



Full wwPDB EM Validation Report ⓘ

Apr 10, 2025 – 04:24 PM EDT

PDB ID : 9N9S / pdb_00009n9s
EMDB ID : EMD-48984
Title : Model of APC/C-CDC20-UBE2C from H3/H4-bound complex
Authors : Skrajna, A.; Bodrug, T.; Brown, N.G.; McGinty, R.K.
Deposited on : 2025-02-11
Resolution : 3.90 Å (reported)

This is a Full wwPDB EM Validation 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.dev117
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) : 2.42

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 8 | K | 620 |  81% 5% 14% |
| 8 | S | 620 |  77% 5% 18% |
| 9 | L | 185 |  92% 6% . |
| 10 | M | 74 |  22% 89% . 8% |
| 11 | N | 720 |  28% 90% . 5% |
| 12 | O | 755 |  10% 87% 7% 6% |
| 13 | Q | 145 |  12% 97% . |
| 14 | R | 499 |  12% 58% 16% . 25% |
| 15 | U | 597 |  14% 86% . 10% |
| 15 | V | 597 |  81% 8% 11% |
| 16 | Y | 565 |  87% . 11% |
| 16 | Z | 565 |  15% 82% . 14% |

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 53106 atoms, of which 17125 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 1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|------|---------|-------|
| | | | Total | C | H | N | O | | |
| 1 | A | 1648 | 9883 | 3296 | 3291 | 1648 | 1648 | 0 | 0 |

There are 21 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|---------------------|------------|
| A | 202 | GLU | SER | engineered mutation | UNP Q9H1A4 |
| A | 286 | GLU | SER | engineered mutation | UNP Q9H1A4 |
| A | 291 | GLU | THR | engineered mutation | UNP Q9H1A4 |
| A | 313 | GLU | SER | engineered mutation | UNP Q9H1A4 |
| A | 316 | GLU | THR | engineered mutation | UNP Q9H1A4 |
| A | 317 | GLU | SER | engineered mutation | UNP Q9H1A4 |
| A | 334 | GLU | SER | engineered mutation | UNP Q9H1A4 |
| A | 341 | GLU | SER | engineered mutation | UNP Q9H1A4 |
| A | 343 | GLU | SER | engineered mutation | UNP Q9H1A4 |
| A | 355 | GLU | SER | engineered mutation | UNP Q9H1A4 |
| A | 362 | GLU | SER | engineered mutation | UNP Q9H1A4 |
| A | 372 | GLU | SER | engineered mutation | UNP Q9H1A4 |
| A | 377 | GLU | SER | engineered mutation | UNP Q9H1A4 |
| A | 537 | GLU | THR | engineered mutation | UNP Q9H1A4 |
| A | 547 | GLU | SER | engineered mutation | UNP Q9H1A4 |
| A | 555 | GLU | SER | engineered mutation | UNP Q9H1A4 |
| A | 569 | GLU | SER | engineered mutation | UNP Q9H1A4 |
| A | 688 | GLU | SER | engineered mutation | UNP Q9H1A4 |
| A | 699 | GLU | SER | engineered mutation | UNP Q9H1A4 |
| A | 916 | GLU | SER | engineered mutation | UNP Q9H1A4 |
| A | 1347 | GLU | SER | engineered mutation | UNP Q9H1A4 |

- Molecule 2 is a protein called Anaphase-promoting complex subunit 11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|----|---------|-------|
| | | | Total | C | H | N | O | | |
| 2 | C | 84 | 508 | 168 | 171 | 84 | 85 | 0 | 0 |

- Molecule 3 is a protein called Anaphase-promoting complex subunit 15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|----|---------|-------|
| | | | Total | C | H | N | O | | |
| 3 | D | 56 | 335 | 112 | 110 | 56 | 57 | 0 | 0 |

- Molecule 4 is a protein called Anaphase-promoting complex subunit CDC26.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|----|---------|-------|
| | | | Total | C | H | N | O | | |
| 4 | G | 27 | 163 | 54 | 55 | 27 | 27 | 0 | 0 |
| 4 | W | 26 | 157 | 52 | 53 | 26 | 26 | 0 | 0 |

There are 6 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|---------------------|------------|
| G | 51 | GLU | SER | engineered mutation | UNP Q8NHZ8 |
| G | 52 | GLU | SER | engineered mutation | UNP Q8NHZ8 |
| G | 82 | GLU | SER | engineered mutation | UNP Q8NHZ8 |
| W | 51 | GLU | SER | engineered mutation | UNP Q8NHZ8 |
| W | 52 | GLU | SER | engineered mutation | UNP Q8NHZ8 |
| W | 82 | GLU | SER | engineered mutation | UNP Q8NHZ8 |

- Molecule 5 is a protein called Anaphase-promoting complex subunit 16.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|----|---------|-------|
| | | | Total | C | H | N | O | | |
| 5 | H | 58 | 348 | 116 | 116 | 58 | 58 | 0 | 0 |

- Molecule 6 is a protein called Anaphase-promoting complex subunit 4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|
| | | | Total | C | H | N | O | | |
| 6 | I | 742 | 4458 | 1484 | 1490 | 742 | 742 | 0 | 0 |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|---------------------|------------|
| I | 777 | GLU | SER | engineered mutation | UNP Q9UJX5 |
| I | 779 | GLU | SER | engineered mutation | UNP Q9UJX5 |

- Molecule 7 is a protein called Cell division cycle protein 27 homolog.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|
| | | | Total | C | H | N | O | | |
| 7 | J | 510 | 3067 | 1020 | 1027 | 510 | 510 | 0 | 0 |
| 7 | P | 496 | 2982 | 992 | 998 | 496 | 496 | 0 | 0 |

There are 28 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|---------------------|------------|
| J | 200 | GLU | THR | engineered mutation | UNP P30260 |
| J | 205 | GLU | THR | engineered mutation | UNP P30260 |
| J | 220 | GLU | SER | engineered mutation | UNP P30260 |
| J | 241 | GLU | SER | engineered mutation | UNP P30260 |
| J | 276 | GLU | SER | engineered mutation | UNP P30260 |
| J | 320 | GLU | SER | engineered mutation | UNP P30260 |
| J | 336 | GLU | SER | engineered mutation | UNP P30260 |
| J | 339 | GLU | SER | engineered mutation | UNP P30260 |
| J | 386 | GLU | SER | engineered mutation | UNP P30260 |
| J | 387 | GLU | SER | engineered mutation | UNP P30260 |
| J | 393 | GLU | SER | engineered mutation | UNP P30260 |
| J | 426 | GLU | SER | engineered mutation | UNP P30260 |
| J | 435 | GLU | SER | engineered mutation | UNP P30260 |
| J | 446 | GLU | THR | engineered mutation | UNP P30260 |
| P | 200 | GLU | THR | engineered mutation | UNP P30260 |
| P | 205 | GLU | THR | engineered mutation | UNP P30260 |
| P | 220 | GLU | SER | engineered mutation | UNP P30260 |
| P | 241 | GLU | SER | engineered mutation | UNP P30260 |
| P | 276 | GLU | SER | engineered mutation | UNP P30260 |
| P | 320 | GLU | SER | engineered mutation | UNP P30260 |
| P | 336 | GLU | SER | engineered mutation | UNP P30260 |
| P | 339 | GLU | SER | engineered mutation | UNP P30260 |
| P | 386 | GLU | SER | engineered mutation | UNP P30260 |
| P | 387 | GLU | SER | engineered mutation | UNP P30260 |
| P | 393 | GLU | SER | engineered mutation | UNP P30260 |
| P | 426 | GLU | SER | engineered mutation | UNP P30260 |
| P | 435 | GLU | SER | engineered mutation | UNP P30260 |
| P | 446 | GLU | THR | engineered mutation | UNP P30260 |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|
| | | | Total | C | H | N | O | | |
| 8 | K | 531 | 3190 | 1062 | 1066 | 531 | 531 | 0 | 0 |

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| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|
| | | | Total | C | H | N | O | | |
| 8 | S | 506 | 3043 | 1012 | 1019 | 506 | 506 | 0 | 0 |

There are 10 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|---------------------|------------|
| K | 112 | GLU | SER | engineered mutation | UNP Q13042 |
| K | 560 | GLU | SER | engineered mutation | UNP Q13042 |
| K | 581 | GLU | THR | engineered mutation | UNP Q13042 |
| K | 585 | GLU | THR | engineered mutation | UNP Q13042 |
| K | 586 | GLU | SER | engineered mutation | UNP Q13042 |
| S | 112 | GLU | SER | engineered mutation | UNP Q13042 |
| S | 560 | GLU | SER | engineered mutation | UNP Q13042 |
| S | 581 | GLU | THR | engineered mutation | UNP Q13042 |
| S | 585 | GLU | THR | engineered mutation | UNP Q13042 |
| S | 586 | GLU | SER | engineered mutation | UNP Q13042 |

- Molecule 9 is a protein called Anaphase-promoting complex subunit 10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|
| | | | Total | C | H | N | O | | |
| 9 | L | 183 | 1097 | 366 | 364 | 183 | 184 | 0 | 0 |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|---------------------|------------|
| L | 3 | GLU | THR | engineered mutation | UNP Q9UM13 |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|----|---------|-------|
| | | | Total | C | H | N | O | | |
| 10 | M | 68 | 409 | 136 | 137 | 68 | 68 | 0 | 0 |

- Molecule 11 is a protein called Anaphase-promoting complex subunit 2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|
| | | | Total | C | H | N | O | | |
| 11 | N | 682 | 4091 | 1364 | 1363 | 682 | 682 | 0 | 0 |

There are 4 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| N | 218 | GLU | SER | conflict | UNP Q9UJX6 |
| N | 314 | GLU | SER | conflict | UNP Q9UJX6 |
| N | 470 | GLU | SER | conflict | UNP Q9UJX6 |
| N | 534 | GLU | SER | conflict | UNP Q9UJX6 |

- Molecule 12 is a protein called Anaphase-promoting complex subunit 5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|
| | | | Total | C | H | N | O | | |
| 12 | O | 707 | 4254 | 1414 | 1425 | 707 | 708 | 0 | 0 |

There are 7 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|---------------------|------------|
| O | 178 | GLU | THR | engineered mutation | UNP Q9UJX4 |
| O | 179 | GLU | SER | engineered mutation | UNP Q9UJX4 |
| O | 195 | GLU | SER | engineered mutation | UNP Q9UJX4 |
| O | 202 | GLU | SER | engineered mutation | UNP Q9UJX4 |
| O | 221 | GLU | SER | engineered mutation | UNP Q9UJX4 |
| O | 232 | GLU | THR | engineered mutation | UNP Q9UJX4 |
| O | 364 | GLU | SER | engineered mutation | UNP Q9UJX4 |

- Molecule 13 is a protein called Ubiquitin-conjugating enzyme E2 C.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|
| | | | Total | C | H | N | O | | |
| 13 | Q | 145 | 870 | 290 | 290 | 145 | 145 | 0 | 0 |

- Molecule 14 is a protein called Cell division cycle protein 20 homolog.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| | | | Total | C | N | O | | |
| 14 | R | 375 | 1845 | 1094 | 375 | 376 | 0 | 0 |

- Molecule 15 is a protein called Cell division cycle protein 23 homolog.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|
| | | | Total | C | H | N | O | | |
| 15 | U | 540 | 3244 | 1080 | 1084 | 540 | 540 | 0 | 0 |
| 15 | V | 534 | 3211 | 1068 | 1075 | 534 | 534 | 0 | 0 |

There are 10 discrepancies between the modelled and reference sequences:

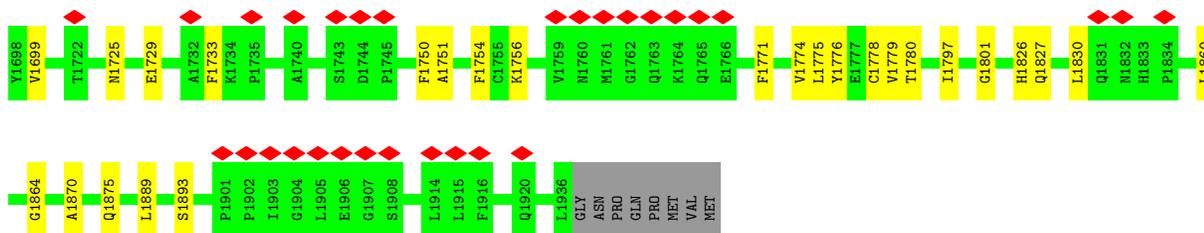
| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|---------------------|------------|
| U | 542 | GLU | THR | engineered mutation | UNP Q9UJX2 |
| U | 562 | GLU | THR | engineered mutation | UNP Q9UJX2 |
| U | 582 | GLU | THR | engineered mutation | UNP Q9UJX2 |
| U | 588 | GLU | SER | engineered mutation | UNP Q9UJX2 |
| U | 596 | GLU | THR | engineered mutation | UNP Q9UJX2 |
| V | 542 | GLU | THR | engineered mutation | UNP Q9UJX2 |
| V | 562 | GLU | THR | engineered mutation | UNP Q9UJX2 |
| V | 582 | GLU | THR | engineered mutation | UNP Q9UJX2 |
| V | 588 | GLU | SER | engineered mutation | UNP Q9UJX2 |
| V | 596 | GLU | THR | engineered mutation | UNP Q9UJX2 |

- Molecule 16 is a protein called Anaphase-promoting complex subunit 7.

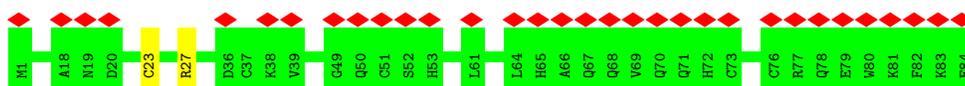
| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|
| 16 | Y | 501 | Total | C | H | N | O | 0 | 0 |
| | | | 3012 | 1002 | 1008 | 501 | 501 | | |
| 16 | Z | 488 | Total | C | H | N | O | 0 | 0 |
| | | | 2935 | 976 | 983 | 488 | 488 | | |

- Molecule 17 is ZINC ION (CCD ID: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| 17 | C | 3 | Total | Zn | 0 |
| | | | 3 | 3 | |
| 17 | N | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |



- Molecule 2: Anaphase-promoting complex subunit 11

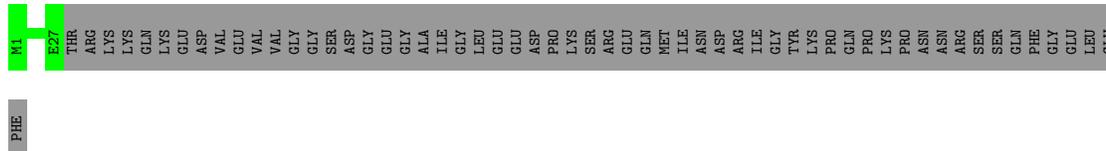


- Molecule 3: Anaphase-promoting complex subunit 15

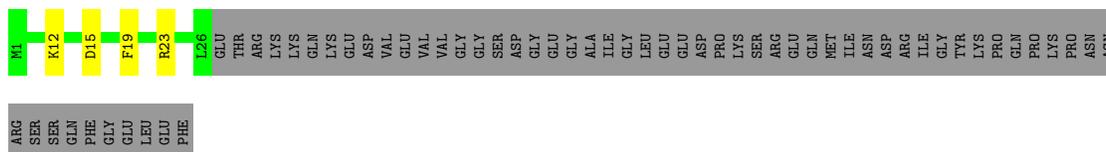


There are no outlier residues recorded for this chain.

- Molecule 4: Anaphase-promoting complex subunit CDC26



- Molecule 4: Anaphase-promoting complex subunit CDC26

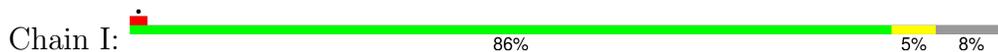


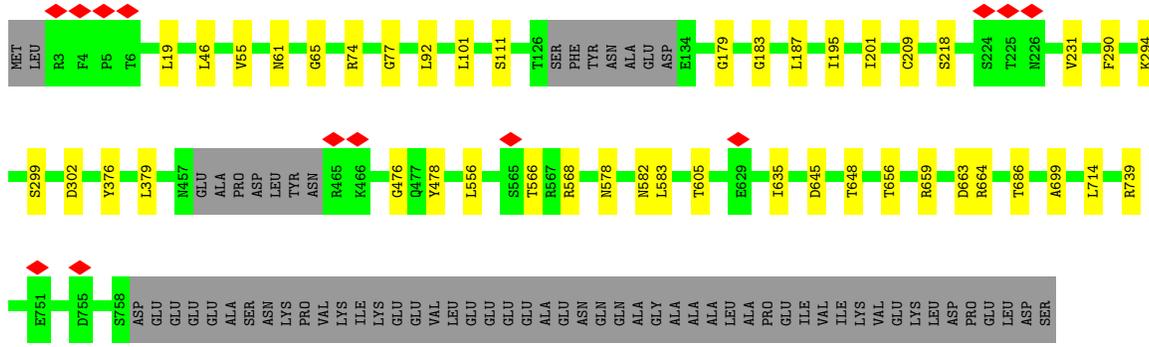
- Molecule 5: Anaphase-promoting complex subunit 16



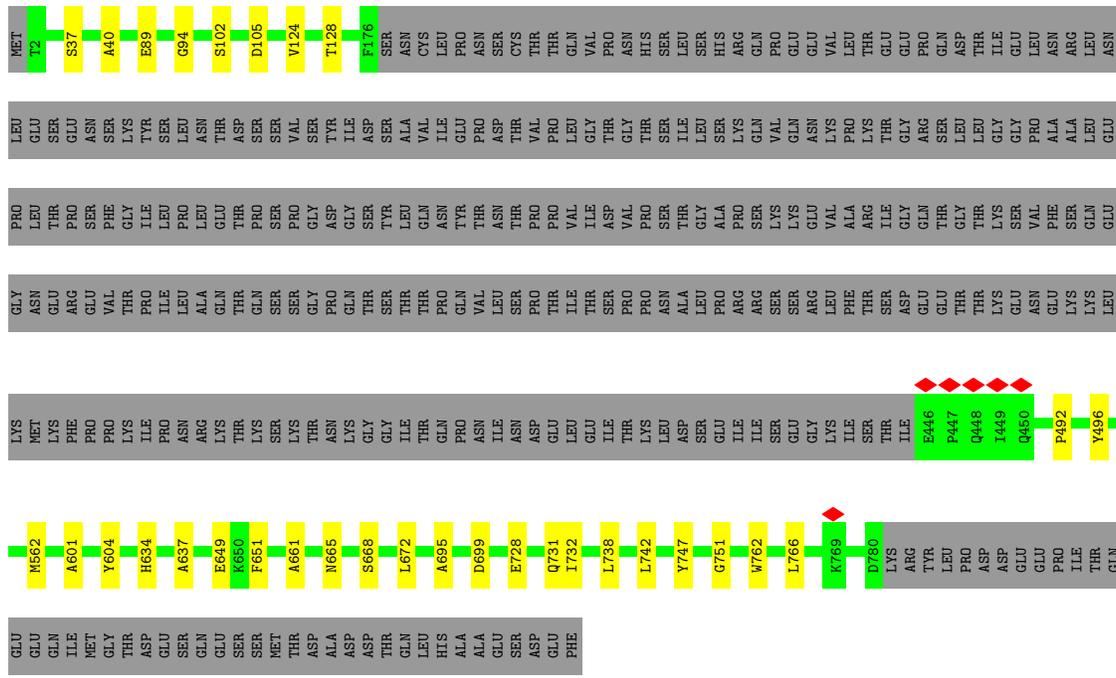
There are no outlier residues recorded for this chain.

- Molecule 6: Anaphase-promoting complex subunit 4

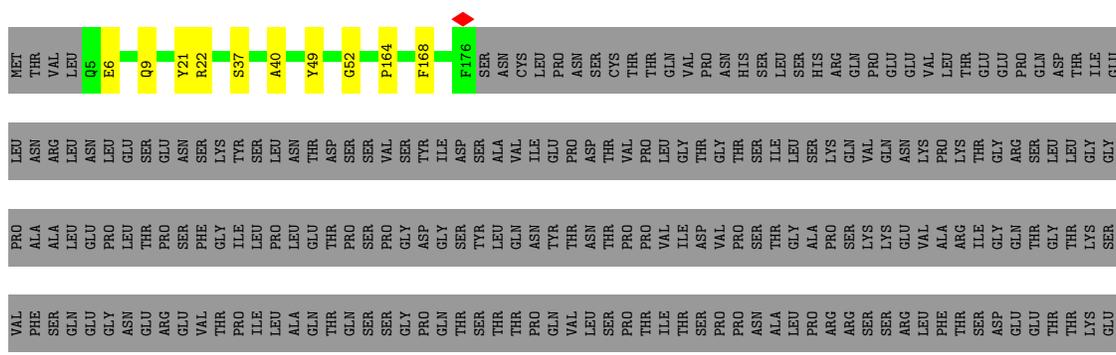




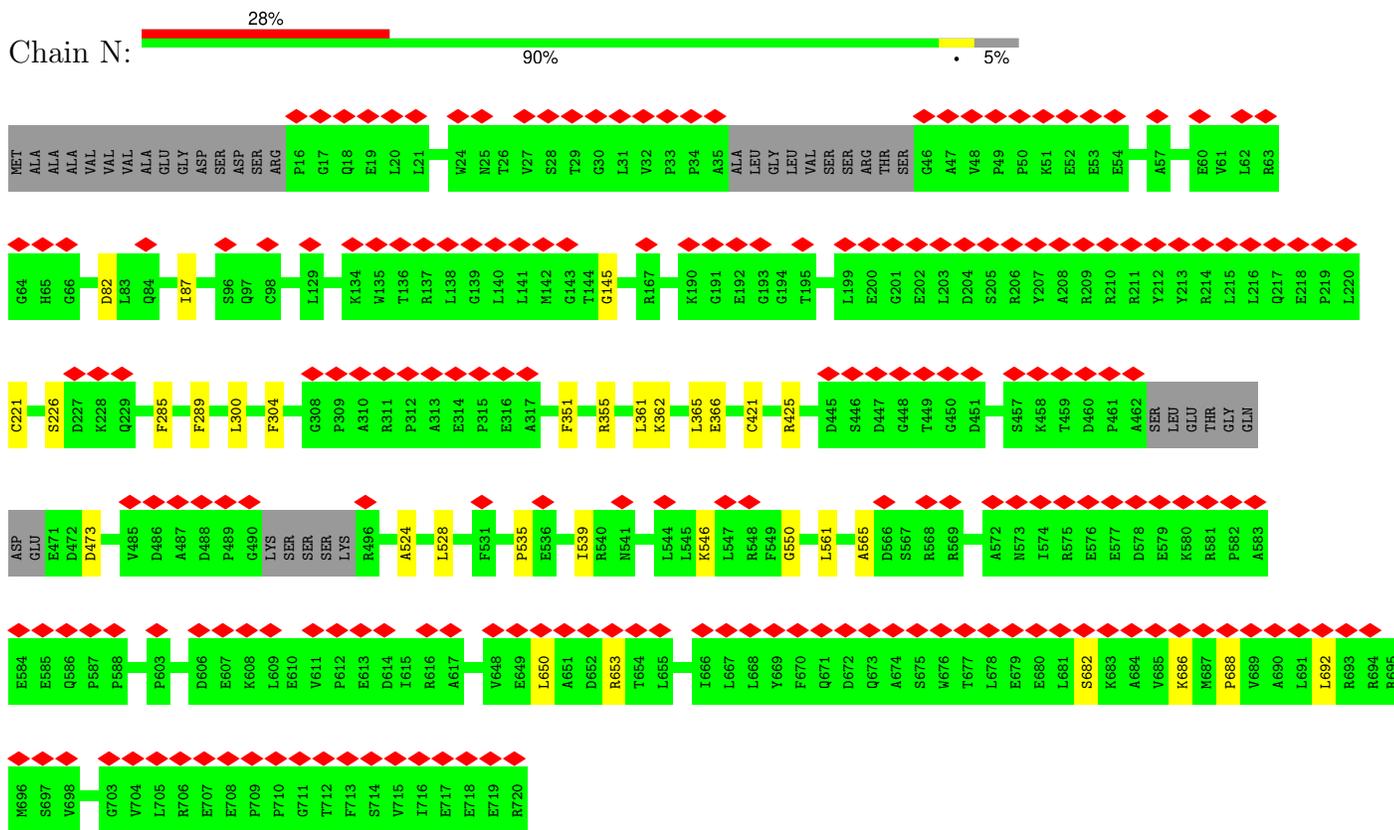
• Molecule 7: Cell division cycle protein 27 homolog



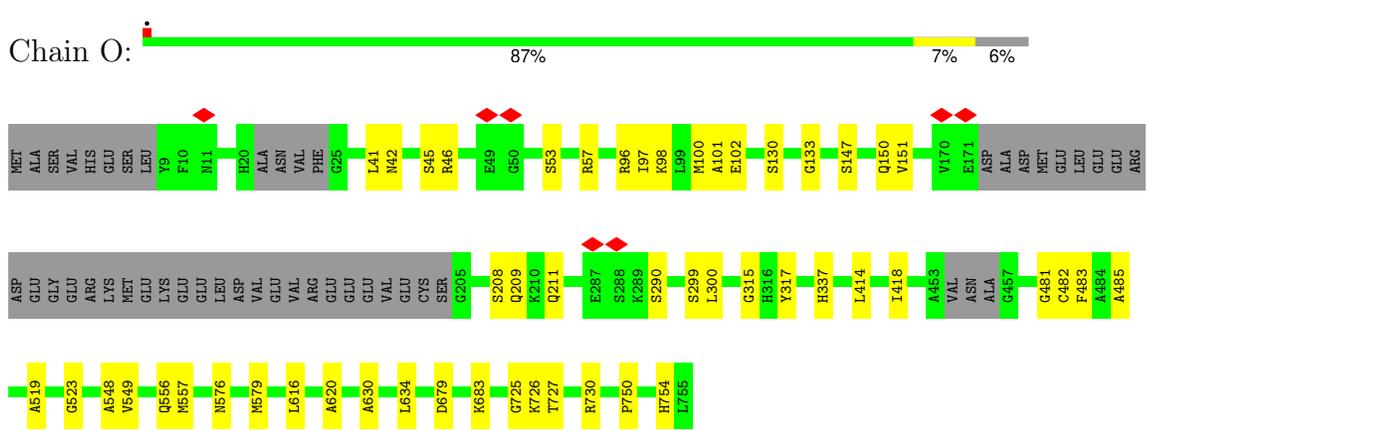
• Molecule 7: Cell division cycle protein 27 homolog



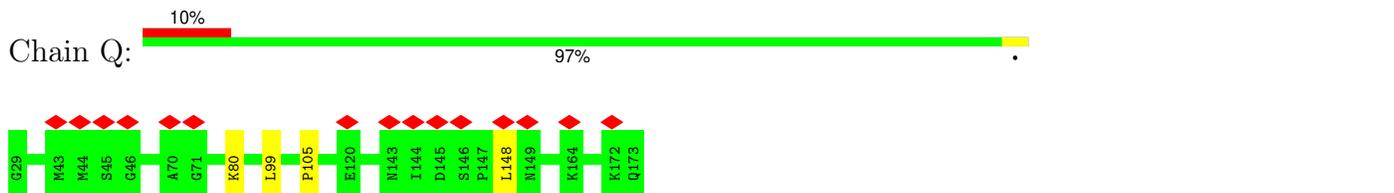
• Molecule 11: Anaphase-promoting complex subunit 2



• Molecule 12: Anaphase-promoting complex subunit 5



• Molecule 13: Ubiquitin-conjugating enzyme E2 C



• Molecule 14: Cell division cycle protein 20 homolog

4 Experimental information

| Property | Value | Source |
|--------------------------------------|---|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 154242 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | FEI TALOS ARCTICA | Depositor |
| Voltage (kV) | 200 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 44 | Depositor |
| Minimum defocus (nm) | 500 | Depositor |
| Maximum defocus (nm) | 3000 | Depositor |
| Magnification | Not provided | |
| Image detector | GATAN K3 (6k x 4k) | Depositor |
| Maximum map value | 0.082 | Depositor |
| Minimum map value | -0.020 | Depositor |
| Average map value | -0.000 | Depositor |
| Map value standard deviation | 0.004 | Depositor |
| Recommended contour level | 0.013 | Depositor |
| Map size (Å) | 422.4, 422.4, 422.4 | wwPDB |
| Map dimensions | 256, 256, 256 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.65, 1.65, 1.65 | Depositor |

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section:
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 | A | 0.26 | 0/6582 | 0.49 | 0/8210 |
| 2 | C | 0.27 | 0/336 | 0.49 | 0/417 |
| 3 | D | 0.25 | 0/224 | 0.44 | 0/277 |
| 4 | G | 0.27 | 0/107 | 0.40 | 0/132 |
| 4 | W | 0.27 | 0/103 | 0.47 | 0/127 |
| 5 | H | 0.23 | 0/231 | 0.42 | 0/287 |
| 6 | I | 0.26 | 0/2965 | 0.50 | 0/3701 |
| 7 | J | 0.26 | 0/2038 | 0.45 | 0/2544 |
| 7 | P | 0.27 | 0/1982 | 0.46 | 0/2474 |
| 8 | K | 0.26 | 0/2121 | 0.45 | 0/2646 |
| 8 | S | 0.26 | 0/2022 | 0.44 | 0/2524 |
| 9 | L | 0.26 | 0/732 | 0.52 | 0/912 |
| 10 | M | 0.26 | 0/271 | 0.50 | 0/337 |
| 11 | N | 0.23 | 0/2724 | 0.43 | 0/3398 |
| 12 | O | 0.26 | 0/2825 | 0.44 | 0/3523 |
| 13 | Q | 0.23 | 0/579 | 0.47 | 0/722 |
| 14 | R | 0.31 | 0/1841 | 0.76 | 16/2551 (0.6%) |
| 15 | U | 0.25 | 0/2157 | 0.44 | 0/2691 |
| 15 | V | 0.27 | 0/2135 | 0.45 | 0/2667 |
| 16 | Y | 0.24 | 0/2002 | 0.42 | 0/2499 |
| 16 | Z | 0.24 | 0/1950 | 0.41 | 0/2434 |
| All | All | 0.26 | 0/35927 | 0.48 | 16/45073 (0.0%) |

There are no bond length outliers.

All (16) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|---------|------|-------------|----------|
| 14 | R | 101 | PRO | N-CA-CB | 6.23 | 110.78 | 103.30 |
| 14 | R | 179 | PRO | N-CA-CB | 6.22 | 110.77 | 103.30 |
| 14 | R | 431 | PRO | N-CA-CB | 6.18 | 110.72 | 103.30 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|---------|-------|-------------|----------|
| 14 | R | 74 | PRO | N-CA-CB | 6.08 | 110.59 | 103.30 |
| 14 | R | 319 | PRO | N-CA-CB | 6.03 | 110.53 | 103.30 |
| 14 | R | 337 | PRO | N-CA-CB | 6.02 | 110.53 | 103.30 |
| 14 | R | 347 | PRO | N-CA-CB | 5.98 | 110.47 | 103.30 |
| 14 | R | 172 | PRO | N-CA-CB | 5.95 | 110.44 | 103.30 |
| 14 | R | 340 | PRO | N-CA-CB | 5.93 | 110.41 | 103.30 |
| 14 | R | 225 | PRO | N-CA-CB | 5.92 | 110.41 | 103.30 |
| 14 | R | 81 | PRO | N-CA-CB | 5.87 | 110.35 | 103.30 |
| 14 | R | 169 | PRO | N-CA-CB | 5.85 | 110.31 | 103.30 |
| 14 | R | 365 | PRO | N-CA-CB | 5.70 | 110.14 | 103.30 |
| 14 | R | 409 | PRO | N-CA-CB | 5.70 | 110.14 | 103.30 |
| 14 | R | 453 | PRO | N-CA-CB | 5.63 | 110.06 | 103.30 |
| 14 | R | 205 | SER | N-CA-CB | -5.19 | 102.72 | 110.50 |

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | A | 6592 | 3291 | 1722 | 90 | 0 |
| 2 | C | 337 | 171 | 92 | 1 | 0 |
| 3 | D | 225 | 110 | 52 | 0 | 0 |
| 4 | G | 108 | 55 | 28 | 0 | 0 |
| 4 | W | 104 | 53 | 27 | 2 | 0 |
| 5 | H | 232 | 116 | 59 | 0 | 0 |
| 6 | I | 2968 | 1490 | 776 | 22 | 0 |
| 7 | J | 2040 | 1027 | 538 | 17 | 0 |
| 7 | P | 1984 | 998 | 522 | 17 | 0 |
| 8 | K | 2124 | 1066 | 552 | 16 | 0 |
| 8 | S | 2024 | 1019 | 531 | 15 | 0 |
| 9 | L | 733 | 364 | 190 | 6 | 0 |
| 10 | M | 272 | 137 | 72 | 1 | 0 |
| 11 | N | 2728 | 1363 | 713 | 17 | 0 |
| 12 | O | 2829 | 1425 | 744 | 27 | 0 |
| 13 | Q | 580 | 290 | 154 | 2 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 14 | R | 1845 | 0 | 858 | 45 | 0 |
| 15 | U | 2160 | 1084 | 561 | 13 | 0 |
| 15 | V | 2136 | 1075 | 560 | 27 | 0 |
| 16 | Y | 2004 | 1008 | 526 | 5 | 0 |
| 16 | Z | 1952 | 983 | 511 | 13 | 0 |
| 17 | C | 3 | 0 | 0 | 0 | 0 |
| 17 | N | 1 | 0 | 0 | 0 | 0 |
| All | All | 35981 | 17125 | 9788 | 333 | 0 |

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (333) 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) |
|------------------|-----------------|--------------------------|-------------------|
| 14:R:335:VAL:O | 14:R:348:LEU:N | 2.08 | 0.86 |
| 12:O:97:ILE:O | 12:O:101:ALA:N | 2.08 | 0.85 |
| 12:O:290:SER:O | 12:O:337:HIS:N | 2.10 | 0.84 |
| 12:O:98:LYS:O | 12:O:102:GLU:N | 2.11 | 0.82 |
| 6:I:46:LEU:O | 6:I:55:VAL:N | 2.13 | 0.81 |
| 16:Y:72:SER:O | 16:Y:76:LYS:N | 2.15 | 0.80 |
| 6:I:582:ASN:O | 6:I:605:THR:N | 2.16 | 0.77 |
| 6:I:92:LEU:O | 6:I:101:LEU:N | 2.18 | 0.77 |
| 1:A:940:THR:O | 1:A:943:ASP:N | 2.17 | 0.77 |
| 9:L:10:GLY:N | 9:L:119:TRP:O | 2.20 | 0.75 |
| 1:A:191:ARG:N | 1:A:209:THR:O | 2.18 | 0.75 |
| 1:A:1775:LEU:O | 1:A:1779:VAL:N | 2.20 | 0.74 |
| 1:A:709:TYR:O | 1:A:713:SER:N | 2.20 | 0.73 |
| 14:R:269:ALA:HB1 | 14:R:286:ARG:CB | 2.18 | 0.73 |
| 14:R:369:ASN:O | 14:R:386:ASN:HA | 1.89 | 0.72 |
| 1:A:1827:GLN:N | 11:N:145:GLY:O | 2.22 | 0.72 |
| 14:R:173:ASP:N | 14:R:469:LEU:O | 2.20 | 0.72 |
| 1:A:1870:ALA:O | 1:A:1875:GLN:N | 2.23 | 0.71 |
| 7:J:661:ALA:O | 7:J:665:ASN:N | 2.24 | 0.71 |
| 12:O:96:ARG:O | 12:O:100:MET:N | 2.21 | 0.71 |
| 1:A:1284:GLU:O | 1:A:1350:TYR:N | 2.23 | 0.70 |
| 1:A:1395:LEU:O | 1:A:1398:PHE:N | 2.25 | 0.70 |
| 6:I:645:ASP:N | 6:I:648:THR:O | 2.25 | 0.70 |
| 16:Z:434:TYR:O | 16:Z:439:ALA:N | 2.24 | 0.70 |
| 1:A:850:SER:O | 1:A:855:GLU:N | 2.24 | 0.70 |
| 14:R:318:ALA:N | 14:R:323:HIS:O | 2.24 | 0.70 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|-----------------|------------------|--------------------------|-------------------|
| 12:O:208:SER:O | 12:O:211:GLN:N | 2.25 | 0.70 |
| 14:R:229:ILE:HA | 14:R:245:THR:HA | 1.74 | 0.69 |
| 12:O:414:LEU:O | 12:O:418:ILE:N | 2.23 | 0.69 |
| 1:A:477:LYS:N | 1:A:491:LEU:O | 2.26 | 0.68 |
| 12:O:147:SER:O | 12:O:151:VAL:N | 2.25 | 0.68 |
| 15:V:539:PHE:O | 15:V:543:ARG:N | 2.26 | 0.68 |
| 1:A:1111:ALA:O | 1:A:1115:ASN:N | 2.27 | 0.68 |
| 1:A:1551:ASN:O | 1:A:1554:PHE:N | 2.26 | 0.67 |
| 14:R:403:CYS:N | 14:R:417:GLY:O | 2.23 | 0.67 |
| 1:A:1320:ASN:O | 1:A:1323:GLU:N | 2.28 | 0.67 |
| 14:R:446:VAL:HA | 14:R:462:ALA:HB2 | 1.76 | 0.67 |
| 1:A:20:PHE:N | 1:A:604:MET:O | 2.27 | 0.67 |
| 15:V:28:ASP:O | 15:V:31:GLU:N | 2.28 | 0.67 |
| 7:J:492:PRO:O | 7:J:496:TYR:N | 2.28 | 0.66 |
| 8:K:91:ASP:O | 8:K:95:MET:N | 2.28 | 0.66 |
| 1:A:1566:PHE:O | 1:A:1569:GLY:N | 2.27 | 0.66 |
| 1:A:1725:ASN:O | 1:A:1729:GLU:N | 2.28 | 0.66 |
| 15:U:259:PHE:O | 15:U:262:SER:N | 2.29 | 0.66 |
| 6:I:635:ILE:O | 6:I:656:THR:N | 2.28 | 0.65 |
| 6:I:299:SER:O | 6:I:302:ASP:N | 2.28 | 0.65 |
| 7:J:559:LEU:O | 7:J:562:MET:N | 2.28 | 0.65 |
| 1:A:428:SER:N | 1:A:445:LEU:O | 2.30 | 0.65 |
| 1:A:1154:ASP:O | 1:A:1157:TRP:N | 2.29 | 0.65 |
| 1:A:1668:VAL:N | 1:A:1676:LEU:O | 2.28 | 0.65 |
| 6:I:61:ASN:O | 6:I:65:GLY:N | 2.25 | 0.65 |
| 9:L:92:SER:N | 9:L:143:ALA:O | 2.24 | 0.64 |
| 7:J:747:TYR:O | 7:J:751:GLY:N | 2.29 | 0.64 |
| 15:V:380:ASN:O | 15:V:383:ALA:N | 2.30 | 0.64 |
| 7:P:645:TYR:O | 7:P:648:GLN:N | 2.30 | 0.64 |
| 1:A:1308:GLY:O | 1:A:1310:GLY:N | 2.31 | 0.64 |
| 7:P:747:TYR:O | 7:P:751:GLY:N | 2.31 | 0.64 |
| 1:A:1290:ASP:O | 1:A:1293:SER:N | 2.31 | 0.63 |
| 16:Y:399:ALA:O | 16:Y:403:ALA:N | 2.32 | 0.63 |
| 1:A:1132:THR:O | 1:A:1135:ALA:N | 2.31 | 0.63 |
| 15:V:168:ASP:O | 15:V:172:LEU:N | 2.29 | 0.63 |
| 16:Z:43:ASP:O | 16:Z:47:ALA:N | 2.32 | 0.63 |
| 1:A:183:THR:N | 1:A:186:GLY:O | 2.32 | 0.62 |
| 1:A:793:LEU:O | 1:A:797:LEU:N | 2.32 | 0.62 |
| 16:Z:354:ARG:O | 16:Z:358:ALA:N | 2.31 | 0.62 |
| 4:W:19:PHE:O | 4:W:23:ARG:N | 2.29 | 0.62 |
| 1:A:675:LEU:O | 1:A:679:ARG:N | 2.30 | 0.62 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|-----------------|-----------------|--------------------------|-------------------|
| 14:R:294:ASP:H | 14:R:300:HIS:HA | 1.66 | 0.61 |
| 6:I:19:LEU:N | 6:I:739:ARG:O | 2.32 | 0.61 |
| 1:A:718:ASN:O | 1:A:722:HIS:N | 2.33 | 0.61 |
| 11:N:682:SER:O | 11:N:686:LYS:N | 2.33 | 0.61 |
| 15:V:77:THR:O | 15:V:81:ALA:N | 2.33 | 0.60 |
| 11:N:421:CYS:O | 11:N:425:ARG:N | 2.29 | 0.60 |
| 6:I:686:THR:N | 6:I:699:ALA:O | 2.33 | 0.60 |
| 12:O:147:SER:O | 12:O:150:GLN:N | 2.35 | 0.60 |
| 1:A:163:SER:O | 1:A:166:GLY:N | 2.30 | 0.60 |
| 1:A:717:GLN:O | 1:A:721:SER:N | 2.35 | 0.60 |
| 1:A:1090:PHE:N | 1:A:1145:LEU:O | 2.35 | 0.60 |
| 13:Q:80:LYS:O | 13:Q:99:LEU:N | 2.35 | 0.60 |
| 6:I:183:GLY:O | 6:I:201:ILE:N | 2.32 | 0.59 |
| 8:K:144:ASP:O | 8:K:146:ARG:N | 2.34 | 0.59 |
| 11:N:650:LEU:N | 11:N:653:ARG:O | 2.35 | 0.59 |
| 16:Z:134:SER:O | 16:Z:137:GLU:N | 2.35 | 0.59 |
| 14:R:205:SER:HA | 14:R:221:GLN:HA | 1.85 | 0.59 |
| 14:R:428:TRP:HA | 14:R:434:ALA:O | 2.02 | 0.59 |
| 1:A:1860:LEU:O | 1:A:1864:GLY:N | 2.35 | 0.58 |
| 14:R:318:ALA:CB | 14:R:323:HIS:H | 2.16 | 0.58 |
| 14:R:384:ILE:O | 14:R:393:LEU:N | 2.31 | 0.58 |
| 15:V:237:ILE:O | 15:V:241:LEU:N | 2.32 | 0.58 |
| 9:L:101:ASN:O | 9:L:104:ASN:N | 2.36 | 0.58 |
| 1:A:798:LYS:O | 1:A:800:GLY:N | 2.35 | 0.58 |
| 15:V:179:LEU:O | 15:V:182:LEU:N | 2.37 | 0.58 |
| 8:K:241:HIS:O | 8:K:246:ASP:N | 2.33 | 0.58 |
| 12:O:679:ASP:O | 12:O:683:LYS:N | 2.35 | 0.58 |
| 1:A:450:LEU:O | 1:A:476:ALA:N | 2.36 | 0.57 |
| 12:O:42:ASN:O | 12:O:46:ARG:N | 2.35 | 0.57 |
| 14:R:233:ALA:N | 14:R:242:ALA:O | 2.33 | 0.57 |
| 14:R:294:ASP:H | 14:R:300:HIS:CA | 2.17 | 0.57 |
| 11:N:221:CYS:N | 11:N:226:SER:O | 2.38 | 0.57 |
| 11:N:285:PHE:O | 11:N:289:PHE:N | 2.32 | 0.57 |
| 14:R:380:ARG:O | 14:R:398:ALA:N | 2.35 | 0.57 |
| 1:A:250:ASN:O | 1:A:254:SER:N | 2.37 | 0.57 |
| 1:A:1130:ASN:O | 1:A:1133:SER:N | 2.36 | 0.57 |
| 8:K:505:ALA:O | 8:K:508:LEU:N | 2.36 | 0.57 |
| 1:A:878:ALA:O | 1:A:882:LEU:N | 2.36 | 0.57 |
| 7:P:6:GLU:O | 7:P:9:GLN:N | 2.38 | 0.57 |
| 1:A:1083:GLY:O | 1:A:1086:MET:N | 2.37 | 0.56 |
| 1:A:1246:PRO:O | 1:A:1249:VAL:N | 2.37 | 0.56 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|-----------------|-----------------|--------------------------|-------------------|
| 1:A:1776:TYR:O | 1:A:1780:THR:N | 2.36 | 0.56 |
| 8:S:315:LYS:O | 8:S:318:HIS:N | 2.38 | 0.56 |
| 8:S:511:ASP:O | 8:S:513:THR:N | 2.37 | 0.56 |
| 12:O:481:GLY:O | 12:O:483:PHE:N | 2.36 | 0.56 |
| 14:R:271:VAL:HA | 14:R:284:GLY:O | 2.06 | 0.56 |
| 7:P:622:ALA:O | 7:P:625:ARG:N | 2.38 | 0.56 |
| 7:P:481:CYS:O | 7:P:484:ALA:N | 2.38 | 0.56 |
| 12:O:726:LYS:O | 12:O:730:ARG:N | 2.35 | 0.56 |
| 1:A:1577:SER:O | 1:A:1580:SER:N | 2.39 | 0.55 |
| 14:R:178:ALA:O | 14:R:465:GLU:HA | 2.06 | 0.55 |
| 8:K:177:THR:O | 8:K:181:GLU:N | 2.39 | 0.55 |
| 12:O:53:SER:O | 12:O:57:ARG:N | 2.39 | 0.55 |
| 13:Q:105:PRO:O | 13:Q:148:LEU:N | 2.40 | 0.55 |
| 15:U:330:ARG:O | 15:U:333:THR:N | 2.38 | 0.55 |
| 11:N:688:PRO:O | 11:N:692:LEU:N | 2.37 | 0.55 |
| 8:S:46:CYS:O | 8:S:50:THR:N | 2.39 | 0.55 |
| 1:A:499:LEU:O | 1:A:506:VAL:N | 2.38 | 0.55 |
| 12:O:750:PRO:O | 12:O:754:HIS:N | 2.35 | 0.55 |
| 1:A:1729:GLU:O | 1:A:1733:PHE:N | 2.35 | 0.55 |
| 9:L:90:THR:O | 9:L:145:HIS:N | 2.27 | 0.55 |
| 16:Z:107:LYS:O | 16:Z:110:LEU:N | 2.39 | 0.55 |
| 1:A:1319:LEU:O | 1:A:1321:VAL:N | 2.35 | 0.55 |
| 14:R:266:SER:CB | 14:R:301:HIS:CB | 2.85 | 0.55 |
| 1:A:1132:THR:O | 1:A:1136:SER:N | 2.36 | 0.55 |
| 1:A:1595:HIS:O | 1:A:1598:ASP:N | 2.33 | 0.55 |
| 8:K:385:LYS:N | 15:V:554:LEU:O | 2.39 | 0.54 |
| 12:O:41:LEU:O | 12:O:45:SER:N | 2.35 | 0.54 |
| 12:O:130:SER:O | 12:O:133:GLY:N | 2.41 | 0.54 |
| 11:N:524:ALA:O | 11:N:528:LEU:N | 2.41 | 0.54 |
| 6:I:659:ARG:O | 6:I:663:ASP:N | 2.41 | 0.54 |
| 11:N:82:ASP:O | 11:N:87:ILE:N | 2.34 | 0.54 |
| 6:I:231:VAL:O | 6:I:556:LEU:N | 2.41 | 0.53 |
| 14:R:358:VAL:HA | 14:R:374:GLY:O | 2.08 | 0.53 |
| 6:I:74:ARG:O | 6:I:77:GLY:N | 2.38 | 0.53 |
| 1:A:27:HIS:O | 1:A:31:HIS:N | 2.41 | 0.53 |
| 6:I:578:ASN:N | 6:I:583:LEU:O | 2.32 | 0.53 |
| 14:R:131:LEU:O | 14:R:133:LEU:N | 2.41 | 0.53 |
| 14:R:402:VAL:HA | 14:R:417:GLY:O | 2.08 | 0.53 |
| 1:A:1375:TYR:O | 1:A:1378:THR:N | 2.35 | 0.53 |
| 7:P:575:ASN:O | 7:P:578:SER:N | 2.37 | 0.53 |
| 15:V:66:PRO:O | 15:V:69:GLU:N | 2.41 | 0.53 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|-----------------|--------------------------|-------------------|
| 16:Z:193:LYS:O | 16:Z:197:ARG:N | 2.39 | 0.53 |
| 9:L:98:VAL:N | 9:L:106:GLN:O | 2.41 | 0.53 |
| 14:R:293:HIS:HA | 14:R:300:HIS:O | 2.09 | 0.53 |
| 15:V:209:LEU:O | 15:V:212:LEU:N | 2.39 | 0.52 |
| 8:K:279:ASN:O | 8:K:281:ALA:N | 2.43 | 0.52 |
| 1:A:1889:LEU:O | 1:A:1893:SER:N | 2.42 | 0.52 |
| 11:N:300:LEU:O | 11:N:304:PHE:N | 2.36 | 0.52 |
| 1:A:1438:SER:O | 1:A:1442:SER:N | 2.42 | 0.52 |
| 12:O:576:ASN:O | 12:O:579:MET:N | 2.43 | 0.52 |
| 14:R:318:ALA:HB3 | 14:R:323:HIS:H | 1.74 | 0.52 |
| 15:U:27:SER:O | 15:U:29:LEU:N | 2.41 | 0.52 |
| 1:A:133:ILE:N | 1:A:146:GLU:O | 2.34 | 0.51 |
| 6:I:111:SER:N | 6:I:179:GLY:O | 2.36 | 0.51 |
| 6:I:664:ARG:O | 6:I:714:LEU:N | 2.37 | 0.51 |
| 12:O:519:ALA:O | 12:O:523:GLY:N | 2.43 | 0.51 |
| 15:U:323:LEU:O | 15:U:326:ILE:N | 2.44 | 0.51 |
| 1:A:1750:PHE:O | 1:A:1754:PHE:N | 2.40 | 0.51 |
| 1:A:260:ASP:N | 1:A:265:VAL:O | 2.40 | 0.51 |
| 1:A:1826:HIS:O | 1:A:1830:LEU:N | 2.39 | 0.51 |
| 7:P:37:SER:O | 7:P:40:ALA:N | 2.43 | 0.51 |
| 14:R:96:SER:O | 14:R:99:ASN:N | 2.43 | 0.51 |
| 14:R:413:GLU:HA | 14:R:430:TYR:H | 1.75 | 0.51 |
| 16:Y:203:LEU:O | 16:Y:206:ILE:N | 2.44 | 0.51 |
| 14:R:199:ALA:HA | 14:R:207:TYR:O | 2.11 | 0.51 |
| 14:R:210:SER:O | 14:R:214:GLY:N | 2.44 | 0.51 |
| 7:J:37:SER:O | 7:J:40:ALA:N | 2.44 | 0.50 |
| 15:U:86:ALA:O | 15:U:87:TYR:C | 2.49 | 0.50 |
| 11:N:535:PRO:O | 11:N:539:ILE:N | 2.42 | 0.50 |
| 1:A:1256:GLY:O | 1:A:1259:LEU:N | 2.45 | 0.50 |
| 7:J:762:TRP:O | 7:J:766:LEU:N | 2.45 | 0.50 |
| 1:A:1774:VAL:O | 1:A:1778:CYS:N | 2.31 | 0.50 |
| 6:I:290:PHE:O | 6:I:294:LYS:N | 2.45 | 0.50 |
| 14:R:384:ILE:O | 14:R:392:CYS:HA | 2.12 | 0.50 |
| 7:J:601:ALA:O | 7:J:604:TYR:N | 2.45 | 0.50 |
| 14:R:376:GLY:HA2 | 14:R:401:GLN:HA | 1.92 | 0.50 |
| 1:A:851:CYS:O | 1:A:854:GLY:N | 2.44 | 0.49 |
| 12:O:725:GLY:O | 12:O:727:THR:N | 2.45 | 0.49 |
| 15:V:361:ASN:O | 15:V:363:ARG:N | 2.46 | 0.49 |
| 1:A:747:LEU:O | 1:A:822:THR:N | 2.44 | 0.49 |
| 7:J:124:VAL:O | 7:J:128:THR:N | 2.45 | 0.49 |
| 15:V:48:LEU:O | 15:V:51:SER:N | 2.46 | 0.49 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 8:S:85:GLU:O | 8:S:89:ALA:N | 2.34 | 0.49 |
| 1:A:1392:THR:O | 1:A:1395:LEU:N | 2.45 | 0.49 |
| 1:A:1622:VAL:N | 1:A:1697:LEU:O | 2.42 | 0.49 |
| 14:R:362:ALA:HB3 | 14:R:372:ALA:HB3 | 1.94 | 0.49 |
| 11:N:361:LEU:O | 11:N:365:LEU:N | 2.42 | 0.49 |
| 1:A:1111:ALA:O | 1:A:1115:ASN:CA | 2.61 | 0.48 |
| 7:J:668:SER:O | 7:J:672:LEU:N | 2.32 | 0.48 |
| 8:K:16:GLN:O | 8:K:18:GLN:N | 2.45 | 0.48 |
| 14:R:231:SER:O | 14:R:244:GLY:N | 2.40 | 0.48 |
| 16:Y:535:ALA:O | 16:Y:539:ASP:N | 2.43 | 0.48 |
| 14:R:446:VAL:HA | 14:R:462:ALA:CB | 2.43 | 0.48 |
| 8:S:394:ALA:O | 8:S:397:ILE:N | 2.45 | 0.48 |
| 7:J:102:SER:O | 7:J:105:ASP:N | 2.47 | 0.48 |
| 2:C:23:CYS:O | 2:C:27:ARG:N | 2.42 | 0.48 |
| 1:A:1201:HIS:O | 1:A:1204:THR:N | 2.46 | 0.48 |
| 15:U:361:ASN:O | 15:U:363:ARG:N | 2.47 | 0.48 |
| 12:O:299:SER:O | 12:O:300:LEU:C | 2.52 | 0.48 |
| 7:P:556:SER:O | 7:P:557:LYS:C | 2.51 | 0.48 |
| 14:R:428:TRP:CB | 14:R:433:MET:HA | 2.44 | 0.48 |
| 1:A:824:ASP:O | 1:A:828:THR:N | 2.46 | 0.47 |
| 15:U:111:SER:O | 15:U:114:ALA:N | 2.47 | 0.47 |
| 15:U:148:ASN:O | 15:U:151:LEU:N | 2.47 | 0.47 |
| 15:V:227:THR:O | 15:V:230:LYS:N | 2.47 | 0.47 |
| 1:A:1622:VAL:O | 1:A:1699:VAL:N | 2.42 | 0.47 |
| 6:I:187:LEU:O | 6:I:195:ILE:N | 2.47 | 0.47 |
| 7:J:649:GLU:O | 7:J:651:PHE:N | 2.47 | 0.47 |
| 8:K:412:ALA:O | 8:K:415:ASN:N | 2.47 | 0.47 |
| 11:N:561:LEU:O | 11:N:565:ALA:N | 2.40 | 0.47 |
| 8:S:512:ASP:O | 8:S:516:VAL:N | 2.39 | 0.47 |
| 8:S:2:ASN:O | 8:S:5:ARG:N | 2.48 | 0.47 |
| 16:Z:163:PRO:O | 16:Z:167:ARG:N | 2.47 | 0.47 |
| 7:J:738:LEU:O | 7:J:742:LEU:N | 2.36 | 0.47 |
| 8:K:29:VAL:O | 8:K:33:SER:N | 2.44 | 0.47 |
| 14:R:233:ALA:HB3 | 14:R:242:ALA:HB3 | 1.96 | 0.47 |
| 15:V:375:TYR:O | 15:V:378:MET:O | 2.32 | 0.47 |
| 1:A:482:VAL:O | 1:A:486:ASP:N | 2.45 | 0.47 |
| 15:U:448:GLN:O | 15:U:452:ALA:N | 2.36 | 0.47 |
| 1:A:1551:ASN:O | 1:A:1552:TYR:C | 2.52 | 0.46 |
| 14:R:429:LYS:O | 14:R:432:THR:N | 2.48 | 0.46 |
| 1:A:1751:ALA:O | 1:A:1756:LYS:N | 2.35 | 0.46 |
| 14:R:248:ALA:HB2 | 14:R:269:ALA:O | 2.15 | 0.46 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|----------------|-----------------|--------------------------|-------------------|
| 8:S:333:TYR:O | 8:S:336:ALA:N | 2.49 | 0.46 |
| 16:Z:445:THR:O | 16:Z:449:THR:N | 2.49 | 0.46 |
| 11:N:362:LYS:O | 11:N:366:GLU:N | 2.41 | 0.46 |
| 7:P:580:GLN:O | 7:P:582:GLU:N | 2.48 | 0.46 |
| 8:S:177:THR:O | 8:S:181:GLU:N | 2.41 | 0.46 |
| 8:K:493:GLY:O | 8:K:495:PHE:N | 2.47 | 0.46 |
| 12:O:616:LEU:O | 12:O:620:ALA:N | 2.36 | 0.46 |
| 7:P:608:GLY:O | 7:P:609:HIS:C | 2.54 | 0.46 |
| 15:V:363:ARG:O | 15:V:365:LEU:N | 2.49 | 0.46 |
| 15:U:398:ASP:O | 15:U:401:ALA:N | 2.49 | 0.45 |
| 15:V:398:ASP:O | 15:V:401:ALA:N | 2.49 | 0.45 |
| 6:I:376:TYR:O | 6:I:379:LEU:N | 2.49 | 0.45 |
| 15:V:455:CYS:O | 15:V:456:TYR:C | 2.54 | 0.45 |
| 8:K:264:HIS:O | 8:K:267:CYS:N | 2.50 | 0.45 |
| 8:S:84:LYS:O | 8:S:86:HIS:N | 2.47 | 0.45 |
| 4:W:12:LYS:O | 4:W:15:ASP:N | 2.47 | 0.45 |
| 16:Z:50:HIS:O | 16:Z:54:ARG:N | 2.44 | 0.45 |
| 1:A:1392:THR:O | 1:A:1394:TYR:N | 2.50 | 0.45 |
| 7:P:631:ASN:O | 7:P:633:ARG:N | 2.50 | 0.45 |
| 10:M:9:GLY:O | 10:M:12:LEU:N | 2.49 | 0.45 |
| 8:S:332:THR:O | 8:S:334:GLY:N | 2.47 | 0.44 |
| 15:U:83:ASP:O | 15:U:84:MET:C | 2.56 | 0.44 |
| 16:Z:72:SER:O | 16:Z:75:GLN:N | 2.50 | 0.44 |
| 14:R:335:VAL:O | 14:R:347:PRO:HA | 2.17 | 0.44 |
| 12:O:482:CYS:O | 12:O:485:ALA:N | 2.50 | 0.44 |
| 7:P:668:SER:O | 7:P:671:LEU:N | 2.50 | 0.44 |
| 15:V:373:HIS:O | 15:V:376:MET:O | 2.35 | 0.44 |
| 1:A:183:THR:O | 1:A:186:GLY:N | 2.46 | 0.44 |
| 1:A:1481:ASN:O | 1:A:1484:ALA:N | 2.51 | 0.44 |
| 6:I:566:THR:O | 6:I:568:ARG:N | 2.50 | 0.44 |
| 7:J:634:HIS:O | 7:J:637:ALA:N | 2.50 | 0.44 |
| 7:P:622:ALA:O | 7:P:623:CYS:C | 2.55 | 0.44 |
| 15:V:520:TYR:O | 15:V:524:LYS:N | 2.51 | 0.44 |
| 7:J:89:GLU:O | 7:J:94:GLY:N | 2.49 | 0.44 |
| 15:V:215:ASP:O | 15:V:218:MET:N | 2.51 | 0.44 |
| 8:S:360:ALA:O | 8:S:364:MET:N | 2.38 | 0.43 |
| 1:A:1544:MET:C | 11:N:473:ASP:CA | 2.87 | 0.43 |
| 16:Z:349:SER:O | 16:Z:353:LYS:N | 2.52 | 0.43 |
| 1:A:1771:PHE:O | 1:A:1775:LEU:N | 2.32 | 0.43 |
| 6:I:476:GLY:O | 6:I:478:TYR:N | 2.51 | 0.43 |
| 11:N:351:PHE:O | 11:N:355:ARG:N | 2.51 | 0.43 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|-----------------|-----------------|--------------------------|-------------------|
| 7:P:49:TYR:O | 7:P:52:GLY:N | 2.34 | 0.43 |
| 1:A:1358:ILE:O | 1:A:1360:VAL:N | 2.51 | 0.43 |
| 1:A:1401:PRO:O | 1:A:1404:LEU:N | 2.52 | 0.43 |
| 14:R:180:GLU:O | 14:R:203:ASP:N | 2.45 | 0.43 |
| 1:A:591:VAL:O | 1:A:592:HIS:C | 2.57 | 0.43 |
| 12:O:630:ALA:O | 12:O:634:LEU:N | 2.45 | 0.43 |
| 15:U:148:ASN:O | 15:U:149:GLU:C | 2.56 | 0.43 |
| 8:K:263:PHE:O | 8:K:265:ALA:N | 2.51 | 0.43 |
| 6:I:209:CYS:N | 6:I:218:SER:O | 2.49 | 0.43 |
| 14:R:286:ARG:HA | 14:R:311:GLU:CB | 2.49 | 0.43 |
| 16:Z:163:PRO:O | 16:Z:166:GLN:N | 2.52 | 0.43 |
| 15:V:425:ALA:O | 15:V:428:LEU:N | 2.49 | 0.42 |
| 16:Y:146:TYR:O | 16:Y:150:LYS:N | 2.52 | 0.42 |
| 7:P:21:TYR:O | 7:P:22:ARG:C | 2.57 | 0.42 |
| 8:S:245:CYS:O | 8:S:247:PHE:N | 2.51 | 0.42 |
| 1:A:1684:THR:O | 1:A:1688:LYS:N | 2.36 | 0.42 |
| 14:R:430:TYR:HA | 14:R:431:PRO:HA | 1.63 | 0.42 |
| 1:A:859:PRO:CA | 1:A:895:TYR:O | 2.67 | 0.42 |
| 15:U:204:GLY:O | 15:U:207:LEU:N | 2.53 | 0.42 |
| 1:A:1019:MET:O | 1:A:1021:HIS:N | 2.51 | 0.42 |
| 7:J:728:GLU:O | 7:J:732:ILE:N | 2.51 | 0.42 |
| 12:O:556:GLN:O | 12:O:557:MET:C | 2.58 | 0.42 |
| 7:P:164:PRO:O | 7:P:168:PHE:N | 2.40 | 0.42 |
| 1:A:1033:ARG:O | 1:A:1036:ASP:N | 2.52 | 0.42 |
| 1:A:1020:ASN:O | 1:A:1022:GLU:N | 2.53 | 0.42 |
| 7:J:695:ALA:O | 7:J:699:ASP:N | 2.50 | 0.42 |
| 9:L:93:LYS:O | 9:L:142:LEU:N | 2.45 | 0.42 |
| 14:R:106:THR:O | 14:R:110:LYS:N | 2.43 | 0.42 |
| 1:A:1246:PRO:O | 1:A:1247:HIS:C | 2.57 | 0.42 |
| 15:V:216:LYS:O | 15:V:219:LEU:N | 2.51 | 0.42 |
| 16:Z:382:ALA:O | 16:Z:386:MET:N | 2.52 | 0.42 |
| 1:A:952:ALA:O | 1:A:953:LEU:C | 2.58 | 0.41 |
| 1:A:1132:THR:O | 1:A:1133:SER:C | 2.59 | 0.41 |
| 1:A:1256:GLY:O | 1:A:1257:ILE:C | 2.58 | 0.41 |
| 8:K:227:LEU:O | 8:K:230:ASN:N | 2.53 | 0.41 |
| 1:A:1363:THR:O | 1:A:1364:CYS:C | 2.58 | 0.41 |
| 15:V:78:GLU:O | 15:V:81:ALA:N | 2.53 | 0.41 |
| 15:V:409:TYR:O | 15:V:412:LEU:O | 2.38 | 0.41 |
| 15:V:397:ARG:O | 15:V:399:TYR:N | 2.53 | 0.41 |
| 8:K:416:GLY:O | 8:K:418:TRP:N | 2.53 | 0.41 |
| 1:A:940:THR:O | 1:A:941:LEU:C | 2.59 | 0.41 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|-----------------|------------------|--------------------------|-------------------|
| 8:S:12:GLN:O | 8:S:16:GLN:N | 2.47 | 0.41 |
| 1:A:12:ILE:O | 1:A:510:PHE:N | 2.49 | 0.41 |
| 1:A:1595:HIS:O | 1:A:1596:SER:C | 2.59 | 0.41 |
| 1:A:1797:ILE:O | 1:A:1801:GLY:N | 2.49 | 0.41 |
| 1:A:1363:THR:O | 1:A:1365:PRO:O | 2.39 | 0.41 |
| 14:R:357:ALA:O | 14:R:375:GLY:HA2 | 2.21 | 0.41 |
| 14:R:461:ALA:HA | 14:R:467:LEU:CB | 2.51 | 0.41 |
| 8:S:369:LEU:O | 8:S:370:PRO:C | 2.59 | 0.41 |
| 15:V:48:LEU:O | 15:V:49:LEU:C | 2.58 | 0.41 |
| 8:K:85:GLU:O | 8:K:86:HIS:C | 2.59 | 0.41 |
| 12:O:208:SER:O | 12:O:209:GLN:C | 2.59 | 0.41 |
| 12:O:548:ALA:O | 12:O:549:VAL:C | 2.60 | 0.41 |
| 12:O:315:GLY:O | 12:O:317:TYR:N | 2.50 | 0.40 |
| 15:V:259:PHE:O | 15:V:262:SER:N | 2.46 | 0.40 |
| 7:J:728:GLU:O | 7:J:731:GLN:N | 2.55 | 0.40 |
| 14:R:314:GLY:O | 14:R:326:SER:HA | 2.20 | 0.40 |
| 1:A:1542:LEU:O | 1:A:1545:LYS:N | 2.54 | 0.40 |
| 1:A:1605:ALA:O | 1:A:1606:LEU:C | 2.59 | 0.40 |
| 7:P:472:GLY:O | 7:P:473:TYR:C | 2.60 | 0.40 |
| 11:N:546:LYS:O | 11:N:550:GLY:N | 2.50 | 0.40 |

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-----------------|------------|----------|----------|-------------|-----|
| 1 | A | 1628/1944 (84%) | 1482 (91%) | 144 (9%) | 2 (0%) | 48 | 80 |
| 2 | C | 82/84 (98%) | 80 (98%) | 2 (2%) | 0 | 100 | 100 |
| 3 | D | 54/56 (96%) | 51 (94%) | 3 (6%) | 0 | 100 | 100 |
| 4 | G | 25/85 (29%) | 24 (96%) | 1 (4%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|------------------|------------|----------|----------|-------------|-----|
| 4 | W | 24/85 (28%) | 23 (96%) | 1 (4%) | 0 | 100 | 100 |
| 5 | H | 56/58 (97%) | 55 (98%) | 1 (2%) | 0 | 100 | 100 |
| 6 | I | 736/808 (91%) | 694 (94%) | 42 (6%) | 0 | 100 | 100 |
| 7 | J | 506/824 (61%) | 476 (94%) | 30 (6%) | 0 | 100 | 100 |
| 7 | P | 492/824 (60%) | 439 (89%) | 53 (11%) | 0 | 100 | 100 |
| 8 | K | 525/620 (85%) | 489 (93%) | 35 (7%) | 1 (0%) | 44 | 75 |
| 8 | S | 502/620 (81%) | 470 (94%) | 32 (6%) | 0 | 100 | 100 |
| 9 | L | 181/185 (98%) | 168 (93%) | 13 (7%) | 0 | 100 | 100 |
| 10 | M | 66/74 (89%) | 57 (86%) | 9 (14%) | 0 | 100 | 100 |
| 11 | N | 674/720 (94%) | 654 (97%) | 20 (3%) | 0 | 100 | 100 |
| 12 | O | 699/755 (93%) | 654 (94%) | 45 (6%) | 0 | 100 | 100 |
| 13 | Q | 143/145 (99%) | 139 (97%) | 4 (3%) | 0 | 100 | 100 |
| 14 | R | 367/499 (74%) | 350 (95%) | 16 (4%) | 1 (0%) | 37 | 70 |
| 15 | U | 534/597 (89%) | 495 (93%) | 39 (7%) | 0 | 100 | 100 |
| 15 | V | 532/597 (89%) | 494 (93%) | 38 (7%) | 0 | 100 | 100 |
| 16 | Y | 497/565 (88%) | 477 (96%) | 20 (4%) | 0 | 100 | 100 |
| 16 | Z | 484/565 (86%) | 470 (97%) | 14 (3%) | 0 | 100 | 100 |
| All | All | 8807/10710 (82%) | 8241 (94%) | 562 (6%) | 4 (0%) | 100 | 100 |

All (4) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 1 | A | 1307 | LEU |
| 8 | K | 264 | HIS |
| 14 | R | 101 | PRO |
| 1 | A | 1359 | ASN |

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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](#)

Of 4 ligands modelled in this entry, 4 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](#)

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 14 | R | 1 |

All chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1 | R | 388:CYS | C | 389:SER | N | 3.46 |

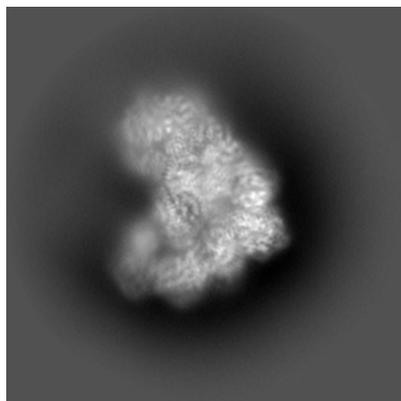
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48984. These allow visual inspection of the internal detail of the map and identification of artifacts.

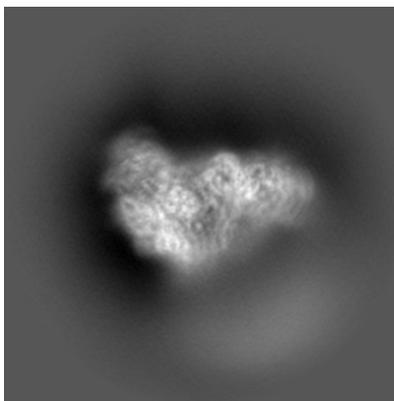
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

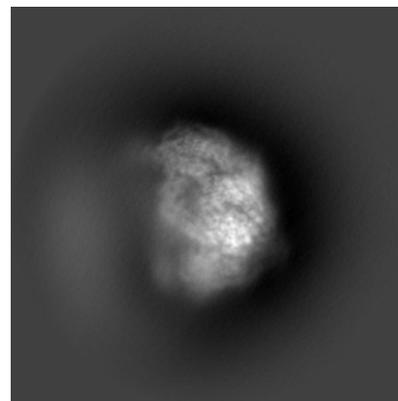
6.1.1 Primary map



X

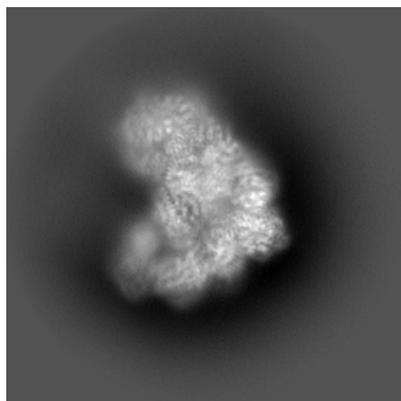


Y

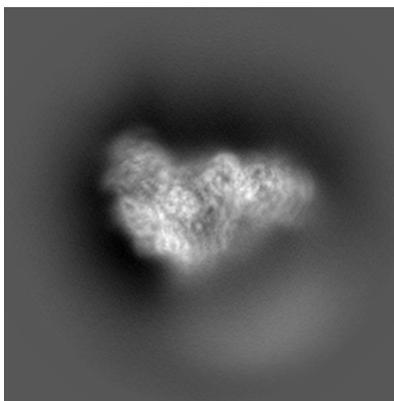


Z

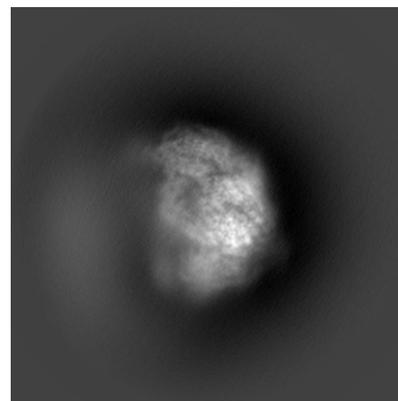
6.1.2 Raw map



X



Y

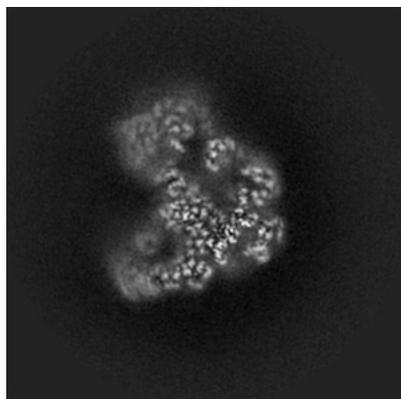


Z

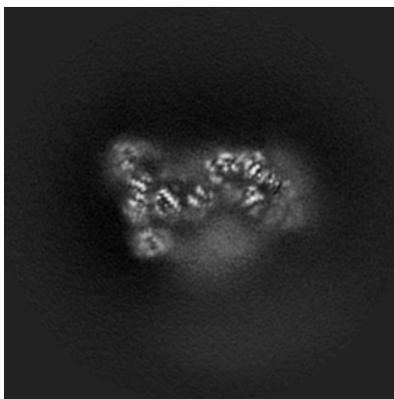
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

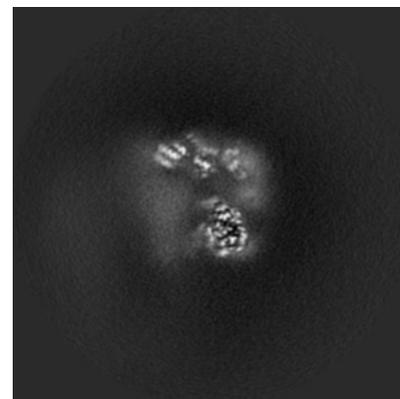
6.2.1 Primary map



X Index: 128

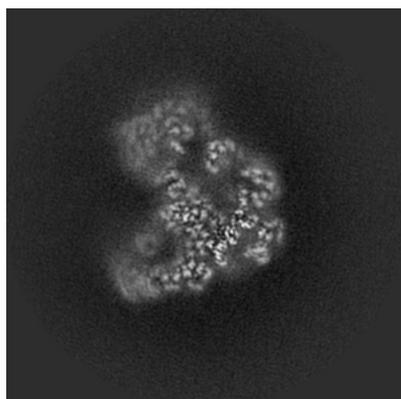


Y Index: 128

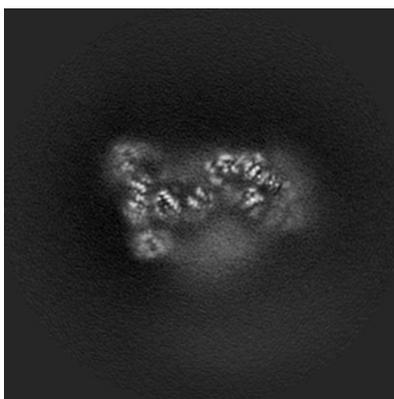


Z Index: 128

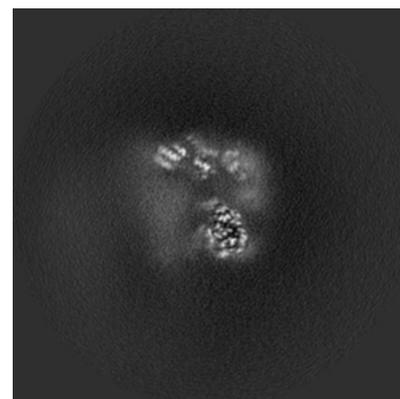
6.2.2 Raw map



X Index: 128



Y Index: 128

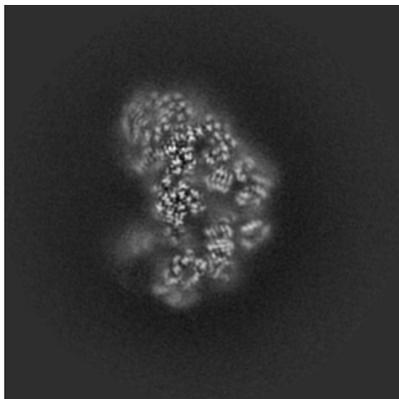


Z Index: 128

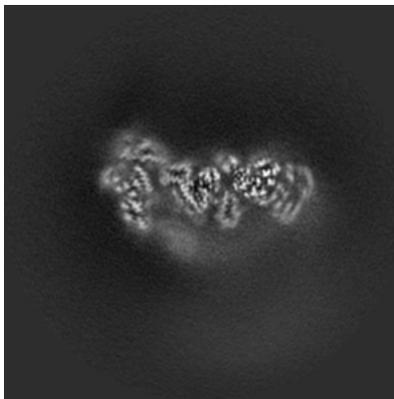
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

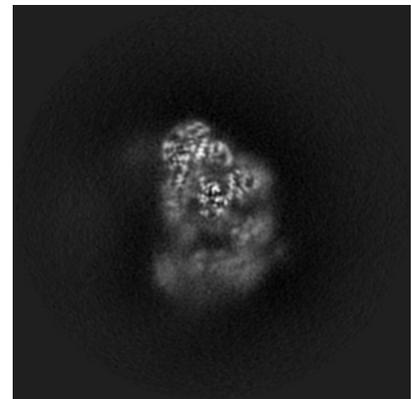
6.3.1 Primary map



X Index: 140

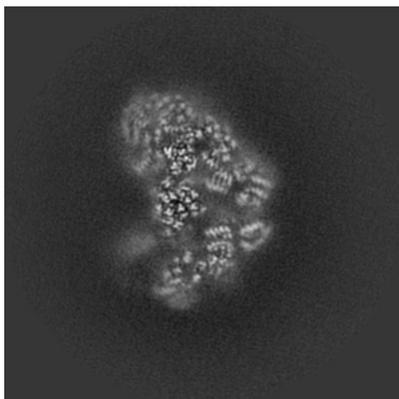


Y Index: 110

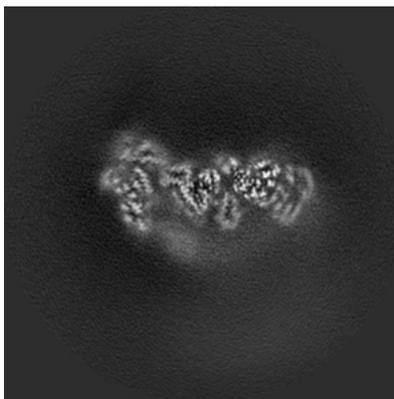


Z Index: 101

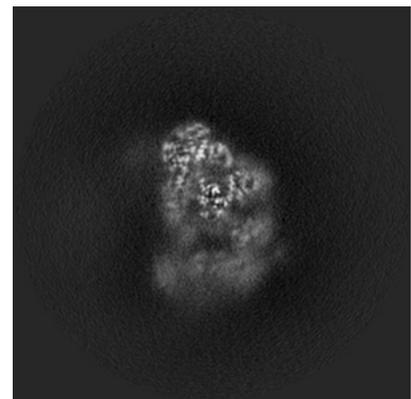
6.3.2 Raw map



X Index: 139



Y Index: 110

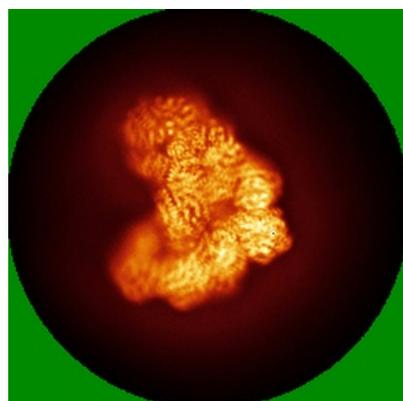


Z Index: 101

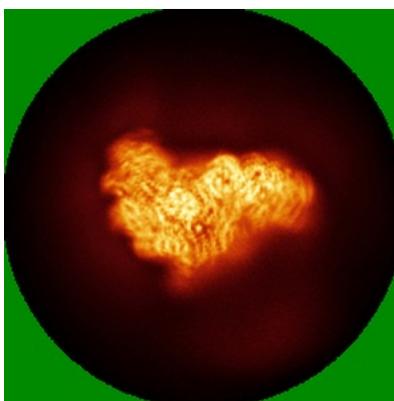
The images above show the largest variance slices of the map in three orthogonal directions.

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

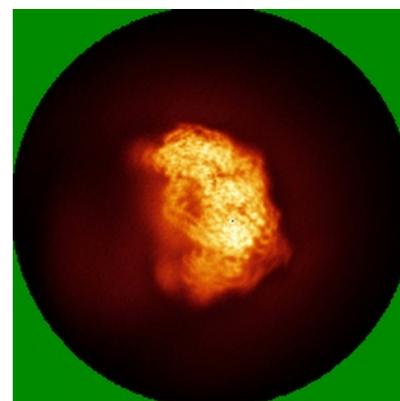
6.4.1 Primary map



X

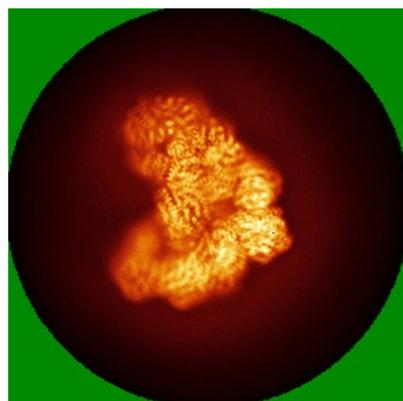


Y

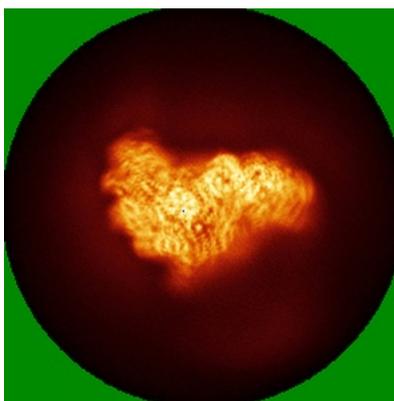


Z

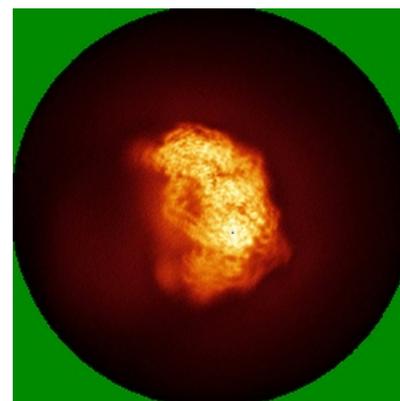
6.4.2 Raw map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.013. 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



X



Y



Z

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.

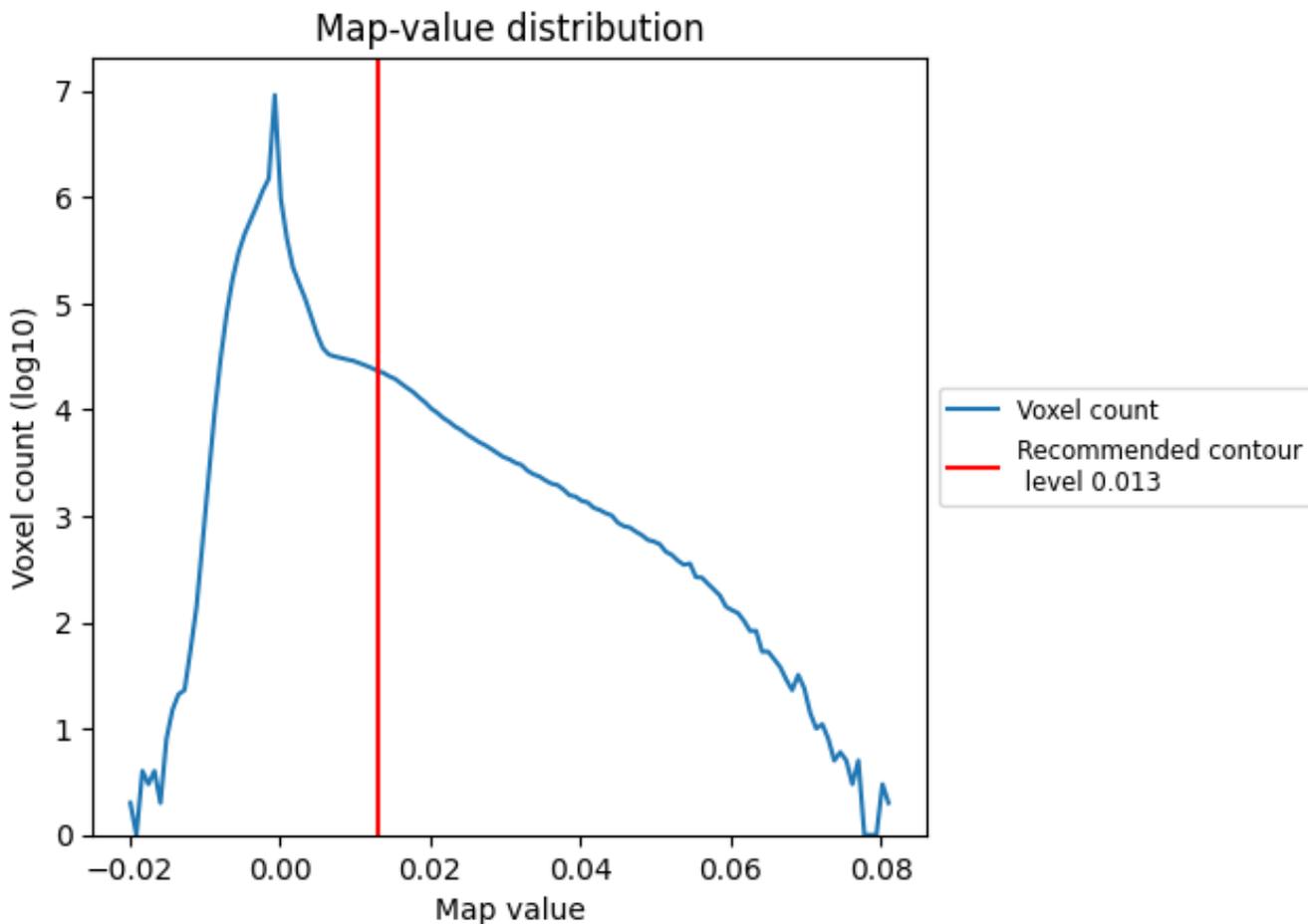
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

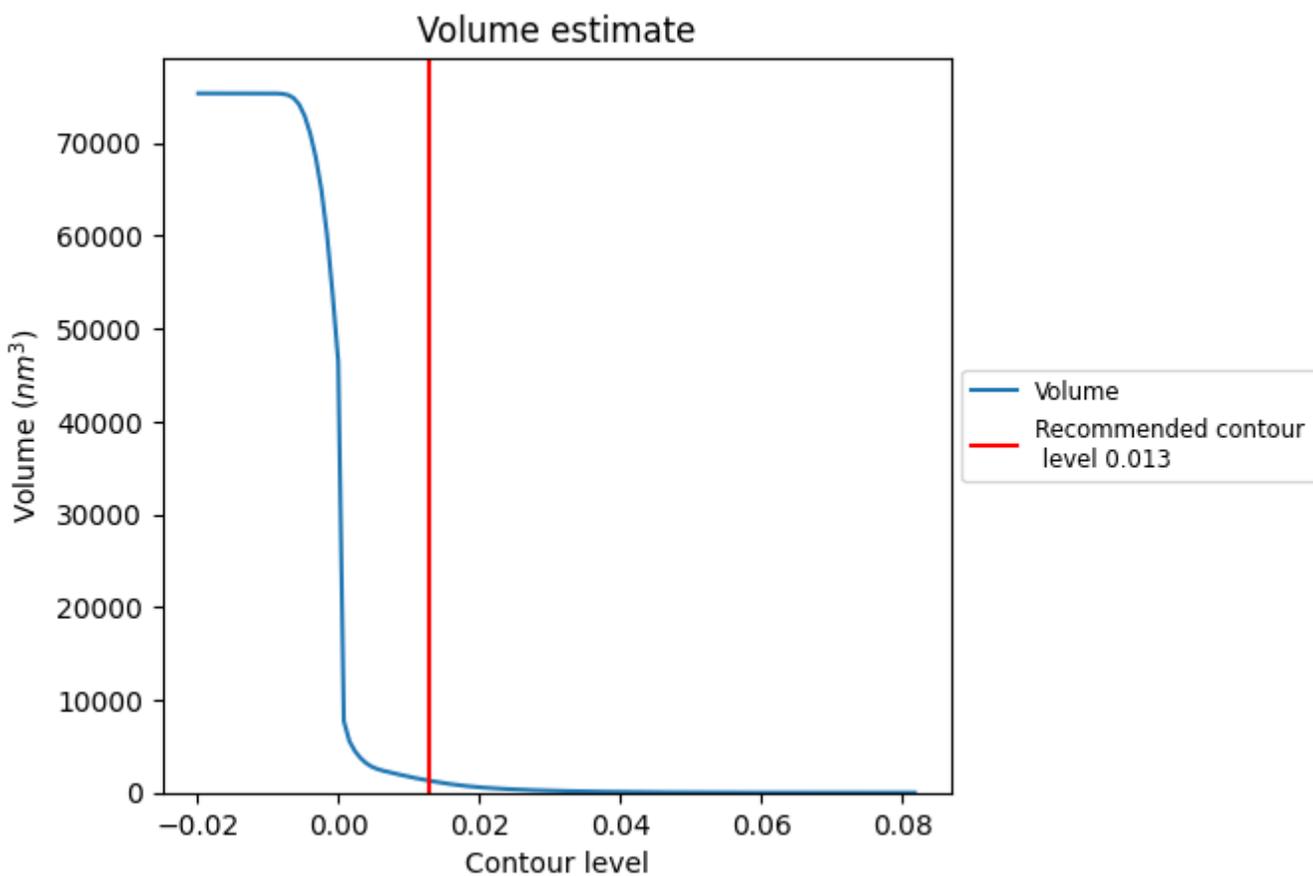
This section contains the results of statistical analysis of the map.

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.

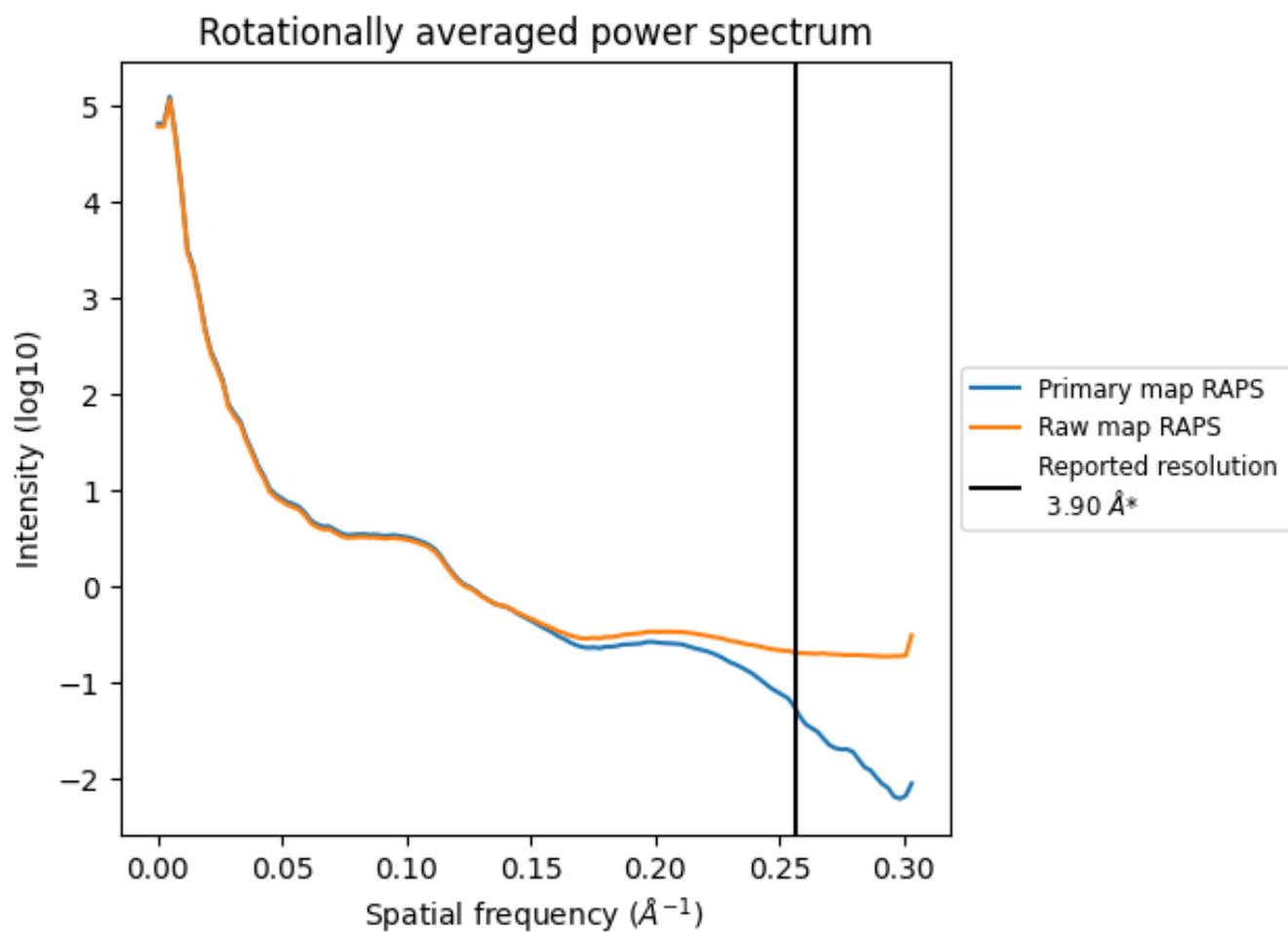
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1277 nm³; this corresponds to an approximate mass of 1153 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

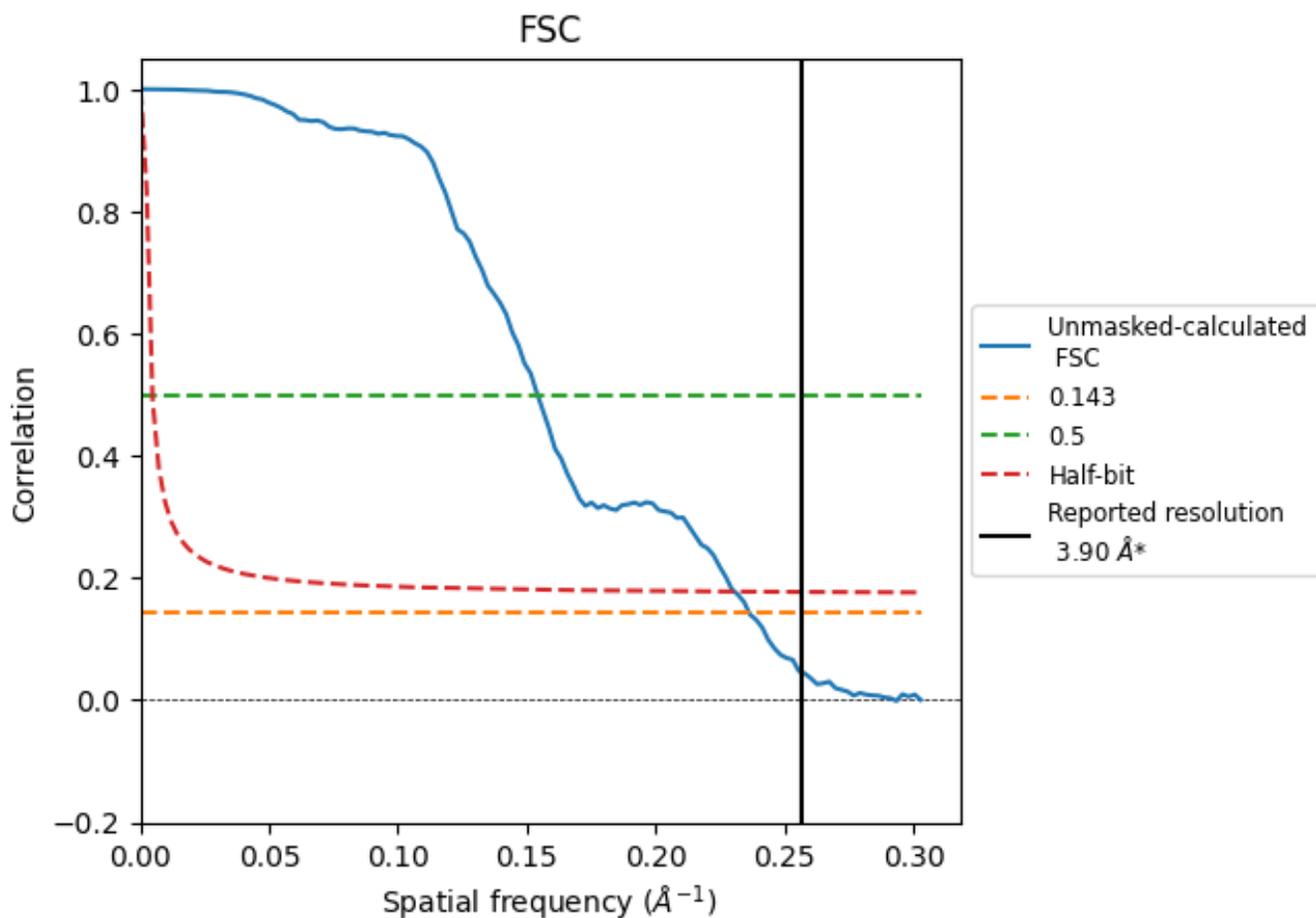


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

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

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

8.1 FSC [\(i\)](#)



*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

8.2 Resolution estimates [i](#)

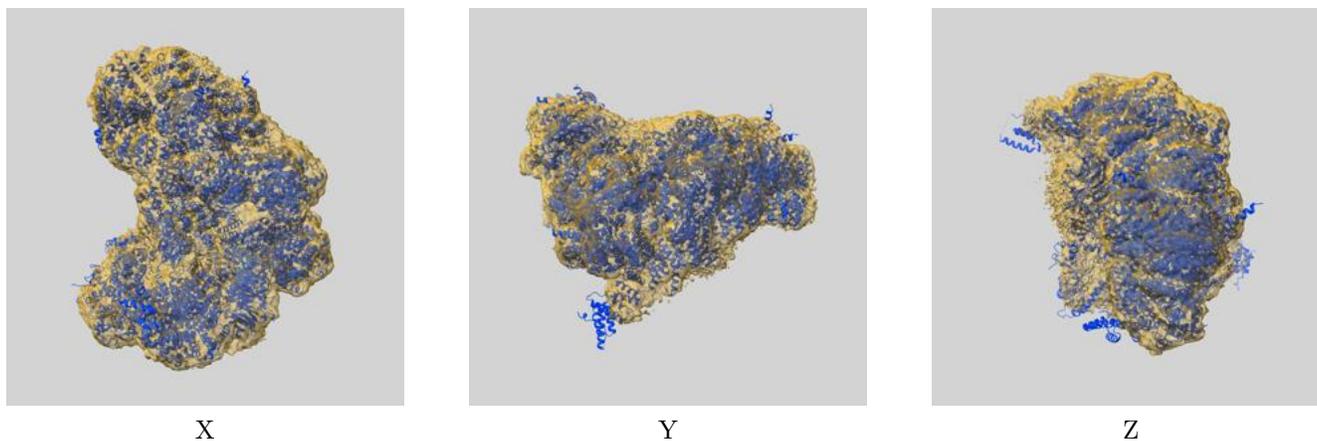
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---------------------------|------------------------------------|------|----------|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 3.90 | - | - |
| Author-provided FSC curve | - | - | - |
| Unmasked-calculated* | 4.23 | 6.49 | 4.33 |

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

9 Map-model fit [i](#)

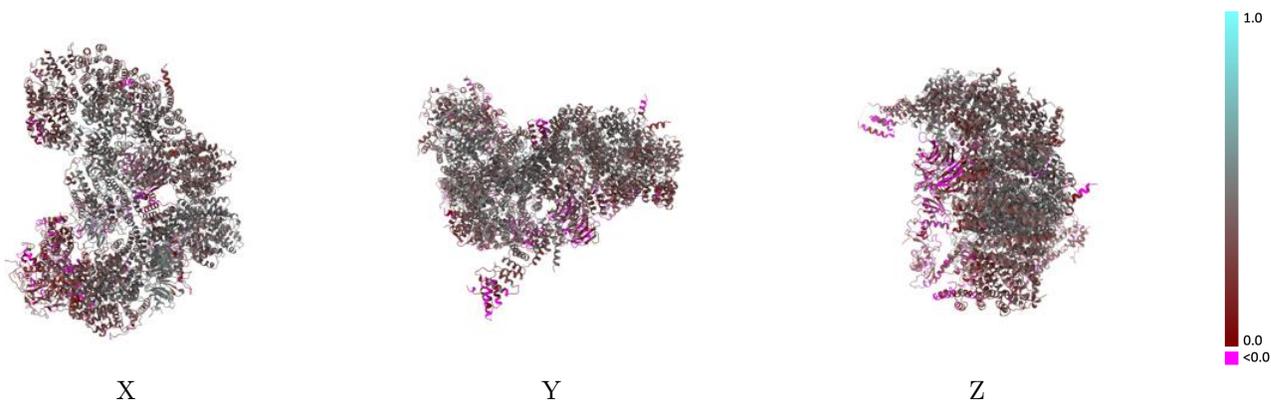
This section contains information regarding the fit between EMDB map EMD-48984 and PDB model 9N9S. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



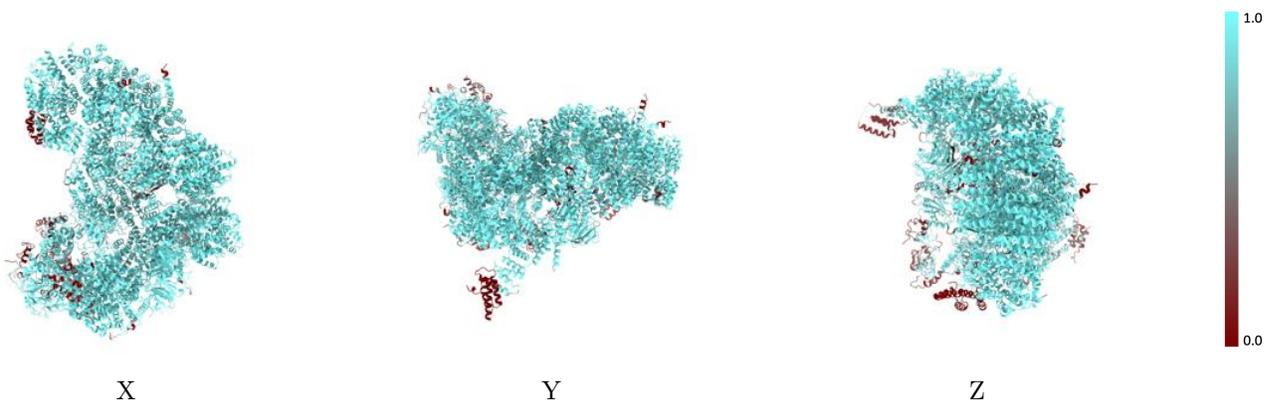
The images above show the 3D surface view of the map at the recommended contour level 0.013 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



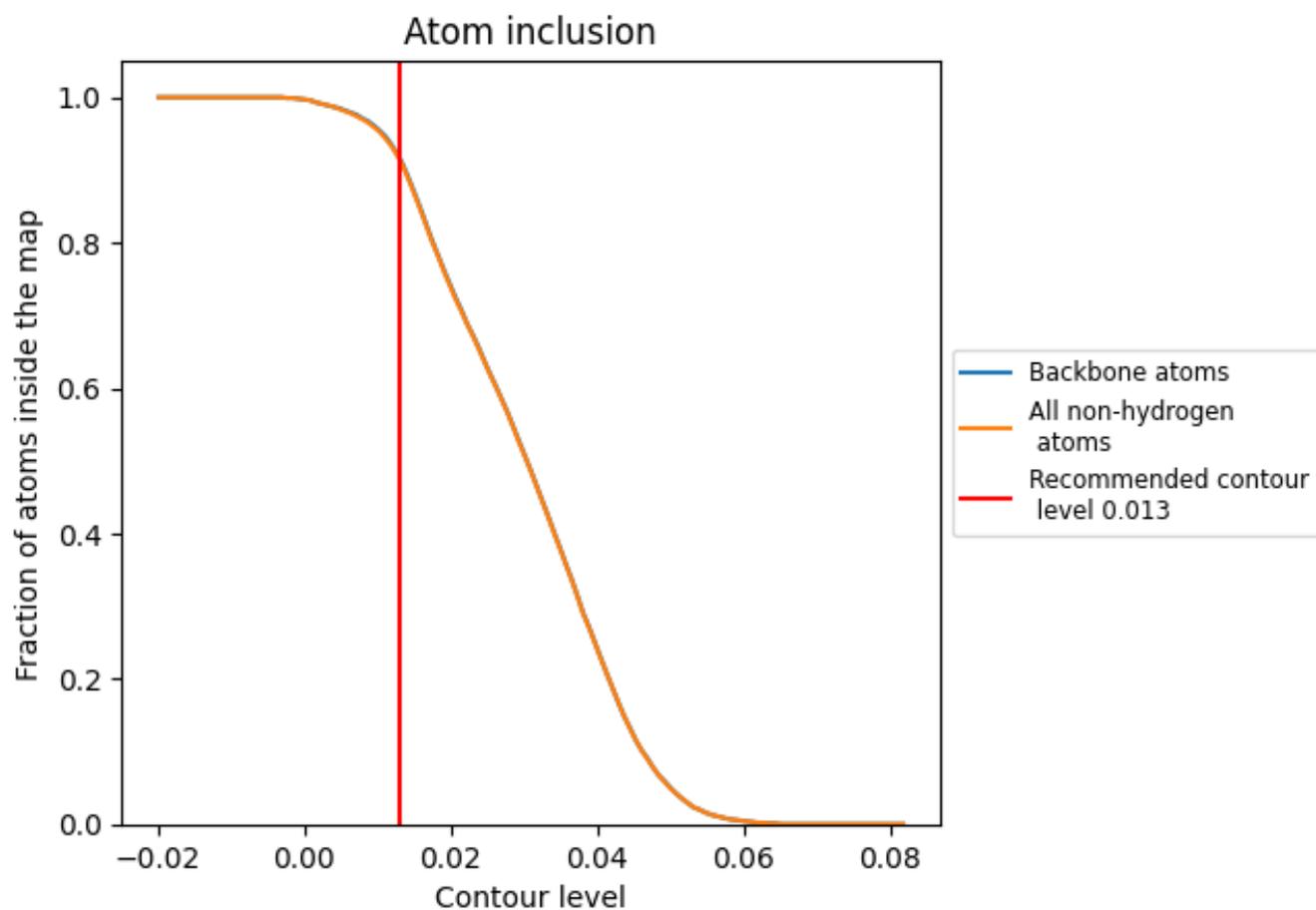
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.013).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 92% 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 (0.013) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|--|--|
| All |  0.9150 |  0.3420 |
| A |  0.9490 |  0.3880 |
| C |  0.5620 |  0.1140 |
| D |  1.0000 |  0.4640 |
| G |  0.9820 |  0.4480 |
| H |  1.0000 |  0.4240 |
| I |  0.9720 |  0.3260 |
| J |  0.9810 |  0.3730 |
| K |  0.9980 |  0.4010 |
| L |  0.9730 |  0.4030 |
| M |  0.7350 |  0.3610 |
| N |  0.6690 |  0.1880 |
| O |  0.9830 |  0.4010 |
| P |  0.9800 |  0.4340 |
| Q |  0.8480 |  0.0890 |
| R |  0.8260 |  0.1430 |
| S |  1.0000 |  0.3790 |
| U |  0.8400 |  0.3720 |
| V |  0.9770 |  0.3950 |
| W |  1.0000 |  0.4770 |
| Y |  0.9610 |  0.3340 |
| Z |  0.8250 |  0.2730 |

