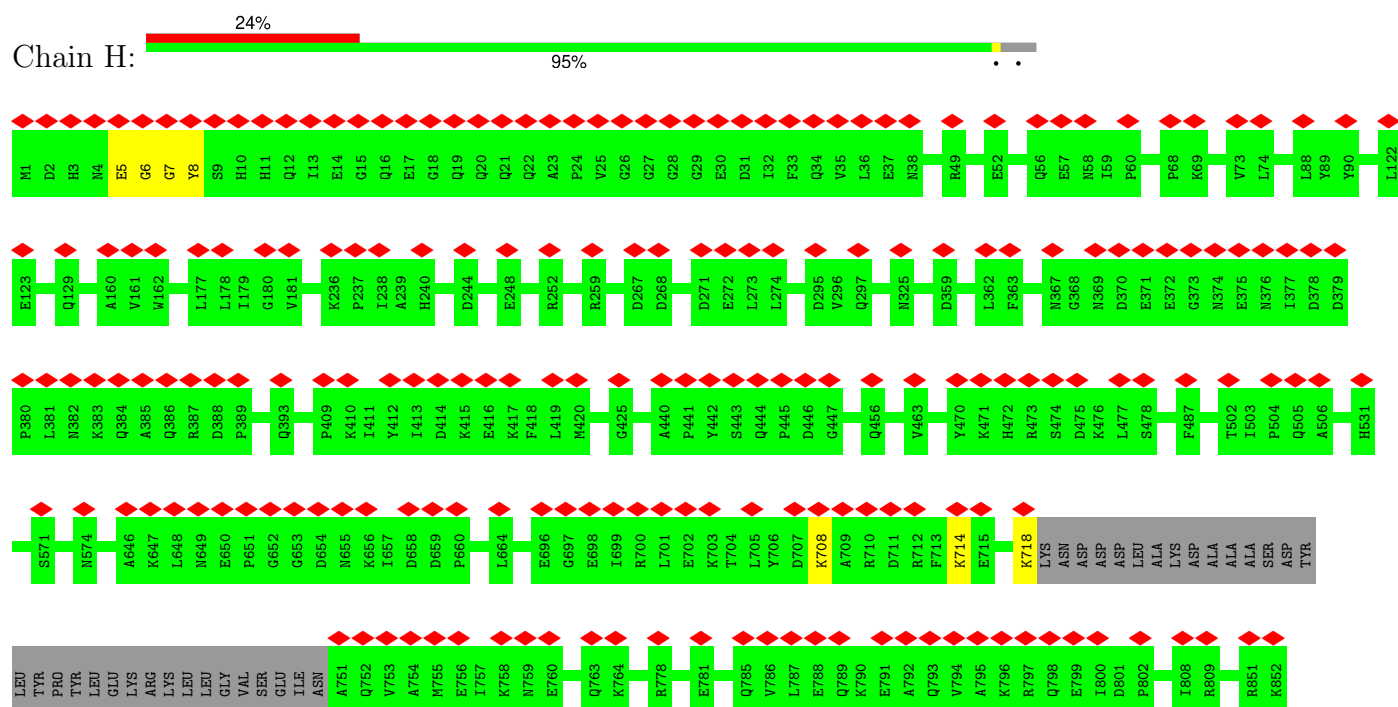
• Molecule 6: Flagellar associated protein



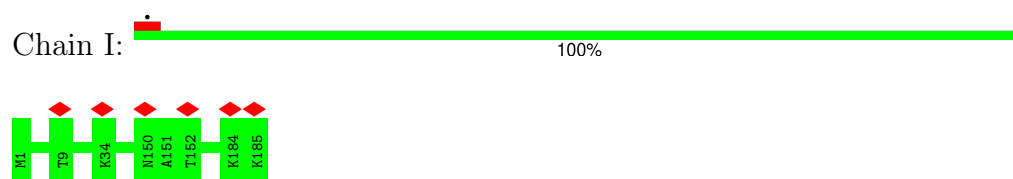
• Molecule 7: Kinase domain protein



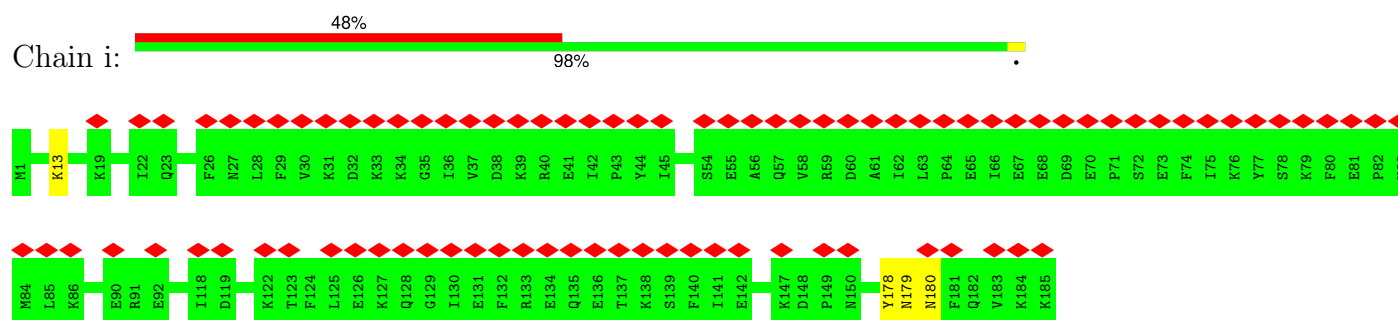
• Molecule 8: Coiled-coil lobo-like protein, putative



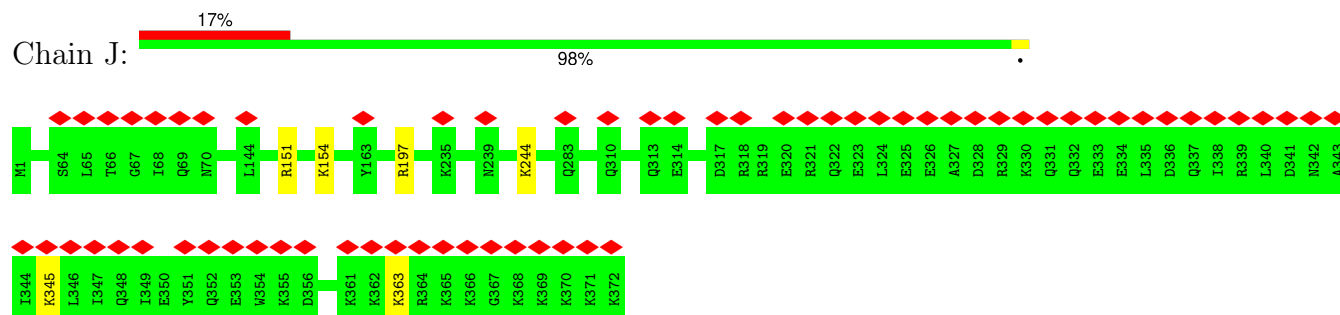
- Molecule 9: EF-hand calcium-binding domain protein



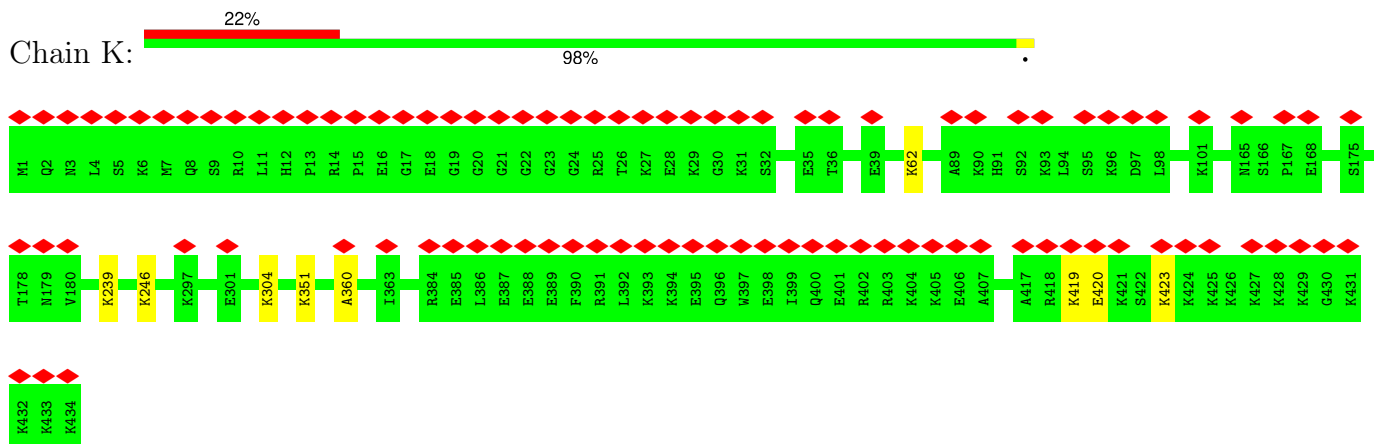
- Molecule 9: EF-hand calcium-binding domain protein



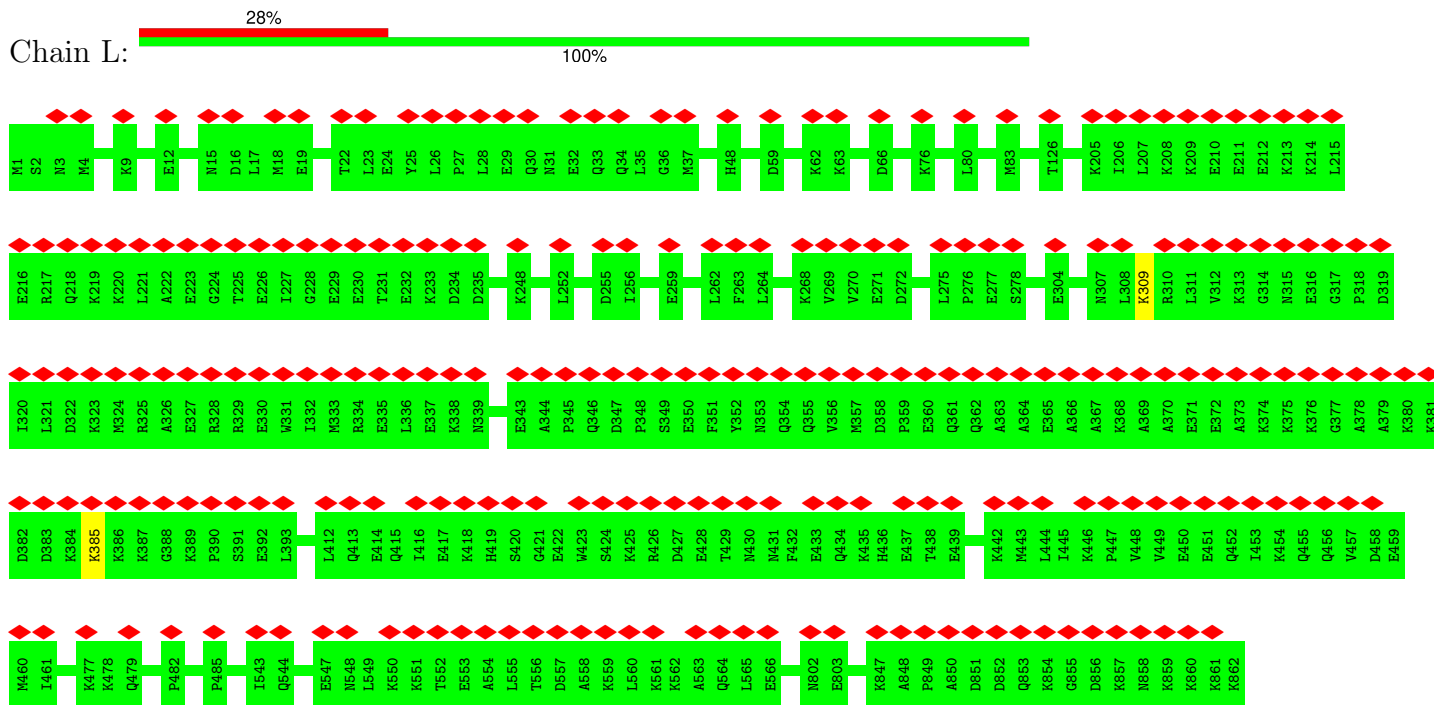
- Molecule 10: Dynein regulatory complex protein 9



Chain K:



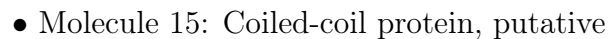
Chain L:



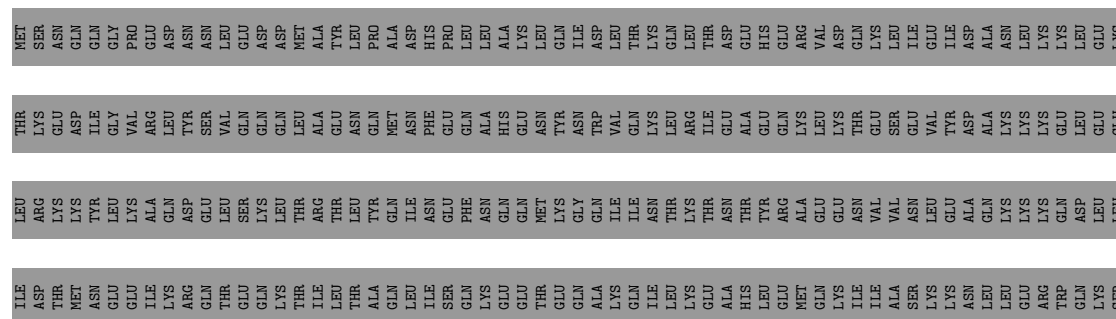
Chain M:



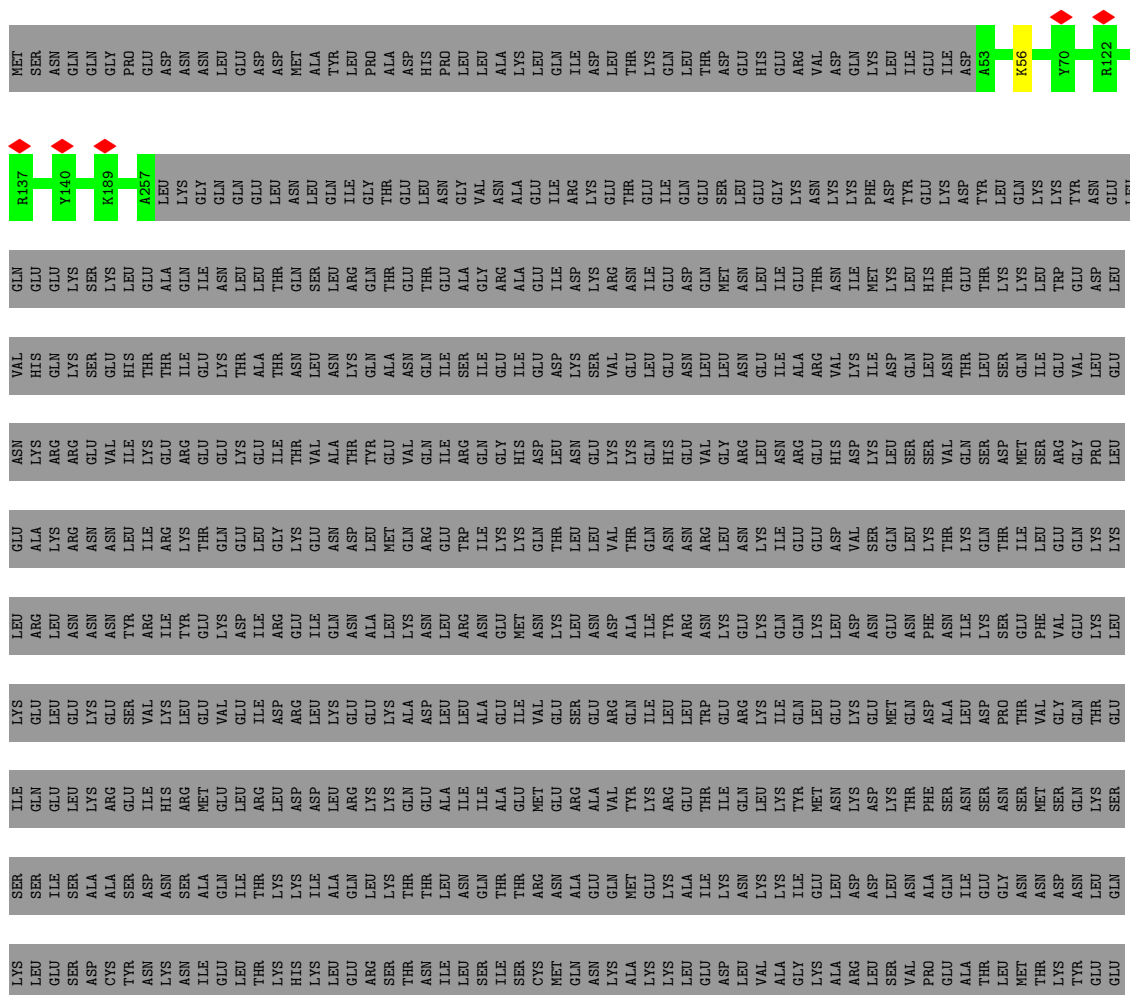
| Response | Percentage |
|----------------------|------------|
| Doing a good job | 22% |
| Not doing a good job | 78% |



| Responsibility | Percentage |
|---------------------|------------|
| Current government | 47% |
| Previous government | 52% |




- Molecule 15: Coiled-coil protein, putative

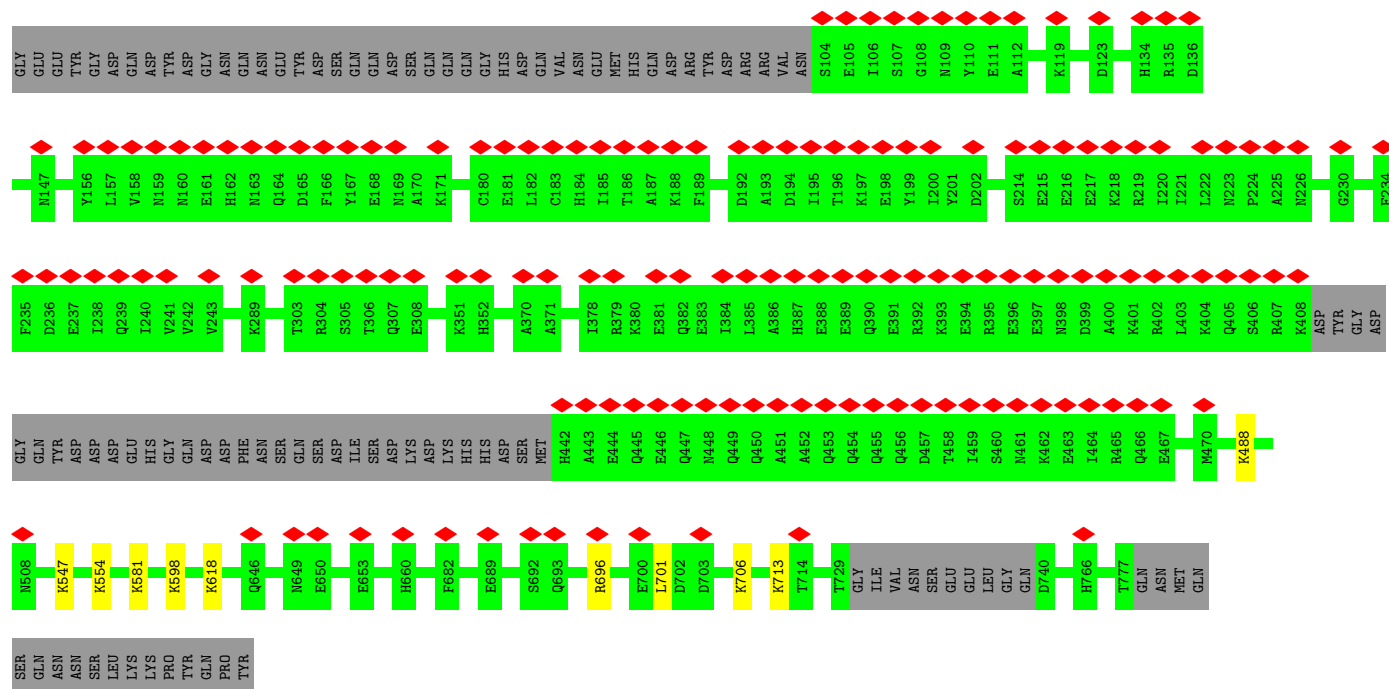


LEU ARG
SER ASP
GLU LYS
ASN
GLN
GLU
ILE
LYS
GLU
ALA
LEU
GLN
GLN
LYS
CYS
ASP
ASP
ALA
PRO
GLN
GLN
TYR
VAL
GLU
VAL
VAL
LEU
ASN
ASN
GLN
GLY
ASP
ASP
ASP
GLU
GLN
GLN
GLN

• Molecule 16: DUF4201 domain-containing protein

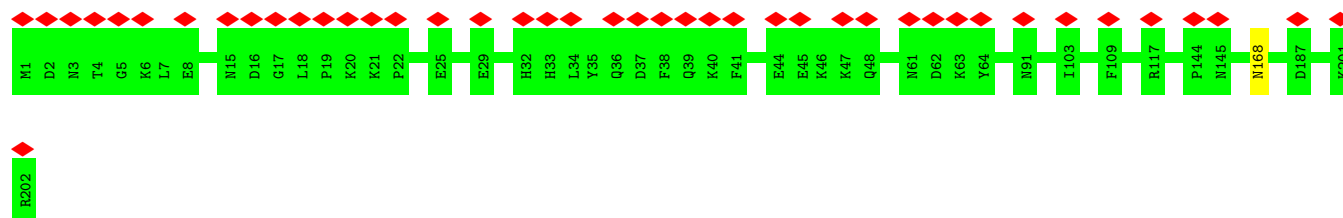
Chain P:  19% 78% 21%

MET
ALA
SER
GLU
ASP
GLY
GLU
MET
PRO
SER
GLN
PHE
GLU
GLY
ILE
ASP
PRO
GLU
GLN
ALA
PRO
GLN
GLN
TYR
VAL
GLU
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GLN
GLY
ASP
ASP
ASP
GLU
GLN
GLN
GLN

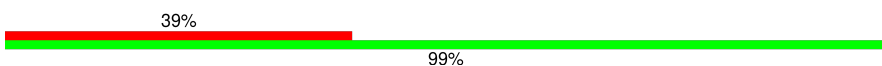


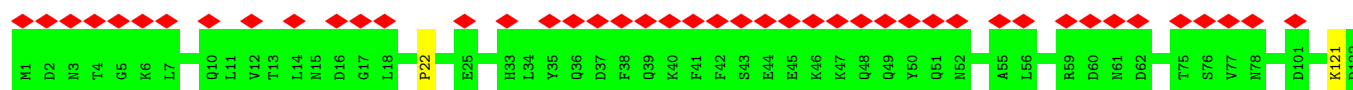
• Molecule 17: Calmodulin 7-2

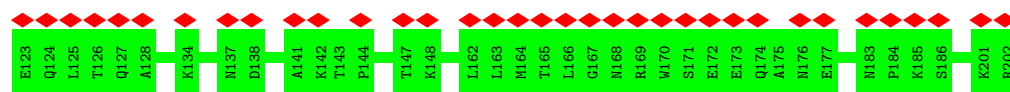
Chain Q:  21% 100%



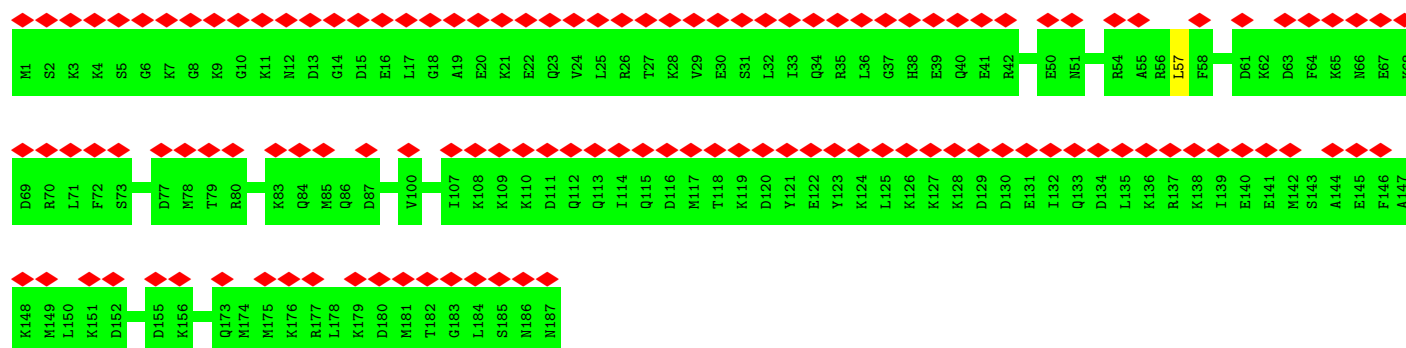
• Molecule 17: Calmodulin 7-2

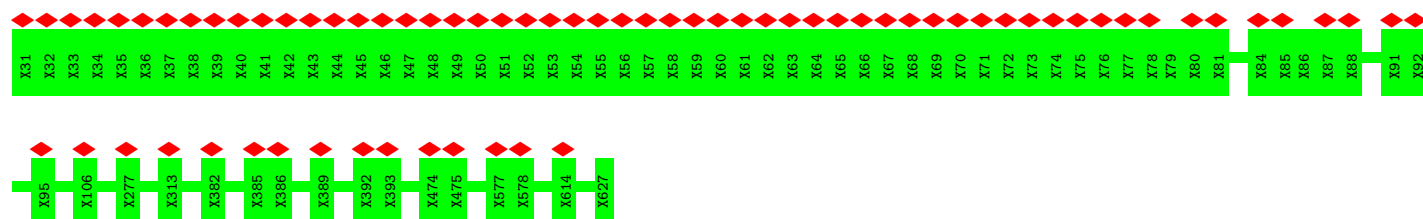
Chain R:  39% 99%





• Molecule 18: Coiled-coil domain-containing protein 153

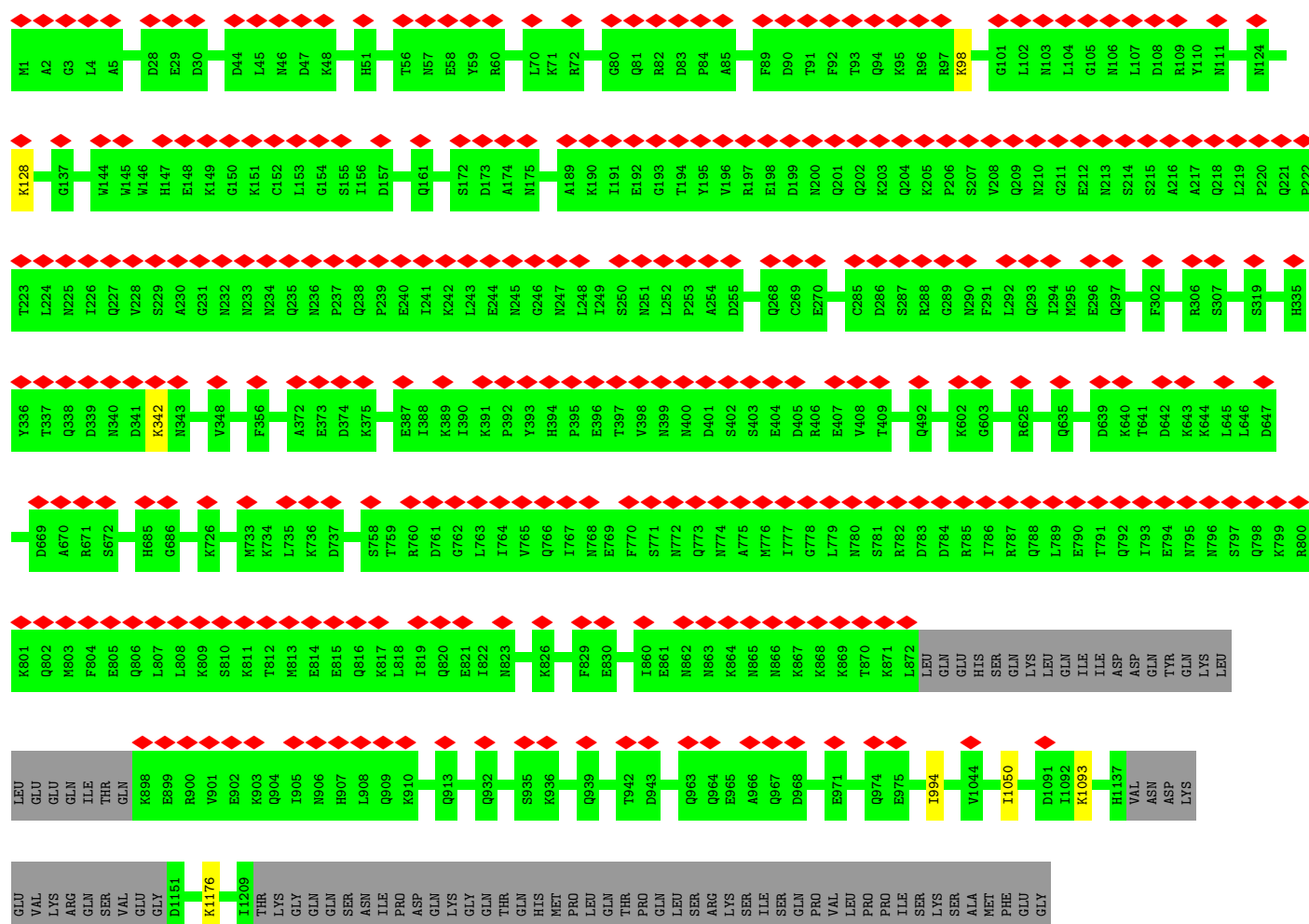
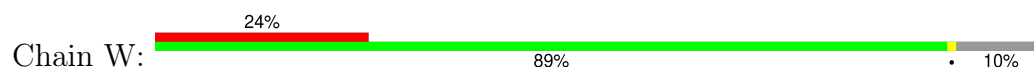


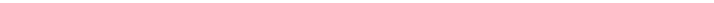


- Molecule 20: L-shape (Unknown-protein)



- Molecule 21: WD40 domain protein



Chain Z:  7% 77% 23%



4 Experimental information

| Property | Value | Source |
|--------------------------------------|---------------------------|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 211502 | Depositor |
| Resolution determination method | OTHER | Depositor |
| CTF correction method | NONE | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 45 | Depositor |
| Minimum defocus (nm) | 1000 | Depositor |
| Maximum defocus (nm) | 3000 | Depositor |
| Magnification | Not provided | |
| Image detector | GATAN K3 (6k x 4k) | Depositor |
| Maximum map value | 3.497 | Depositor |
| Minimum map value | -1.582 | Depositor |
| Average map value | 0.007 | Depositor |
| Map value standard deviation | 0.240 | Depositor |
| Recommended contour level | 0.545 | Depositor |
| Map size (\AA) | 1293.28, 1293.28, 1293.28 | wwPDB |
| Map dimensions | 472, 472, 472 | wwPDB |
| Map angles ($^\circ$) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (\AA) | 2.74, 2.74, 2.74 | Depositor |

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|------------------|-------------|------------------|
| | | RMSZ | $\# Z > 5$ | RMSZ | $\# Z > 5$ |
| 1 | A | 1.82 | 12/3988 (0.3%) | 0.50 | 0/5310 |
| 2 | B | 0.57 | 3/3918 (0.1%) | 0.57 | 3/5221 (0.1%) |
| 3 | C | 0.25 | 0/4482 | 0.43 | 0/6008 |
| 4 | D | 0.81 | 6/3911 (0.2%) | 0.50 | 0/5225 |
| 5 | E | 0.97 | 1/3903 (0.0%) | 0.53 | 3/5211 (0.1%) |
| 6 | F | 0.25 | 0/3768 | 0.43 | 0/5071 |
| 7 | G | 0.24 | 0/2821 | 0.43 | 1/3772 (0.0%) |
| 8 | H | 1.20 | 8/6994 (0.1%) | 0.51 | 2/9419 (0.0%) |
| 9 | I | 0.26 | 0/1586 | 0.41 | 0/2128 |
| 9 | i | 0.26 | 0/1586 | 0.43 | 0/2128 |
| 10 | J | 0.24 | 0/3173 | 0.49 | 0/4219 |
| 11 | K | 0.24 | 0/3620 | 0.45 | 0/4803 |
| 12 | L | 0.25 | 0/7234 | 0.42 | 0/9693 |
| 13 | M | 0.27 | 0/1387 | 0.55 | 0/1843 |
| 14 | N | 0.30 | 0/3633 | 0.50 | 0/4835 |
| 14 | n | 0.26 | 0/1759 | 0.47 | 0/2350 |
| 15 | O | 0.28 | 0/3625 | 0.52 | 0/4840 |
| 15 | o | 0.29 | 0/1719 | 0.47 | 0/2295 |
| 16 | P | 0.26 | 0/5379 | 0.50 | 1/7204 (0.0%) |
| 17 | Q | 0.27 | 0/1705 | 0.43 | 0/2290 |
| 17 | R | 0.24 | 0/1705 | 0.45 | 0/2290 |
| 18 | S | 0.24 | 0/1552 | 0.44 | 0/2057 |
| 18 | s | 0.23 | 0/1552 | 0.45 | 0/2057 |
| 19 | T | 0.25 | 0/2798 | 0.46 | 0/3711 |
| 21 | W | 0.24 | 0/9685 | 0.45 | 0/13007 |
| 22 | Z | 0.25 | 0/6876 | 0.48 | 0/9303 |
| 23 | g | 0.27 | 0/1591 | 0.57 | 0/2149 |
| 24 | w | 0.25 | 0/9986 | 0.45 | 0/13371 |
| All | All | 0.58 | 30/105936 (0.0%) | 0.47 | 10/141810 (0.0%) |

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

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 1 | A | 0 | 1 |
| 2 | B | 0 | 4 |
| 4 | D | 0 | 1 |
| 5 | E | 0 | 2 |
| 8 | H | 0 | 1 |
| 9 | i | 0 | 3 |
| 10 | J | 0 | 1 |
| 11 | K | 0 | 2 |
| 15 | O | 0 | 1 |
| 17 | Q | 0 | 1 |
| 20 | V | 0 | 1 |
| 21 | W | 0 | 1 |
| All | All | 0 | 19 |

The worst 5 of 30 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|---------|-------|-------------|----------|
| 1 | A | 295 | TYR | CD1-CE1 | 59.37 | 2.28 | 1.39 |
| 5 | E | 259 | ILE | CB-CG2 | 57.89 | 3.32 | 1.52 |
| 1 | A | 295 | TYR | CD2-CE2 | 55.10 | 2.22 | 1.39 |
| 8 | H | 8 | TYR | CD2-CE2 | 53.55 | 2.19 | 1.39 |
| 8 | H | 8 | TYR | CD1-CE1 | 51.13 | 2.16 | 1.39 |

The worst 5 of 10 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-----------|-------|-------------|----------|
| 8 | H | 5 | GLU | C-N-CA | 15.37 | 154.58 | 122.30 |
| 2 | B | 289 | HIS | CA-CB-CG | 12.06 | 134.10 | 113.60 |
| 8 | H | 6 | GLY | N-CA-C | 8.42 | 134.15 | 113.10 |
| 5 | E | 259 | ILE | CA-CB-CG2 | 7.79 | 126.47 | 110.90 |
| 16 | P | 701 | LEU | CA-CB-CG | 7.20 | 131.86 | 115.30 |

There are no chirality outliers.

5 of 19 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 1 | A | 291 | ASP | Peptide |
| 2 | B | 16 | GLY | Peptide |
| 2 | B | 17 | GLY | Peptide |
| 2 | B | 275 | LYS | Peptide |
| 2 | B | 276 | LYS | Peptide |

5.2 Too-close contacts ⓘ

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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 | |
|-----|-------|----------------|------------|----------|----------|-------------|-----|
| 1 | A | 454/826 (55%) | 417 (92%) | 35 (8%) | 2 (0%) | 30 | 63 |
| 2 | B | 456/506 (90%) | 405 (89%) | 50 (11%) | 1 (0%) | 44 | 73 |
| 3 | C | 529/575 (92%) | 500 (94%) | 29 (6%) | 0 | 100 | 100 |
| 4 | D | 457/472 (97%) | 435 (95%) | 21 (5%) | 1 (0%) | 44 | 73 |
| 5 | E | 462/468 (99%) | 419 (91%) | 40 (9%) | 3 (1%) | 22 | 55 |
| 6 | F | 459/461 (100%) | 440 (96%) | 19 (4%) | 0 | 100 | 100 |
| 7 | G | 343/345 (99%) | 318 (93%) | 25 (7%) | 0 | 100 | 100 |
| 8 | H | 816/852 (96%) | 752 (92%) | 64 (8%) | 0 | 100 | 100 |
| 9 | I | 183/185 (99%) | 177 (97%) | 6 (3%) | 0 | 100 | 100 |
| 9 | i | 183/185 (99%) | 172 (94%) | 11 (6%) | 0 | 100 | 100 |
| 10 | J | 370/372 (100%) | 346 (94%) | 23 (6%) | 1 (0%) | 37 | 67 |
| 11 | K | 432/434 (100%) | 403 (93%) | 27 (6%) | 2 (0%) | 25 | 59 |
| 12 | L | 860/862 (100%) | 819 (95%) | 41 (5%) | 0 | 100 | 100 |
| 13 | M | 160/644 (25%) | 140 (88%) | 17 (11%) | 3 (2%) | 6 | 35 |
| 14 | N | 428/963 (44%) | 419 (98%) | 7 (2%) | 2 (0%) | 25 | 59 |
| 14 | n | 206/963 (21%) | 206 (100%) | 0 | 0 | 100 | 100 |
| 15 | O | 424/893 (48%) | 411 (97%) | 10 (2%) | 3 (1%) | 19 | 53 |
| 15 | o | 203/893 (23%) | 203 (100%) | 0 | 0 | 100 | 100 |
| 16 | P | 625/794 (79%) | 591 (95%) | 34 (5%) | 0 | 100 | 100 |
| 17 | Q | 200/202 (99%) | 184 (92%) | 16 (8%) | 0 | 100 | 100 |
| 17 | R | 200/202 (99%) | 184 (92%) | 15 (8%) | 1 (0%) | 25 | 59 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-------------------|-------------|----------|----------|-------------|-----|
| 18 | S | 185/187 (99%) | 176 (95%) | 8 (4%) | 1 (0%) | 25 | 59 |
| 18 | s | 185/187 (99%) | 179 (97%) | 6 (3%) | 0 | 100 | 100 |
| 19 | T | 329/361 (91%) | 326 (99%) | 3 (1%) | 0 | 100 | 100 |
| 21 | W | 1165/1308 (89%) | 1117 (96%) | 47 (4%) | 1 (0%) | 48 | 79 |
| 22 | Z | 828/1079 (77%) | 754 (91%) | 72 (9%) | 2 (0%) | 44 | 73 |
| 23 | g | 185/195 (95%) | 145 (78%) | 40 (22%) | 0 | 100 | 100 |
| 24 | w | 1186/1293 (92%) | 1141 (96%) | 43 (4%) | 2 (0%) | 44 | 73 |
| All | All | 12513/16707 (75%) | 11779 (94%) | 709 (6%) | 25 (0%) | 45 | 73 |

5 of 25 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 237 | LYS |
| 2 | B | 279 | ILE |
| 5 | E | 241 | ASN |
| 5 | E | 299 | LYS |
| 10 | J | 154 | LYS |

5.3.2 Protein sidechains ⓘ

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

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|------------|----------|-------------|-----|
| 1 | A | 434/766 (57%) | 431 (99%) | 3 (1%) | 81 | 90 |
| 2 | B | 430/473 (91%) | 425 (99%) | 5 (1%) | 67 | 82 |
| 3 | C | 499/540 (92%) | 496 (99%) | 3 (1%) | 84 | 92 |
| 4 | D | 428/438 (98%) | 423 (99%) | 5 (1%) | 67 | 82 |
| 5 | E | 430/434 (99%) | 422 (98%) | 8 (2%) | 52 | 73 |
| 6 | F | 414/414 (100%) | 412 (100%) | 2 (0%) | 86 | 93 |
| 7 | G | 310/310 (100%) | 309 (100%) | 1 (0%) | 91 | 96 |
| 8 | H | 759/786 (97%) | 756 (100%) | 3 (0%) | 89 | 95 |
| 9 | I | 170/170 (100%) | 170 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-------------------|-------------|----------|-------------|-----|
| 9 | i | 170/170 (100%) | 169 (99%) | 1 (1%) | 84 | 92 |
| 10 | J | 350/350 (100%) | 346 (99%) | 4 (1%) | 70 | 83 |
| 11 | K | 403/403 (100%) | 398 (99%) | 5 (1%) | 67 | 82 |
| 12 | L | 776/776 (100%) | 774 (100%) | 2 (0%) | 91 | 96 |
| 13 | M | 147/590 (25%) | 146 (99%) | 1 (1%) | 81 | 90 |
| 14 | N | 394/884 (45%) | 386 (98%) | 8 (2%) | 50 | 72 |
| 14 | n | 189/884 (21%) | 189 (100%) | 0 | 100 | 100 |
| 15 | O | 405/829 (49%) | 400 (99%) | 5 (1%) | 67 | 82 |
| 15 | o | 188/829 (23%) | 187 (100%) | 1 (0%) | 86 | 93 |
| 16 | P | 589/733 (80%) | 580 (98%) | 9 (2%) | 60 | 78 |
| 17 | Q | 189/189 (100%) | 189 (100%) | 0 | 100 | 100 |
| 17 | R | 189/189 (100%) | 188 (100%) | 1 (0%) | 86 | 93 |
| 18 | S | 172/172 (100%) | 172 (100%) | 0 | 100 | 100 |
| 18 | s | 172/172 (100%) | 171 (99%) | 1 (1%) | 84 | 92 |
| 19 | T | 309/335 (92%) | 304 (98%) | 5 (2%) | 58 | 76 |
| 21 | W | 1070/1200 (89%) | 1065 (100%) | 5 (0%) | 86 | 93 |
| 22 | Z | 761/994 (77%) | 759 (100%) | 2 (0%) | 91 | 96 |
| 23 | g | 175/182 (96%) | 174 (99%) | 1 (1%) | 84 | 92 |
| 24 | w | 1103/1201 (92%) | 1097 (100%) | 6 (0%) | 86 | 93 |
| All | All | 11625/15413 (75%) | 11538 (99%) | 87 (1%) | 80 | 90 |

5 of 87 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 16 | P | 554 | LYS |
| 21 | W | 128 | LYS |
| 16 | P | 598 | LYS |
| 19 | T | 108 | LYS |
| 22 | Z | 377 | LYS |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 137 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 21 | W | 1192 | ASN |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 22 | Z | 805 | HIS |
| 24 | w | 468 | HIS |
| 8 | H | 527 | HIS |
| 8 | H | 332 | ASN |

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

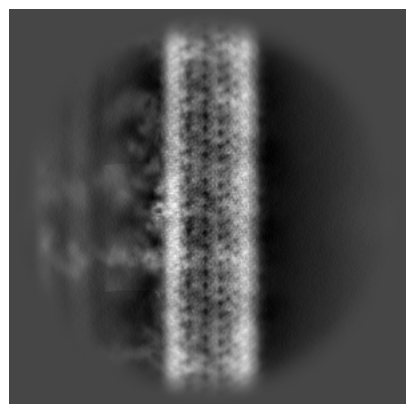
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41284. These allow visual inspection of the internal detail of the map and identification of artifacts.

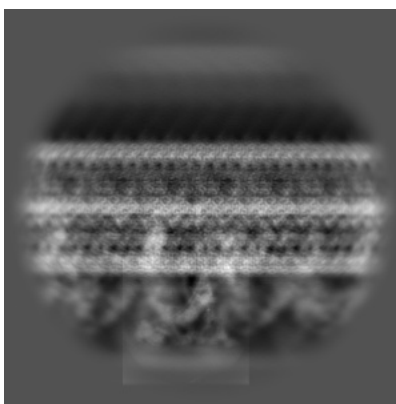
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

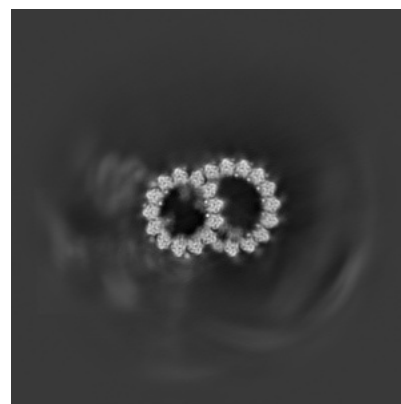
6.1.1 Primary map



X

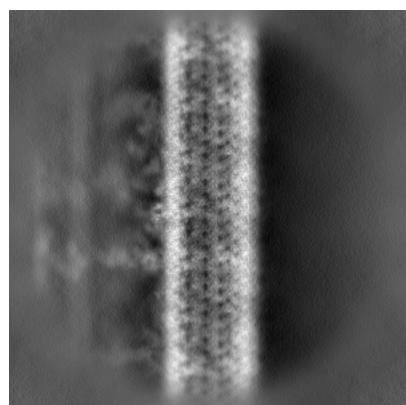


Y

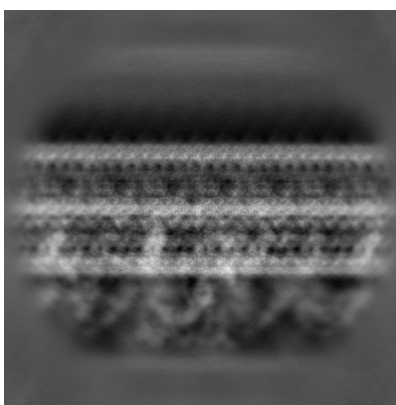


Z

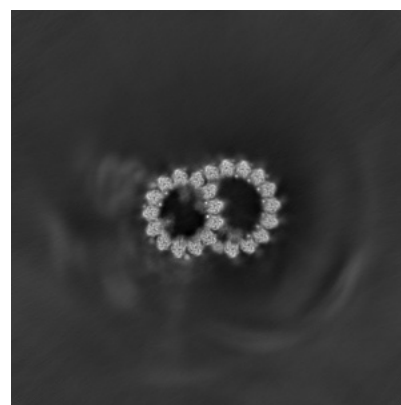
6.1.2 Raw map



X



Y

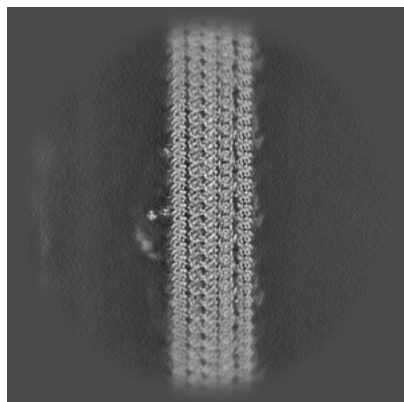


Z

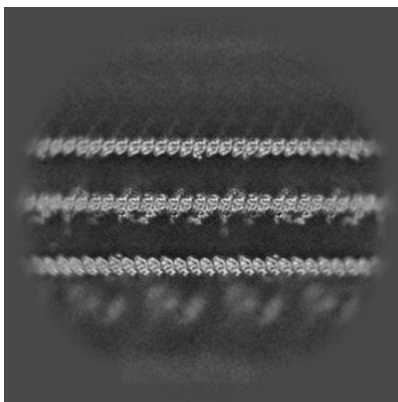
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

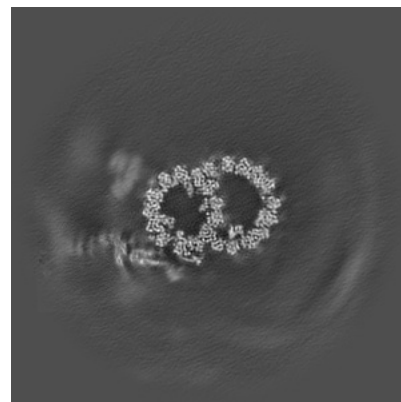
6.2.1 Primary map



X Index: 236

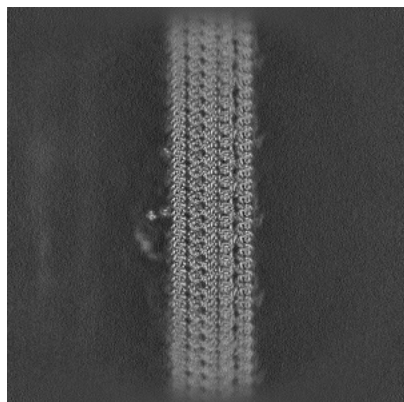


Y Index: 236

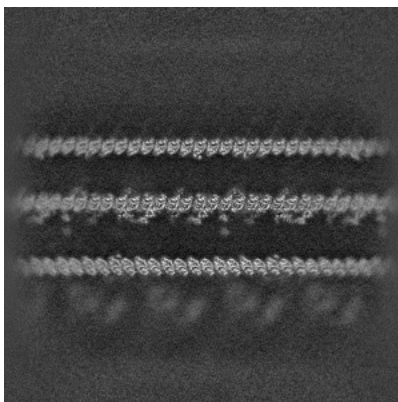


Z Index: 236

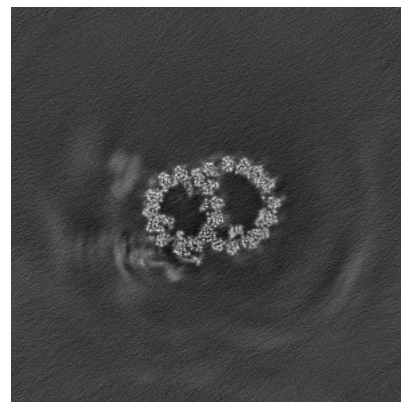
6.2.2 Raw map



X Index: 235



Y Index: 235

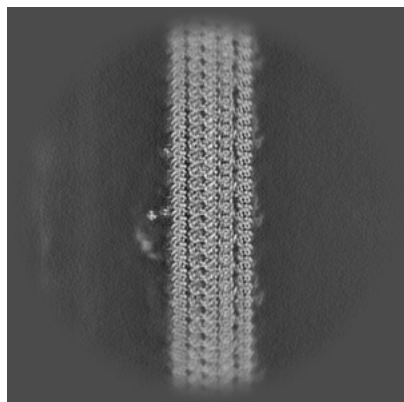


Z Index: 235

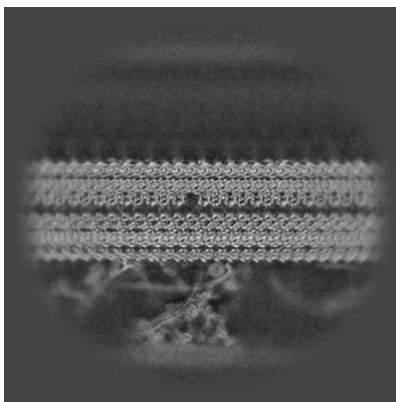
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

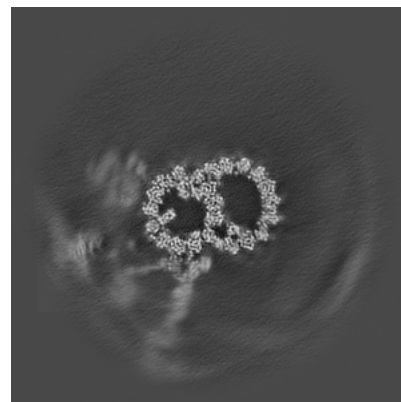
6.3.1 Primary map



X Index: 236

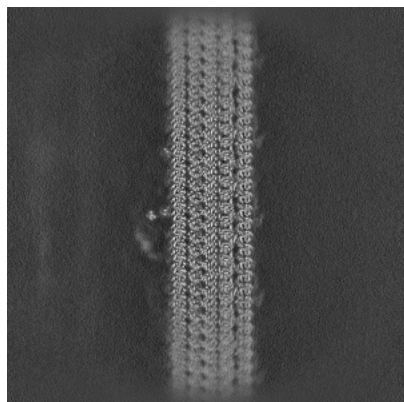


Y Index: 192

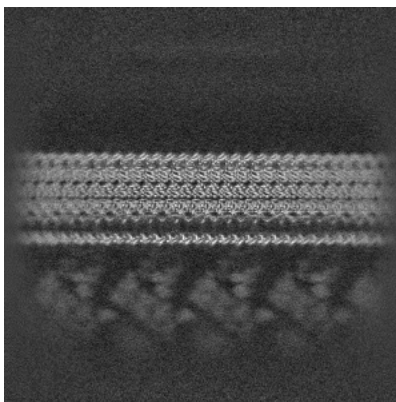


Z Index: 180

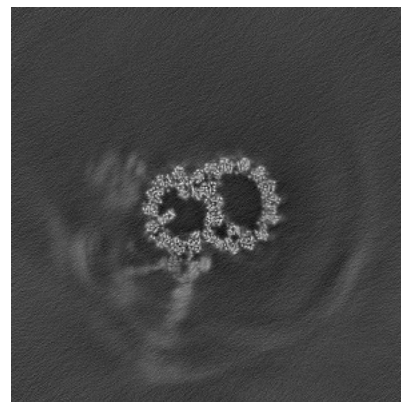
6.3.2 Raw map



X Index: 235



Y Index: 280

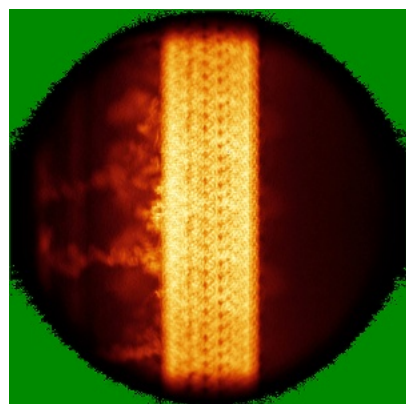


Z Index: 179

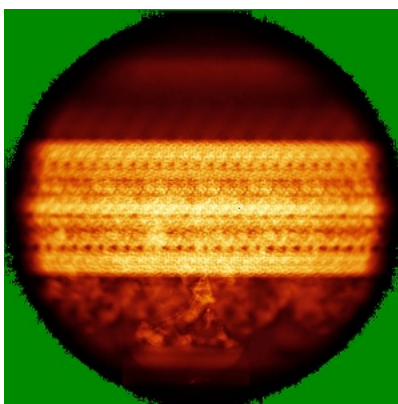
The images above show the largest variance slices of the map in three orthogonal directions.

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

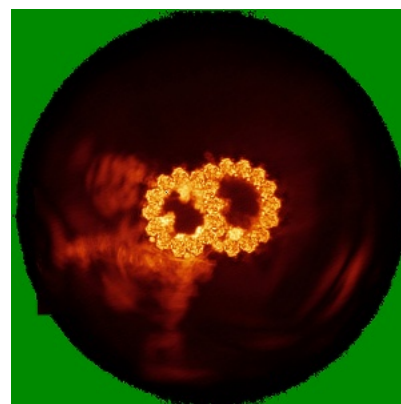
6.4.1 Primary map



X

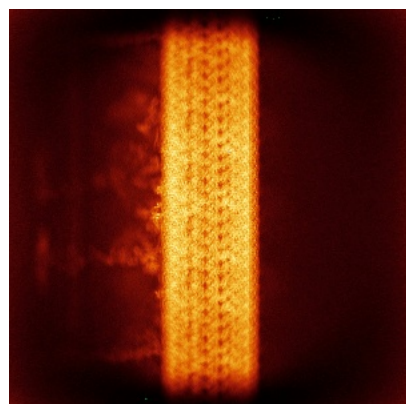


Y

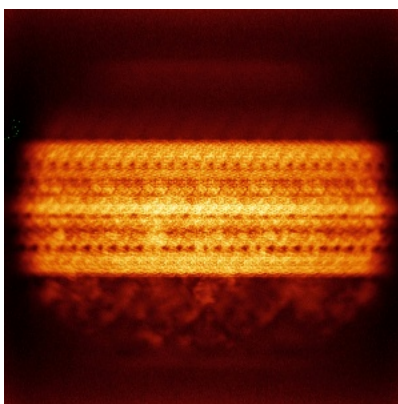


Z

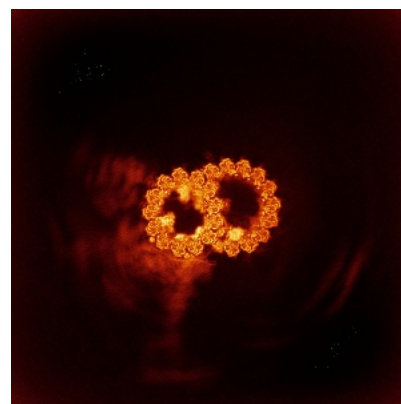
6.4.2 Raw map



X



Y

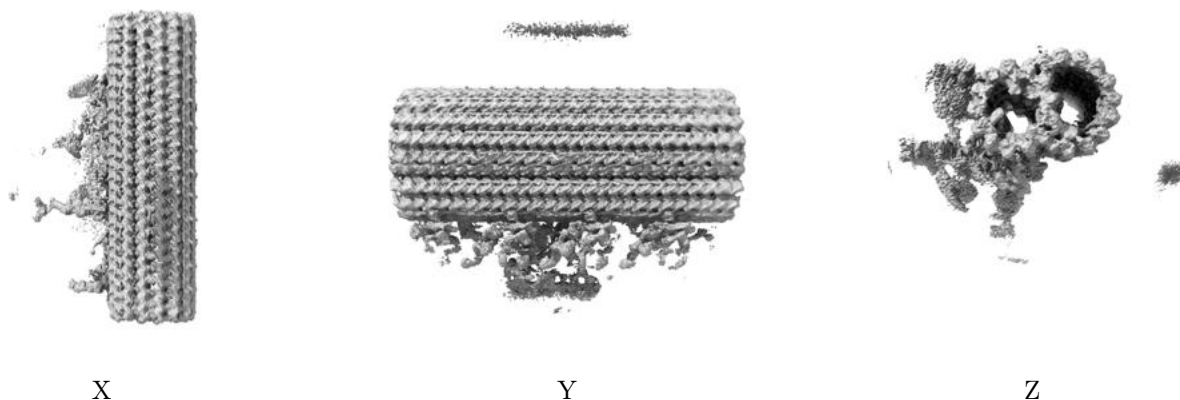


Z

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.

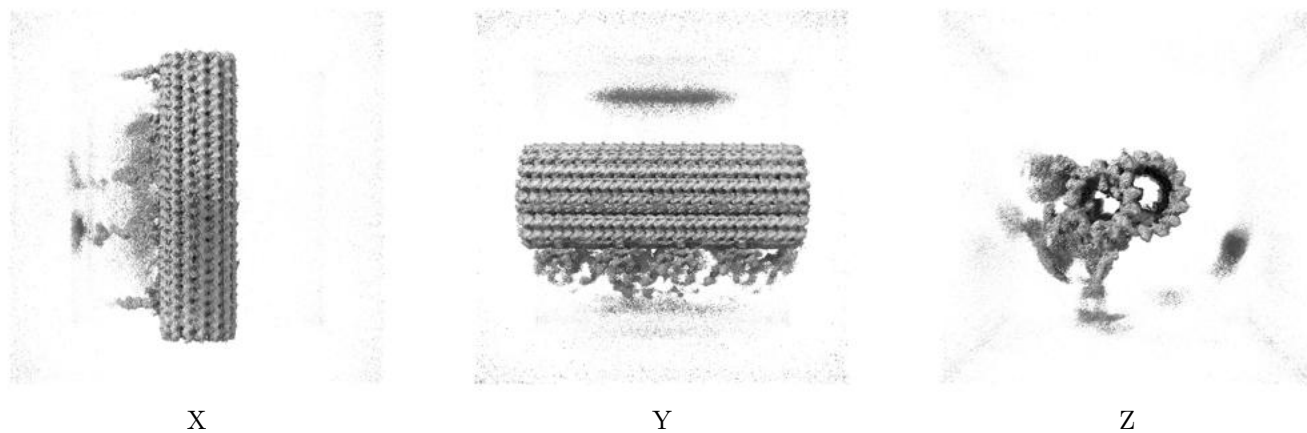
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.545. 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.

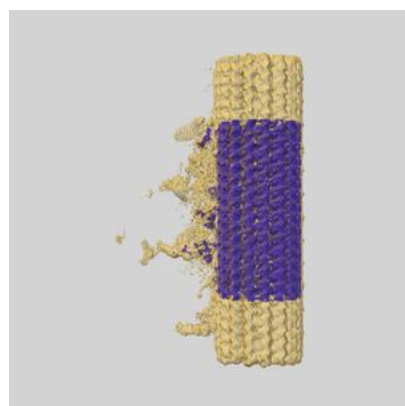
6.6 Mask visualisation [i](#)

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

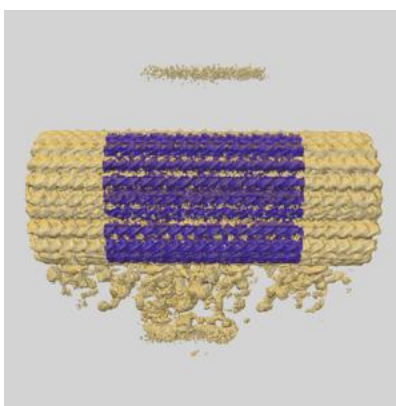
A mask typically either:

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

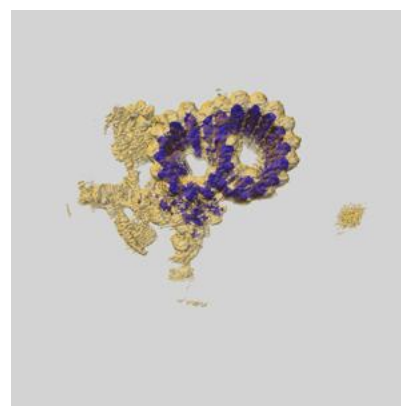
6.6.1 emd_41284_msk_1.map [i](#)



X



Y

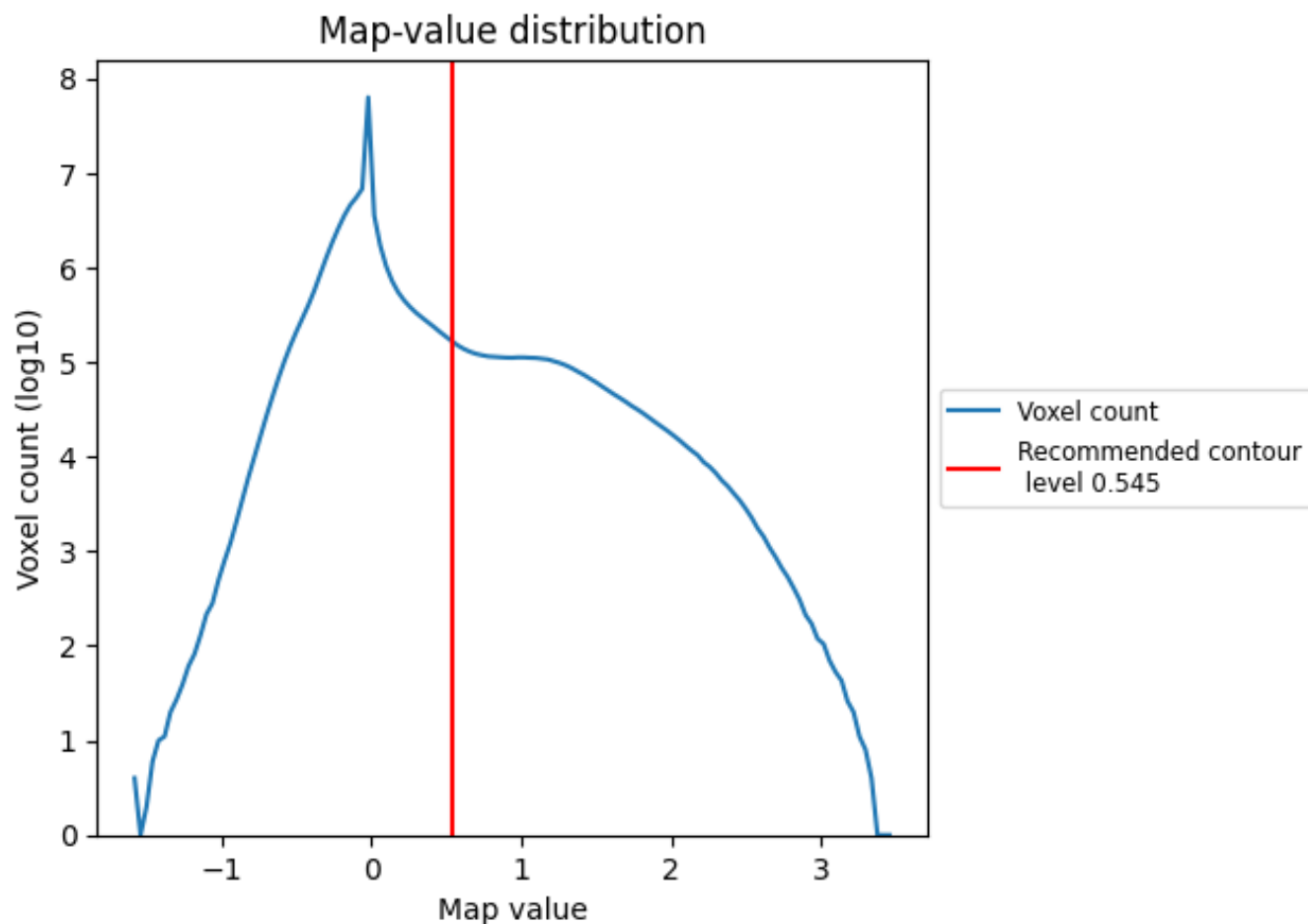


Z

7 Map analysis [i](#)

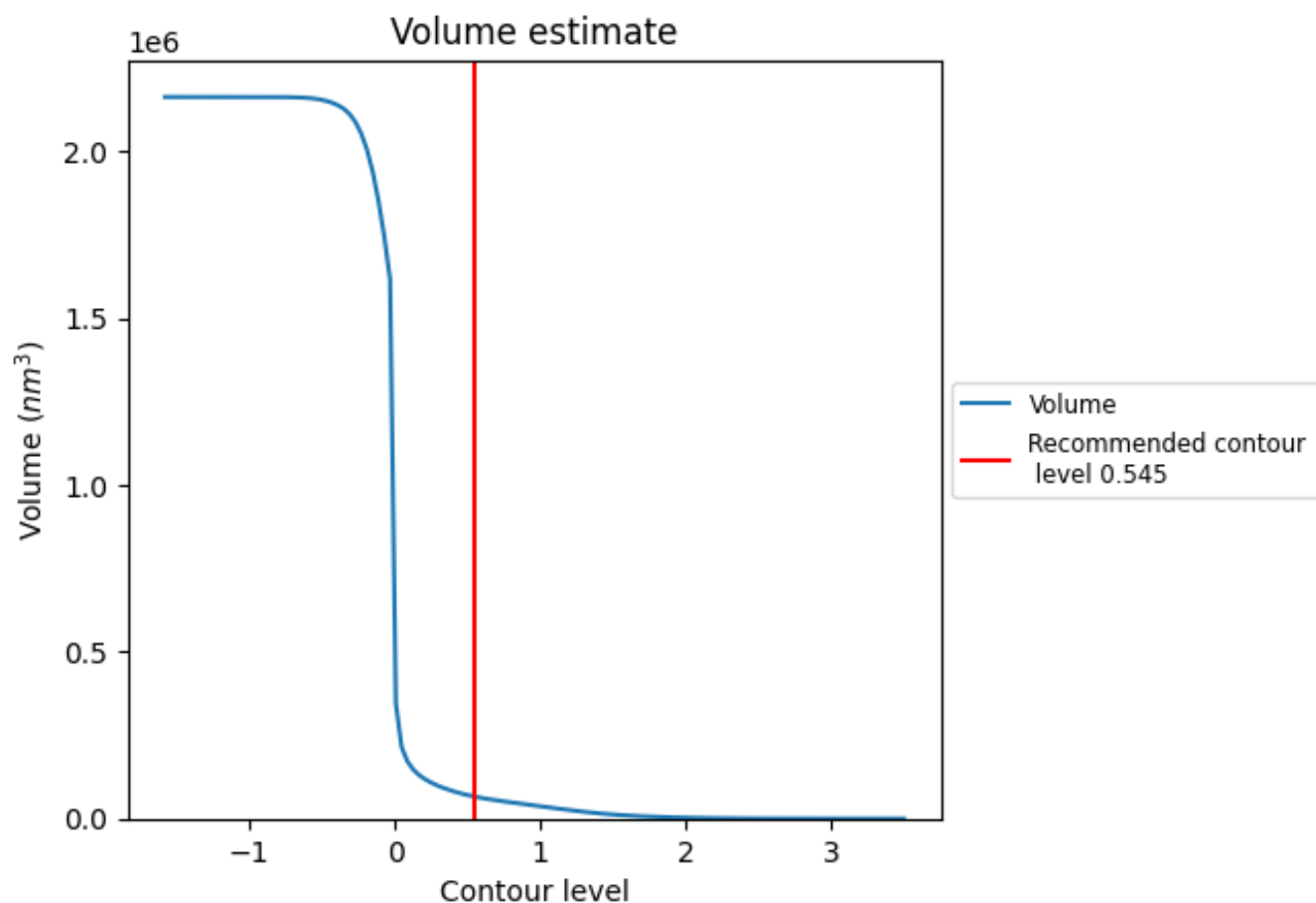
This section contains the results of statistical analysis of the map.

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.

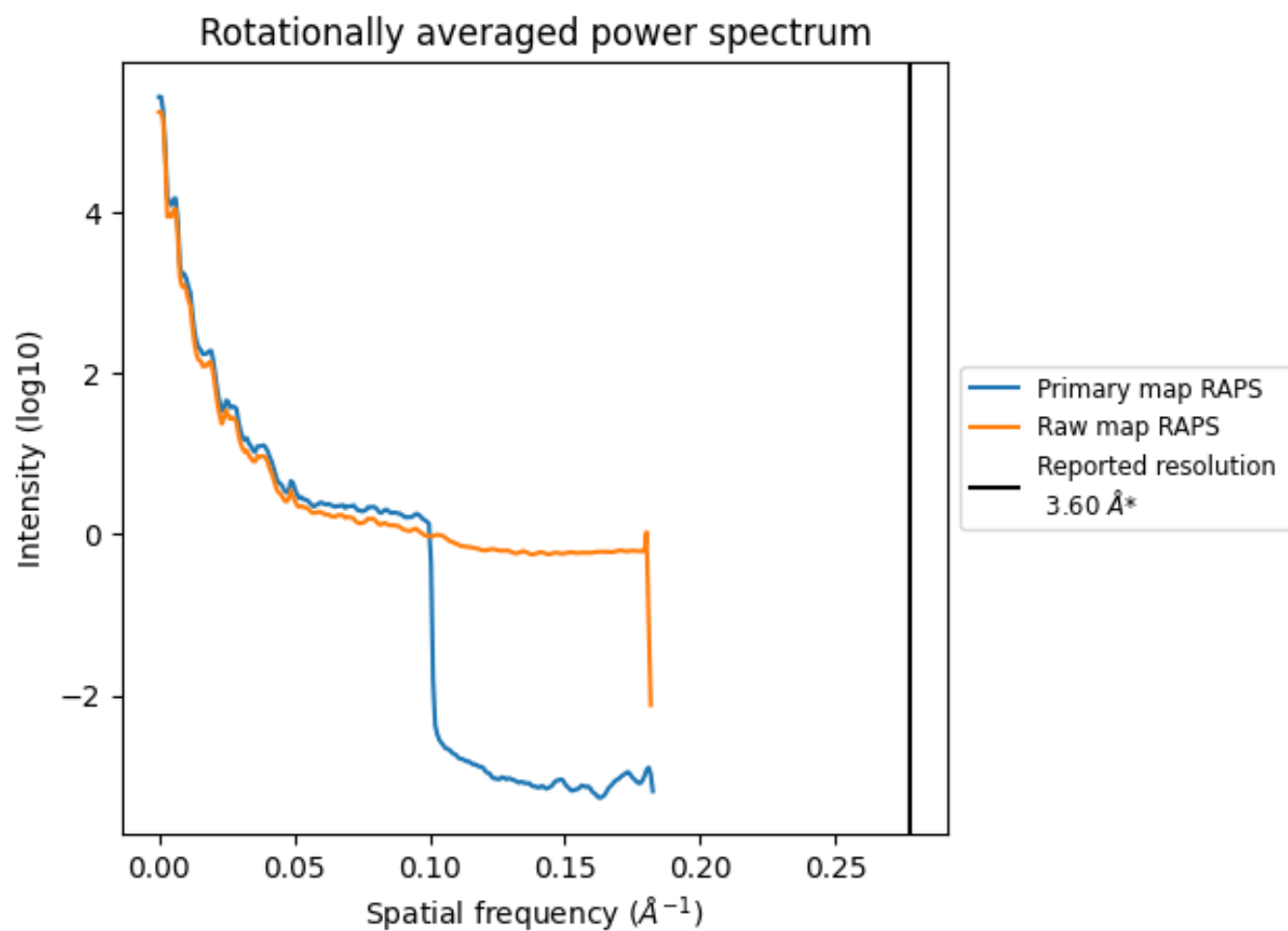
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 66091 nm³; this corresponds to an approximate mass of 59702 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](#)

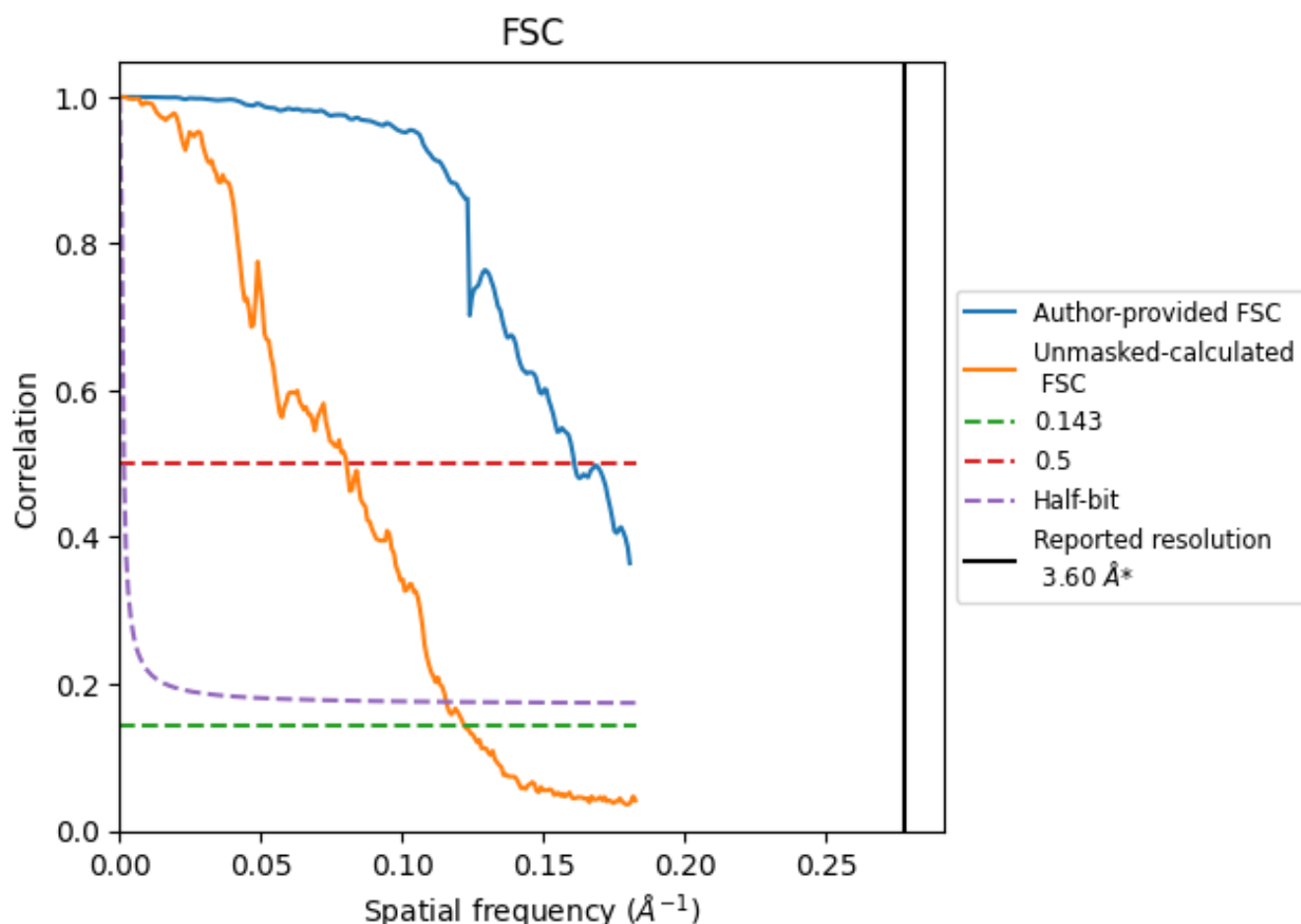


*Reported resolution corresponds to spatial frequency of 0.278 \AA^{-1}

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 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

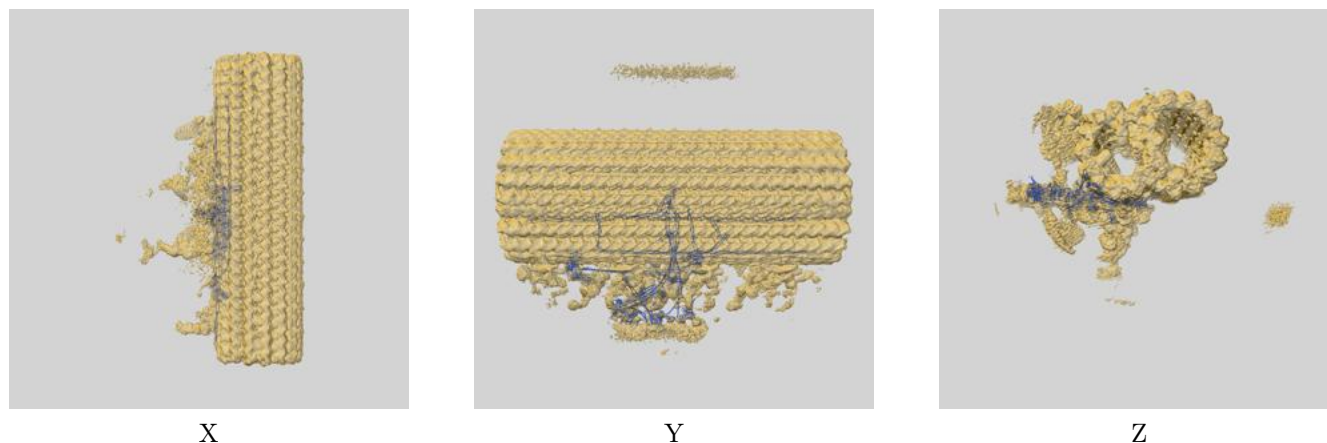
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | | |
|---------------------------|------------------------------------|-------|----------|-------|
| | 0.143 | 0.5 | Half-bit | Other |
| Reported by author | - | - | - | 3.60 |
| Author-provided FSC curve | - | 6.22 | - | - |
| Unmasked-calculated* | 8.20 | 12.45 | 8.65 | - |

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

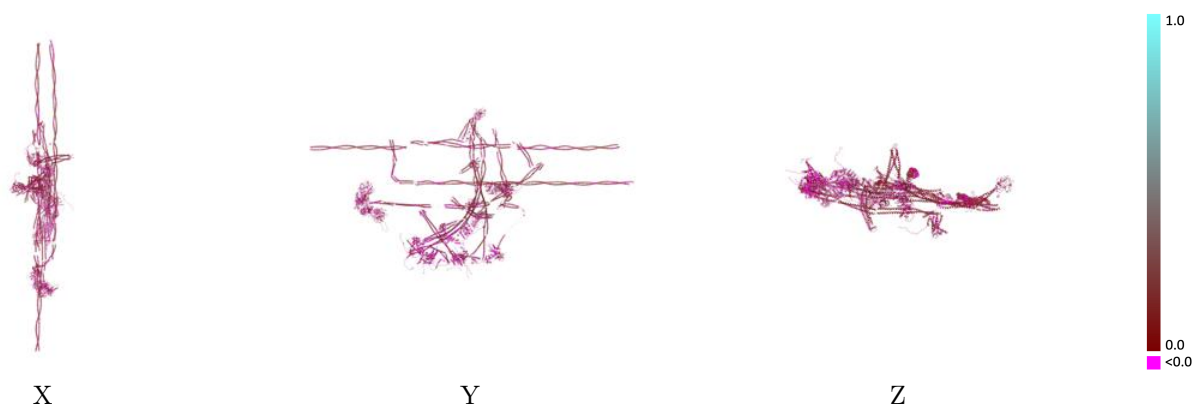
This section contains information regarding the fit between EMDB map EMD-41284 and PDB model 8TID. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



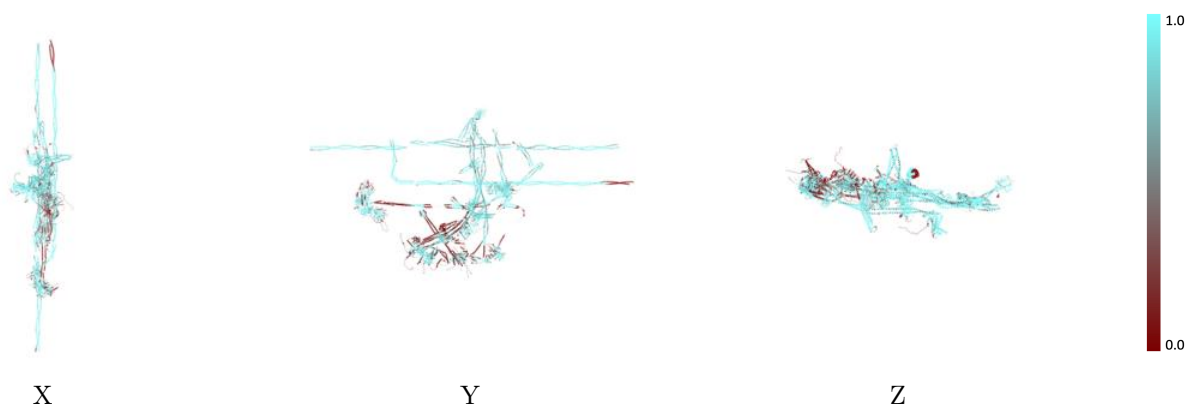
The images above show the 3D surface view of the map at the recommended contour level 0.545 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



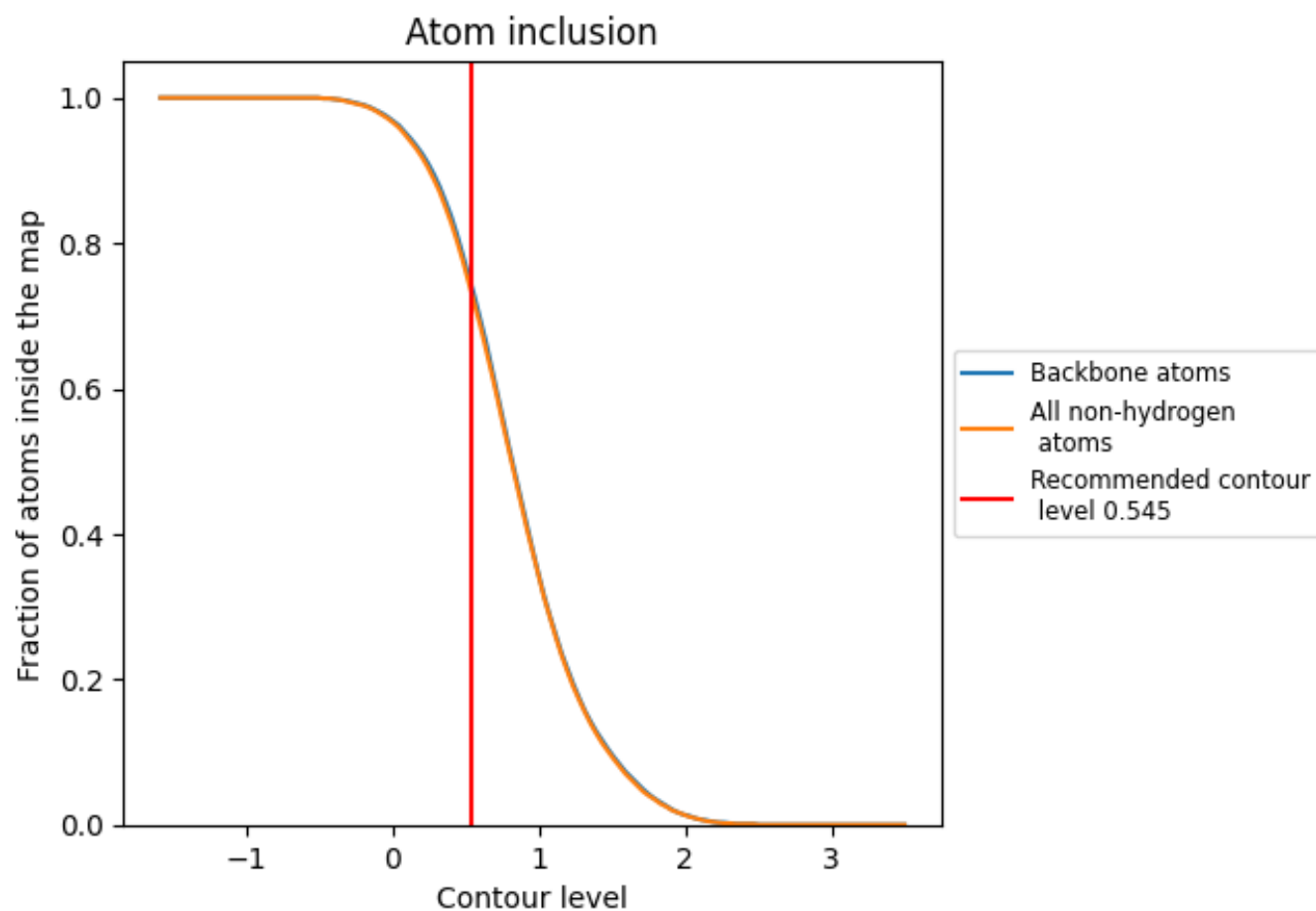
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.545).































































9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 73% 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 (0.545) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|--|--|
| All |  0.7290 |  0.0720 |
| A |  0.6230 |  0.0950 |
| B |  0.5970 |  0.0830 |
| C |  0.9270 |  0.0770 |
| D |  0.7550 |  0.0730 |
| E |  0.8160 |  0.0820 |
| F |  0.2470 |  0.0370 |
| G |  0.7240 |  0.0260 |
| H |  0.7160 |  0.0520 |
| I |  0.9500 |  0.0550 |
| J |  0.7650 |  0.0910 |
| K |  0.7430 |  0.0850 |
| L |  0.6950 |  0.0270 |
| M |  0.8070 |  0.1190 |
| N |  0.8400 |  0.0930 |
| O |  0.8500 |  0.1080 |
| P |  0.7040 |  0.0780 |
| Q |  0.7370 |  0.0350 |
| R |  0.5740 |  0.0500 |
| S |  0.2970 |  0.0610 |
| T |  0.7580 |  0.0850 |
| U |  0.8690 |  0.1310 |
| V |  0.8790 |  0.1240 |
| W |  0.6990 |  0.0670 |
| Z |  0.8920 |  0.0660 |
| g |  0.8900 |  0.0900 |
| i |  0.5020 |  0.0310 |
| n |  0.8830 |  0.0990 |
| o |  0.9210 |  0.1230 |
| s |  0.2660 |  0.0440 |
| w |  0.6180 |  0.0630 |

