



## wwPDB EM Validation Summary Report ⓘ

Mar 16, 2026 – 02:27 PM UTC

PDB ID : 9GAW / pdb\_00009gaw  
EMDB ID : EMD-51190  
Title : High-resolution structure of the Anaphase-promoting complex/cyclosome (APC/C) bound to co-activator Cdh1  
Authors : Hoefler, A.; Yu, J.; Chang, L.; Zhang, Z.; Yang, J.; Boland, A.; Barford, D.  
Deposited on : 2024-07-29  
Resolution : 2.90 Å(reported)  
Based on initial model : 4UI9

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

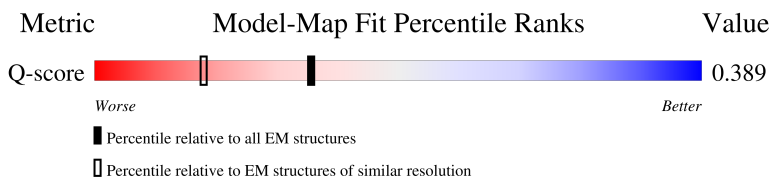
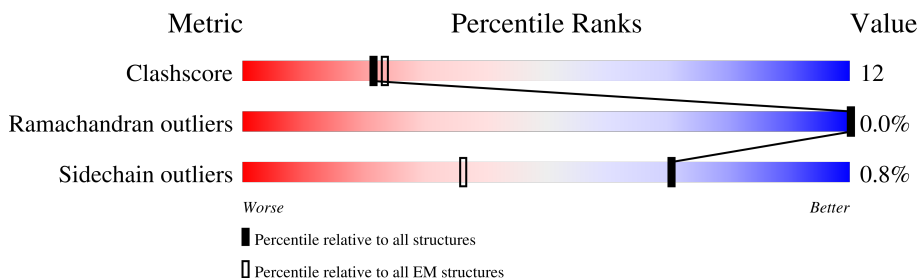
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins)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

# 1 Overall quality at a glance

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

The reported resolution of this entry is 2.90 Å.

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



| Metric                | Whole archive<br>(#Entries) | EM structures<br>(#Entries) | Similar EM resolution<br>(#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|-----------------------------|----------------------------------------------------------|
| Clashscore            | 229148                      | 23984                       | -                                                        |
| Ramachandran outliers | 224038                      | 23583                       | -                                                        |
| Sidechain outliers    | 223484                      | 23102                       | -                                                        |
| Q-score               | -                           | 25397                       | 15020 ( 2.70 - 3.70 )                                    |

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

| Mol | Chain | Length | Quality of chain                                                                     |
|-----|-------|--------|--------------------------------------------------------------------------------------|
| 1   | L     | 185    |  |
| 2   | D     | 121    |  |
| 3   | A     | 1944   |  |
| 4   | N     | 822    |  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 5   | I     | 814    |                  |
| 6   | O     | 755    |                  |
| 7   | S     | 447    |                  |
| 8   | K     | 620    |                  |
| 8   | Q     | 620    |                  |
| 9   | G     | 85     |                  |
| 9   | W     | 85     |                  |
| 10  | M     | 74     |                  |
| 11  | H     | 110    |                  |
| 12  | J     | 824    |                  |
| 12  | P     | 824    |                  |
| 13  | Y     | 599    |                  |
| 13  | Z     | 599    |                  |
| 14  | U     | 597    |                  |
| 14  | V     | 597    |                  |
| 15  | R     | 496    |                  |
| 16  | C     | 84     |                  |

## 2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 66640 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 Anaphase-promoting complex subunit 10.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 1   | L     | 178      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1404  | 882 | 254 | 261 | 7 |         |       |

- Molecule 2 is a protein called Anaphase-promoting complex subunit 15.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 2   | D     | 56       | Total | C   | N  | O  | 1       | 0     |
|     |       |          | 446   | 286 | 75 | 85 |         |       |

- Molecule 3 is a protein called Anaphase-promoting complex subunit 1.

| Mol | Chain | Residues | Atoms |      |      |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| 3   | A     | 1602     | Total | C    | N    | O    | S  | 0       | 0     |
|     |       |          | 12378 | 7932 | 2079 | 2284 | 83 |         |       |

- Molecule 4 is a protein called Anaphase-promoting complex subunit 2.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 4   | N     | 632      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 4632  | 2942 | 828 | 840 | 22 |         |       |

- Molecule 5 is a protein called Anaphase-promoting complex subunit 4.

| Mol | Chain | Residues | Atoms |      |     |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|------|----|---------|-------|
| 5   | I     | 721      | Total | C    | N   | O    | S  | 0       | 0     |
|     |       |          | 5675  | 3641 | 948 | 1054 | 32 |         |       |

There are 6 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| I     | 809     | GLU      | -      | expression tag | UNP Q9UJX5 |
| I     | 810     | ASN      | -      | expression tag | UNP Q9UJX5 |
| I     | 811     | LEU      | -      | expression tag | UNP Q9UJX5 |

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| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| I     | 812     | TYR      | -      | expression tag | UNP Q9UJX5 |
| I     | 813     | PHE      | -      | expression tag | UNP Q9UJX5 |
| I     | 814     | GLN      | -      | expression tag | UNP Q9UJX5 |

- Molecule 6 is a protein called Anaphase-promoting complex subunit 5.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 6   | O     | 699      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 5473  | 3492 | 954 | 999 | 28 |         |       |

- Molecule 7 is a protein called F-box only protein 5.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 7   | S     | 94       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 655   | 399 | 123 | 125 | 8 |         |       |

- Molecule 8 is a protein called Cell division cycle protein 16 homolog.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 8   | K     | 518      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 4164  | 2676 | 702 | 760 | 26 |         |       |
| 8   | Q     | 505      | Total | C    | N   | O   | S  | 1       | 0     |
|     |       |          | 4064  | 2606 | 691 | 743 | 24 |         |       |

- Molecule 9 is a protein called Anaphase-promoting complex subunit CDC26.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 9   | G     | 26       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 221   | 137 | 41 | 42 | 1 |         |       |
| 9   | W     | 26       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 222   | 139 | 42 | 40 | 1 |         |       |

- Molecule 10 is a protein called Anaphase-promoting complex subunit 13.

| Mol | Chain | Residues | Atoms |     |    |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|-----|---|---------|-------|
| 10  | M     | 64       | Total | C   | N  | O   | S | 0       | 0     |
|     |       |          | 514   | 323 | 83 | 106 | 2 |         |       |

- Molecule 11 is a protein called Anaphase-promoting complex subunit 16.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 11  | H     | 58       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 469   | 298 | 79 | 90 | 2 |         |       |

- Molecule 12 is a protein called Cell division cycle protein 27 homolog.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 12  | J     | 499      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 3957  | 2545 | 667 | 719 | 26 |         |       |
| 12  | P     | 491      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 3929  | 2526 | 660 | 717 | 26 |         |       |

- Molecule 13 is a protein called Anaphase-promoting complex subunit 7.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 13  | Y     | 499      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 3696  | 2335 | 637 | 701 | 23 |         |       |
| 13  | Z     | 455      | Total | C    | N   | O   | S  | 1       | 0     |
|     |       |          | 3247  | 2044 | 569 | 613 | 21 |         |       |

- Molecule 14 is a protein called Cell division cycle protein 23 homolog.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 14  | U     | 488      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 3888  | 2501 | 659 | 709 | 19 |         |       |
| 14  | V     | 493      | Total | C    | N   | O   | S  | 1       | 0     |
|     |       |          | 4012  | 2588 | 677 | 726 | 21 |         |       |

- Molecule 15 is a protein called Fizzy-related protein homolog.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 15  | R     | 415      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 3015  | 1904 | 542 | 559 | 10 |         |       |

- Molecule 16 is a protein called Anaphase-promoting complex subunit 11.

| Mol | Chain | Residues | Atoms |     |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|----|---------|-------|
| 16  | C     | 81       | Total | C   | N   | O  | S  | 0       | 0     |
|     |       |          | 573   | 368 | 102 | 91 | 12 |         |       |

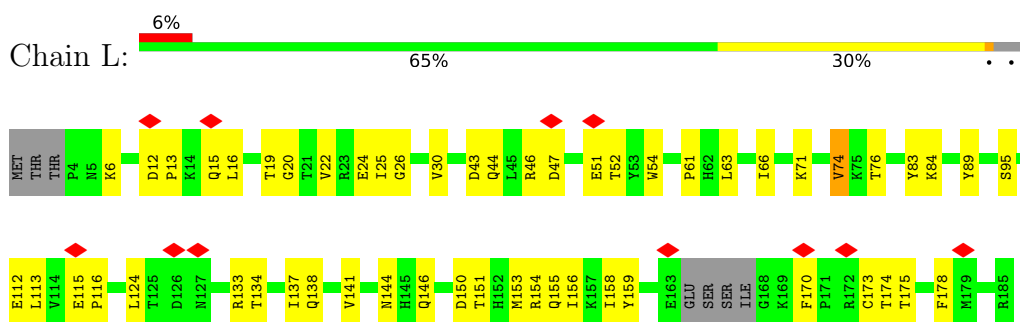
- Molecule 17 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

| Mol | Chain | Residues | Atoms      |         | AltConf |
|-----|-------|----------|------------|---------|---------|
| 17  | N     | 1        | Total<br>1 | Zn<br>1 | 0       |
| 17  | S     | 2        | Total<br>2 | Zn<br>2 | 0       |
| 17  | C     | 3        | Total<br>3 | Zn<br>3 | 0       |

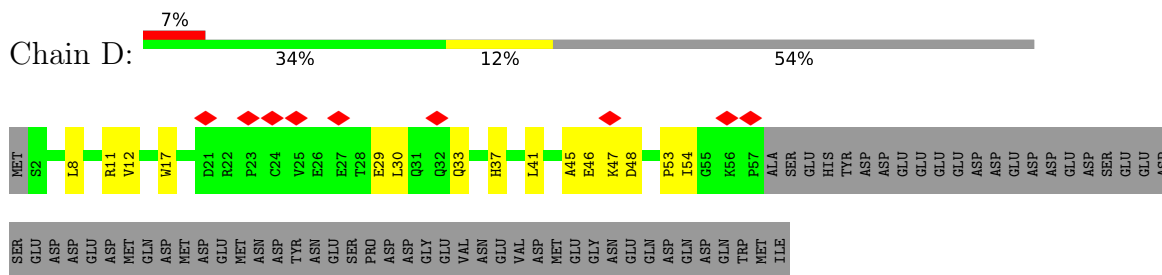
### 3 Residue-property plots

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

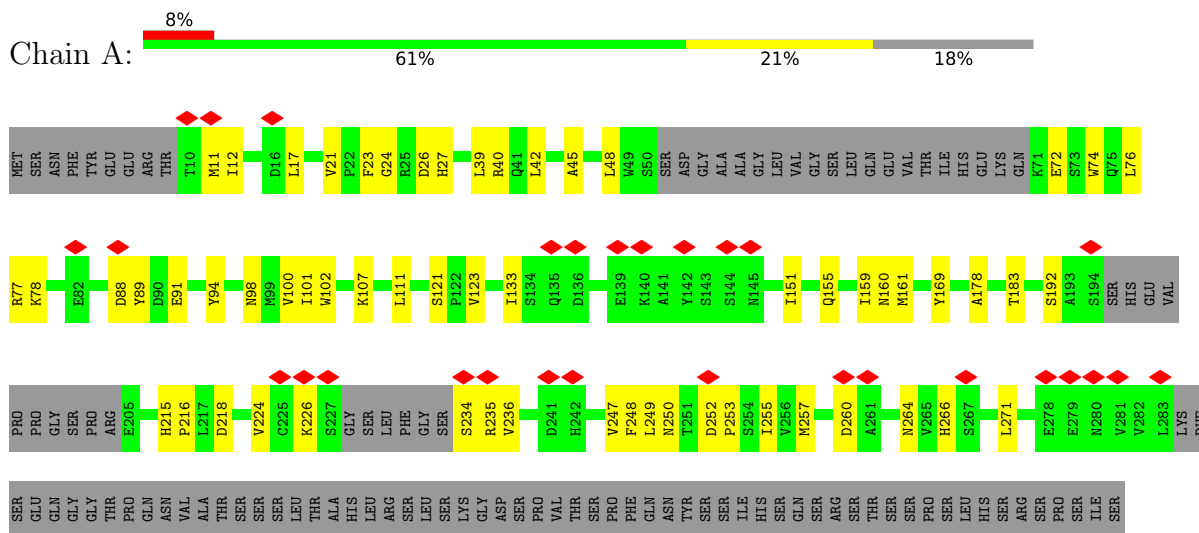
- Molecule 1: Anaphase-promoting complex subunit 10



- Molecule 2: Anaphase-promoting complex subunit 15



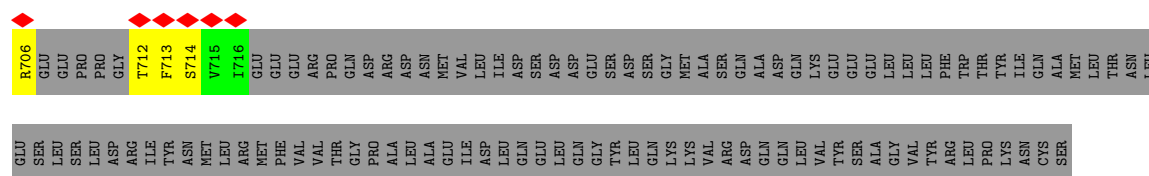
- Molecule 3: Anaphase-promoting complex subunit 1



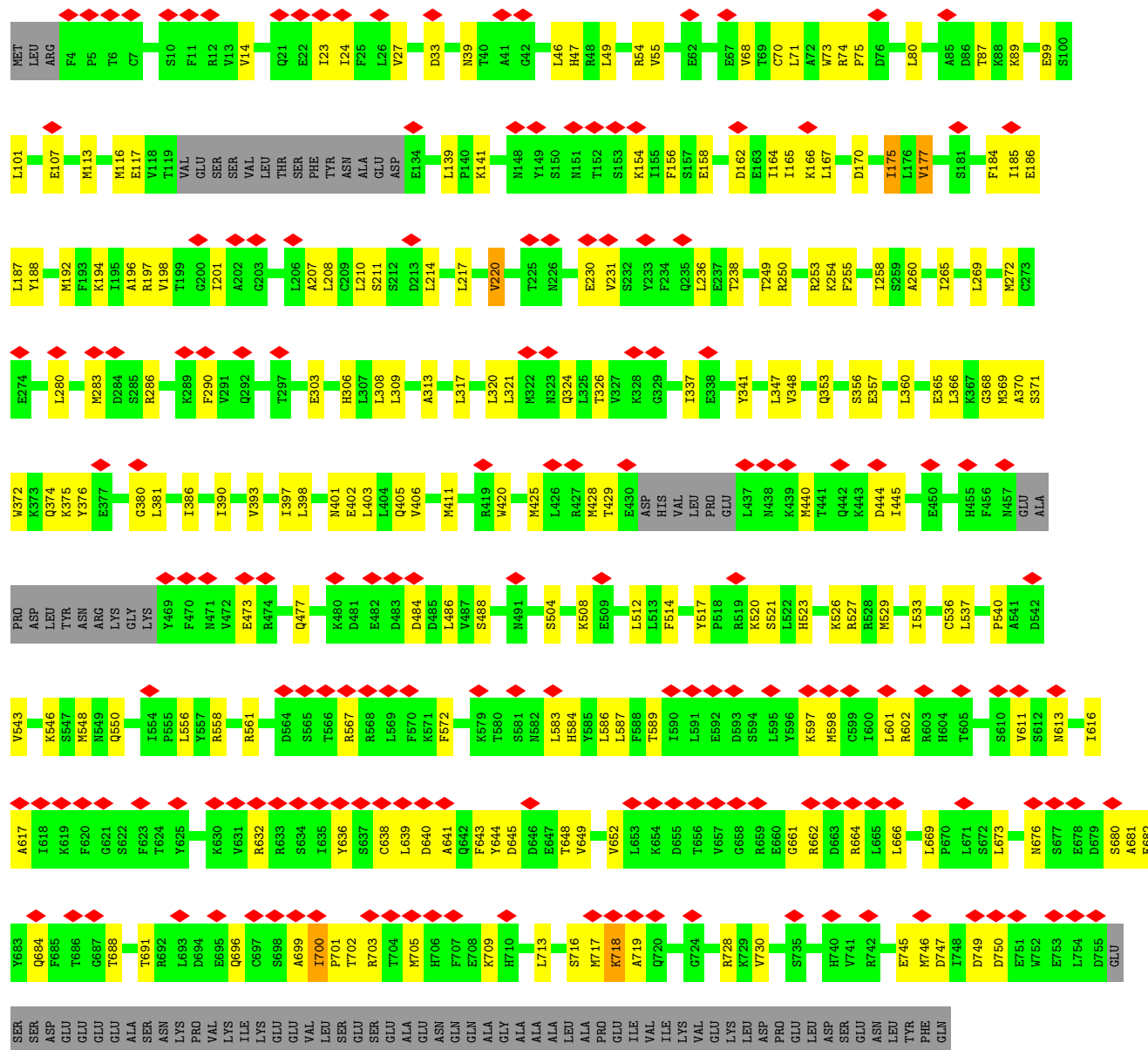






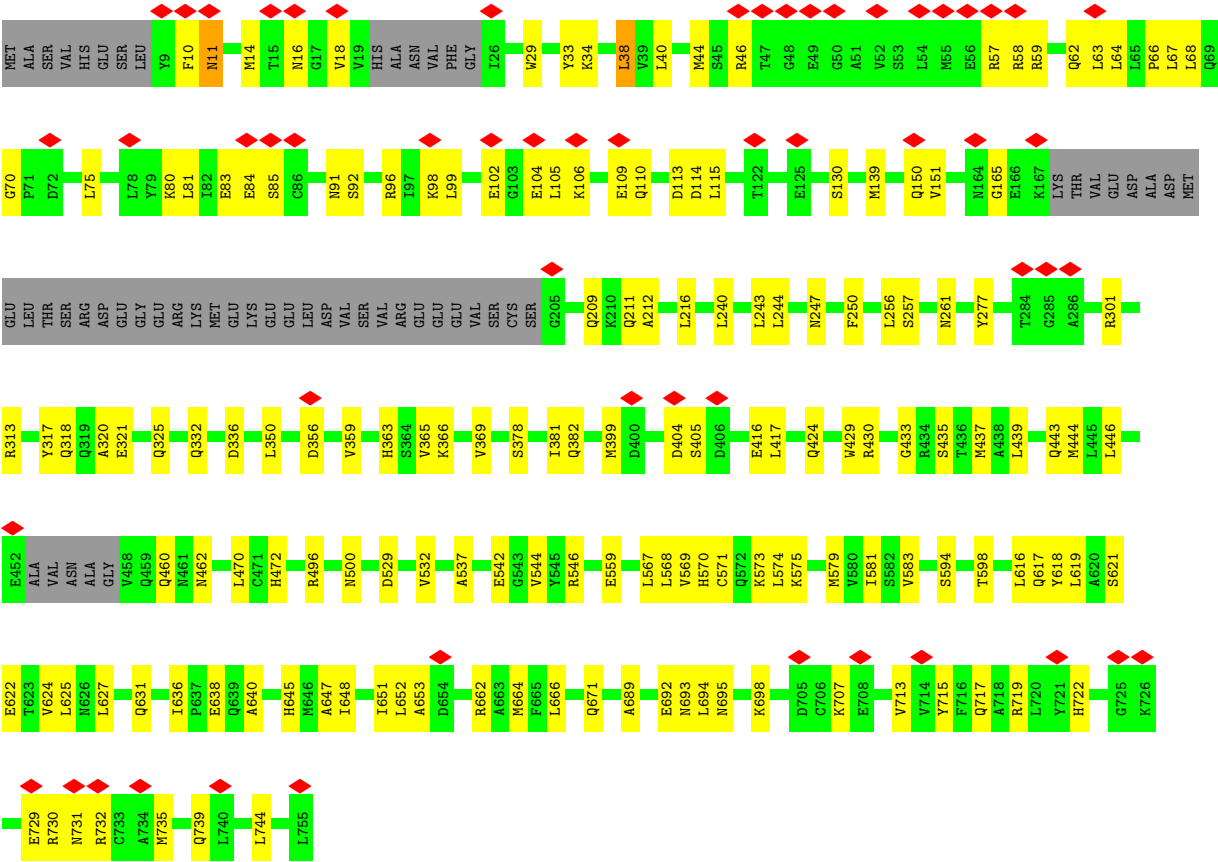


• Molecule 5: Anaphase-promoting complex subunit 4

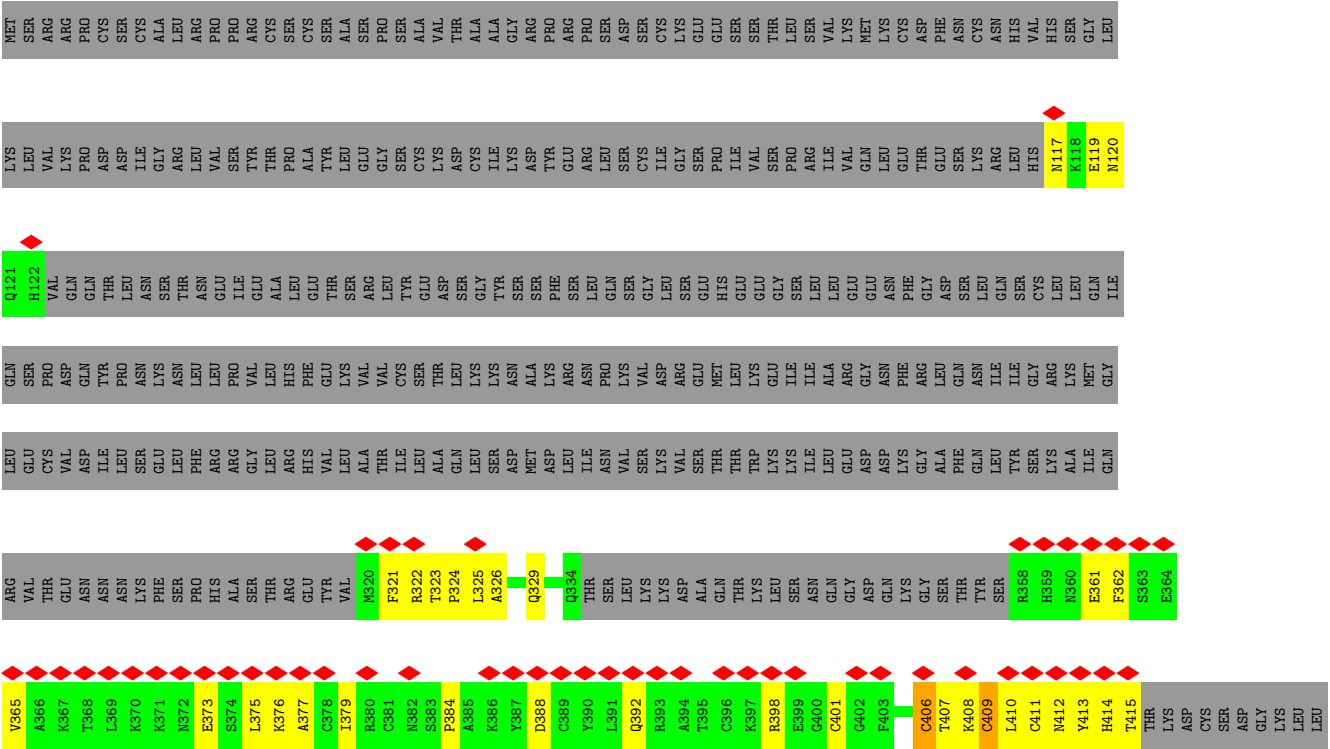


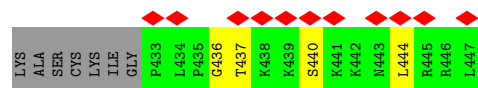
• Molecule 6: Anaphase-promoting complex subunit 5



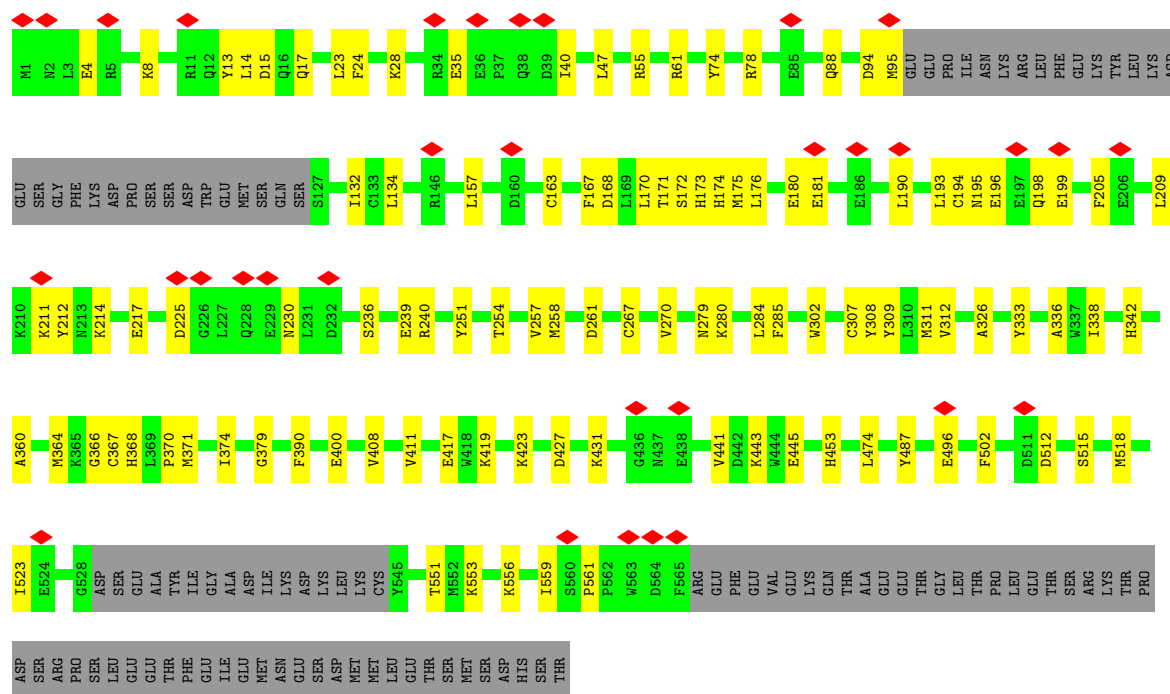


• Molecule 7: F-box only protein 5

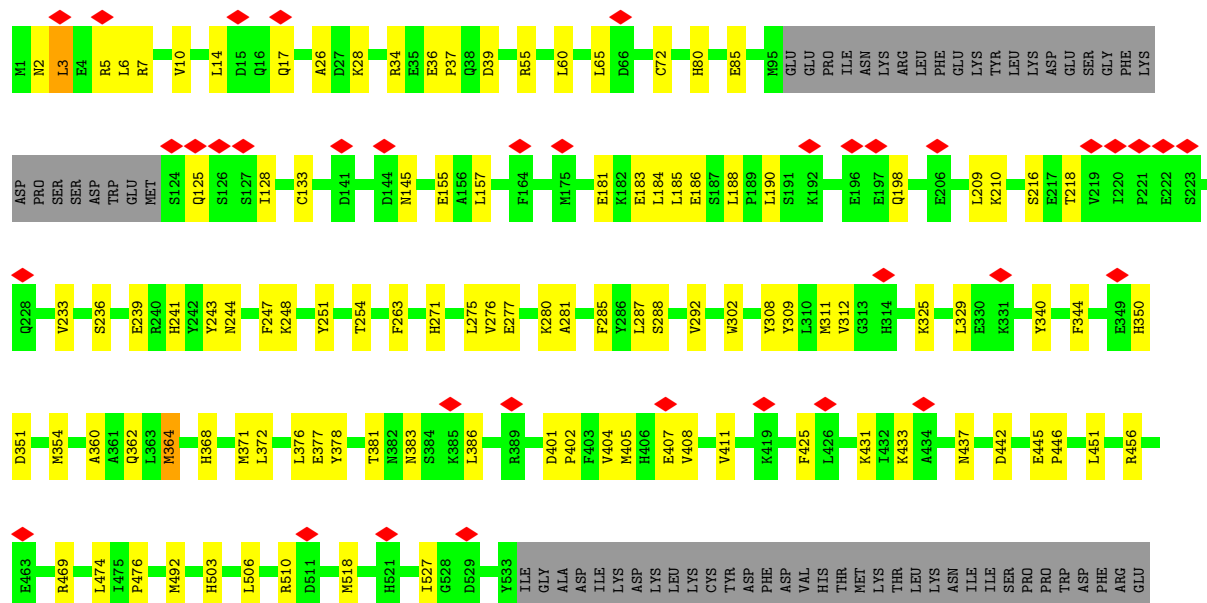




• Molecule 8: Cell division cycle protein 16 homolog



• Molecule 8: Cell division cycle protein 16 homolog



PHE GLU VAL GLU LYS LYS THR ALA GLU THR GLY LEU THR PRO LEU GLU THR SER ARG LYS THR PRO ASP SER ARG PRO SER SER LEU GLU ASP GLU THR PHE GLU ILE GLU MET ASN GLU SER SER MET MET LEU GLU THR MET SER ASP HIS THR

• Molecule 9: Anaphase-promoting complex subunit CDC26

Chain G:  7% 21% 9% 69%

M1 L2 R3 R4 R8 L9 E10 L11 D14 D15 I16 E17 E20 K24 D25 L26 GLU THR ARG LYS LYS GLN LYS LEU ASP VAL GLU VAL ILE GLU MET ASN GLU SER SER MET MET LEU GLU THR MET SER ASP HIS THR

TYR LYS PRO GLN LYS PRO ASN ARG SER SER GLN PHE GLY SER LEU GLU PHE

• Molecule 9: Anaphase-promoting complex subunit CDC26

Chain W:  22% 8% 69%

M1 L2 K5 R8 L9 E10 L11 D15 I16 E17 K23 K24 K25 L26 GLU THR ARG LYS LYS GLN LYS ASP VAL GLU VAL ILE GLU MET ASN GLU SER SER LEU GLU PHE

PRO GLN PRO LYS PRO ASN ASN ARG SER SER PHE GLY SER LEU PHE

• Molecule 10: Anaphase-promoting complex subunit 13

Chain M:  7% 58% 26% 14%

H1 D2 S3 E4 V5 Q6 R7 D8 C9 R10 R11 L12 D13 H19 D22 E27 I31 F32 L33 L36 F37 E38 F39 E40 E41 ASP ASN GLY T46 T47 E48 S49 E52 D59 L60 Q63 Y64 R68 VAL PRO PRO ILE GLY ASN

• Molecule 11: Anaphase-promoting complex subunit 16

Chain H:  10% 30% 23% 47%

MET ALA ALA SER SER SER SER SER ALA GLY VAL VAL THR GLY GLY PHE SER VAL SER ASP E38 ALA PRO PRO ARG LYS ALA LEU PHE THR TYR PRO LYS GLY ALA GLY MET LEU GLU ASP GLY SER E51 E52 F53 L54 S57 Y61 Q62 V63

L67 K68 Q69 V70 K71 Q75 W79 R80 K81 L82 L85 V86 E87 E88 L89 E90 A91 D92 E93 F96 K97 P98 Y99 E100 Q101 L102 T106 P107 S108 GLY

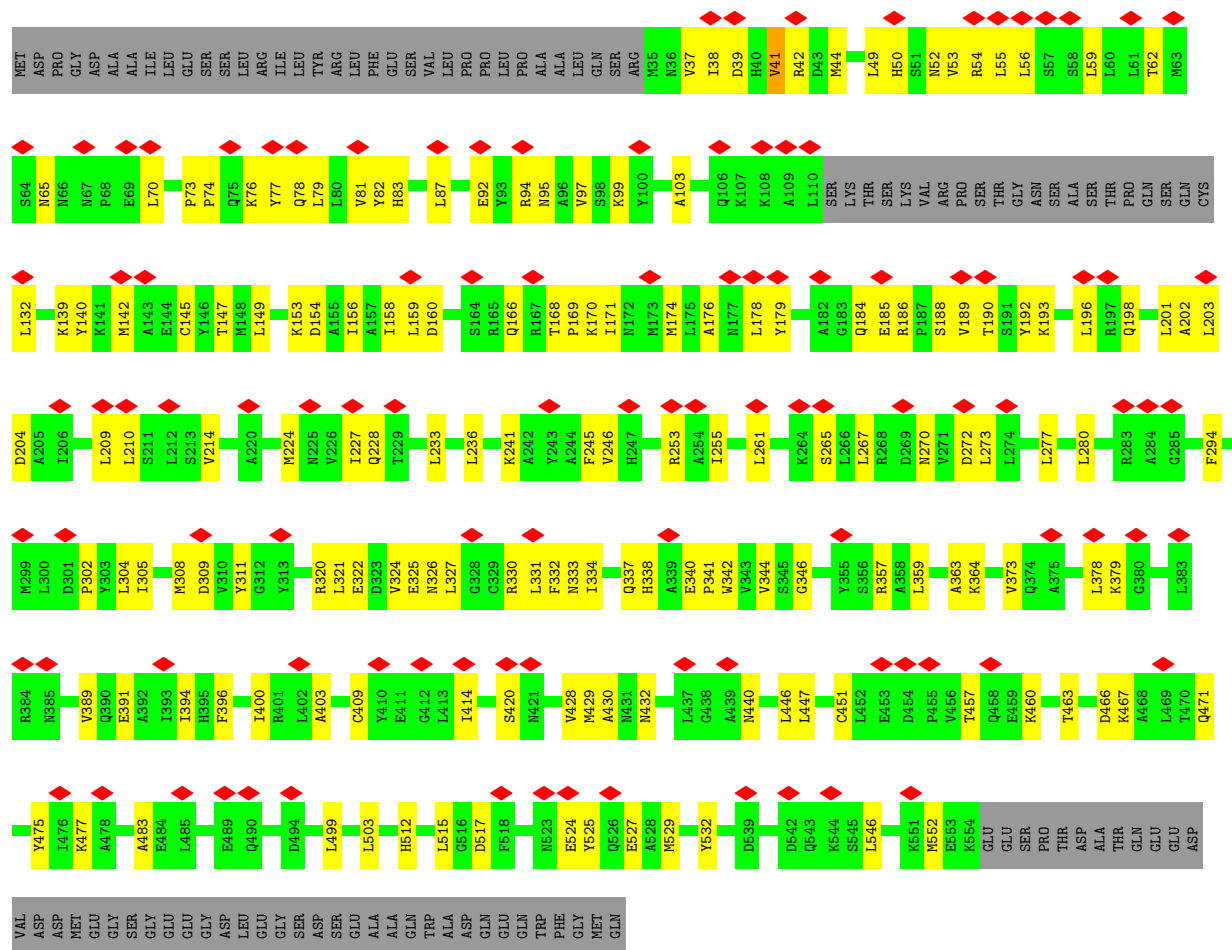
• Molecule 12: Cell division cycle protein 27 homolog

Chain J:  45% 15% 39%

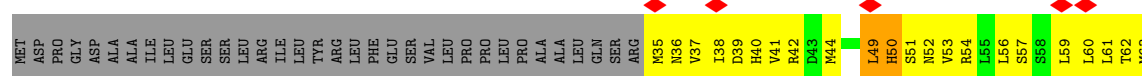
MET THR V3 L4 Q5 E6 Q9 A15 L16 H17 H18 D23 F26 L27 A28 E29 E34 F42 Y49 R50 Y55 Y58 R59 T68 F69 Q70 C71 K72 Y73 L74 L75 C78 D81 L82 L85 I91 L92 S93 G94 G95 V96 F97 H103 D104



- Molecule 13: Anaphase-promoting complex subunit 7



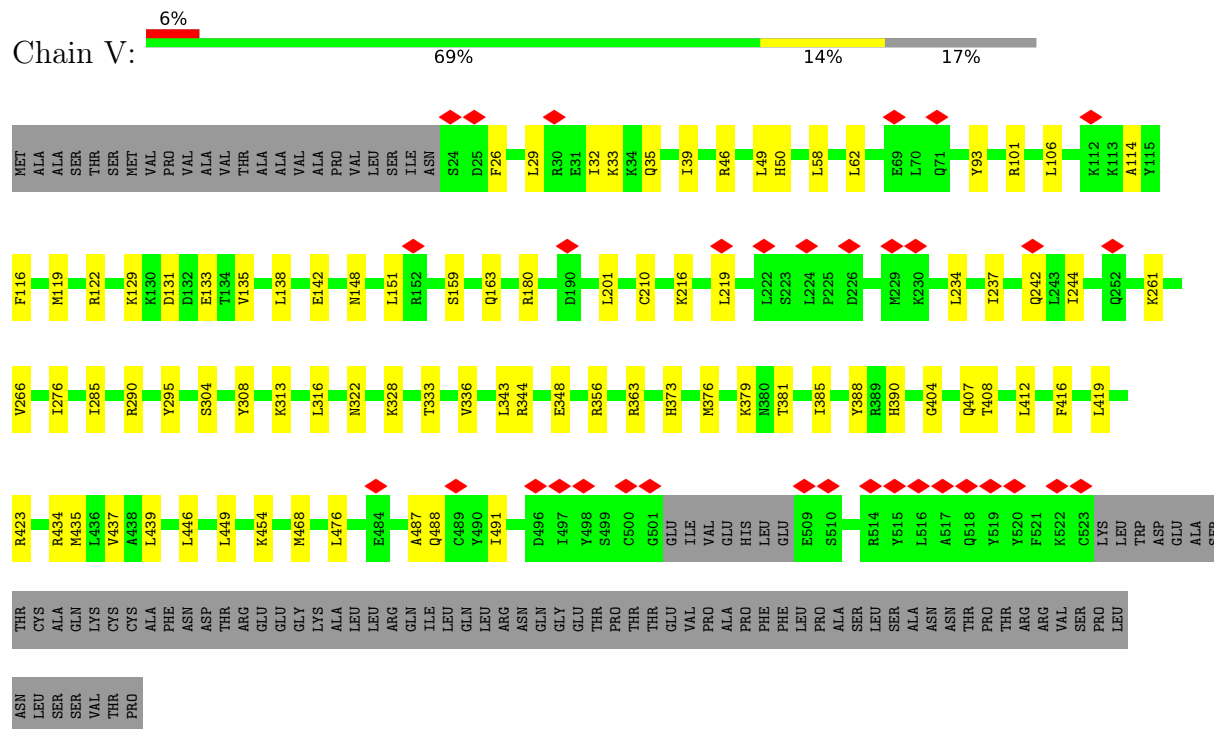
- Molecule 13: Anaphase-promoting complex subunit 7



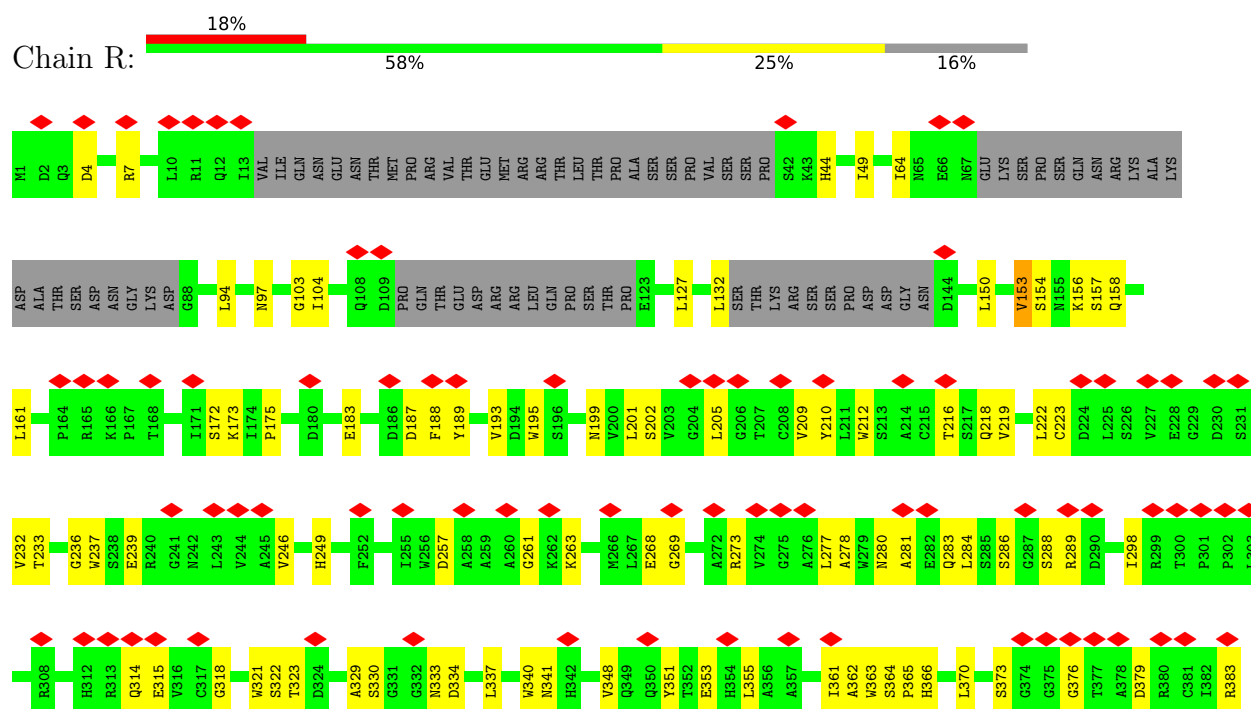


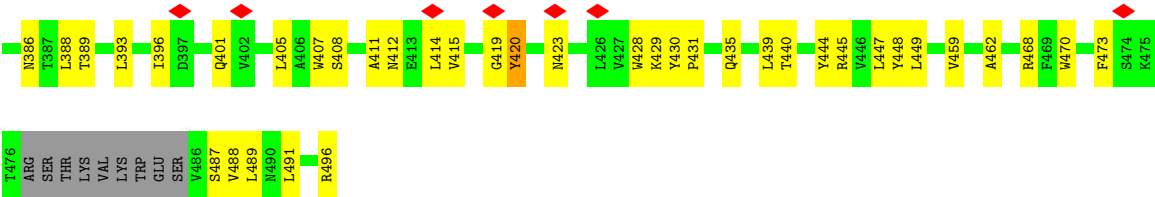


- Molecule 14: Cell division cycle protein 23 homolog

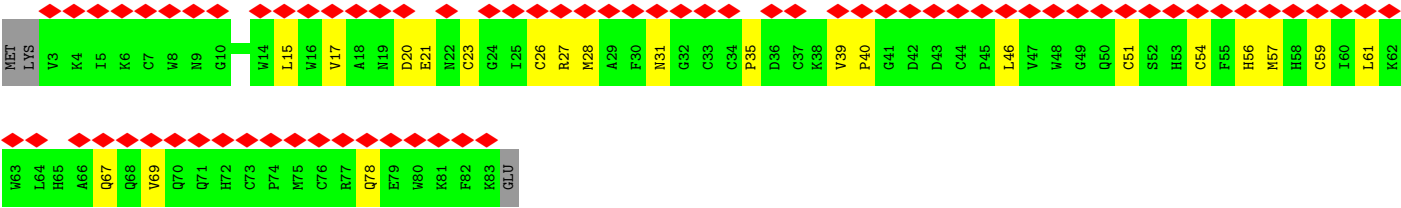
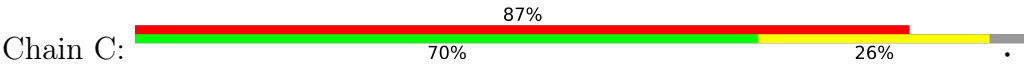


- Molecule 15: Fizzy-related protein homolog





● Molecule 16: Anaphase-promoting complex subunit 11



## 4 Experimental information

| Property                             | Value                                   | Source    |
|--------------------------------------|-----------------------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE                         | Depositor |
| Imposed symmetry                     | POINT, Not provided                     |           |
| Number of particles used             | 364331                                  | 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 ( $e^-/\text{\AA}^2$ ) | 40                                      | Depositor |
| Minimum defocus (nm)                 | 1500                                    | Depositor |
| Maximum defocus (nm)                 | 3500                                    | Depositor |
| Magnification                        | Not provided                            |           |
| Image detector                       | FEI FALCON III (4k x 4k)                | Depositor |
| Maximum map value                    | 2.019                                   | Depositor |
| Minimum map value                    | -0.063                                  | Depositor |
| Average map value                    | 0.003                                   | Depositor |
| Map value standard deviation         | 0.038                                   | Depositor |
| Recommended contour level            | 0.18                                    | Depositor |
| Map size (Å)                         | 385.2, 385.2, 385.2                     | wwPDB     |
| Map dimensions                       | 360, 360, 360                           | wwPDB     |
| Map angles (°)                       | 90.0, 90.0, 90.0                        | wwPDB     |
| Pixel spacing (Å)                    | 1.07, 1.07, 1.07                        | Depositor |

## 5 Model quality

### 5.1 Standard geometry

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

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   | L     | 0.26         | 0/1436  | 0.47        | 0/1949         |
| 2   | D     | 0.39         | 0/460   | 0.71        | 0/630          |
| 3   | A     | 0.18         | 0/12662 | 0.37        | 3/17244 (0.0%) |
| 4   | N     | 0.30         | 0/4717  | 0.52        | 0/6429         |
| 5   | I     | 0.26         | 0/5795  | 0.44        | 0/7855         |
| 6   | O     | 0.23         | 0/5574  | 0.37        | 0/7538         |
| 7   | S     | 0.45         | 0/662   | 0.70        | 0/896          |
| 8   | K     | 0.16         | 0/4265  | 0.32        | 0/5777         |
| 8   | Q     | 0.20         | 0/4165  | 0.35        | 0/5640         |
| 9   | G     | 0.18         | 0/222   | 0.46        | 0/295          |
| 9   | W     | 0.25         | 0/223   | 0.47        | 0/295          |
| 10  | M     | 0.19         | 0/523   | 0.51        | 0/711          |
| 11  | H     | 0.27         | 0/477   | 0.61        | 0/642          |
| 12  | J     | 0.17         | 0/4051  | 0.34        | 0/5482         |
| 12  | P     | 0.22         | 0/4023  | 0.35        | 0/5440         |
| 13  | Y     | 0.23         | 0/3753  | 0.48        | 0/5113         |
| 13  | Z     | 0.31         | 0/3298  | 0.60        | 0/4498         |
| 14  | U     | 0.20         | 0/3975  | 0.36        | 0/5380         |
| 14  | V     | 0.17         | 0/4108  | 0.32        | 0/5552         |
| 15  | R     | 0.31         | 0/3075  | 0.53        | 0/4192         |
| 16  | C     | 0.15         | 0/595   | 0.41        | 0/822          |
| All | All   | 0.23         | 0/68059 | 0.42        | 3/92380 (0.0%) |

There are no bond length outliers.

All (3) bond angle outliers are listed below:

| Mol | Chain | Res  | Type | Atoms   | Z     | Observed(°) | Ideal(°) |
|-----|-------|------|------|---------|-------|-------------|----------|
| 3   | A     | 1652 | MET  | CA-C-N  | 5.49  | 129.02      | 120.68   |
| 3   | A     | 1652 | MET  | C-N-CA  | 5.49  | 129.02      | 120.68   |
| 3   | A     | 1284 | GLU  | CB-CA-C | -5.19 | 110.57      | 116.54   |

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

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

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1   | L     | 1404  | 0        | 1359     | 38      | 0            |
| 2   | D     | 446   | 0        | 414      | 15      | 0            |
| 3   | A     | 12378 | 0        | 12145    | 290     | 0            |
| 4   | N     | 4632  | 0        | 4265     | 129     | 0            |
| 5   | I     | 5675  | 0        | 5585     | 154     | 0            |
| 6   | O     | 5473  | 0        | 5491     | 120     | 0            |
| 7   | S     | 655   | 0        | 557      | 32      | 0            |
| 8   | K     | 4164  | 0        | 4077     | 80      | 0            |
| 8   | Q     | 4064  | 0        | 3961     | 84      | 0            |
| 9   | G     | 221   | 0        | 224      | 11      | 0            |
| 9   | W     | 222   | 0        | 233      | 9       | 0            |
| 10  | M     | 514   | 0        | 479      | 22      | 0            |
| 11  | H     | 469   | 0        | 462      | 28      | 0            |
| 12  | J     | 3957  | 0        | 3876     | 95      | 0            |
| 12  | P     | 3929  | 0        | 3866     | 74      | 0            |
| 13  | Y     | 3696  | 0        | 3569     | 128     | 0            |
| 13  | Z     | 3247  | 0        | 3015     | 141     | 0            |
| 14  | U     | 3888  | 0        | 3745     | 80      | 0            |
| 14  | V     | 4012  | 0        | 3949     | 60      | 0            |
| 15  | R     | 3015  | 0        | 2800     | 95      | 0            |
| 16  | C     | 573   | 0        | 457      | 14      | 0            |
| 17  | C     | 3     | 0        | 0        | 0       | 0            |
| 17  | N     | 1     | 0        | 0        | 0       | 0            |
| 17  | S     | 2     | 0        | 0        | 0       | 0            |
| All | All   | 66640 | 0        | 64529    | 1528    | 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 12.

The worst 5 of 1528 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) |
|-------------------|-------------------|--------------------------|-------------------|
| 3:A:703:SER:HB3   | 6:O:731:ASN:HB3   | 1.50                     | 0.94              |
| 3:A:1802:ARG:HG3  | 3:A:1804:GLU:HG2  | 1.48                     | 0.94              |
| 5:I:664:ARG:NH1   | 5:I:718:LYS:HA    | 1.82                     | 0.94              |
| 11:H:97:LYS:HZ3   | 11:H:101:GLN:HB3  | 1.34                     | 0.93              |
| 13:Y:414:ILE:HD12 | 13:Y:446:LEU:HD21 | 1.51                     | 0.90              |

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   | L     | 174/185 (94%)   | 166 (95%)  | 8 (5%)  | 0        | 100         | 100 |
| 2   | D     | 55/121 (46%)    | 49 (89%)   | 6 (11%) | 0        | 100         | 100 |
| 3   | A     | 1574/1944 (81%) | 1526 (97%) | 48 (3%) | 0        | 100         | 100 |
| 4   | N     | 616/822 (75%)   | 593 (96%)  | 23 (4%) | 0        | 100         | 100 |
| 5   | I     | 713/814 (88%)   | 689 (97%)  | 23 (3%) | 1 (0%)   | 48          | 77  |
| 6   | O     | 691/755 (92%)   | 680 (98%)  | 11 (2%) | 0        | 100         | 100 |
| 7   | S     | 86/447 (19%)    | 78 (91%)   | 8 (9%)  | 0        | 100         | 100 |
| 8   | K     | 512/620 (83%)   | 499 (98%)  | 13 (2%) | 0        | 100         | 100 |
| 8   | Q     | 502/620 (81%)   | 494 (98%)  | 8 (2%)  | 0        | 100         | 100 |
| 9   | G     | 24/85 (28%)     | 24 (100%)  | 0       | 0        | 100         | 100 |
| 9   | W     | 24/85 (28%)     | 24 (100%)  | 0       | 0        | 100         | 100 |
| 10  | M     | 60/74 (81%)     | 60 (100%)  | 0       | 0        | 100         | 100 |
| 11  | H     | 56/110 (51%)    | 56 (100%)  | 0       | 0        | 100         | 100 |
| 12  | J     | 495/824 (60%)   | 484 (98%)  | 11 (2%) | 0        | 100         | 100 |
| 12  | P     | 487/824 (59%)   | 477 (98%)  | 10 (2%) | 0        | 100         | 100 |
| 13  | Y     | 495/599 (83%)   | 483 (98%)  | 12 (2%) | 0        | 100         | 100 |

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| Mol | Chain | Analysed         | Favoured   | Allowed  | Outliers | Percentiles |     |
|-----|-------|------------------|------------|----------|----------|-------------|-----|
| 13  | Z     | 452/599 (76%)    | 431 (95%)  | 20 (4%)  | 1 (0%)   | 43          | 72  |
| 14  | U     | 484/597 (81%)    | 465 (96%)  | 19 (4%)  | 0        | 100         | 100 |
| 14  | V     | 490/597 (82%)    | 480 (98%)  | 10 (2%)  | 0        | 100         | 100 |
| 15  | R     | 403/496 (81%)    | 371 (92%)  | 31 (8%)  | 1 (0%)   | 43          | 72  |
| 16  | C     | 79/84 (94%)      | 74 (94%)   | 5 (6%)   | 0        | 100         | 100 |
| All | All   | 8472/11302 (75%) | 8203 (97%) | 266 (3%) | 3 (0%)   | 100         | 100 |

All (3) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 15  | R     | 420 | TYR  |
| 13  | Z     | 50  | HIS  |
| 5   | I     | 718 | 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   | L     | 153/170 (90%)   | 152 (99%)  | 1 (1%)   | 76          | 92  |
| 2   | D     | 47/115 (41%)    | 47 (100%)  | 0        | 100         | 100 |
| 3   | A     | 1343/1720 (78%) | 1333 (99%) | 10 (1%)  | 76          | 92  |
| 4   | N     | 433/724 (60%)   | 429 (99%)  | 4 (1%)   | 70          | 90  |
| 5   | I     | 619/736 (84%)   | 613 (99%)  | 6 (1%)   | 68          | 89  |
| 6   | O     | 582/650 (90%)   | 574 (99%)  | 8 (1%)   | 59          | 85  |
| 7   | S     | 60/403 (15%)    | 58 (97%)   | 2 (3%)   | 33          | 67  |
| 8   | K     | 441/548 (80%)   | 439 (100%) | 2 (0%)   | 81          | 93  |
| 8   | Q     | 426/548 (78%)   | 423 (99%)  | 3 (1%)   | 76          | 92  |
| 9   | G     | 24/77 (31%)     | 24 (100%)  | 0        | 100         | 100 |
| 9   | W     | 24/77 (31%)     | 24 (100%)  | 0        | 100         | 100 |
| 10  | M     | 55/67 (82%)     | 52 (94%)   | 3 (6%)   | 19          | 50  |

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| Mol | Chain | Analysed        | Rotameric  | Outliers | Percentiles |     |
|-----|-------|-----------------|------------|----------|-------------|-----|
| 11  | H     | 51/89 (57%)     | 51 (100%)  | 0        | 100         | 100 |
| 12  | J     | 415/727 (57%)   | 414 (100%) | 1 (0%)   | 87          | 96  |
| 12  | P     | 418/727 (58%)   | 417 (100%) | 1 (0%)   | 87          | 96  |
| 13  | Y     | 375/513 (73%)   | 373 (100%) | 2 (0%)   | 81          | 93  |
| 13  | Z     | 303/513 (59%)   | 297 (98%)  | 6 (2%)   | 48          | 78  |
| 14  | U     | 389/520 (75%)   | 387 (100%) | 2 (0%)   | 81          | 93  |
| 14  | V     | 415/520 (80%)   | 415 (100%) | 0        | 100         | 100 |
| 15  | R     | 292/431 (68%)   | 290 (99%)  | 2 (1%)   | 76          | 92  |
| 16  | C     | 50/75 (67%)     | 49 (98%)   | 1 (2%)   | 48          | 78  |
| All | All   | 6915/9950 (70%) | 6861 (99%) | 54 (1%)  | 70          | 90  |

5 of 54 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 6   | O     | 638 | GLU  |
| 10  | M     | 60  | LEU  |
| 13  | Z     | 203 | LEU  |
| 7   | S     | 406 | CYS  |
| 8   | K     | 312 | VAL  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 96 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 8   | Q     | 314 | HIS  |
| 14  | U     | 268 | GLN  |
| 8   | Q     | 393 | GLN  |
| 13  | Y     | 270 | ASN  |
| 14  | V     | 287 | ASN  |

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 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.

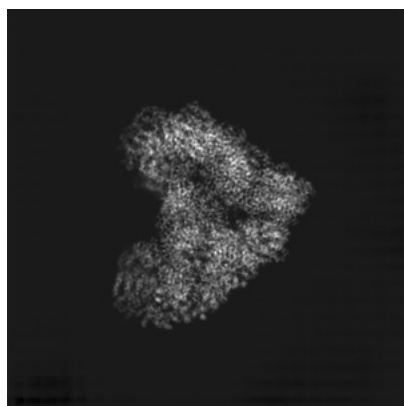
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51190. These allow visual inspection of the internal detail of the map and identification of artifacts.

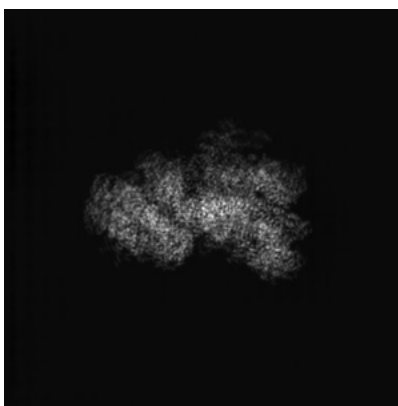
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

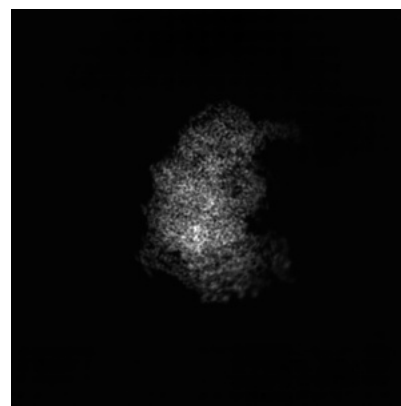
#### 6.1.1 Primary map



X

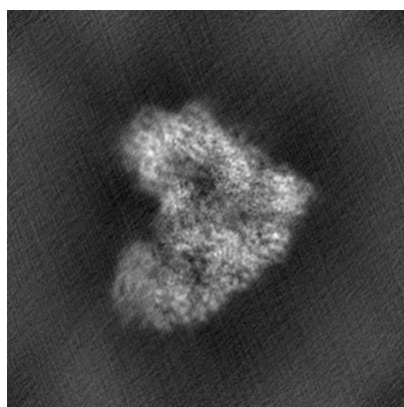


Y

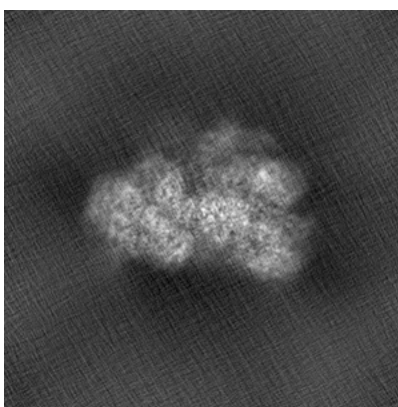


Z

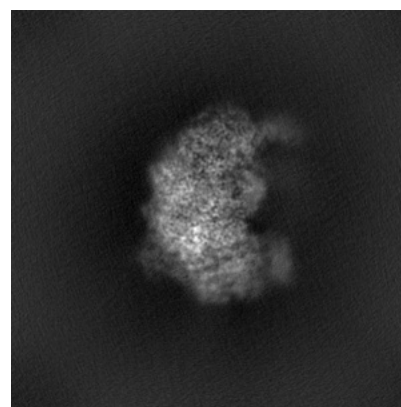
#### 6.1.2 Raw map



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: 180

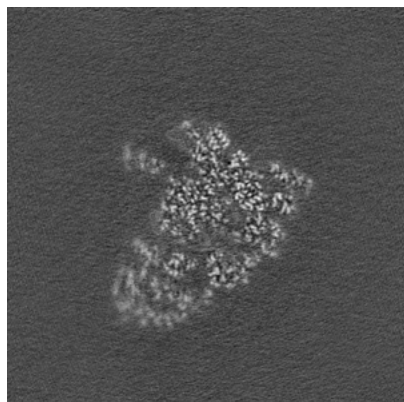


Y Index: 180

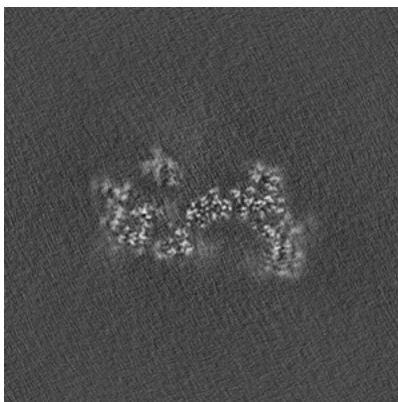


Z Index: 180

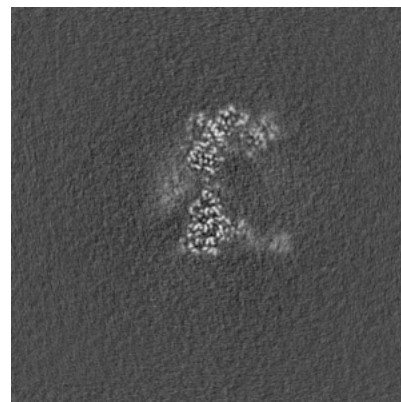
### 6.2.2 Raw map



X Index: 180



Y Index: 180



Z Index: 180

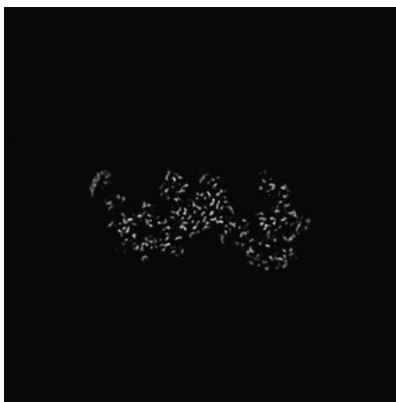
The images above show central slices of the map in three orthogonal directions.

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

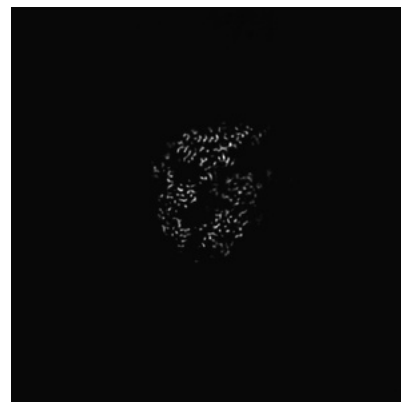
### 6.3.1 Primary map



X Index: 175

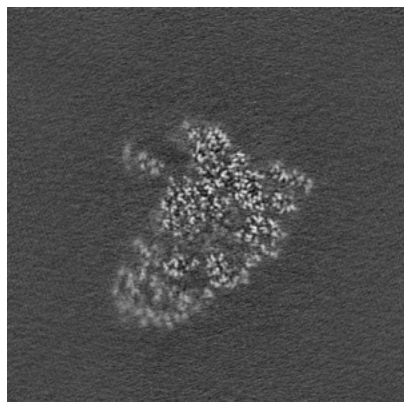


Y Index: 163

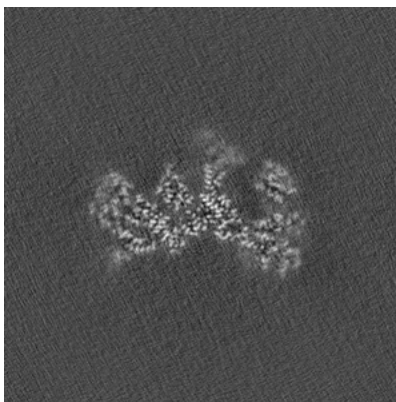


Z Index: 155

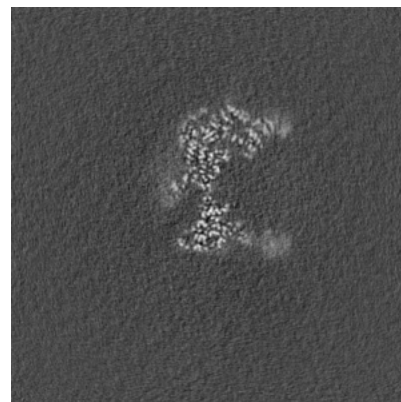
### 6.3.2 Raw map



X Index: 179



Y Index: 155

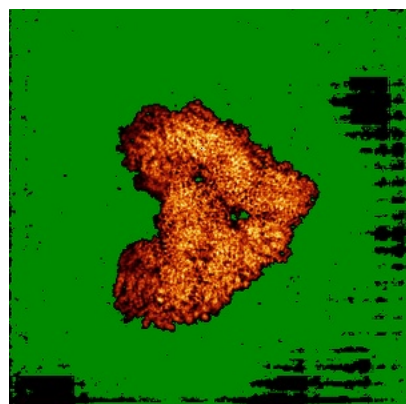


Z Index: 187

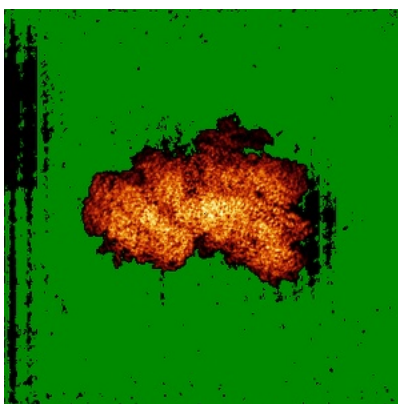
The images above show the largest variance slices of the map in three orthogonal directions.

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

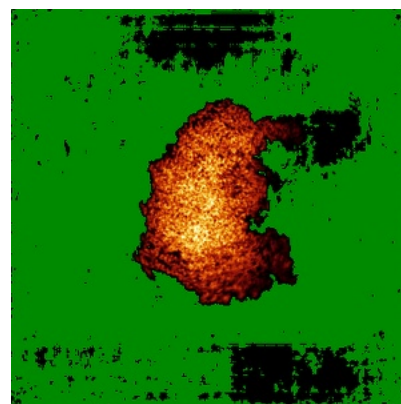
### 6.4.1 Primary map



X

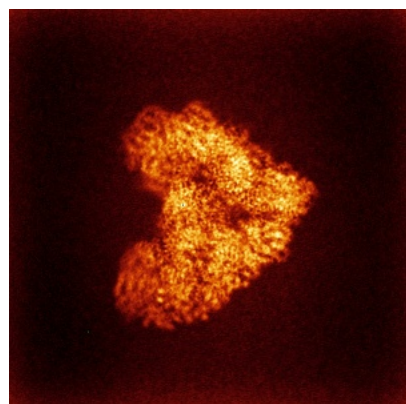


Y

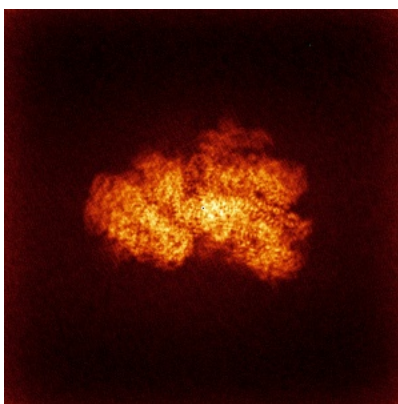


Z

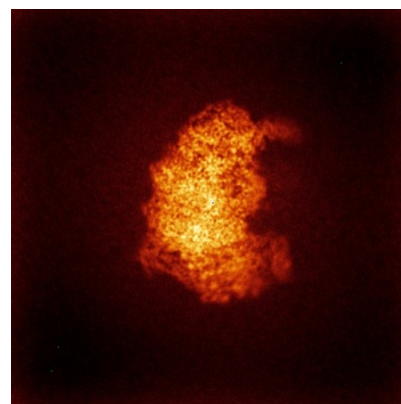
### 6.4.2 Raw map



X



Y



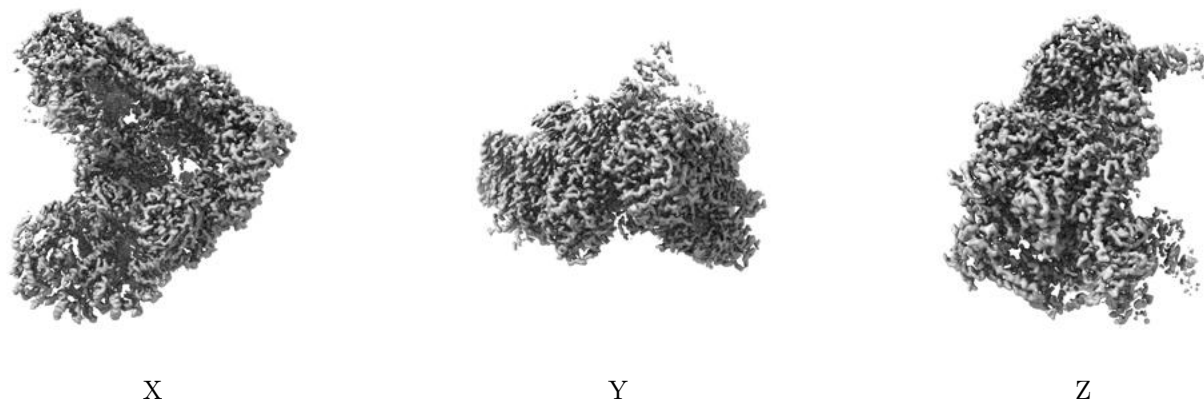
Z

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.



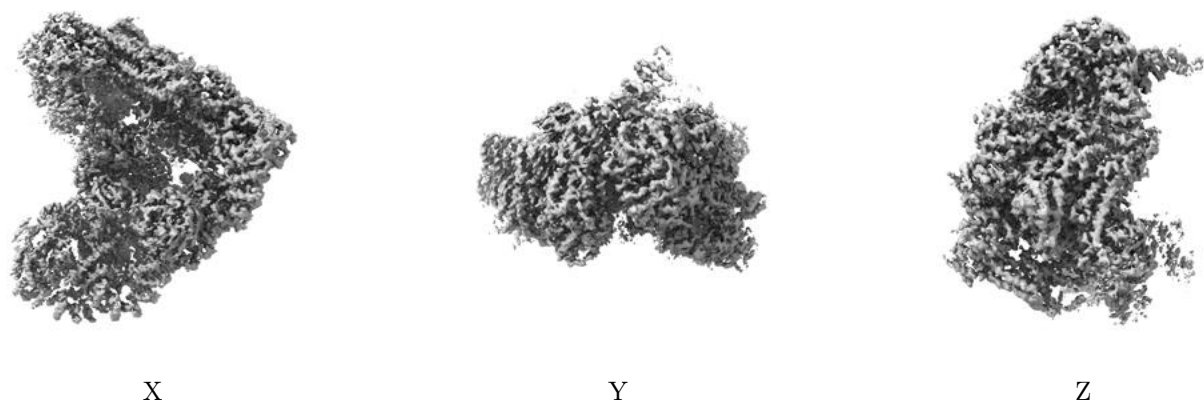
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.18. 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.

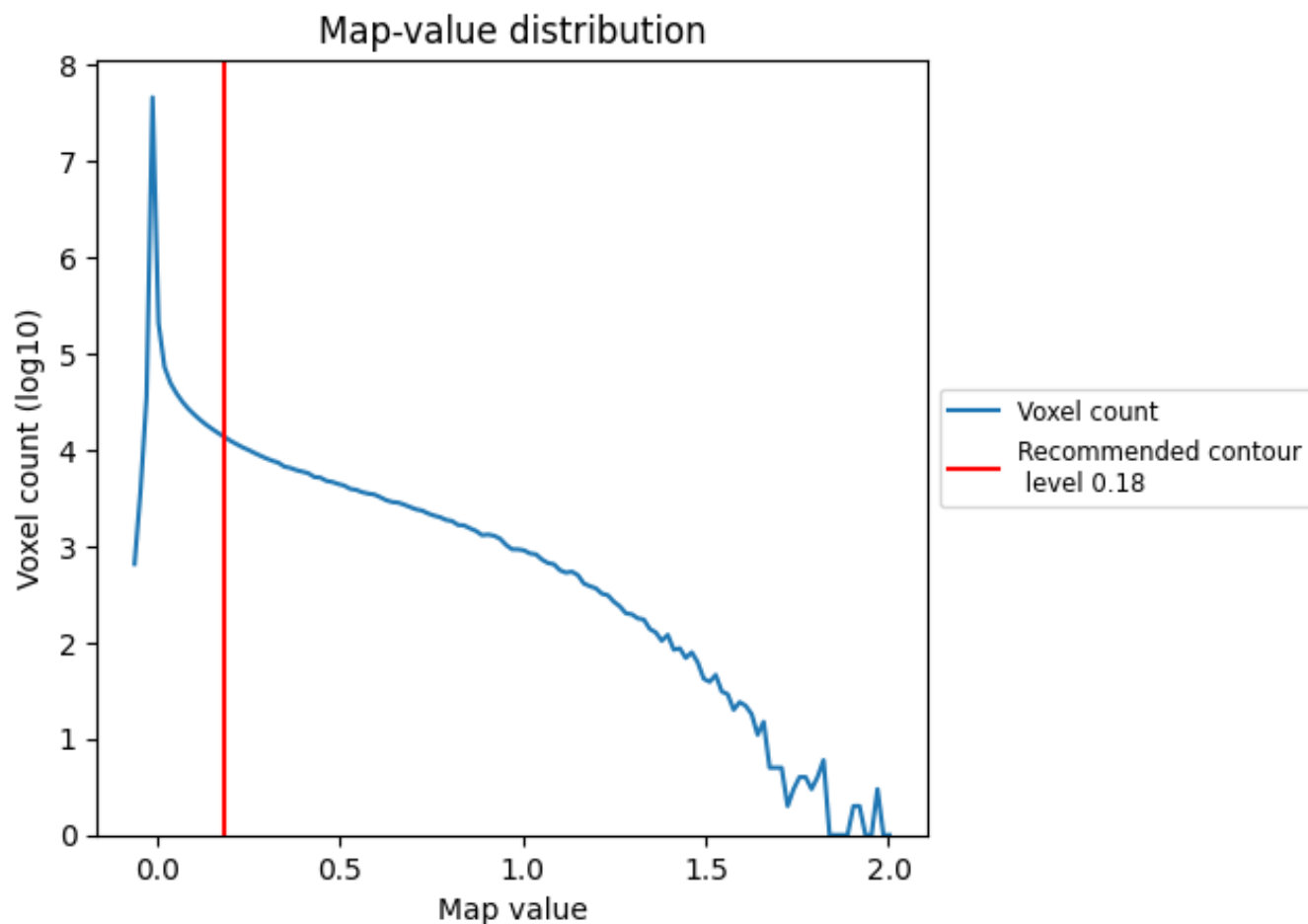
## 6.6 Mask visualisation [i](#)

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.

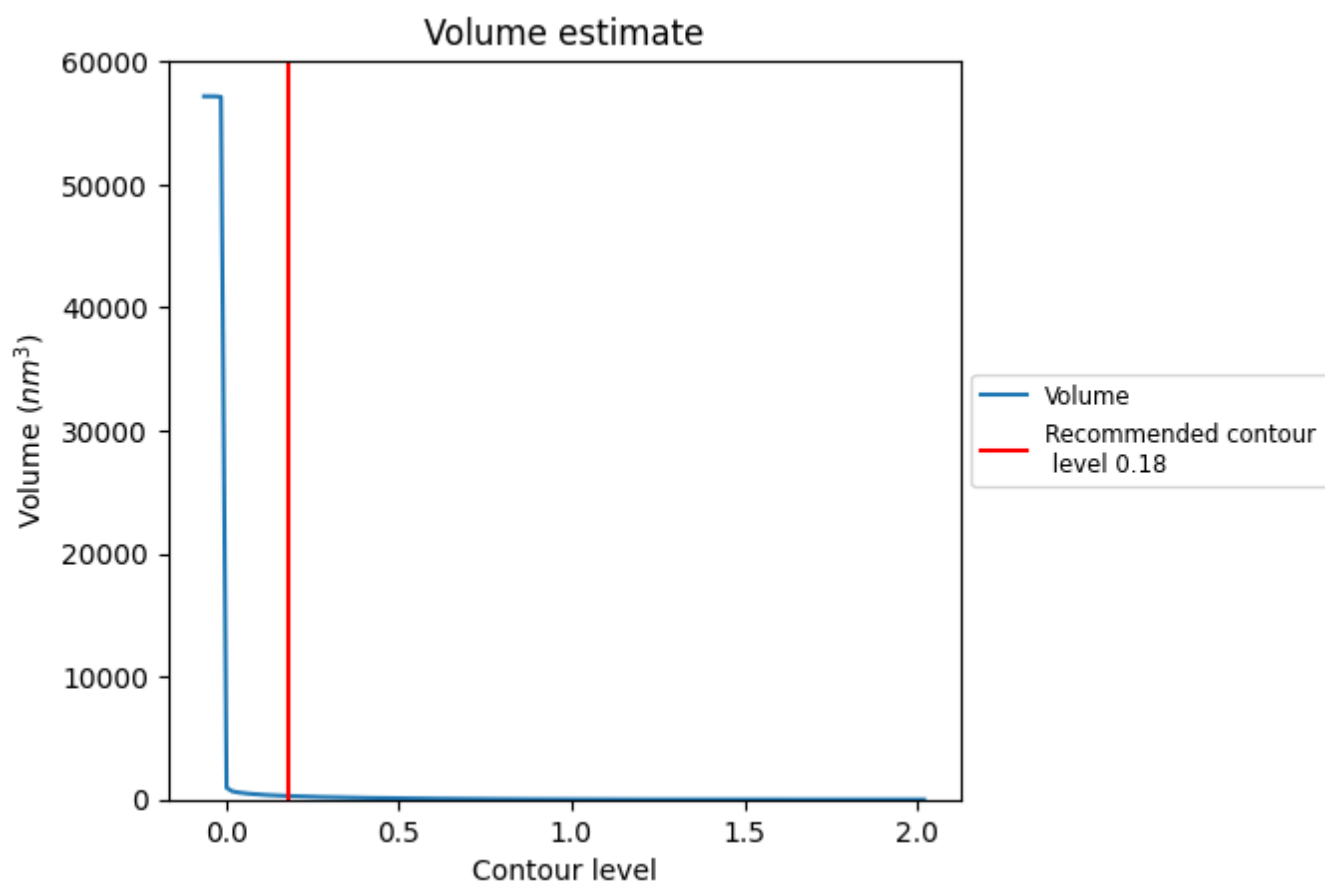
### 7.1 Map-value distribution [i](#)



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.



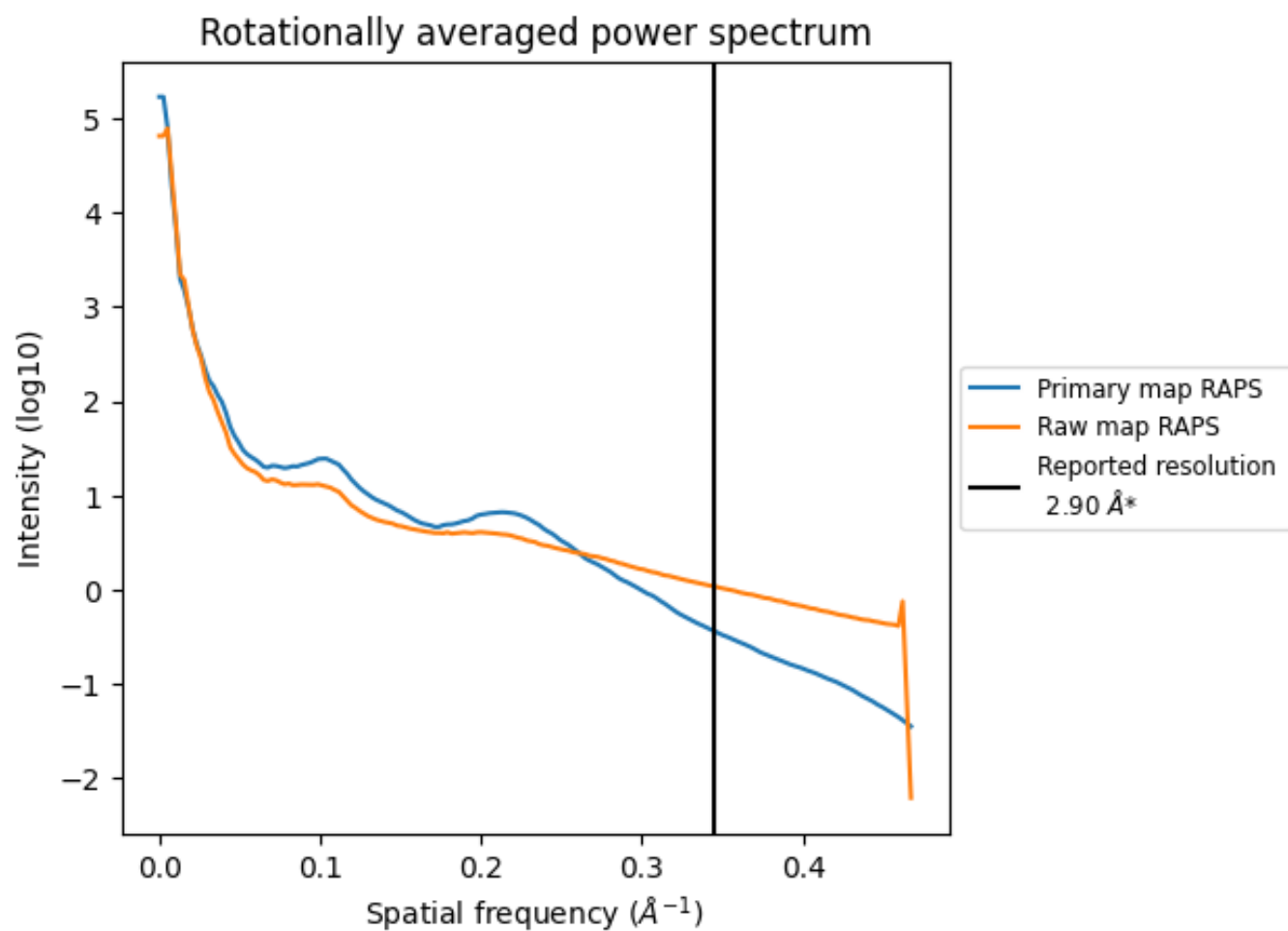
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 291  $\text{nm}^3$ ; this corresponds to an approximate mass of 263 kDa.

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

### 7.3 Rotationally averaged power spectrum ⓘ

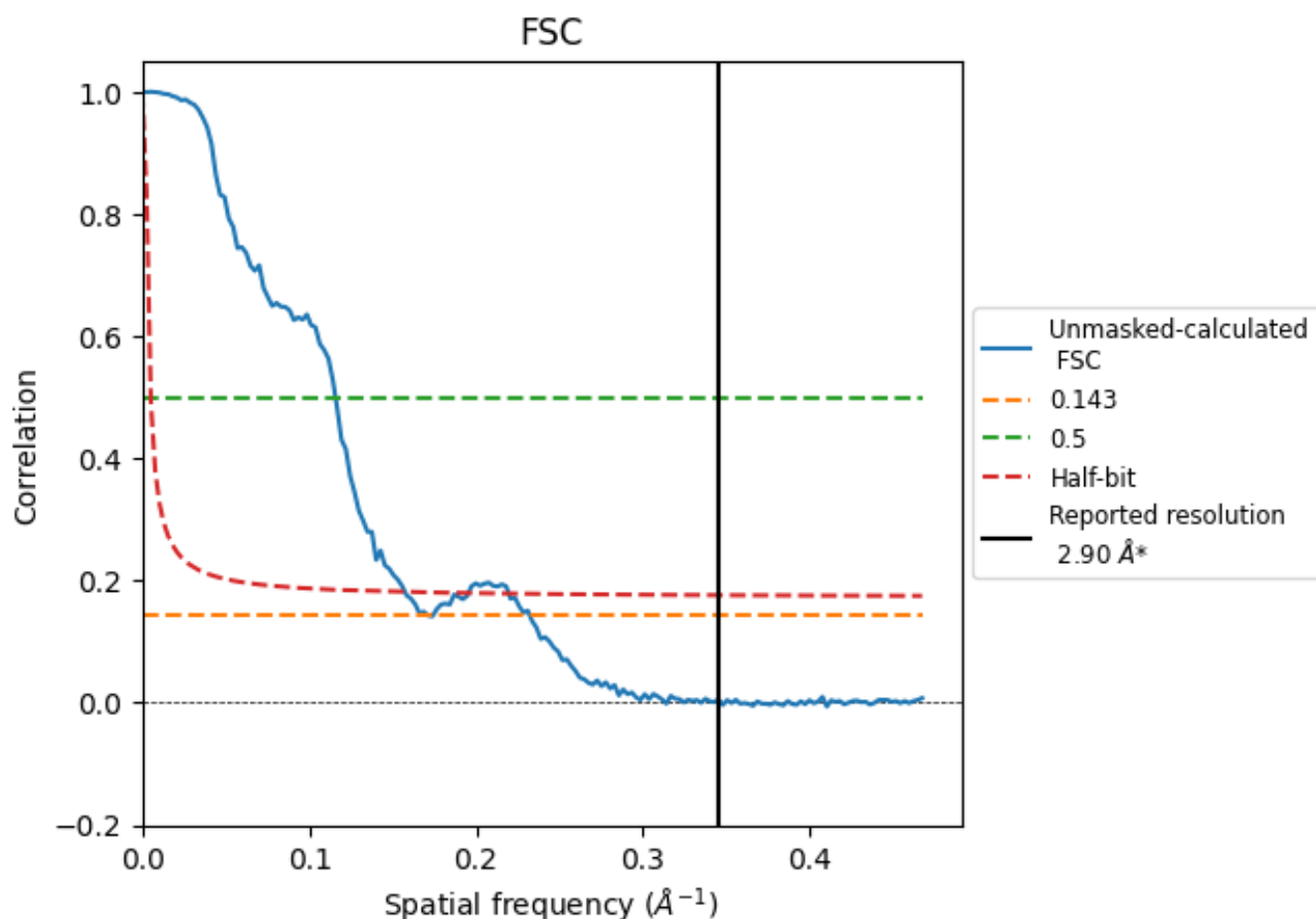


\*Reported resolution corresponds to spatial frequency of 0.345 Å<sup>-1</sup>

## 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 0.345 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

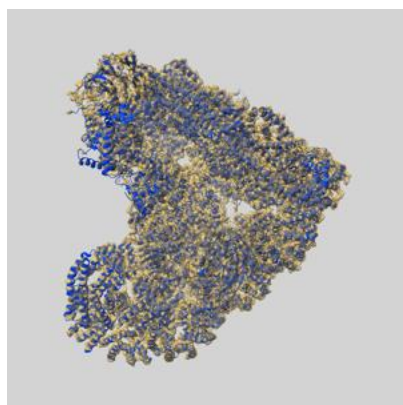
| Resolution estimate (Å)   | Estimation criterion (FSC cut-off) |      |          |
|---------------------------|------------------------------------|------|----------|
|                           | 0.143                              | 0.5  | Half-bit |
| Reported by author        | 2.90                               | -    | -        |
| Author-provided FSC curve | -                                  | -    | -        |
| Unmasked-calculated*      | 5.84                               | 8.64 | 6.35     |

\*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 5.84 differs from the reported value 2.9 by more than 10 %

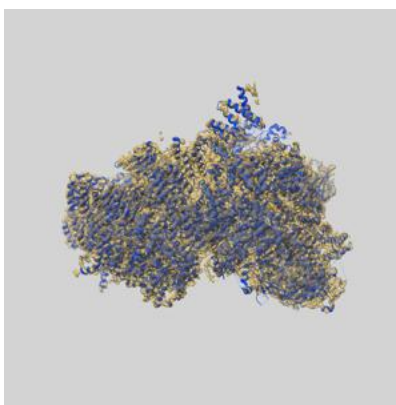
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51190 and PDB model 9GAW. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

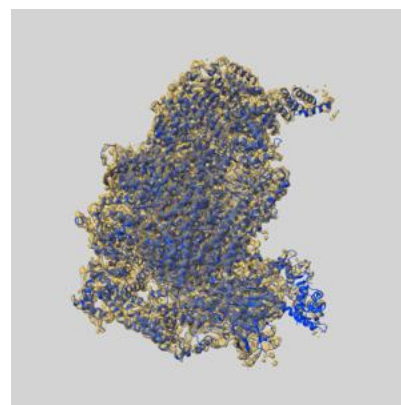
### 9.1 Map-model overlay [i](#)



X



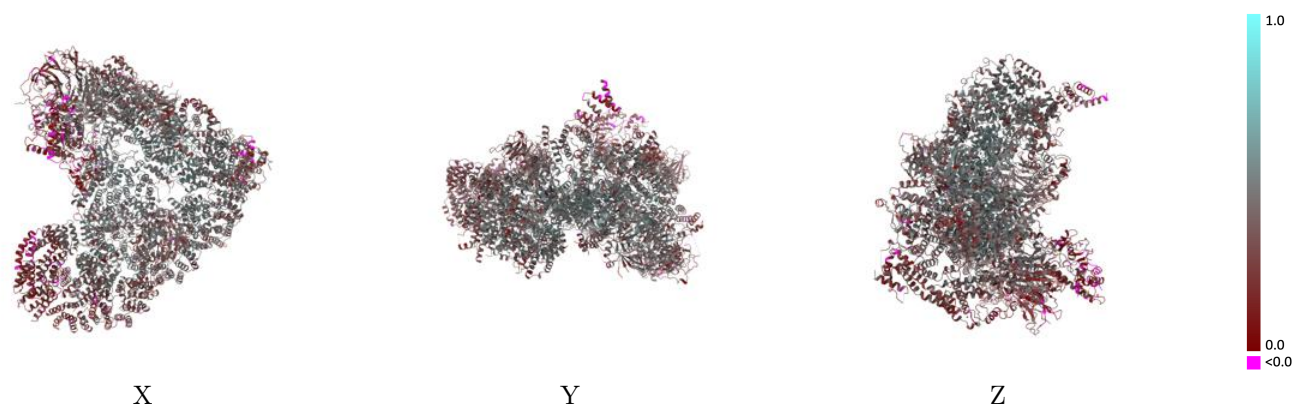
Y



Z

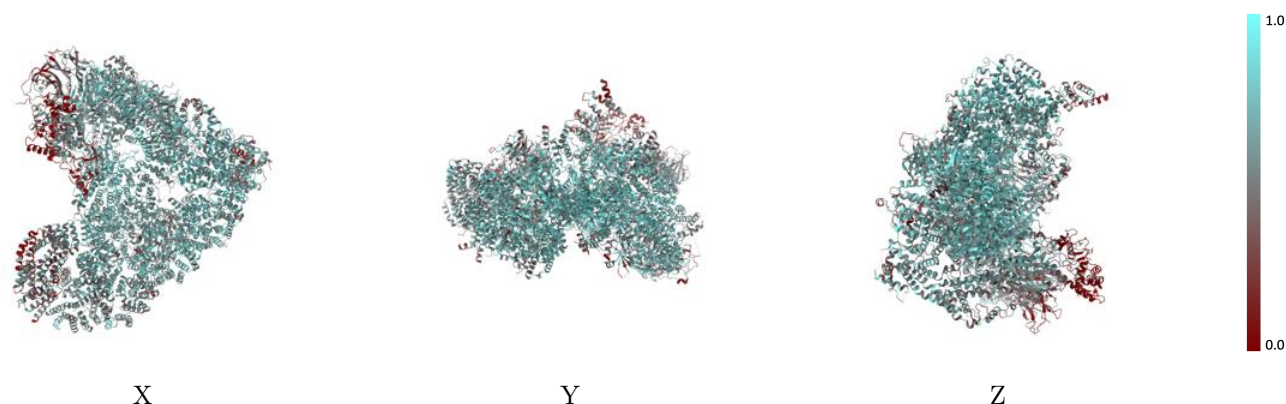
The images above show the 3D surface view of the map at the recommended contour level 0.18 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



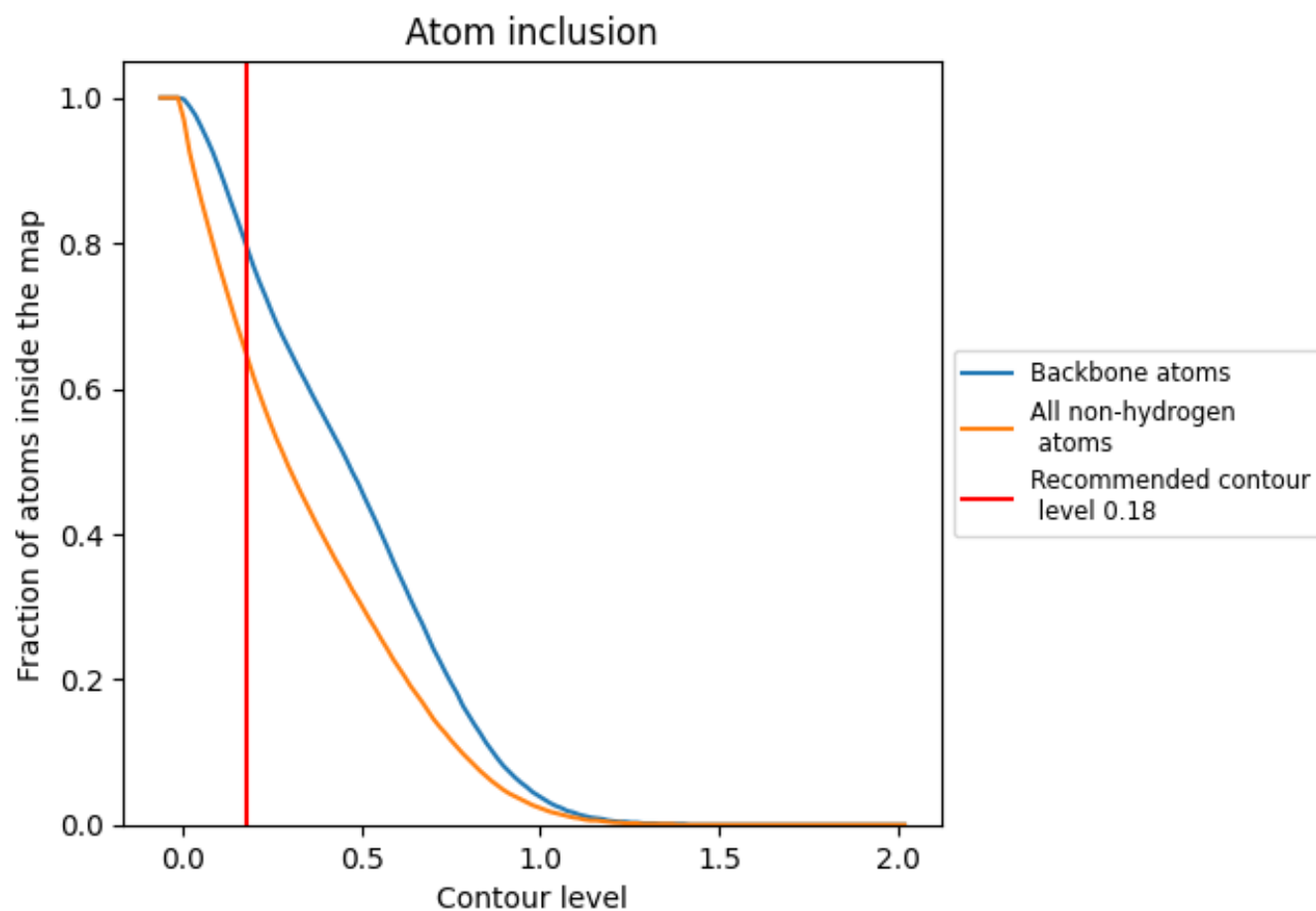
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.18).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 64% 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 (0.18) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion                                                                             | Q-score                                                                                    |
|-------|--------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|
| All   |  0.6430   |  0.3890   |
| A     |  0.6950   |  0.4290   |
| C     |  0.1370   |  0.1550   |
| D     |  0.6570   |  0.4290   |
| G     |  0.6150   |  0.4000   |
| H     |  0.6440   |  0.3640   |
| I     |  0.5530   |  0.3460   |
| J     |  0.7130   |  0.4110   |
| K     |  0.7200   |  0.4590   |
| L     |  0.7040   |  0.4300   |
| M     |  0.6610   |  0.4160   |
| N     |  0.4920   |  0.2810   |
| O     |  0.7110   |  0.4400   |
| P     |  0.7080   |  0.4320   |
| Q     |  0.7110  |  0.4380  |
| R     |  0.5940 |  0.3590 |
| S     |  0.3320 |  0.2330 |
| U     |  0.6670 |  0.4110 |
| V     |  0.7320 |  0.4650 |
| W     |  0.6310 |  0.4570 |
| Y     |  0.5630 |  0.2790 |
| Z     |  0.4720 |  0.2350 |

