# wwPDB EM Validation Summary Report (i)

Sep 8, 2026 – 05:48 am BST

| | | |
|---|---|---|
| PDB ID | : | 6GEJ / pdb_00006gej |
| EMDB ID | : | EMD-4395 |
| Title | : | Chromatin remodeller-nucleosome complex at 3.6 A resolution. |
| Authors | : | Willhoft, O.; Chua, E.Y.D.; Wilkinson, M.; Wigley, D.B. |
| Deposited on | : | 2018-04-26 |
| Resolution | : | 3.60 Å(reported) |

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

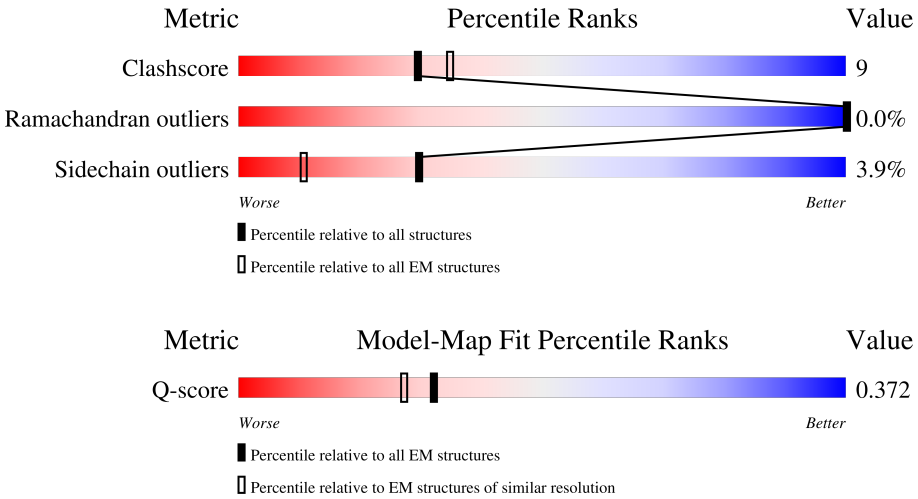
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.1.dev133 |
| Mogul | : | 1.8.4, CSD as541be (2020) |
| MolProbity | : | 4-5-2 with Phenix2.0 |
| Buster-report | : | wwPDB partial adaption of 1.1.7 (2018) |
| Percentile statistics | : | 20250101.v01 (using entries in the PDB archive January 1st 2025) |
| EM percentile statistics | : | 202505.v01 (Using data in the EMDB archive up until May 2025) |
| MapQ | : | 1.9.13 |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.50 |

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.60 Å.

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







| Metric | Whole archive (#Entries) | EM structures (#Entries) | Similar EM resolution (#Entries, resolution range(Å)) |
|---|---|---|---|
| Clashscore | 229148 | 23984 | - |
| Ramachandran outliers | 224038 | 23583 | - |
| Sidechain outliers | 223484 | 23102 | - |
| Q-score | - | 25397 | 12797 ( 3.10 - 4.10 ) |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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 | Z | 131 | 95% 5% |
| 2 | A | 136 | 60% 11% 29% |
| 2 | B | 136 | 60% 12% 29% |
| 3 | C | 103 | 61% 17% 20% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 3 | D | 103 | 62% 15% 22% |
| 4 | E | 132 | 65% 12% 22% |
| 4 | F | 132 | 66% 10% 23% |
| 5 | G | 131 | 60% 13% 27% |
| 5 | H | 131 | 59% 11% 31% |
| 6 | I | 154 | 39% 61% |
| 7 | J | 154 | 46% 54% |
| 8 | M | 1514 | 34% 11% 55% |
| 9 | R | 438 | 74% 19% 6% |
| 10 | S | 280 | 58% 16% 26% |
| 11 | T | 463 | 75% 19% |
| 11 | V | 463 | 69% 23% 6% |
| 11 | X | 463 | 70% 24% 5% |
| 12 | U | 471 | 66% 23% 9% |
| 12 | W | 471 | 69% 21% 8% |
| 12 | Y | 471 | 75% 19% 5% |

# 2 Entry composition (i)

There are 16 unique types of molecules in this entry. The entry contains 43702 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 Vacuolar protein sorting-associated protein 72.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 1 | Z | 131 | Total<br>655 | C<br>393 | N<br>131 | O<br>131 | 0 | 0 |

- Molecule 2 is a protein called Histone H3.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 2 | A | 97 | Total<br>796 | C<br>506 | N<br>152 | O<br>138 | 0 | 0 |
| 2 | B | 97 | Total<br>796 | C<br>506 | N<br>152 | O<br>138 | 0 | 0 |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| A | 123 | GLU | ASP | conflict | UNP P61830 |
| B | 123 | GLU | ASP | conflict | UNP P61830 |

- Molecule 3 is a protein called Histone H4.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 3 | C | 82 | Total<br>651 | C<br>410 | N<br>126 | O<br>115 | 0 | 0 |
| 3 | D | 80 | Total<br>638 | C<br>401 | N<br>124 | O<br>113 | 0 | 0 |

- Molecule 4 is a protein called Histone H2A.1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 4 | E | 103 | Total<br>795 | C<br>499 | N<br>156 | O<br>140 | 0 | 0 |
| 4 | F | 101 | Total<br>779 | C<br>489 | N<br>153 | O<br>137 | 0 | 0 |

- Molecule 5 is a protein called Histone H2B.1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 5 | G | 96 | Total | C | N | O | S | 0 | 0 |
| | | | 746 | 468 | 131 | 146 | 1 | | |
| 5 | H | 91 | Total | C | N | O | S | 0 | 0 |
| | | | 712 | 449 | 125 | 137 | 1 | | |

- Molecule 6 is a DNA chain called DNA (154-MER).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 6 | I | 154 | Total | C | N | O | P | 0 | 0 |
| | | | 3137 | 1489 | 569 | 925 | 154 | | |

- Molecule 7 is a DNA chain called DNA (154-MER).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 7 | J | 154 | Total | C | N | O | P | 0 | 0 |
| | | | 3177 | 1502 | 598 | 923 | 154 | | |

- Molecule 8 is a protein called Helicase SWR1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 8 | M | 688 | Total | C | N | O | S | 0 | 0 |
| | | | 5398 | 3438 | 960 | 974 | 26 | | |

- Molecule 9 is a protein called Actin-like protein ARP6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 9 | R | 411 | Total | C | N | O | S | 0 | 0 |
| | | | 3335 | 2156 | 544 | 619 | 16 | | |

- Molecule 10 is a protein called Vacuolar protein sorting-associated protein 71.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 10 | S | 208 | Total | C | N | O | S | 0 | 0 |
| | | | 1695 | 1071 | 302 | 312 | 10 | | |

- Molecule 11 is a protein called RuvB-like protein 1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 11 | T | 443 | Total | C | N | O | S | 0 | 0 |
| | | | 3391 | 2140 | 584 | 657 | 10 | | |

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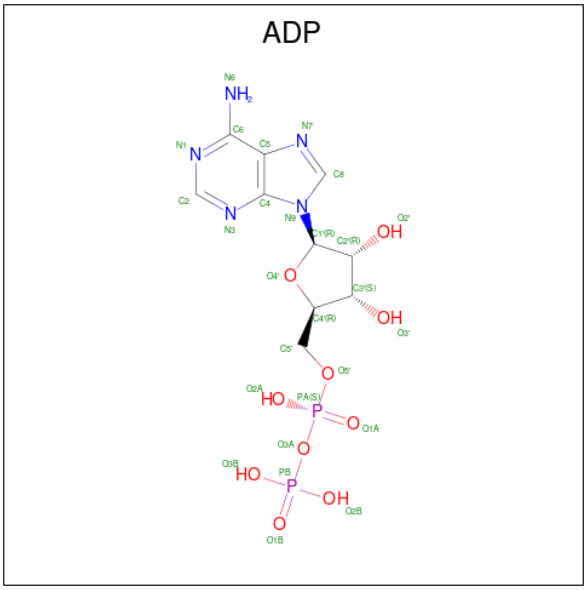
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| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 11 | V | 434 | Total | C | N | O | S | 0 | 0 |
| | | | 3336 | 2107 | 574 | 645 | 10 | | |
| 11 | X | 442 | Total | C | N | O | S | 0 | 0 |
| | | | 3397 | 2144 | 584 | 659 | 10 | | |

- Molecule 12 is a protein called RuvB-like protein 2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 12 | U | 430 | Total | C | N | O | S | 0 | 0 |
| | | | 3299 | 2063 | 570 | 655 | 11 | | |
| 12 | W | 433 | Total | C | N | O | S | 0 | 0 |
| | | | 3325 | 2085 | 572 | 657 | 11 | | |
| 12 | Y | 447 | Total | C | N | O | S | 0 | 0 |
| | | | 3410 | 2133 | 590 | 675 | 12 | | |

- Molecule 13 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



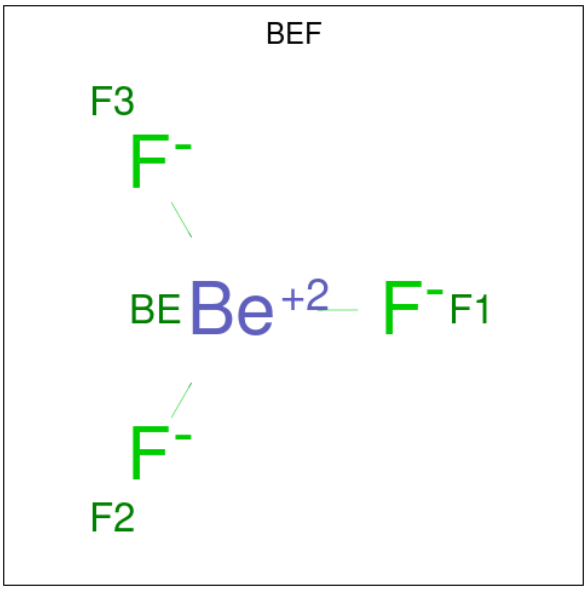

| Mol | Chain | Residues | Atoms | | | | | AltConf |
|---|---|---|---|---|---|---|---|---|
| 13 | M | 1 | Total | C | N | O | P | 0 |
| | | | 27 | 10 | 5 | 10 | 2 | |
| 13 | R | 1 | Total | C | N | O | P | 0 |
| | | | 27 | 10 | 5 | 10 | 2 | |
| 13 | T | 1 | Total | C | N | O | P | 0 |
| | | | 27 | 10 | 5 | 10 | 2 | |
| 13 | U | 1 | Total | C | N | O | P | 0 |
| | | | 27 | 10 | 5 | 10 | 2 | |

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| Mol | Chain | Residues | Atoms | | | | | AltConf |
|---|---|---|---|---|---|---|---|---|
| 13 | V | 1 | Total | C | N | O | P | 0 |
| | | | 27 | 10 | 5 | 10 | 2 | |
| 13 | W | 1 | Total | C | N | O | P | 0 |
| | | | 27 | 10 | 5 | 10 | 2 | |
| 13 | X | 1 | Total | C | N | O | P | 0 |
| | | | 27 | 10 | 5 | 10 | 2 | |
| 13 | Y | 1 | Total | C | N | O | P | 0 |
| | | | 27 | 10 | 5 | 10 | 2 | |

- Molecule 14 is BERYLLIUM TRIFLUORIDE ION (CCD ID: BEF) (formula: $BeF_3$).




| Mol | Chain | Residues | Atoms | | | AltConf |
|---|---|---|---|---|---|---|
| 14 | M | 1 | Total | Be | F | 0 |
| | | | 4 | 1 | 3 | |
| 14 | R | 1 | Total | Be | F | 0 |
| | | | 4 | 1 | 3 | |

- Molecule 15 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | | AltConf |
|---|---|---|---|---|---|
| 15 | M | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 15 | R | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 15 | U | 2 | Total | Mg | 0 |
| | | | 2 | 2 | |

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| Mol | Chain | Residues | Atoms | AltConf |
|---|---|---|---|---|
| 15 | V | 1 | Total Mg<br>1 1 | 0 |
| 15 | W | 1 | Total Mg<br>1 1 | 0 |
| 15 | X | 1 | Total Mg<br>1 1 | 0 |
| 15 | Y | 1 | Total Mg<br>1 1 | 0 |

- Molecule 16 is ZINC ION (CCD ID: ZN) (formula: Zn).

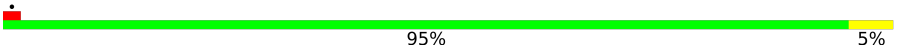
| Mol | Chain | Residues | Atoms | AltConf |
|---|---|---|---|---|
| 16 | S | 2 | Total Zn<br>2 2 | 0 |

# 3 Residue-property plots (i)

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

• Molecule 1: Vacuolar protein sorting-associated protein 72

Chain Z:







• Molecule 2: Histone H3

Chain A:










• Molecule 2: Histone H3

Chain B:





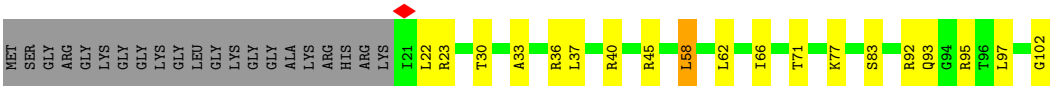





• Molecule 3: Histone H4

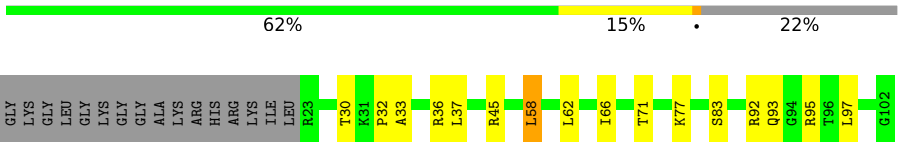
Chain C:



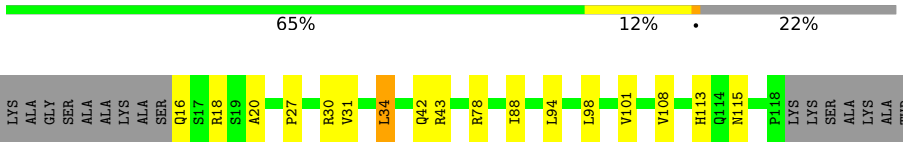

• Molecule 3: Histone H4

Chain D:



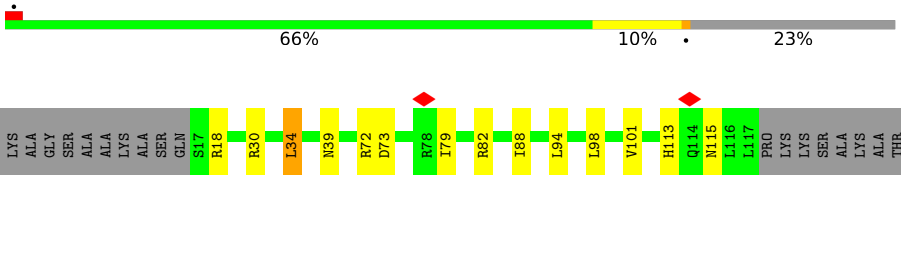

• Molecule 4: Histone H2A.1

Chain E:



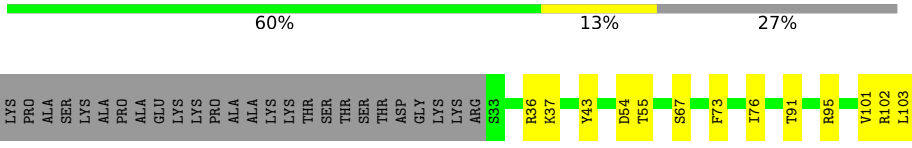

• Molecule 4: Histone H2A.1

Chain F:



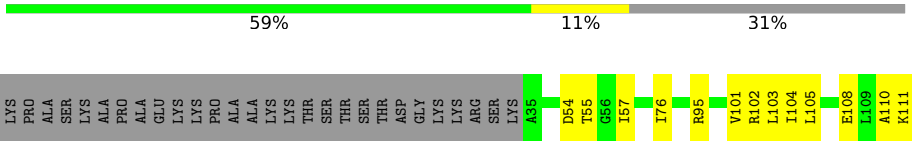

• Molecule 5: Histone H2B.1

Chain G:




• Molecule 5: Histone H2B.1

Chain H:




• Molecule 6: DNA (154-MER)

Chain I:

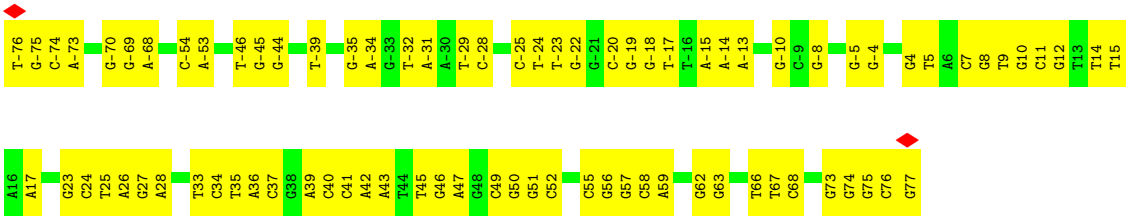





• Molecule 7: DNA (154-MER)

Chain J:

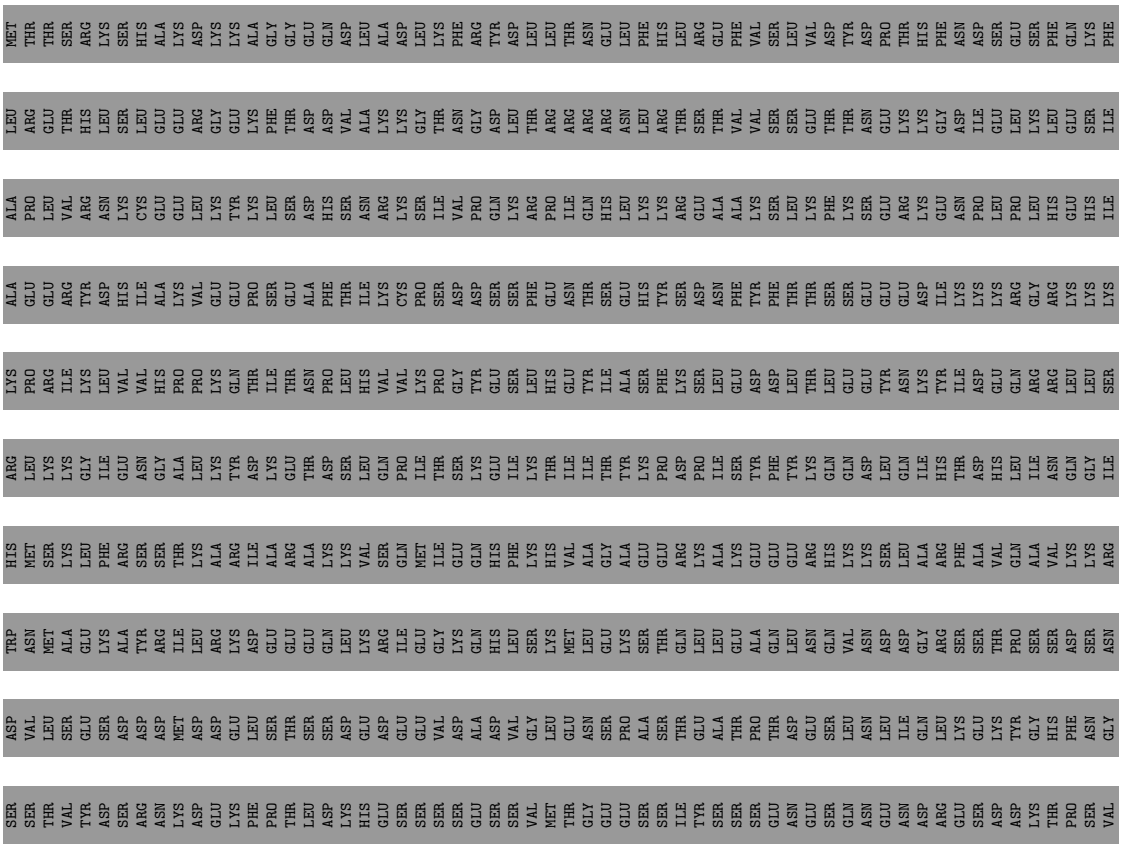


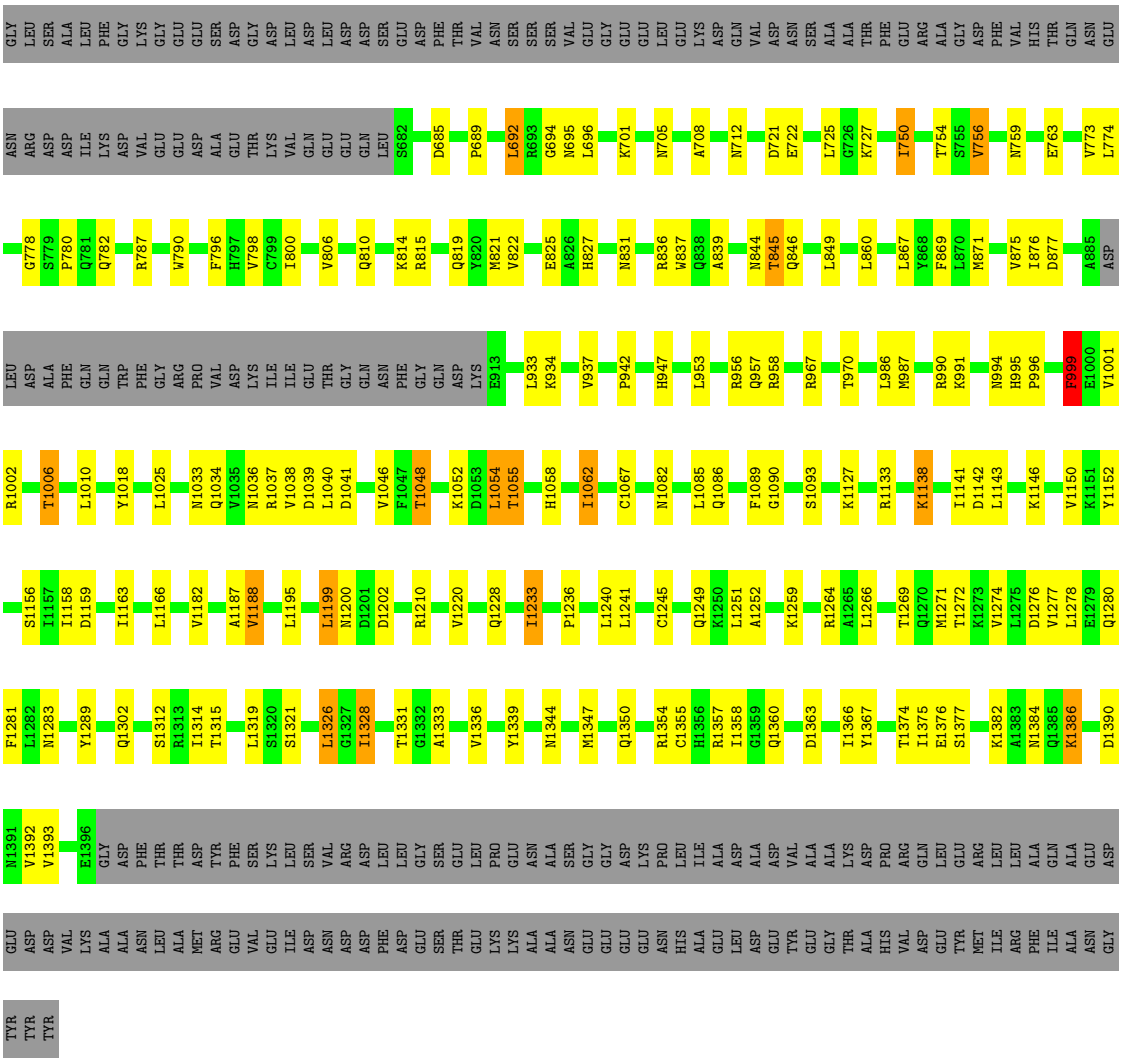




• Molecule 8: Helicase SWR1

Chain M:



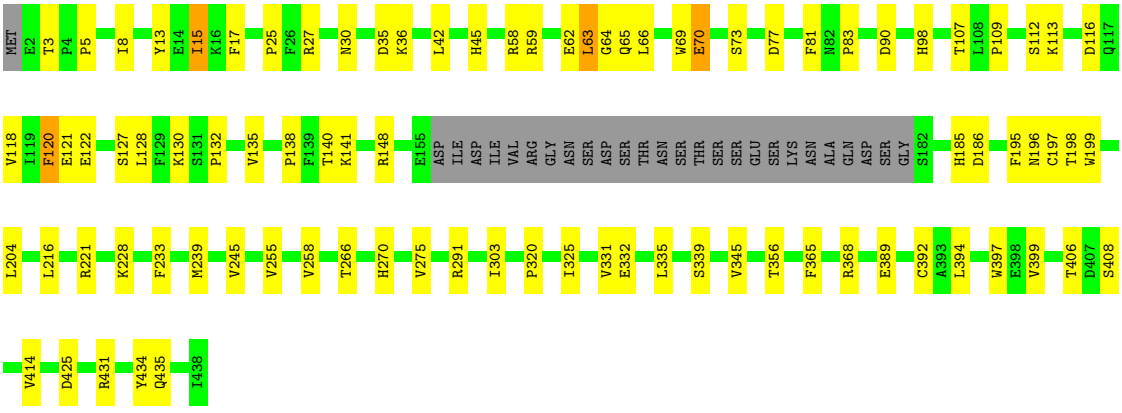





• Molecule 9: Actin-like protein ARP6

Chain R:

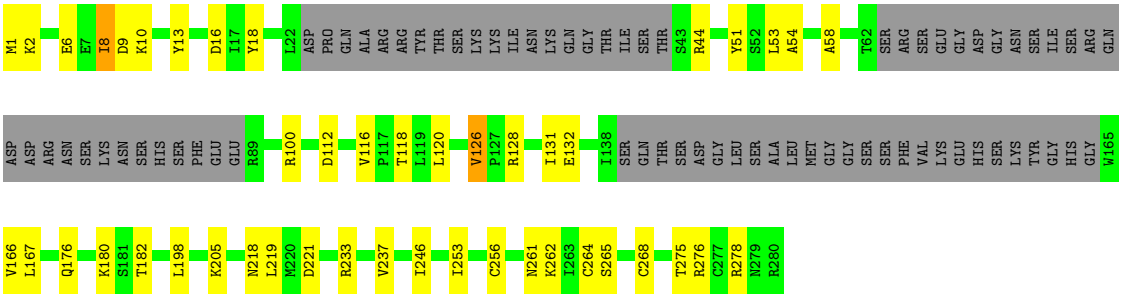


• Molecule 10: Vacuolar protein sorting-associated protein 71

Chain S:





• Molecule 11: RuvB-like protein 1

Chain T:

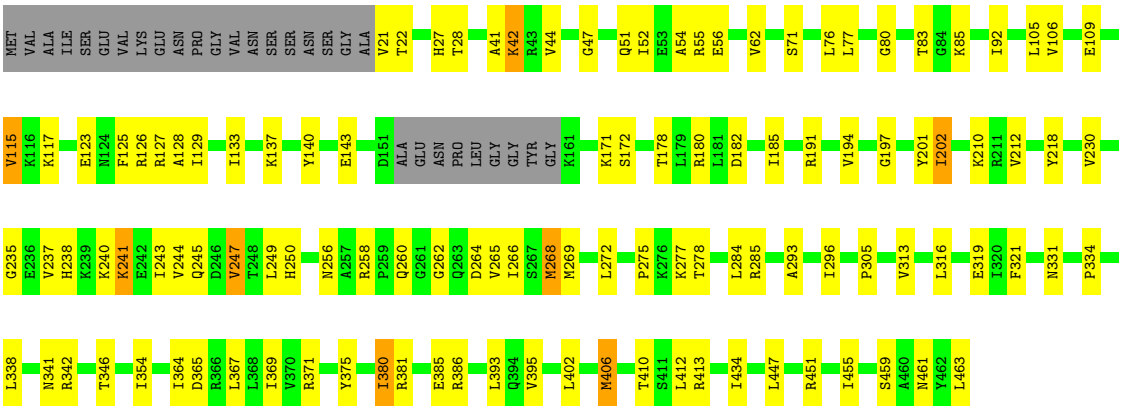





• Molecule 11: RuvB-like protein 1

Chain V:

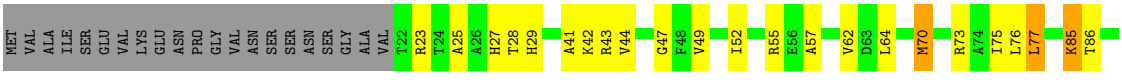


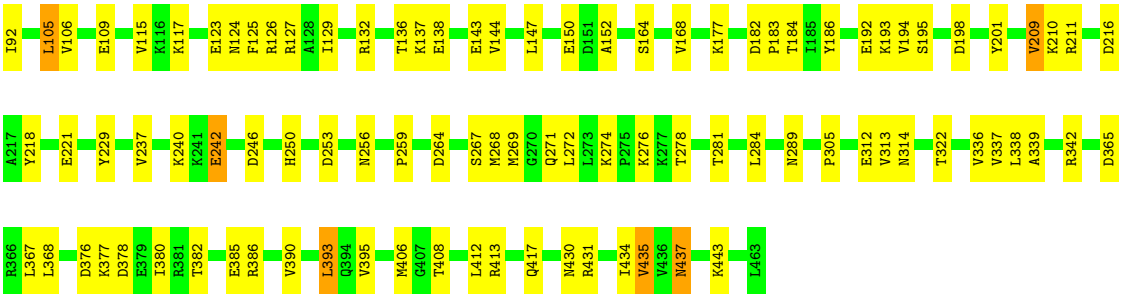



• Molecule 11: RuvB-like protein 1

Chain X:



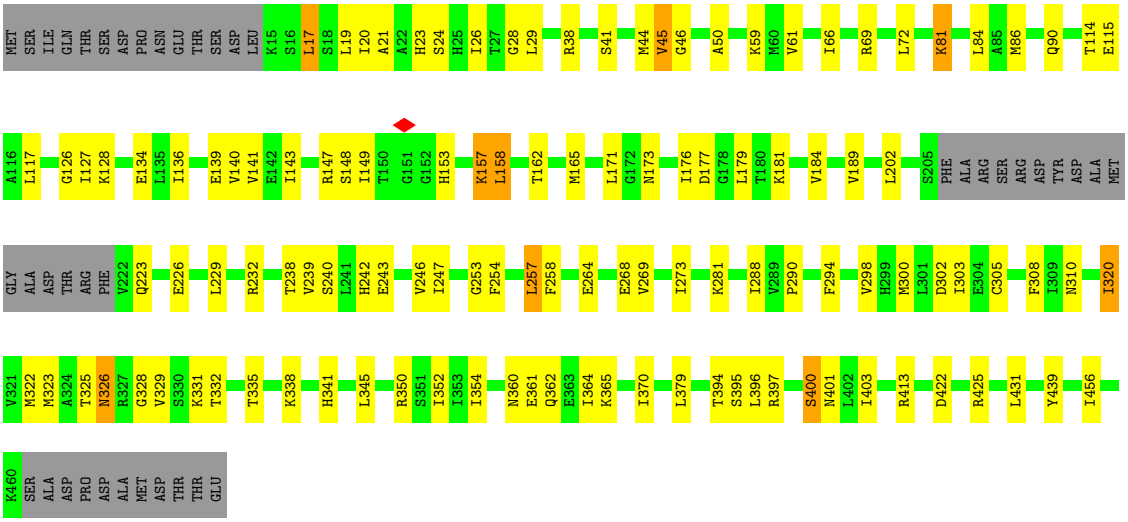





• Molecule 12: RuvB-like protein 2

Chain U:

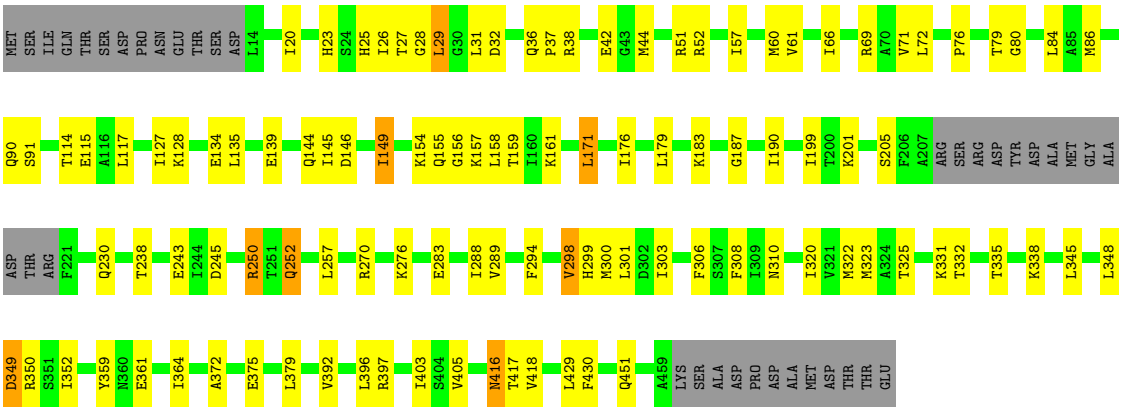


• Molecule 12: RuvB-like protein 2

Chain W:

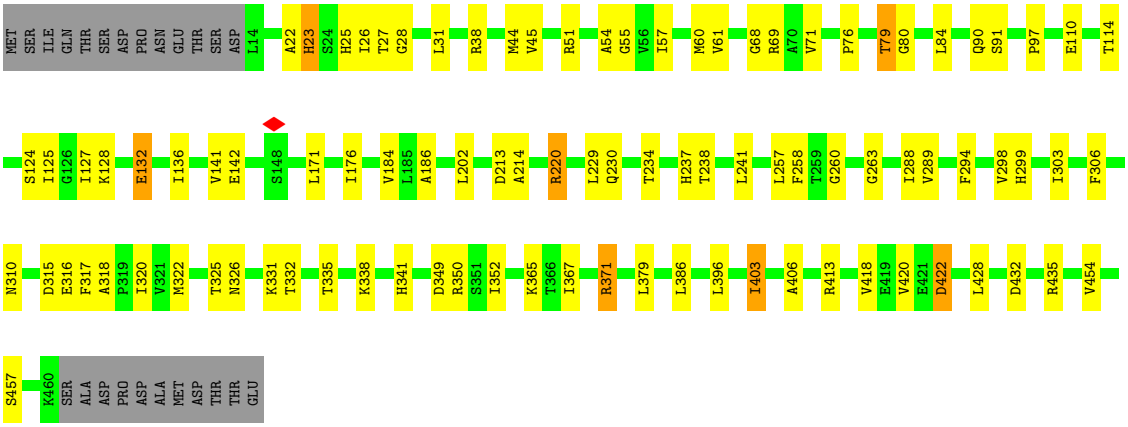


• Molecule 12: RuvB-like protein 2

Chain Y:




MET SER ILE GLN THR SER ASP PRO ASN GLU THR SER ASP L14 A22 H23 S24 H25 I26 T27 G28 L31 R38 M44 V45 R51 A54 G55 V56 I57 M60 V61 G68 R69 A70 V71 P76 T79 G80 L84 Q90 S91 P97 E110 T114
S124 I125 G126 I127 K128 E132 I136 V141 E142 S148 L171 I176 V184 L185 A186 L202 D213 A214 R220 L229 Q230 T234 H237 T238 L241 L257 F258 T259 G260 G263 I288 V289 F294 V298 H299 I303 F306
N310 D315 E316 F317 A318 P319 I320 V321 M322 T325 N326 K331 T332 T335 K338 H341 D349 R350 S351 I352 K365 T366 I367 R371 L379 L386 L396 I403 A406 R413 V418 E419 V420 E421 D422 L428 D432 R435 V454
S457 K460 SER ALA ASP PRO ASP ALA MET ASP THR THR GLU

# 4 Experimental information (i)

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, C1 | Depositor |
| Number of particles used | 98529 | 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 ($e^-/Å^2$) | 1.71794871794872 | Depositor |
| Minimum defocus (nm) | Not provided | |
| Maximum defocus (nm) | Not provided | |
| Magnification | Not provided | |
| Image detector | FEI FALCON III (4k x 4k) | Depositor |
| Maximum map value | 0.358 | Depositor |
| Minimum map value | -0.160 | Depositor |
| Average map value | 0.001 | Depositor |
| Map value standard deviation | 0.008 | Depositor |
| Recommended contour level | 0.0295 | Depositor |
| Map size (Å) | 426.24, 426.24, 426.24 | wwPDB |
| Map dimensions | 384, 384, 384 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.11, 1.11, 1.11 | Depositor |

# 5 Model quality

## 5.1 Standard geometry

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

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 | $\#\|Z\| > 5$ |
| 2 | A | 0.09 | 0/807 | 0.28 | 0/1081 |
| 2 | B | 0.09 | 0/807 | 0.28 | 0/1081 |
| 3 | C | 0.11 | 0/658 | 0.31 | 0/880 |
| 3 | D | 0.11 | 0/645 | 0.31 | 0/862 |
| 4 | E | 0.09 | 0/806 | 0.26 | 0/1091 |
| 4 | F | 0.09 | 0/789 | 0.26 | 0/1067 |
| 5 | G | 0.08 | 0/756 | 0.26 | 0/1017 |
| 5 | H | 0.08 | 0/722 | 0.25 | 0/972 |
| 6 | I | 0.18 | 0/3514 | 0.40 | 0/5416 |
| 7 | J | 0.16 | 0/3568 | 0.34 | 0/5510 |
| 8 | M | 0.11 | 0/5495 | 0.35 | 0/7442 |
| 9 | R | 0.08 | 0/3429 | 0.25 | 0/4650 |
| 10 | S | 0.08 | 0/1722 | 0.28 | 0/2320 |
| 11 | T | 0.14 | 0/3433 | 0.41 | 0/4646 |
| 11 | V | 0.14 | 0/3375 | 0.42 | 0/4565 |
| 11 | X | 0.14 | 0/3439 | 0.40 | 0/4652 |
| 12 | U | 0.13 | 0/3333 | 0.42 | 0/4492 |
| 12 | W | 0.14 | 0/3361 | 0.41 | 0/4530 |
| 12 | Y | 0.15 | 0/3447 | 0.41 | 0/4649 |
| All | All | 0.13 | 0/44106 | 0.36 | 0/60923 |

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

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|---|---|---|---|
| 1 | Z | 0 | 1 |
| 8 | M | 0 | 2 |
| All | All | 0 | 3 |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 8 | M | 1344 | ASN | Peptide |
| 8 | M | 692 | LEU | Peptide |
| 1 | Z | 188 | UNK | Peptide |

## 5.2 Too-close contacts (i)

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

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 1 | Z | 655 | 0 | 144 | 3 | 0 |
| 2 | A | 796 | 0 | 841 | 14 | 0 |
| 2 | B | 796 | 0 | 841 | 12 | 0 |
| 3 | C | 651 | 0 | 690 | 14 | 0 |
| 3 | D | 638 | 0 | 677 | 15 | 0 |
| 4 | E | 795 | 0 | 834 | 16 | 0 |
| 4 | F | 779 | 0 | 819 | 12 | 0 |
| 5 | G | 746 | 0 | 771 | 16 | 0 |
| 5 | H | 712 | 0 | 736 | 11 | 0 |
| 6 | I | 3137 | 0 | 1728 | 81 | 0 |
| 7 | J | 3177 | 0 | 1727 | 81 | 0 |
| 8 | M | 5398 | 0 | 5352 | 123 | 0 |
| 9 | R | 3335 | 0 | 3256 | 60 | 0 |
| 10 | S | 1695 | 0 | 1746 | 36 | 0 |
| 11 | T | 3391 | 0 | 3513 | 62 | 0 |
| 11 | V | 3336 | 0 | 3475 | 77 | 0 |
| 11 | X | 3397 | 0 | 3533 | 70 | 0 |
| 12 | U | 3299 | 0 | 3387 | 78 | 0 |
| 12 | W | 3325 | 0 | 3413 | 67 | 0 |
| 12 | Y | 3410 | 0 | 3465 | 62 | 0 |
| 13 | M | 27 | 0 | 12 | 3 | 0 |
| 13 | R | 27 | 0 | 12 | 1 | 0 |
| 13 | T | 27 | 0 | 12 | 2 | 0 |
| 13 | U | 27 | 0 | 12 | 2 | 0 |
| 13 | V | 27 | 0 | 12 | 0 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 13 | W | 27 | 0 | 12 | 1 | 0 |
| 13 | X | 27 | 0 | 12 | 1 | 0 |
| 13 | Y | 27 | 0 | 12 | 4 | 0 |
| 14 | M | 4 | 0 | 0 | 1 | 0 |
| 14 | R | 4 | 0 | 0 | 1 | 0 |
| 15 | M | 1 | 0 | 0 | 0 | 0 |
| 15 | R | 1 | 0 | 0 | 0 | 0 |
| 15 | U | 2 | 0 | 0 | 0 | 0 |
| 15 | V | 1 | 0 | 0 | 0 | 0 |
| 15 | W | 1 | 0 | 0 | 0 | 0 |
| 15 | X | 1 | 0 | 0 | 0 | 0 |
| 15 | Y | 1 | 0 | 0 | 0 | 0 |
| 16 | S | 2 | 0 | 0 | 0 | 0 |
| All | All | 43702 | 0 | 41044 | 773 | 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 9.

The worst 5 of 773 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) |
|---|---|---|---|
| 11:T:406:MET:SD | 11:T:443:LYS:NZ | 2.29 | 1.06 |
| 9:R:77:ASP:O | 9:R:81:PHE:HB2 | 1.68 | 0.93 |
| 11:X:406:MET:SD | 11:X:443:LYS:HD2 | 2.08 | 0.93 |
| 10:S:176:GLN:O | 10:S:180:LYS:HB2 | 1.72 | 0.89 |
| 11:X:406:MET:SD | 11:X:443:LYS:CD | 2.67 | 0.83 |

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 | |
|---|---|---|---|---|---|---|---|
| 2 | A | 95/136 (70%) | 90 (95%) | 5 (5%) | 0 | 100 | 100 |
| 2 | B | 95/136 (70%) | 90 (95%) | 5 (5%) | 0 | 100 | 100 |
| 3 | C | 80/103 (78%) | 75 (94%) | 5 (6%) | 0 | 100 | 100 |
| 3 | D | 78/103 (76%) | 73 (94%) | 5 (6%) | 0 | 100 | 100 |
| 4 | E | 101/132 (76%) | 99 (98%) | 2 (2%) | 0 | 100 | 100 |
| 4 | F | 99/132 (75%) | 97 (98%) | 2 (2%) | 0 | 100 | 100 |
| 5 | G | 94/131 (72%) | 87 (93%) | 7 (7%) | 0 | 100 | 100 |
| 5 | H | 89/131 (68%) | 84 (94%) | 5 (6%) | 0 | 100 | 100 |
| 8 | M | 684/1514 (45%) | 621 (91%) | 62 (9%) | 1 (0%) | 48 | 79 |
| 9 | R | 407/438 (93%) | 396 (97%) | 11 (3%) | 0 | 100 | 100 |
| 10 | S | 200/280 (71%) | 195 (98%) | 5 (2%) | 0 | 100 | 100 |
| 11 | T | 441/463 (95%) | 423 (96%) | 17 (4%) | 1 (0%) | 43 | 72 |
| 11 | V | 430/463 (93%) | 414 (96%) | 16 (4%) | 0 | 100 | 100 |
| 11 | X | 440/463 (95%) | 422 (96%) | 18 (4%) | 0 | 100 | 100 |
| 12 | U | 426/471 (90%) | 405 (95%) | 21 (5%) | 0 | 100 | 100 |
| 12 | W | 429/471 (91%) | 420 (98%) | 9 (2%) | 0 | 100 | 100 |
| 12 | Y | 445/471 (94%) | 427 (96%) | 18 (4%) | 0 | 100 | 100 |
| All | All | 4633/6038 (77%) | 4418 (95%) | 213 (5%) | 2 (0%) | 100 | 100 |

All (2) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 8 | M | 999 | PHE |
| 11 | T | 236 | GLU |

### 5.3.2 Protein sidechains (i)

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

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 2 | A | 84/113 (74%) | 84 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 2 | B | 84/113 (74%) | 84 (100%) | 0 | 100 | 100 |
| 3 | C | 68/81 (84%) | 65 (96%) | 3 (4%) | 25 | 52 |
| 3 | D | 67/81 (83%) | 64 (96%) | 3 (4%) | 24 | 51 |
| 4 | E | 82/99 (83%) | 81 (99%) | 1 (1%) | 63 | 73 |
| 4 | F | 80/99 (81%) | 79 (99%) | 1 (1%) | 61 | 72 |
| 5 | G | 83/109 (76%) | 83 (100%) | 0 | 100 | 100 |
| 5 | H | 78/109 (72%) | 78 (100%) | 0 | 100 | 100 |
| 8 | M | 574/1376 (42%) | 538 (94%) | 36 (6%) | 16 | 44 |
| 9 | R | 372/396 (94%) | 362 (97%) | 10 (3%) | 39 | 61 |
| 10 | S | 199/261 (76%) | 196 (98%) | 3 (2%) | 57 | 70 |
| 11 | T | 371/391 (95%) | 360 (97%) | 11 (3%) | 36 | 59 |
| 11 | V | 368/391 (94%) | 350 (95%) | 18 (5%) | 22 | 49 |
| 11 | X | 374/391 (96%) | 347 (93%) | 27 (7%) | 13 | 40 |
| 12 | U | 367/403 (91%) | 351 (96%) | 16 (4%) | 25 | 52 |
| 12 | W | 369/403 (92%) | 355 (96%) | 14 (4%) | 29 | 55 |
| 12 | Y | 372/403 (92%) | 358 (96%) | 14 (4%) | 29 | 55 |
| All | All | 3992/5219 (76%) | 3835 (96%) | 157 (4%) | 30 | 54 |

5 of 157 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 12 | W | 451 | GLN |
| 12 | Y | 23 | HIS |
| 11 | X | 85 | LYS |
| 11 | X | 242 | GLU |
| 12 | Y | 341 | HIS |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 9 | R | 374 | GLN |
| 12 | Y | 63 | ASN |
| 12 | U | 252 | GLN |
| 12 | Y | 36 | GLN |
| 12 | Y | 455 | GLN |

### 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 20 ligands modelled in this entry, 10 are monoatomic - leaving 10 for Mogul analysis.

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

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Counts | RMSZ | $\#\|Z\| > 2$ | Counts | RMSZ | $\#\|Z\| > 2$ |
| 13 | ADP | V | 501 | 15 | 27,29,29 | 1.36 | 4 (14%) | 42,45,45 | 1.99 | 12 (28%) |
| 13 | ADP | R | 501 | 14,15 | 27,29,29 | 1.36 | 4 (14%) | 42,45,45 | 1.91 | 10 (23%) |
| 13 | ADP | T | 501 | 15 | 27,29,29 | 1.35 | 4 (14%) | 42,45,45 | 1.98 | 11 (26%) |
| 13 | ADP | X | 501 | 15 | 27,29,29 | 1.38 | 4 (14%) | 42,45,45 | 2.00 | 10 (23%) |
| 13 | ADP | M | 1601 | 14 | 27,29,29 | 1.36 | 4 (14%) | 42,45,45 | 1.92 | 10 (23%) |
| 14 | BEF | R | 502 | 13 | 0,3,3 | - | - | - | | |
| 14 | BEF | M | 1602 | 13 | 0,3,3 | - | - | - | | |
| 13 | ADP | W | 501 | 15 | 27,29,29 | 1.37 | 4 (14%) | 42,45,45 | 2.04 | 10 (23%) |
| 13 | ADP | Y | 501 | - | 27,29,29 | 1.38 | 4 (14%) | 42,45,45 | 1.98 | 10 (23%) |
| 13 | ADP | U | 502 | - | 27,29,29 | 1.36 | 4 (14%) | 42,45,45 | 1.98 | 10 (23%) |

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

| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|---|---|---|---|---|---|---|---|
| 13 | ADP | V | 501 | 15 | - | 3/16/32/32 | 0/3/3/3 |
| 13 | ADP | R | 501 | 14,15 | - | 6/16/32/32 | 0/3/3/3 |
| 13 | ADP | T | 501 | 15 | - | 4/16/32/32 | 0/3/3/3 |
| 13 | ADP | X | 501 | 15 | - | 2/16/32/32 | 0/3/3/3 |
| 13 | ADP | M | 1601 | 14 | - | 6/16/32/32 | 0/3/3/3 |
| 13 | ADP | W | 501 | 15 | - | 5/16/32/32 | 0/3/3/3 |
| 13 | ADP | Y | 501 | - | - | 2/16/32/32 | 0/3/3/3 |
| 13 | ADP | U | 502 | - | - | 4/16/32/32 | 0/3/3/3 |

The worst 5 of 32 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 13 | X | 501 | ADP | C5-C4 | 4.62 | 1.47 | 1.39 |
| 13 | Y | 501 | ADP | C5-C4 | 4.62 | 1.47 | 1.39 |
| 13 | W | 501 | ADP | C5-C4 | 4.57 | 1.47 | 1.39 |
| 13 | R | 501 | ADP | C5-C4 | 4.56 | 1.47 | 1.39 |
| 13 | M | 1601 | ADP | C5-C4 | 4.51 | 1.47 | 1.39 |

The worst 5 of 83 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 13 | W | 501 | ADP | C5-C4-N3 | -6.56 | 118.19 | 126.75 |
| 13 | Y | 501 | ADP | C5-C4-N3 | -6.40 | 118.39 | 126.75 |
| 13 | X | 501 | ADP | C5-C4-N3 | -6.39 | 118.41 | 126.75 |
| 13 | U | 502 | ADP | C5-C4-N3 | -6.25 | 118.59 | 126.75 |
| 13 | M | 1601 | ADP | C5-C4-N3 | -6.18 | 118.69 | 126.75 |

There are no chirality outliers.

5 of 32 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 13 | M | 1601 | ADP | PA-O3A-PB-O2B |
| 13 | M | 1601 | ADP | C5'-O5'-PA-O1A |
| 13 | M | 1601 | ADP | C5'-O5'-PA-O2A |
| 13 | R | 501 | ADP | PA-O3A-PB-O2B |
| 13 | R | 501 | ADP | PA-O3A-PB-O3B |

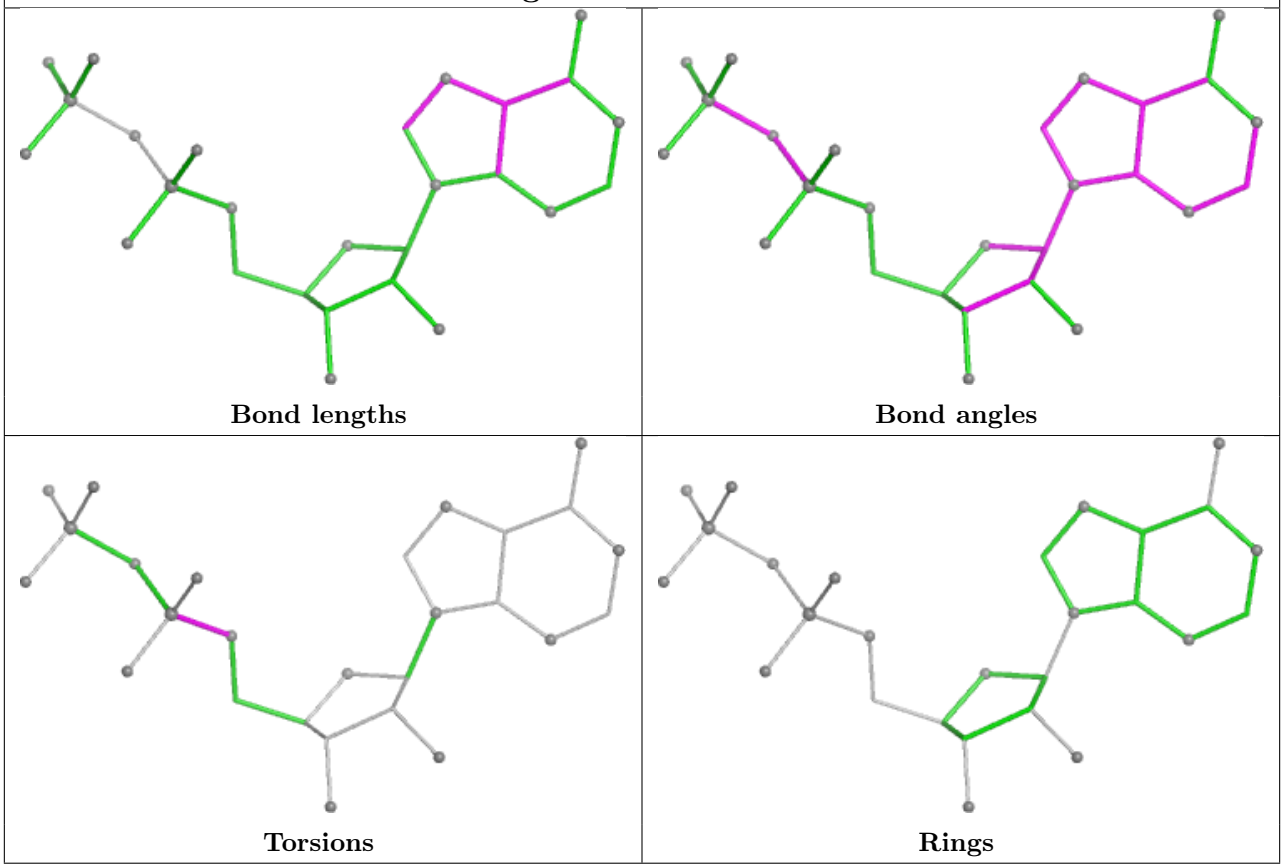
There are no ring outliers.

9 monomers are involved in 15 short contacts:

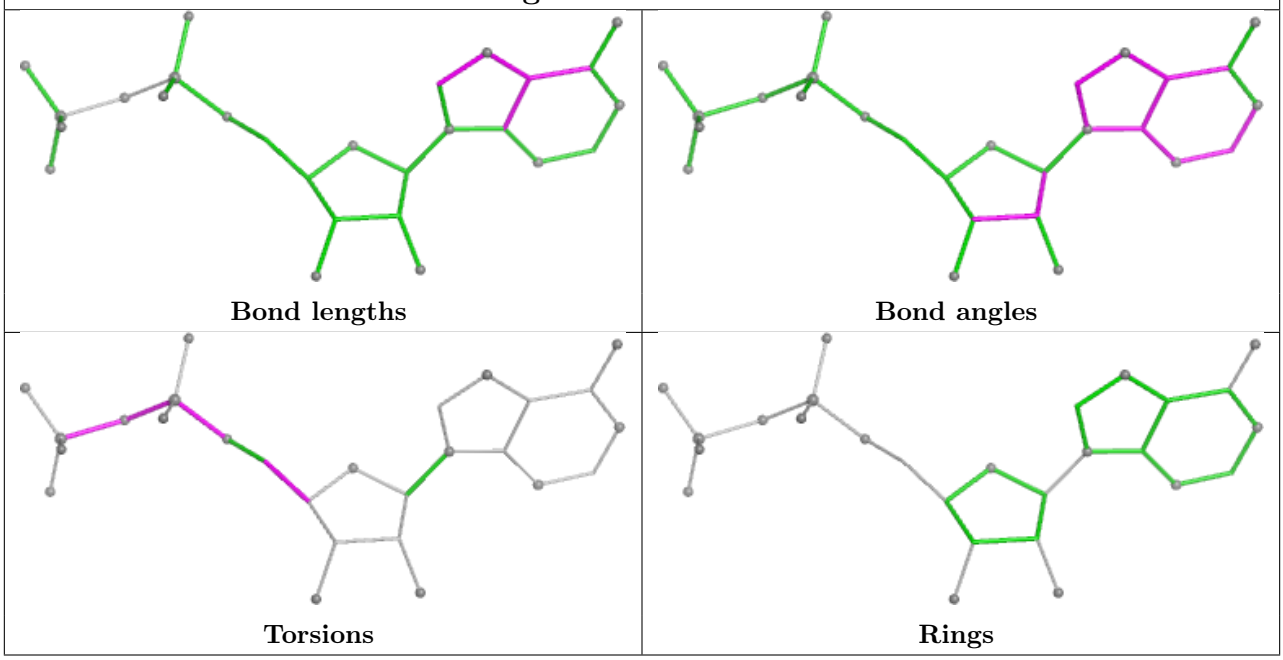
| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|---|---|---|---|---|---|
| 13 | R | 501 | ADP | 1 | 0 |
| 13 | T | 501 | ADP | 2 | 0 |
| 13 | X | 501 | ADP | 1 | 0 |
| 13 | M | 1601 | ADP | 3 | 0 |
| 14 | R | 502 | BEF | 1 | 0 |
| 14 | M | 1602 | BEF | 1 | 0 |
| 13 | W | 501 | ADP | 1 | 0 |
| 13 | Y | 501 | ADP | 4 | 0 |
| 13 | U | 502 | ADP | 2 | 0 |

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight $> 250$ and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

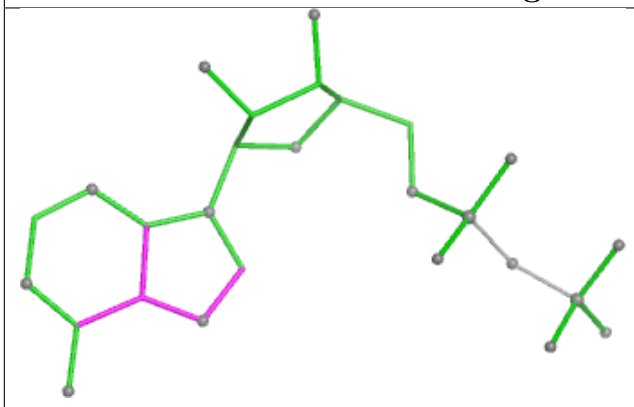
**Ligand ADP V 501**



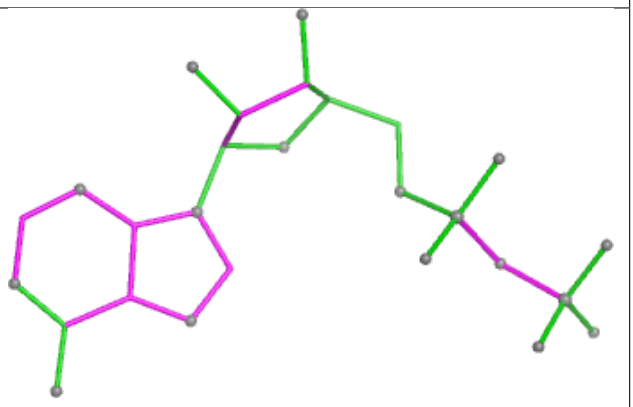

**Ligand ADP R 501**



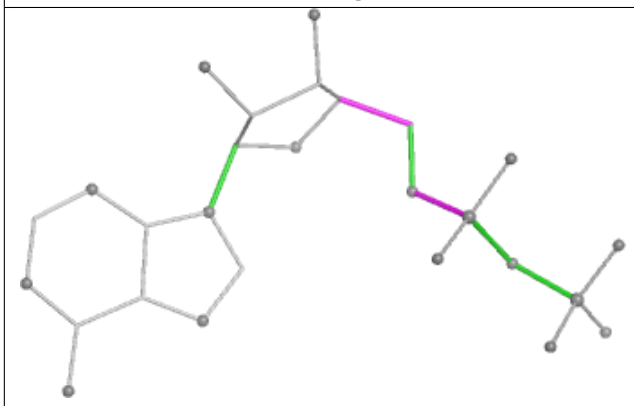
## Ligand ADP T 501



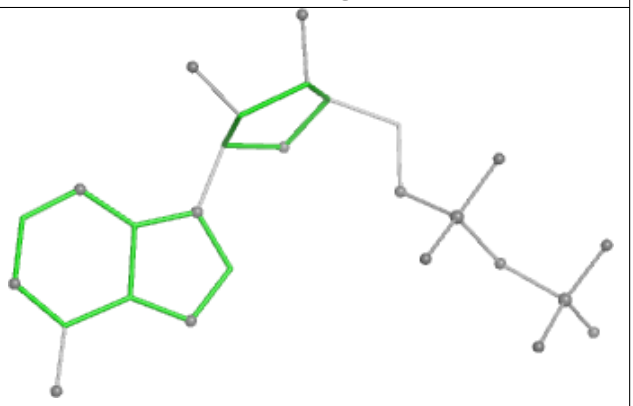
Bond lengths



Bond angles

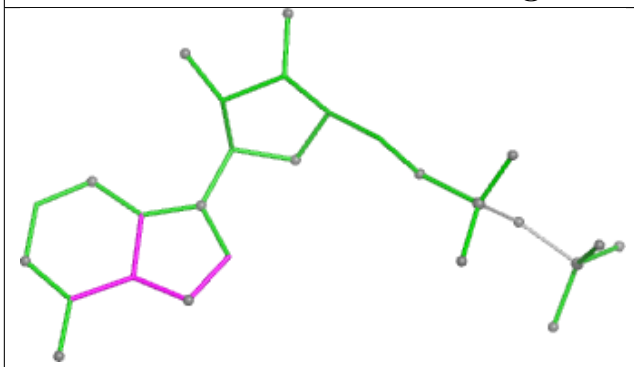


Torsions

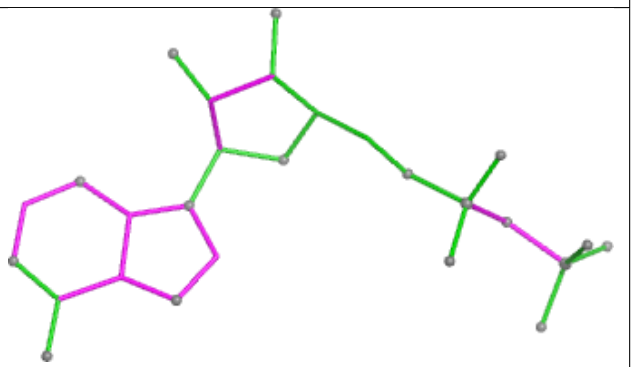


Rings

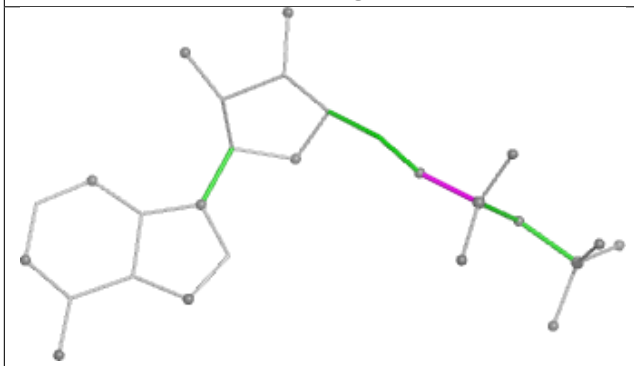
## Ligand ADP X 501



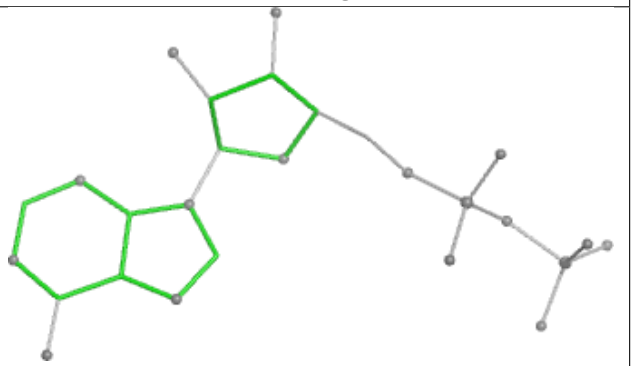
Bond lengths



Bond angles

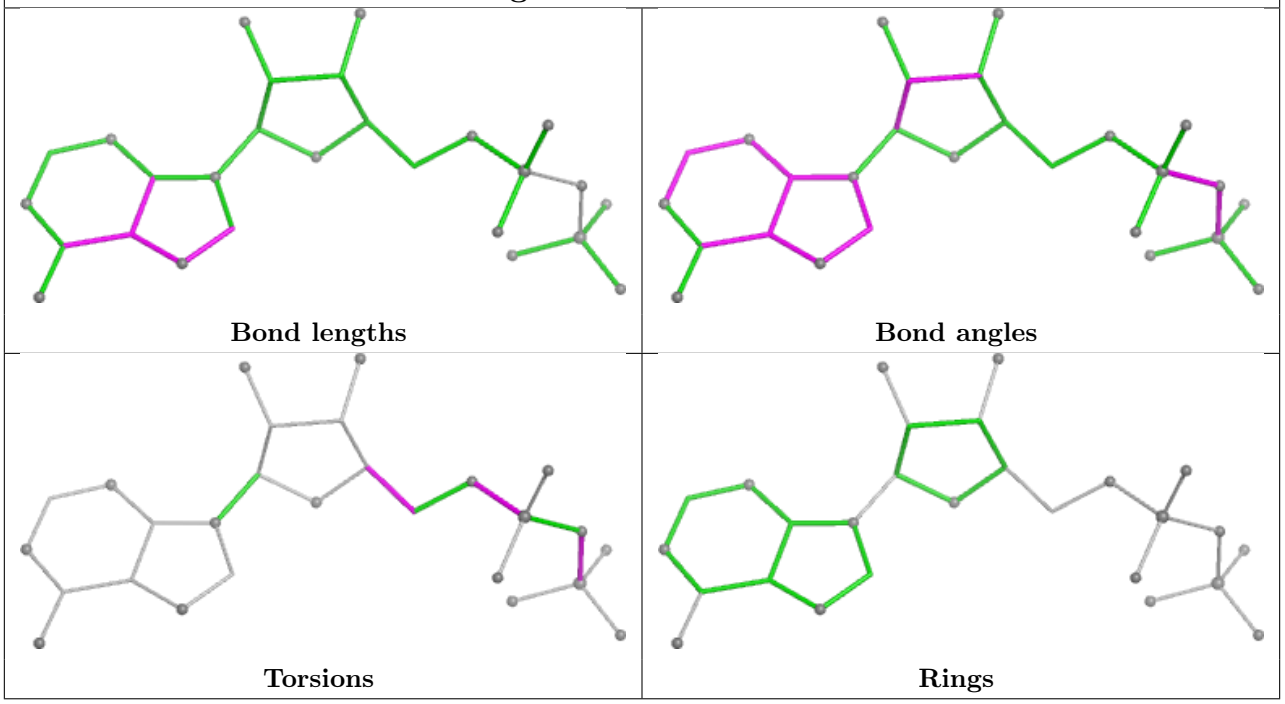


Torsions

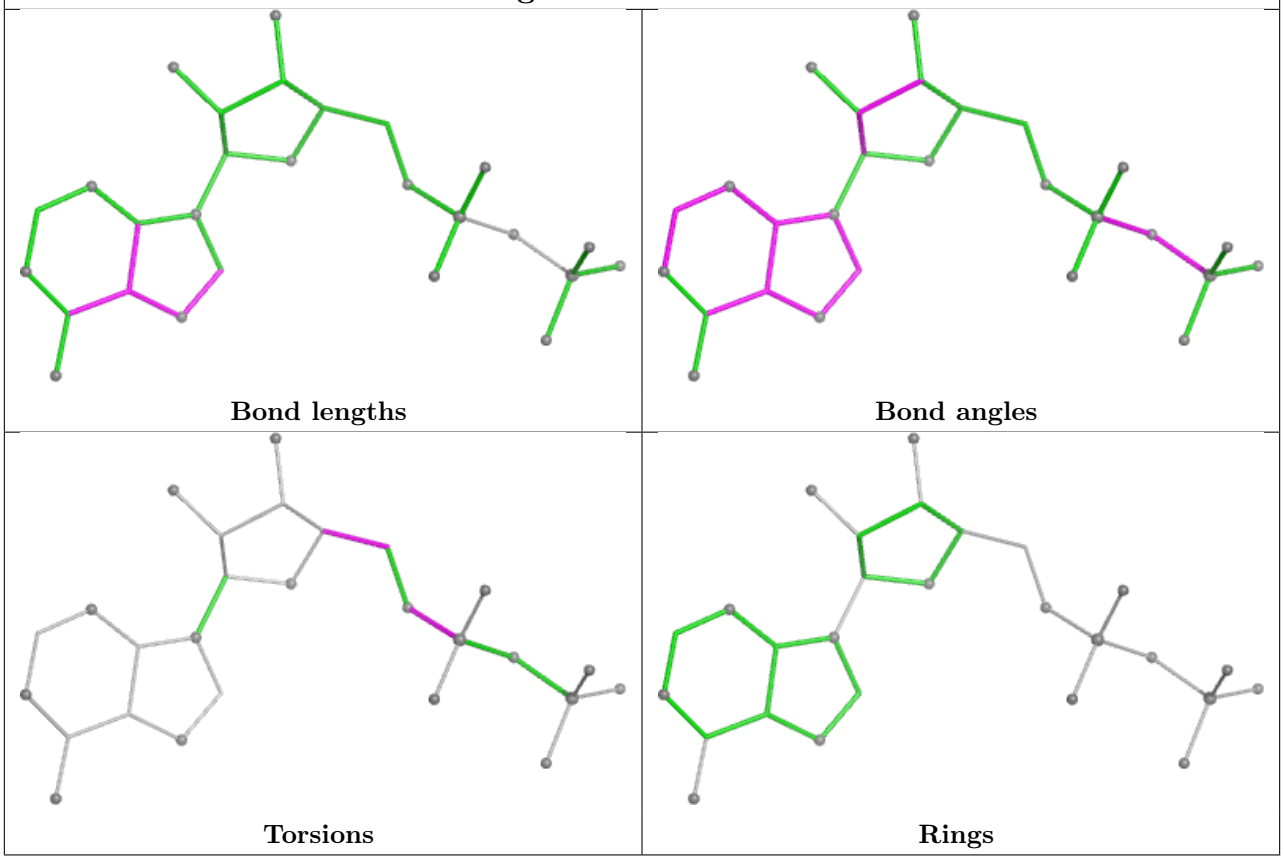


Rings

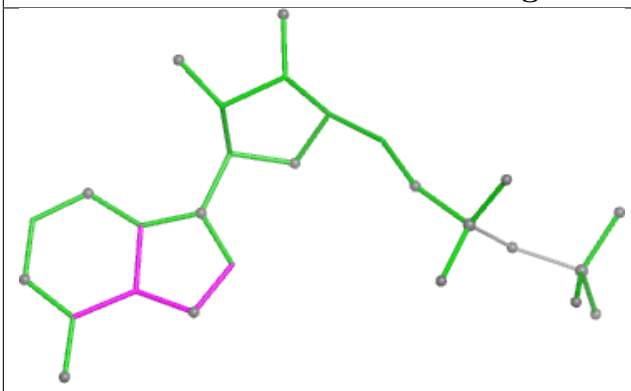
**Ligand ADP M 1601**



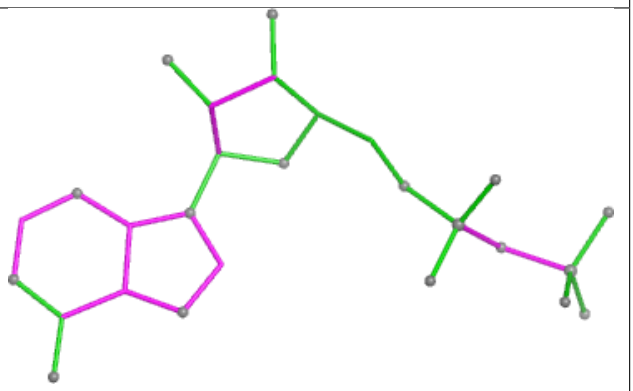

**Ligand ADP W 501**



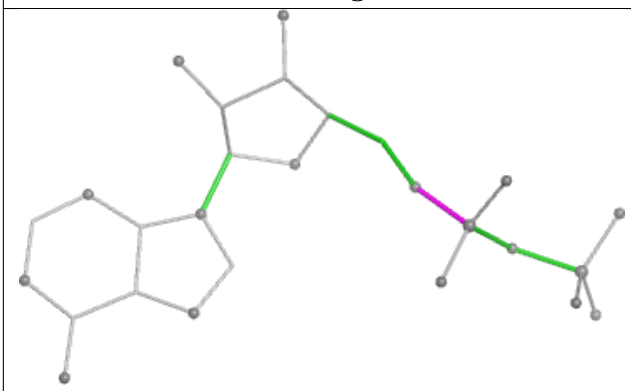
**Ligand ADP Y 501**



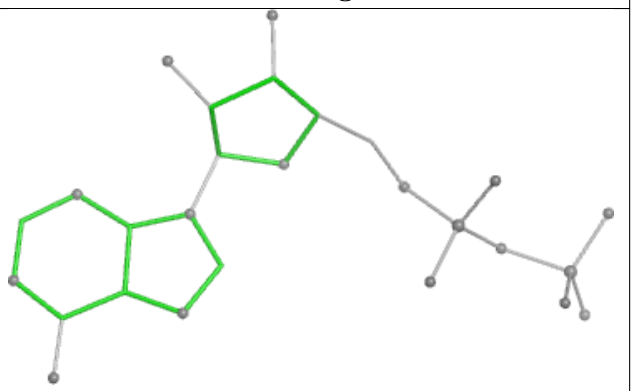
**Bond lengths**



**Bond angles**

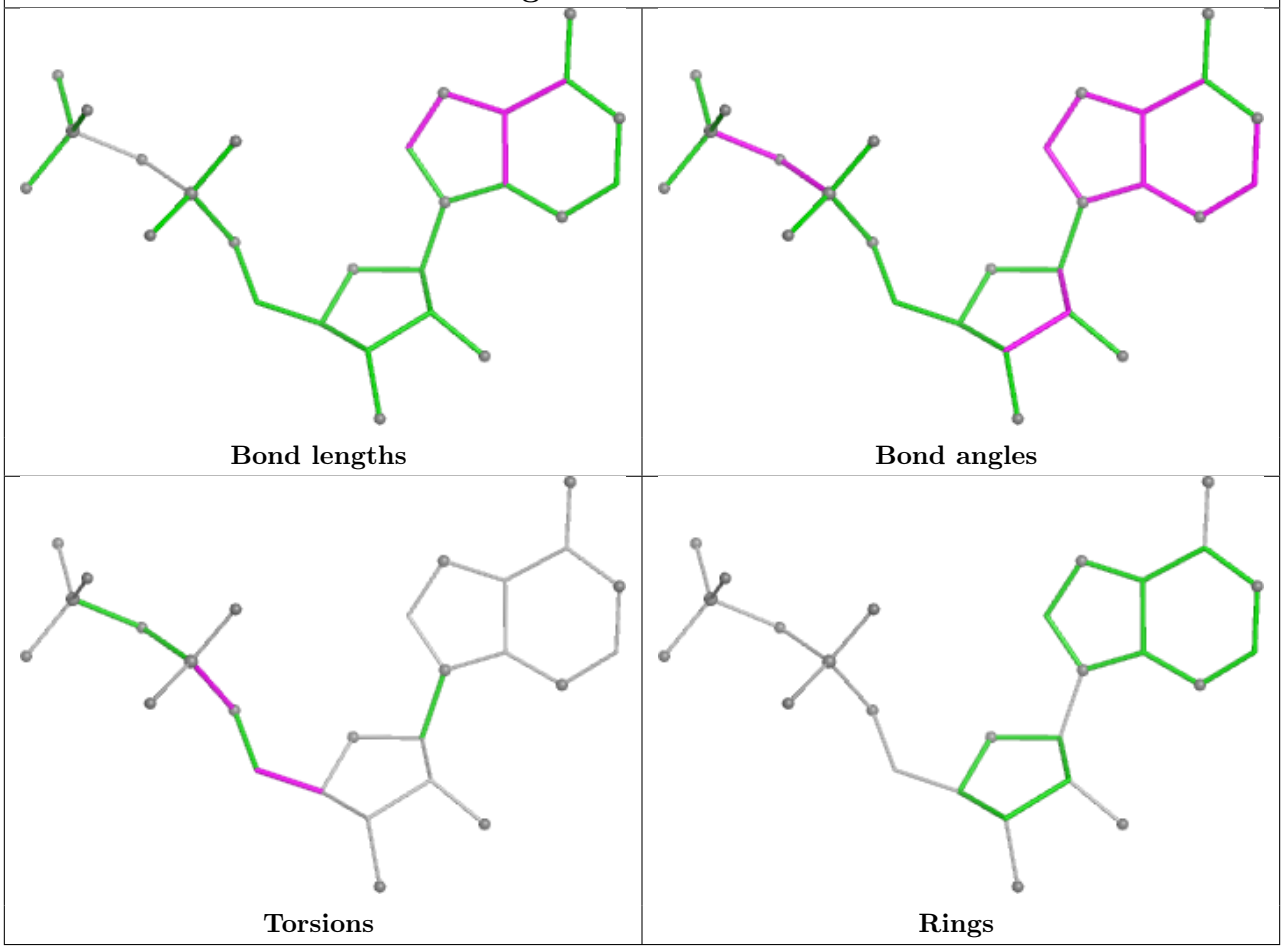


**Torsions**



**Rings**

**Ligand ADP U 502**




## 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.

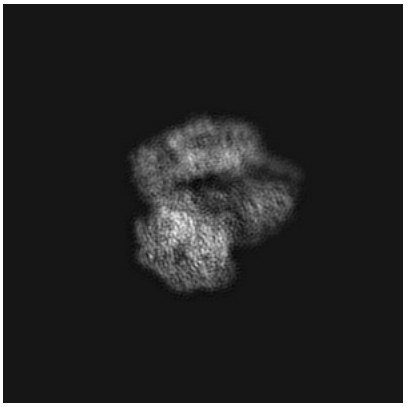
# 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-4395. These allow visual inspection of the internal detail of the map and identification of artifacts.

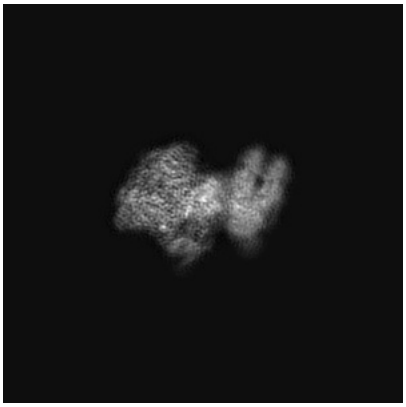
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

## 6.1 Orthogonal projections

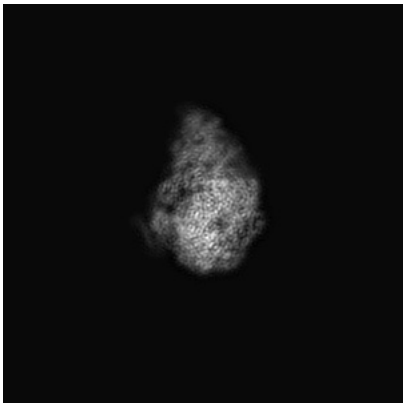
### 6.1.1 Primary map



X



Y

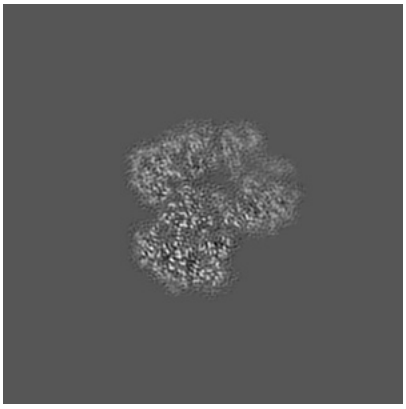


Z

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

## 6.2 Central slices

### 6.2.1 Primary map



X Index: 192



Y Index: 192

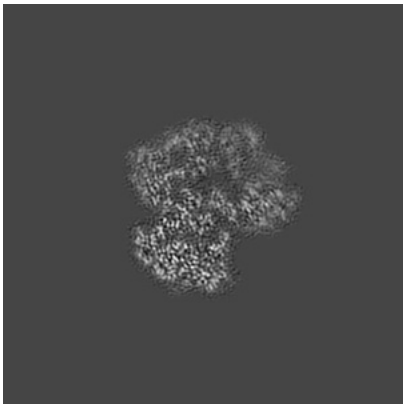


Z Index: 192

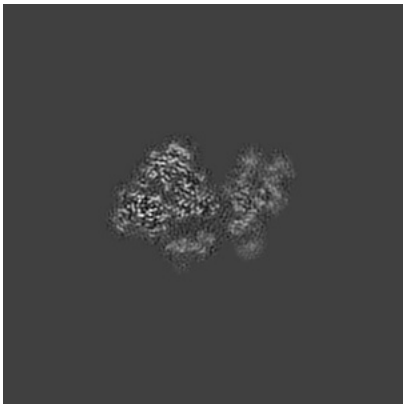
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices (i)

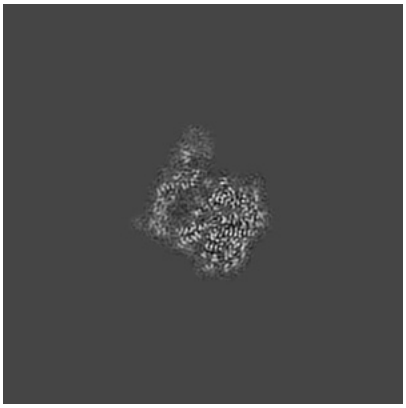
### 6.3.1 Primary map



X Index: 195



Y Index: 181

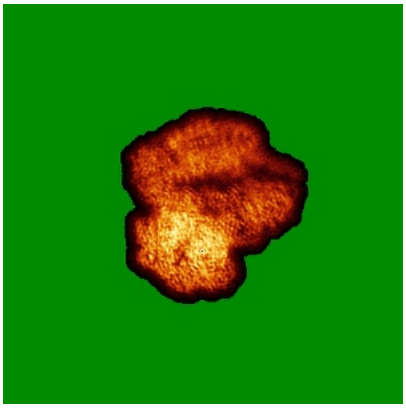


Z Index: 164

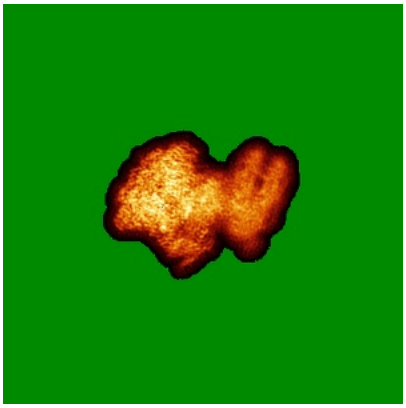
The images above show the largest variance slices of the map in three orthogonal directions.

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

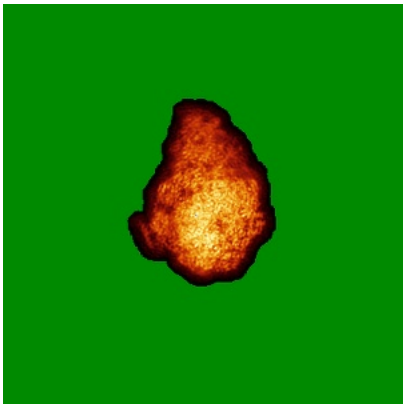
### 6.4.1 Primary map



X



Y

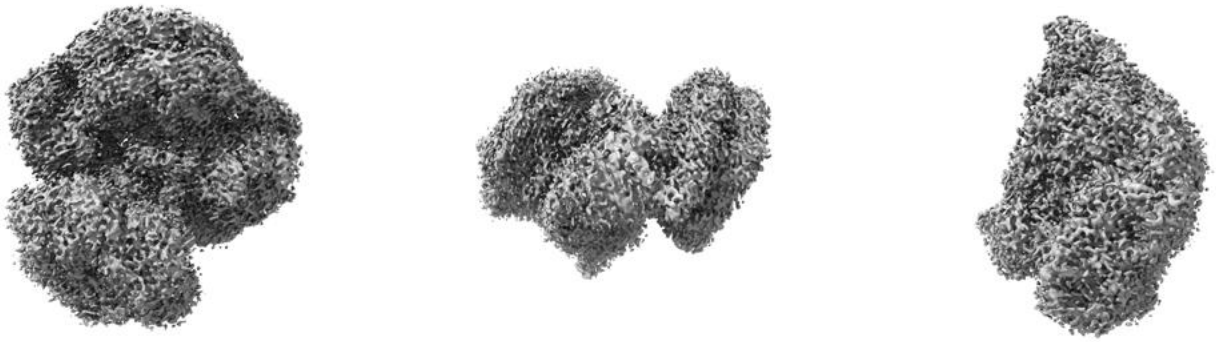


Z

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 0.0295. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

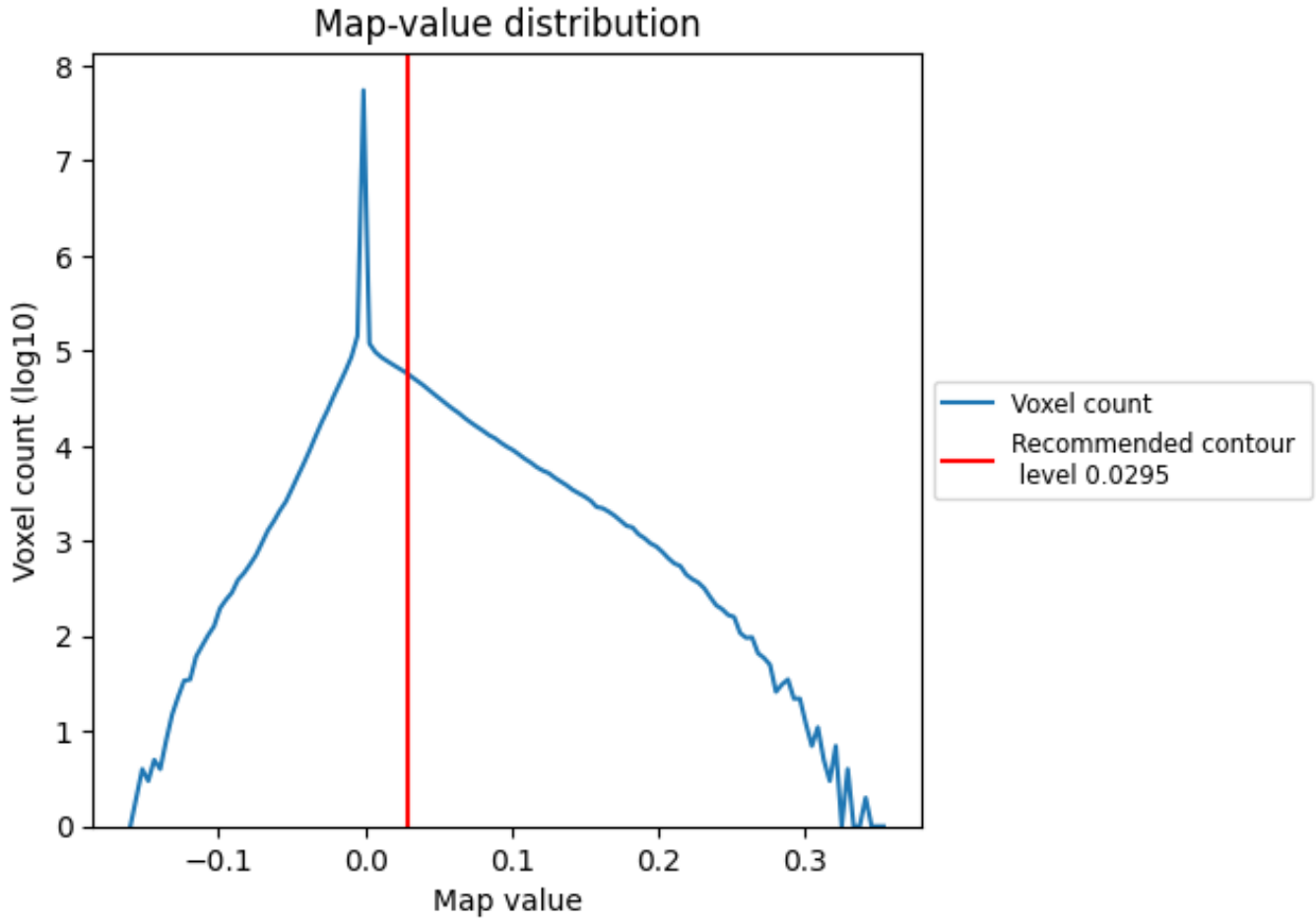
## 6.6 Mask visualisation (i)

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

# 7 Map analysis

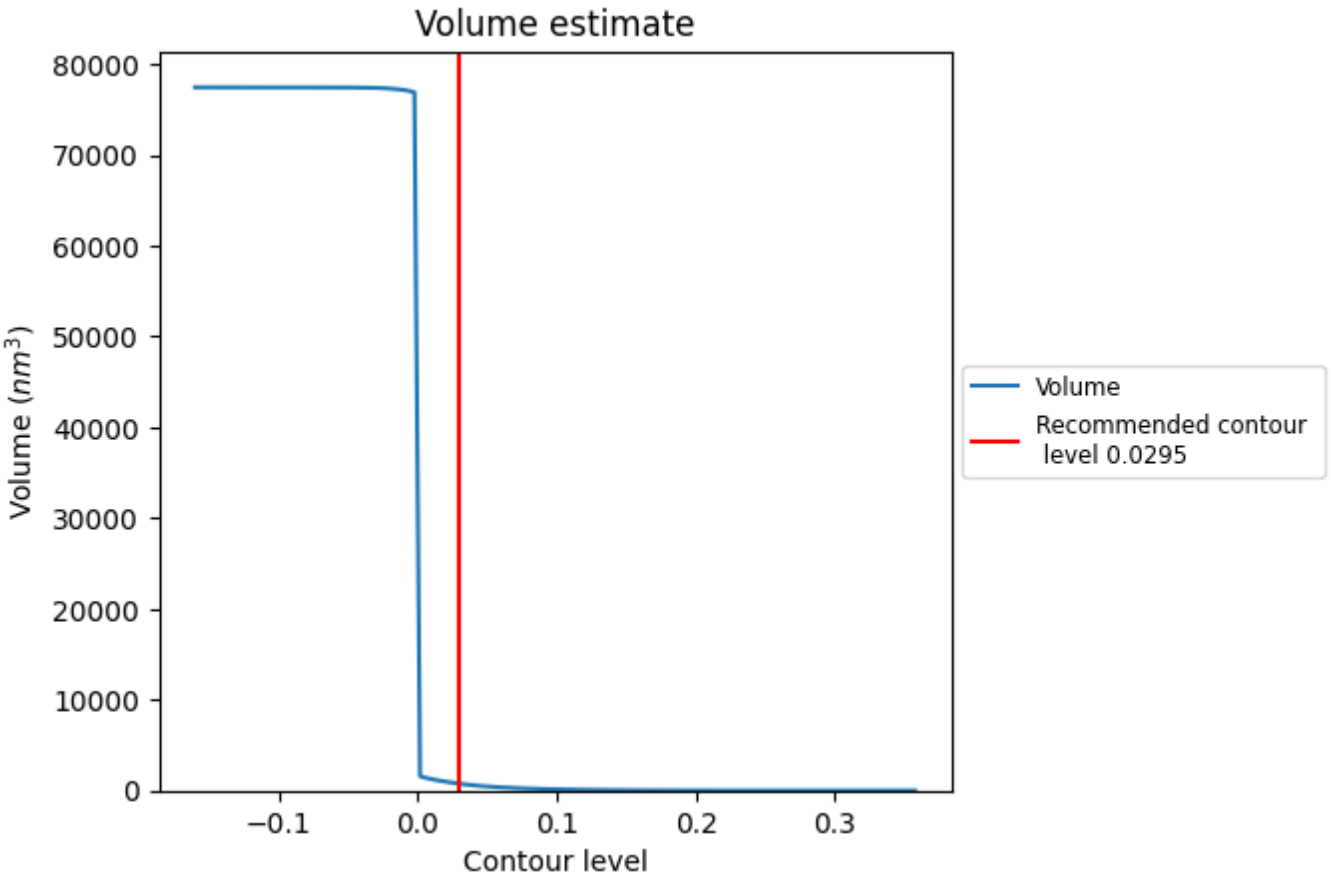
This section contains the results of statistical analysis of the map.

## 7.1 Map-value distribution




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.

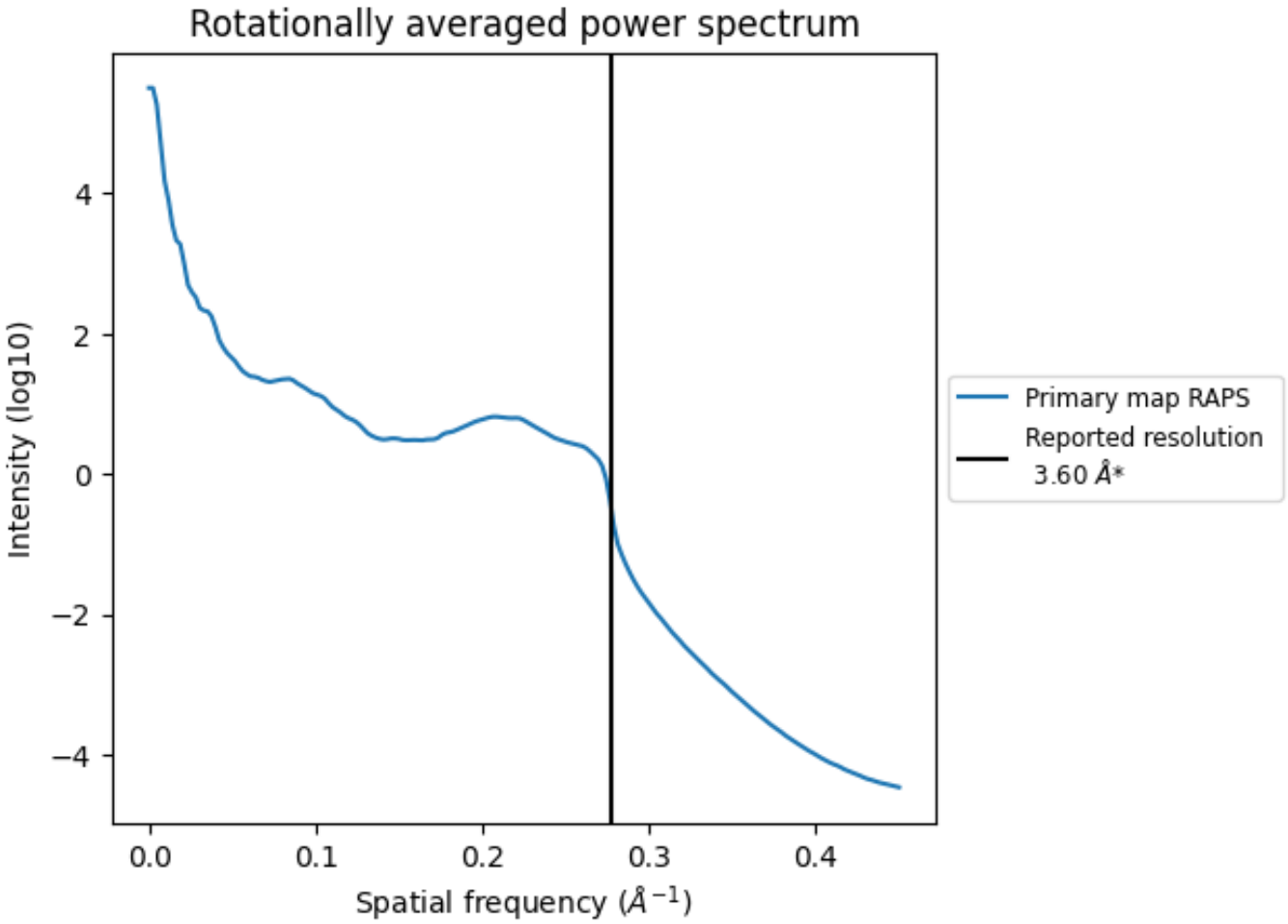
## 7.2 Volume estimate (i)




The volume at the recommended contour level is 765 $nm^3$; this corresponds to an approximate mass of 691 kDa.

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

## 7.3 Rotationally averaged power spectrum (i)




*Reported resolution corresponds to spatial frequency of 0.278 Å$^{-1}$

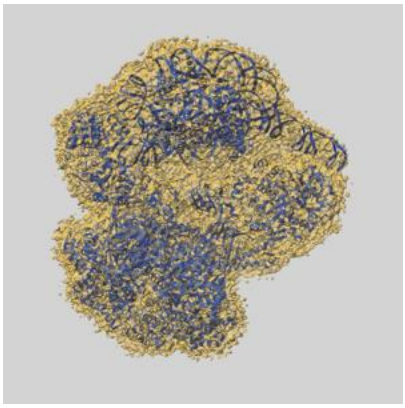
# 8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

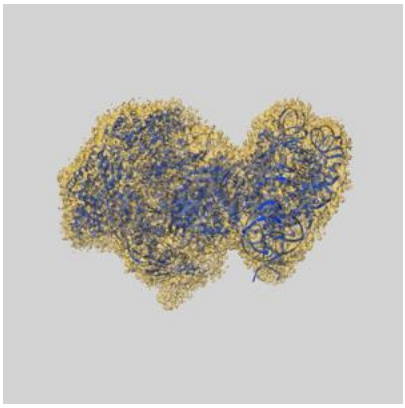
# 9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-4395 and PDB model 6GEJ. Per-residue inclusion information can be found in section 3 on page 9.

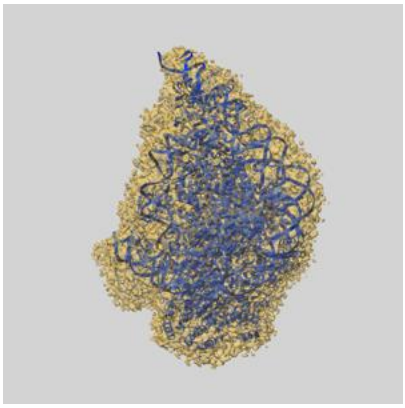
## 9.1 Map-model overlay



X



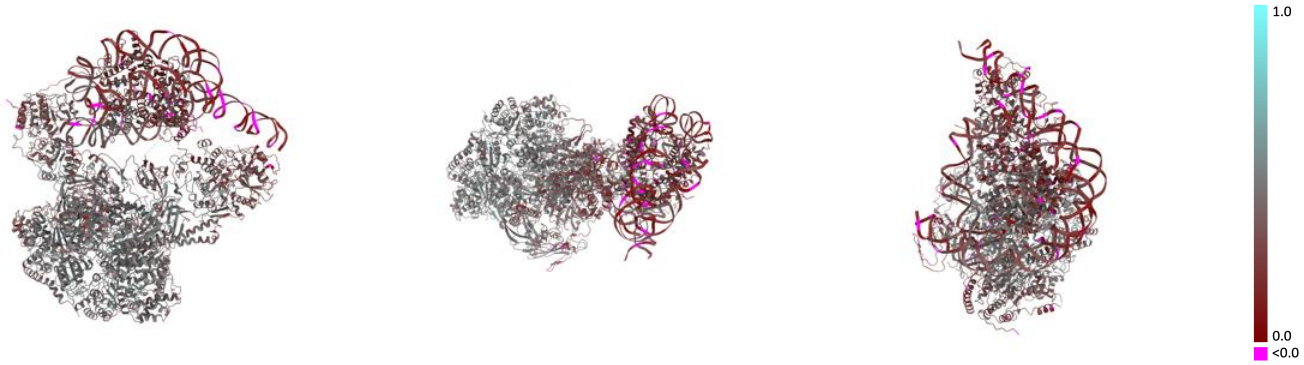
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0295 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.

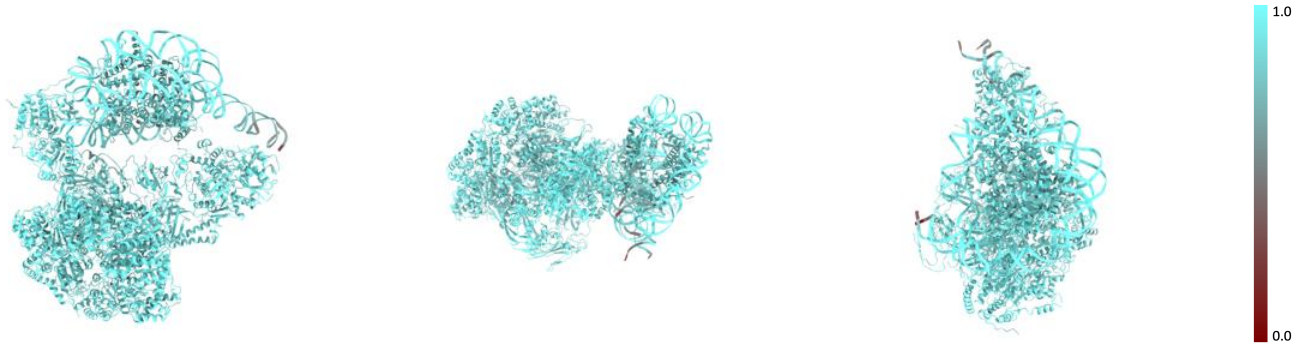
## 9.2 Q-score mapped to coordinate model




X Y Z

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.

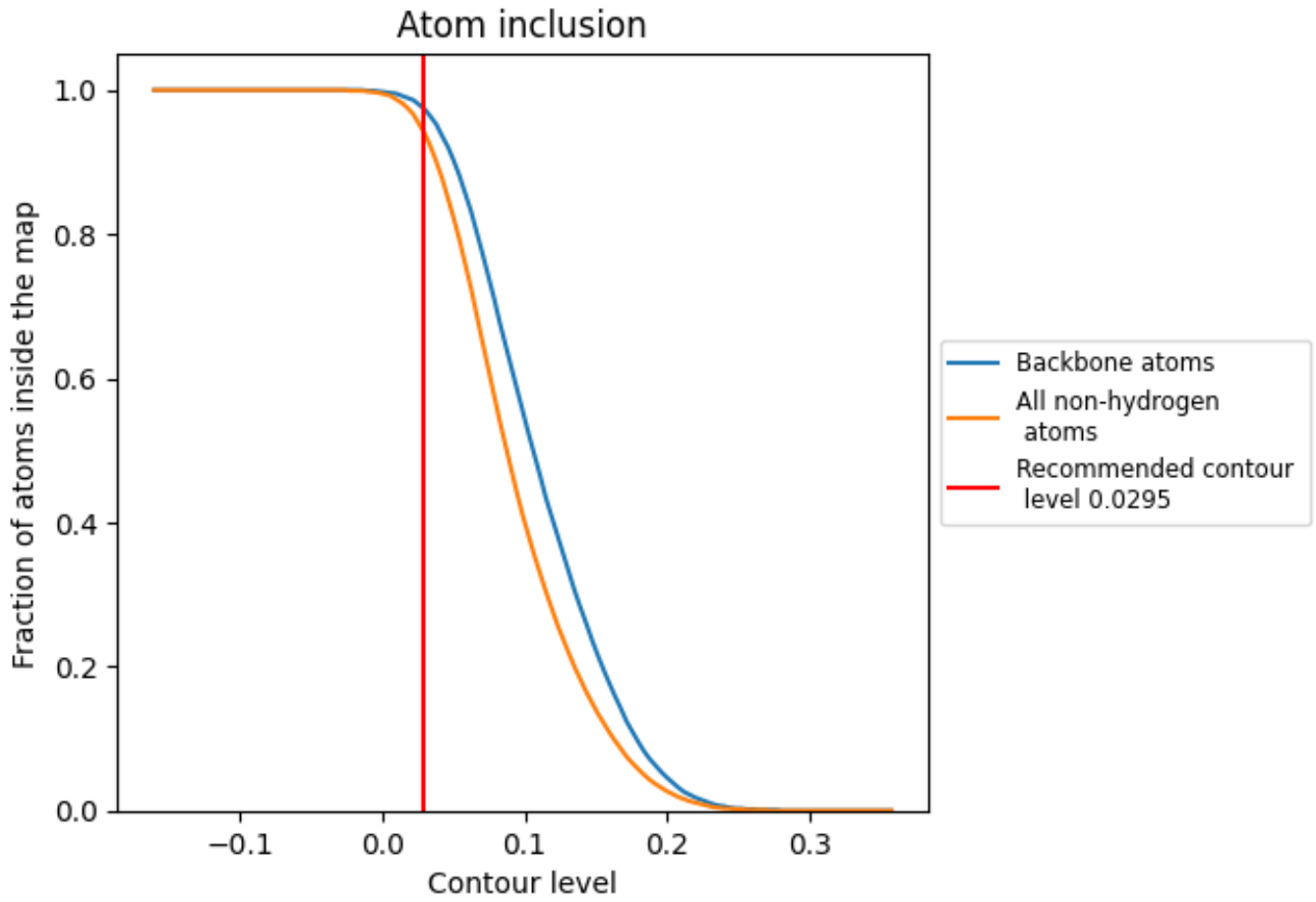
## 9.3 Atom inclusion mapped to coordinate model




X Y Z

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 (0.0295).

## 9.4 Atom inclusion (i)




At the recommended contour level, 97% of all backbone atoms, 94% 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 (0.0295) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|---|---|---|
| All | 0.9410 | 0.3720 |
| A | 0.9050 | 0.2700 |
| B | 0.9220 | 0.3700 |
| C | 0.9090 | 0.3840 |
| D | 0.8940 | 0.2810 |
| E | 0.9340 | 0.3170 |
| F | 0.8800 | 0.2360 |
| G | 0.9170 | 0.2980 |
| H | 0.8790 | 0.2390 |
| I | 0.9220 | 0.2000 |
| J | 0.9340 | 0.2240 |
| M | 0.9560 | 0.3960 |
| R | 0.9420 | 0.3640 |
| S | 0.8890 | 0.3130 |
| T | 0.9560 | 0.4520 |
| U | 0.9470 | 0.4380 |
| V | 0.9520 | 0.4460 |
| W | 0.9600 | 0.4570 |
| X | 0.9580 | 0.4440 |
| Y | 0.9650 | 0.4540 |
| Z | 0.9210 | 0.2110 |

