



## wwPDB EM Validation Summary Report ⓘ

Mar 4, 2026 – 08:26 PM UTC

PDB ID : 7ZTS / pdb\_00007zts  
EMDB ID : EMD-14963  
Title : Saccharomyces cerevisiae L-BC virus, open particle, asymmetric reconstruction  
Authors : Grybchuk, D.; Prochazkova, M.; Fuzik, T.; Konovalovas, A.; Serva, S.; Yurchenko, V.; Plevka, P.  
Deposited on : 2022-05-11  
Resolution : 16.00 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

The types of validation reports are described at

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

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

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

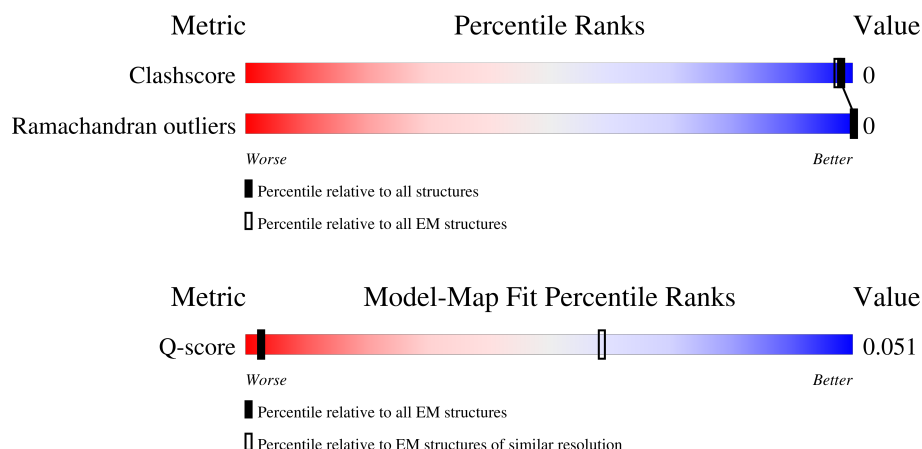
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 16.00 Å.

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



| Metric                | Whole archive<br>(#Entries) | EM structures<br>(#Entries) | Similar EM resolution<br>(#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|-----------------------------|----------------------------------------------------------|
| Clashscore            | 229148                      | 23984                       | -                                                        |
| Ramachandran outliers | 224038                      | 23583                       | -                                                        |
| Q-score               | -                           | 25397                       | 41 ( 15.50 - 16.50 )                                     |

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

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1   | AA    | 697    |                  |
| 1   | AB    | 697    |                  |
| 1   | AC    | 697    |                  |
| 1   | AD    | 697    |                  |
| 1   | AE    | 697    |                  |

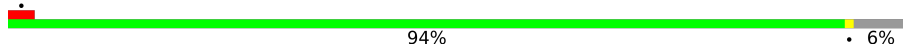
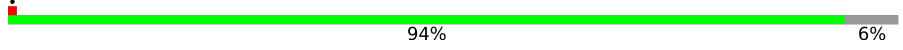
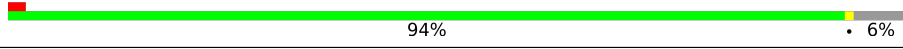
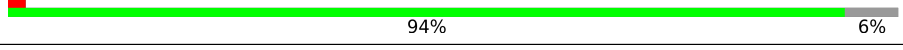
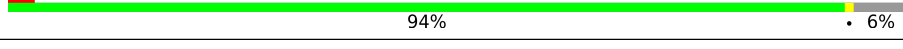
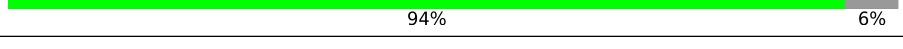
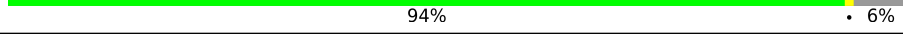
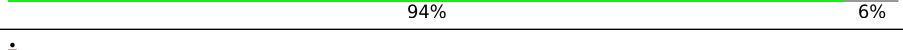
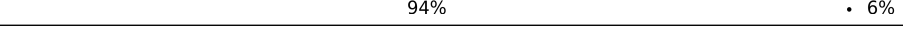
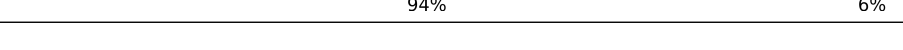
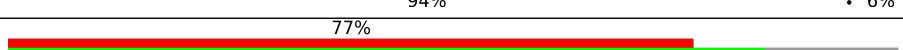
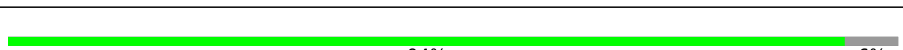
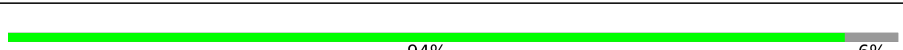
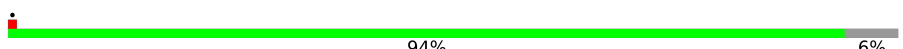
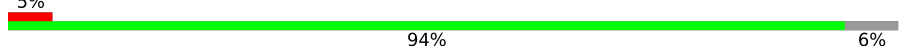
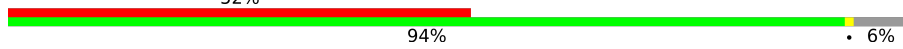
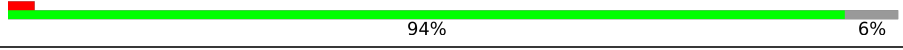
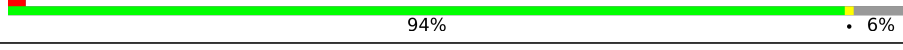
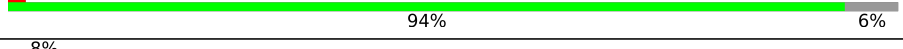
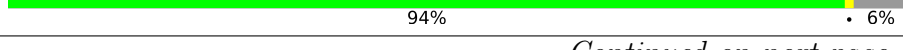
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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1   | AF    | 697    |                  |
| 1   | AG    | 697    |                  |
| 1   | AH    | 697    |                  |
| 1   | AI    | 697    |                  |
| 1   | AJ    | 697    |                  |
| 1   | AK    | 697    |                  |
| 1   | AL    | 697    |                  |
| 1   | AM    | 697    |                  |
| 1   | AN    | 697    |                  |
| 1   | AO    | 697    |                  |
| 1   | AP    | 697    |                  |
| 1   | AQ    | 697    |                  |
| 1   | AR    | 697    |                  |
| 1   | AS    | 697    |                  |
| 1   | AT    | 697    |                  |
| 1   | AU    | 697    |                  |
| 1   | AV    | 697    |                  |
| 1   | AW    | 697    |                  |
| 1   | AX    | 697    |                  |
| 1   | AY    | 697    |                  |
| 1   | AZ    | 697    |                  |
| 1   | BA    | 697    |                  |
| 1   | BB    | 697    |                  |
| 1   | BC    | 697    |                  |
| 1   | BD    | 697    |                  |

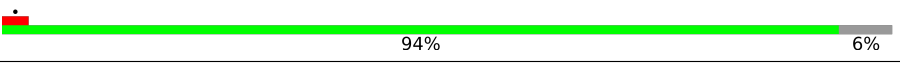
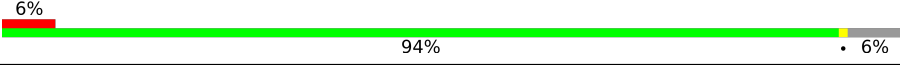
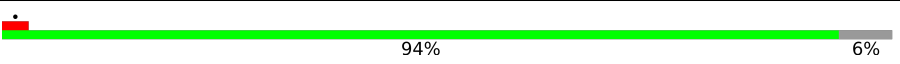
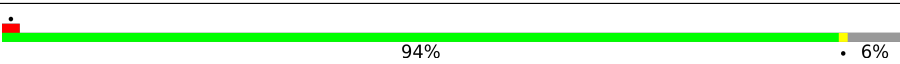
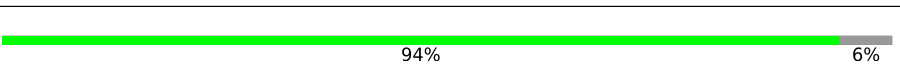
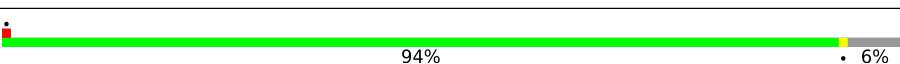
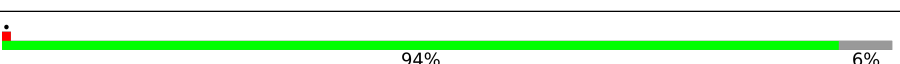
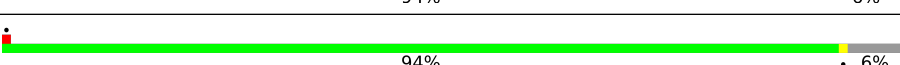
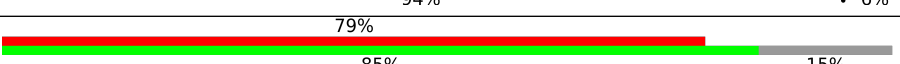
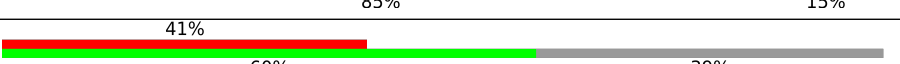
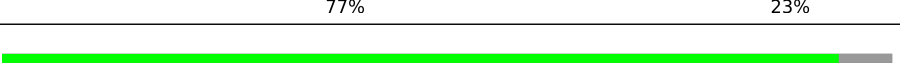
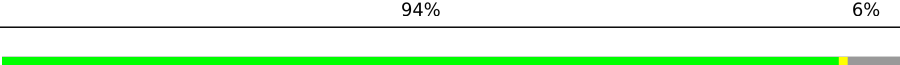
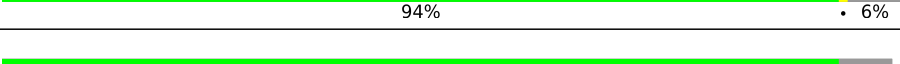
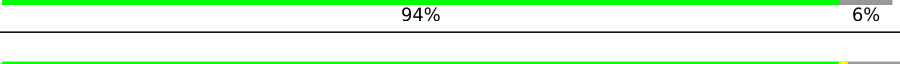
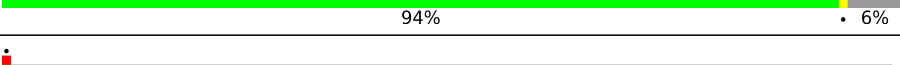
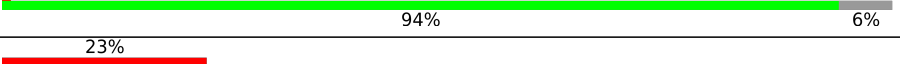
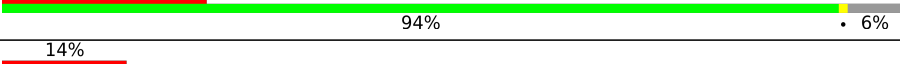
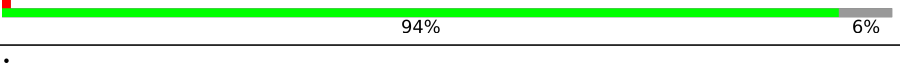
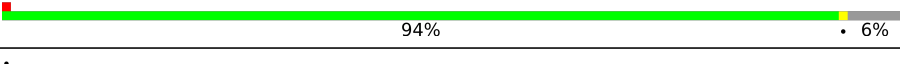
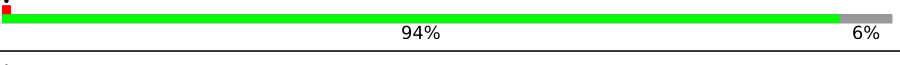
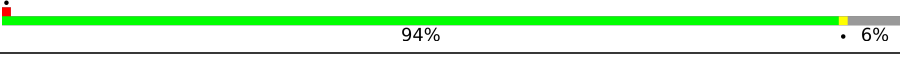
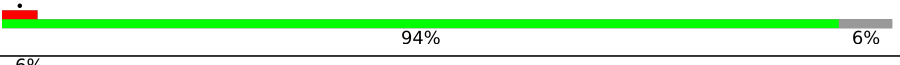
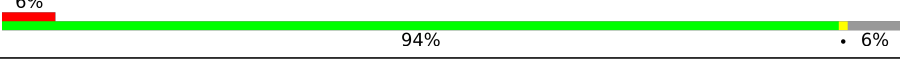
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| Mol | Chain | Length | Quality of chain                                                                     |
|-----|-------|--------|--------------------------------------------------------------------------------------|
| 1   | BE    | 697    |    |
| 1   | BF    | 697    |    |
| 1   | BG    | 697    |    |
| 1   | BH    | 697    |    |
| 1   | BI    | 697    |    |
| 1   | BJ    | 697    |    |
| 1   | BK    | 697    |    |
| 1   | BL    | 697    |    |
| 1   | BM    | 697    |    |
| 1   | BN    | 697    |    |
| 1   | BO    | 697    |    |
| 1   | BP    | 697    |  |
| 1   | BQ    | 697    |  |
| 1   | BR    | 697    |  |
| 1   | BS    | 697    |  |
| 1   | BT    | 697    |  |
| 1   | BU    | 697    |  |
| 1   | BV    | 697    |  |
| 1   | BW    | 697    |  |
| 1   | BX    | 697    |  |
| 1   | BY    | 697    |  |
| 1   | BZ    | 697    |  |
| 1   | CA    | 697    |  |
| 1   | CB    | 697    |  |
| 1   | CC    | 697    |  |

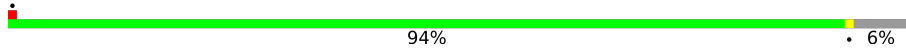
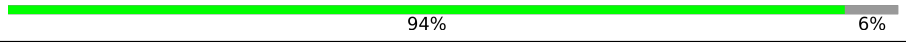
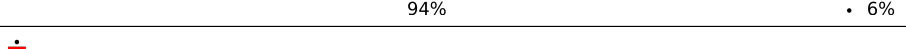
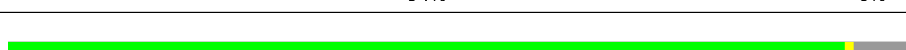
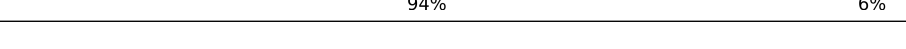
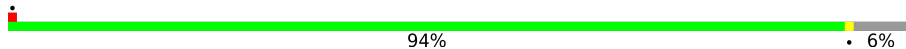
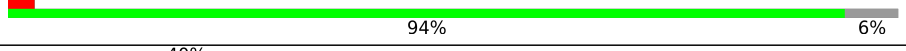
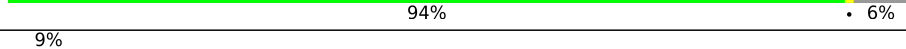
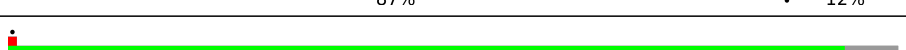
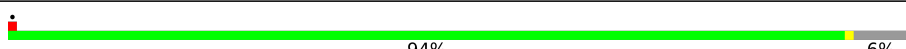
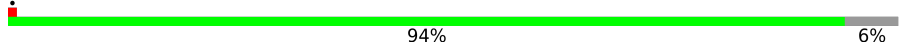
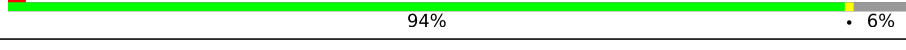
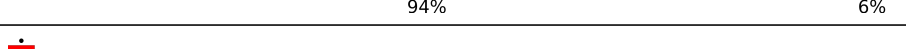
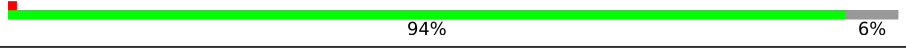
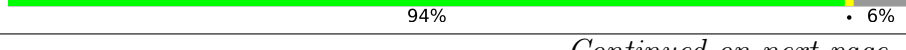
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| Mol | Chain | Length | Quality of chain                                                                     |
|-----|-------|--------|--------------------------------------------------------------------------------------|
| 1   | CD    | 697    |    |
| 1   | CE    | 697    |    |
| 1   | CF    | 697    |    |
| 1   | CG    | 697    |    |
| 1   | CH    | 697    |    |
| 1   | CI    | 697    |    |
| 1   | CJ    | 697    |    |
| 1   | CK    | 697    |    |
| 1   | CL    | 697    |    |
| 1   | CM    | 697    |    |
| 1   | CN    | 697    |    |
| 1   | CO    | 697    |    |
| 1   | CP    | 697    |   |
| 1   | CQ    | 697    |  |
| 1   | CR    | 697    |  |
| 1   | CS    | 697    |  |
| 1   | CT    | 697    |  |
| 1   | CU    | 697    |  |
| 1   | CV    | 697    |  |
| 1   | CW    | 697    |  |
| 1   | CX    | 697    |  |
| 1   | CY    | 697    |  |
| 1   | CZ    | 697    |  |
| 1   | DA    | 697    |  |
| 1   | DB    | 697    |  |

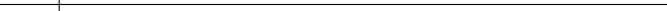
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| Mol | Chain | Length | Quality of chain                                                                     |
|-----|-------|--------|--------------------------------------------------------------------------------------|
| 1   | DC    | 697    |    |
| 1   | DD    | 697    |    |
| 1   | DE    | 697    |    |
| 1   | DF    | 697    |    |
| 1   | DG    | 697    |    |
| 1   | DH    | 697    |    |
| 1   | DI    | 697    |    |
| 1   | DJ    | 697    |    |
| 1   | DK    | 697    |    |
| 1   | DL    | 697    |   |
| 1   | DM    | 697    |  |
| 1   | DN    | 697    |  |
| 1   | DO    | 697    |  |
| 1   | DP    | 697    |  |
| 1   | DQ    | 697    |  |
| 1   | DR    | 697    |  |
| 1   | DS    | 697    |  |
| 1   | DT    | 697    |  |
| 1   | DU    | 697    |  |
| 1   | DV    | 697    |  |
| 1   | DW    | 697    |  |
| 1   | DX    | 697    |  |
| 1   | DY    | 697    |  |
| 1   | DZ    | 697    |  |
| 1   | EA    | 697    |  |

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| Mol | Chain | Length | Quality of chain                                                                   |
|-----|-------|--------|------------------------------------------------------------------------------------|
| 1   | EB    | 697    |  |
| 1   | EC    | 697    |  |
| 1   | ED    | 697    |  |
| 1   | EE    | 697    |  |
| 1   | EF    | 697    |  |

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 280400 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 Major capsid protein.

| Mol | Chain | Residues | Atoms |      |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 1   | AA    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | AB    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | AC    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | AD    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | AE    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | AF    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | AG    | 613      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2452  | 1226 | 613 | 613 |         |       |
| 1   | AH    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | AI    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | AJ    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | AK    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | AL    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | AM    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | AN    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | AO    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | AP    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | AQ    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |

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| Mol | Chain | Residues | Atoms |      |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 1   | AR    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | AS    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | AT    | 593      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2372  | 1186 | 593 | 593 |         |       |
| 1   | AU    | 422      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 1692  | 846  | 423 | 423 |         |       |
| 1   | AV    | 538      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2152  | 1076 | 538 | 538 |         |       |
| 1   | AW    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | AX    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | AY    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | AZ    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | BA    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | BB    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | BC    | 613      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2452  | 1226 | 613 | 613 |         |       |
| 1   | BD    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | BE    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | BF    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | BG    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | BH    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | BI    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | BJ    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | BK    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | BL    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |

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| Mol | Chain | Residues | Atoms |      |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 1   | BM    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | BN    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | BO    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | BP    | 593      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2372  | 1186 | 593 | 593 |         |       |
| 1   | BQ    | 422      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 1692  | 846  | 423 | 423 |         |       |
| 1   | BR    | 538      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2152  | 1076 | 538 | 538 |         |       |
| 1   | BS    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | BT    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | BU    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | BV    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | BW    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | BX    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | BY    | 613      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2452  | 1226 | 613 | 613 |         |       |
| 1   | BZ    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | CA    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | CB    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | CC    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | CD    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | CE    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | CF    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | CG    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |

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| Mol | Chain | Residues | Atoms |      |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 1   | CH    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | CI    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | CJ    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | CK    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | CL    | 593      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2372  | 1186 | 593 | 593 |         |       |
| 1   | CM    | 422      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 1692  | 846  | 423 | 423 |         |       |
| 1   | CN    | 538      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2152  | 1076 | 538 | 538 |         |       |
| 1   | CO    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | CP    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | CQ    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | CR    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | CS    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | CT    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | CU    | 613      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2452  | 1226 | 613 | 613 |         |       |
| 1   | CV    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | CW    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | CX    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | CY    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | CZ    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | DA    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | DB    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |

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| Mol | Chain | Residues | Atoms |      |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 1   | DC    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | DD    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | DE    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | DF    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | DG    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | DH    | 593      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2372  | 1186 | 593 | 593 |         |       |
| 1   | DI    | 422      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 1692  | 846  | 423 | 423 |         |       |
| 1   | DJ    | 538      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2152  | 1076 | 538 | 538 |         |       |
| 1   | DK    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | DL    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | DM    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | DN    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | DO    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | DP    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | DQ    | 613      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2452  | 1226 | 613 | 613 |         |       |
| 1   | DR    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | DS    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | DT    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | DU    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | DV    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | DW    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |

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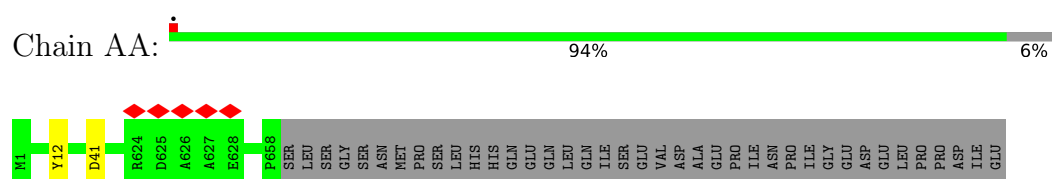
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| Mol | Chain | Residues | Atoms |      |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 1   | DX    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | DY    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | DZ    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | EA    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | EB    | 658      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 2636  | 1318 | 659 | 659 |         |       |
| 1   | EC    | 658      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2632  | 1316 | 658 | 658 |         |       |
| 1   | ED    | 593      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2372  | 1186 | 593 | 593 |         |       |
| 1   | EE    | 422      | Total | C    | N   | O   | 1       | 0     |
|     |       |          | 1692  | 846  | 423 | 423 |         |       |
| 1   | EF    | 538      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 2152  | 1076 | 538 | 538 |         |       |

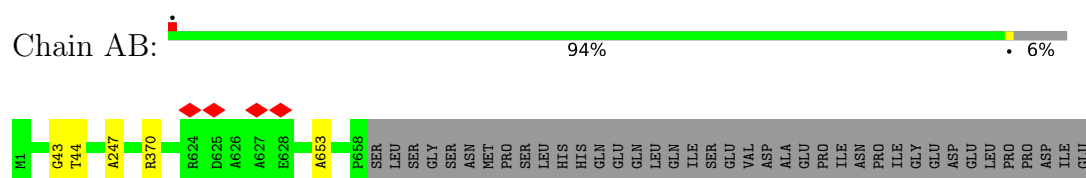
### 3 Residue-property plots

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

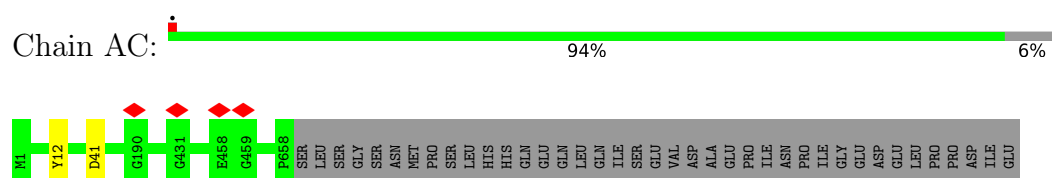
- Molecule 1: Major capsid protein



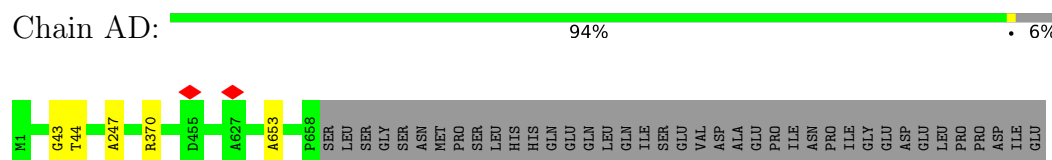
- Molecule 1: Major capsid protein



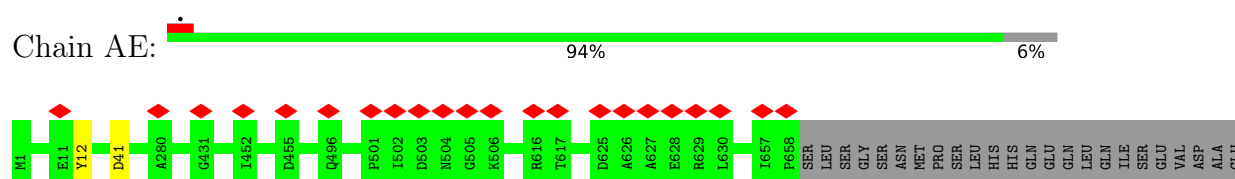
- Molecule 1: Major capsid protein



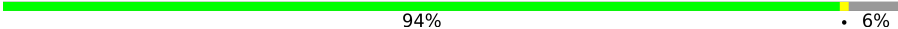
- Molecule 1: Major capsid protein

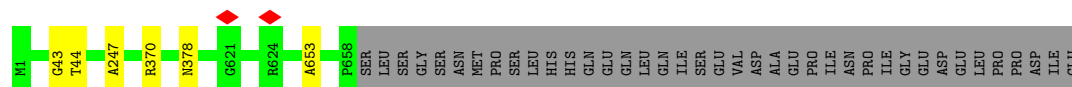


- Molecule 1: Major capsid protein

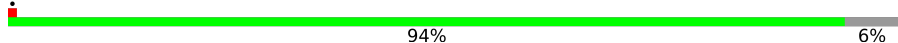


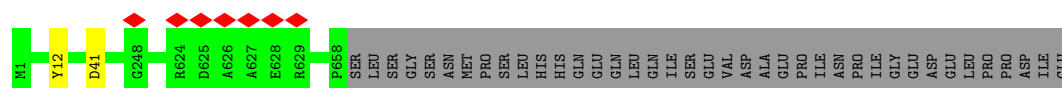


Chain AI:  94% 6%

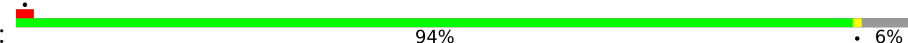


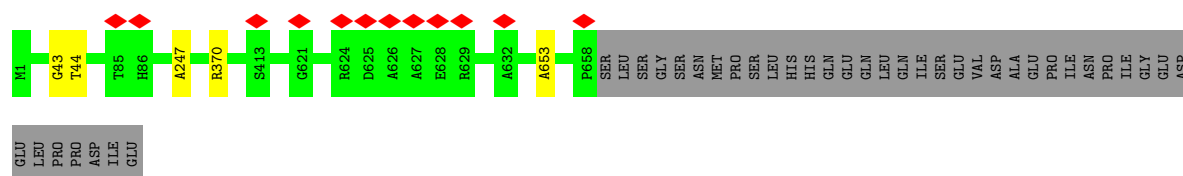
- Molecule 1: Major capsid protein

Chain AJ:  94% 6%

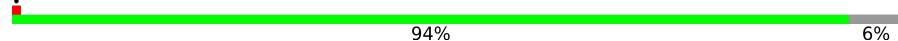


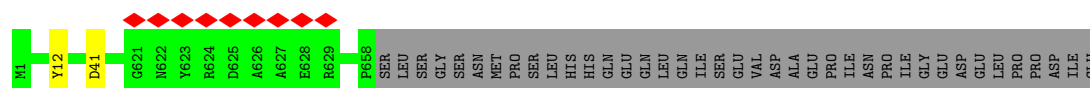
- Molecule 1: Major capsid protein

Chain AK:  94% 6%

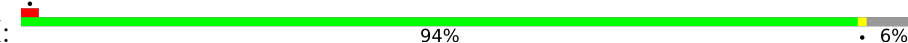


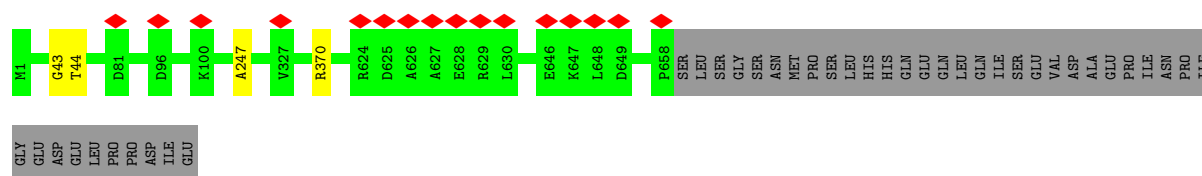
- Molecule 1: Major capsid protein

Chain AL:  94% 6%

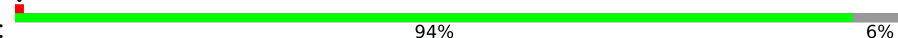


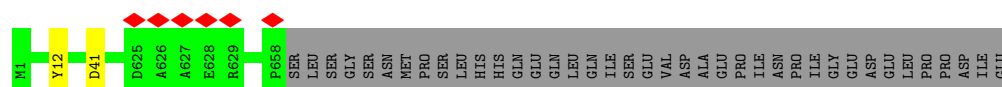
- Molecule 1: Major capsid protein

Chain AM:  94% 6%



- Molecule 1: Major capsid protein

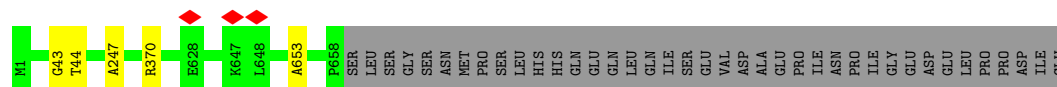
Chain AN:  94% 6%



- Molecule 1: Major capsid protein

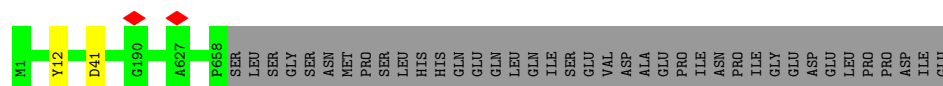


Chain AO:  94% 6%



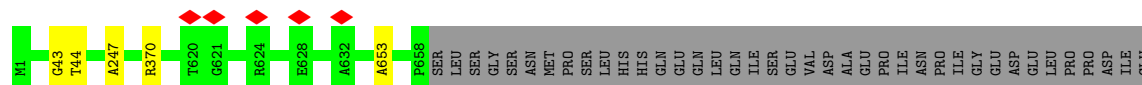
- Molecule 1: Major capsid protein

Chain AP:  94% 6%



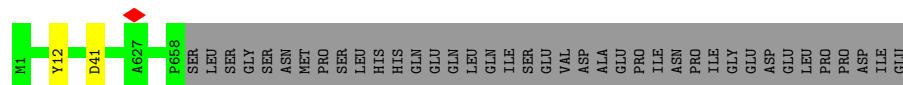
- Molecule 1: Major capsid protein

Chain AQ:  94% 6%



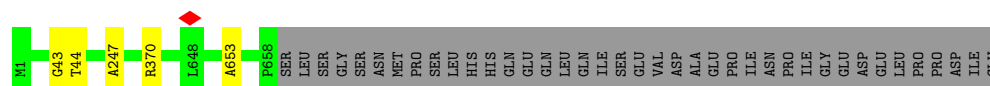
- Molecule 1: Major capsid protein

Chain AR:  94% 6%



- Molecule 1: Major capsid protein

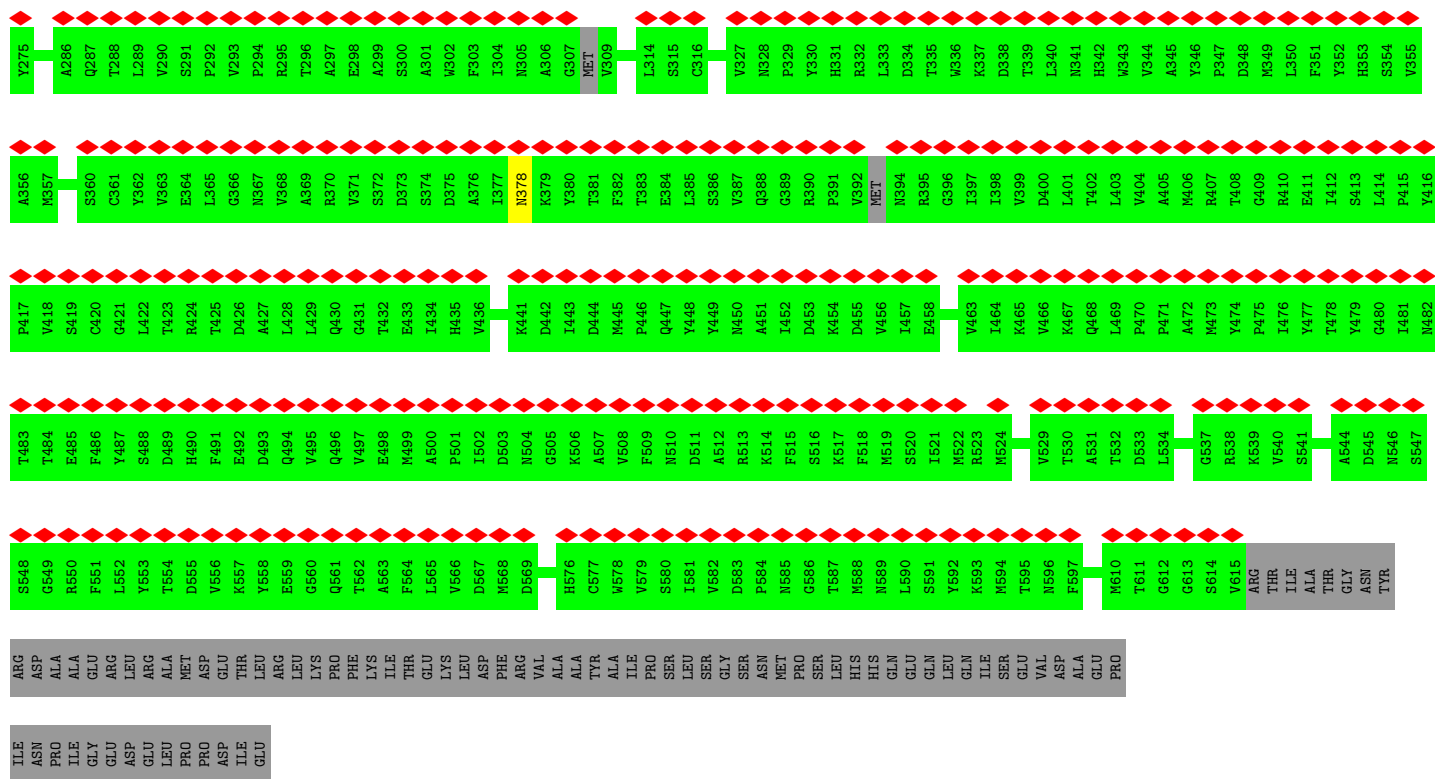
Chain AS:  94% 6%



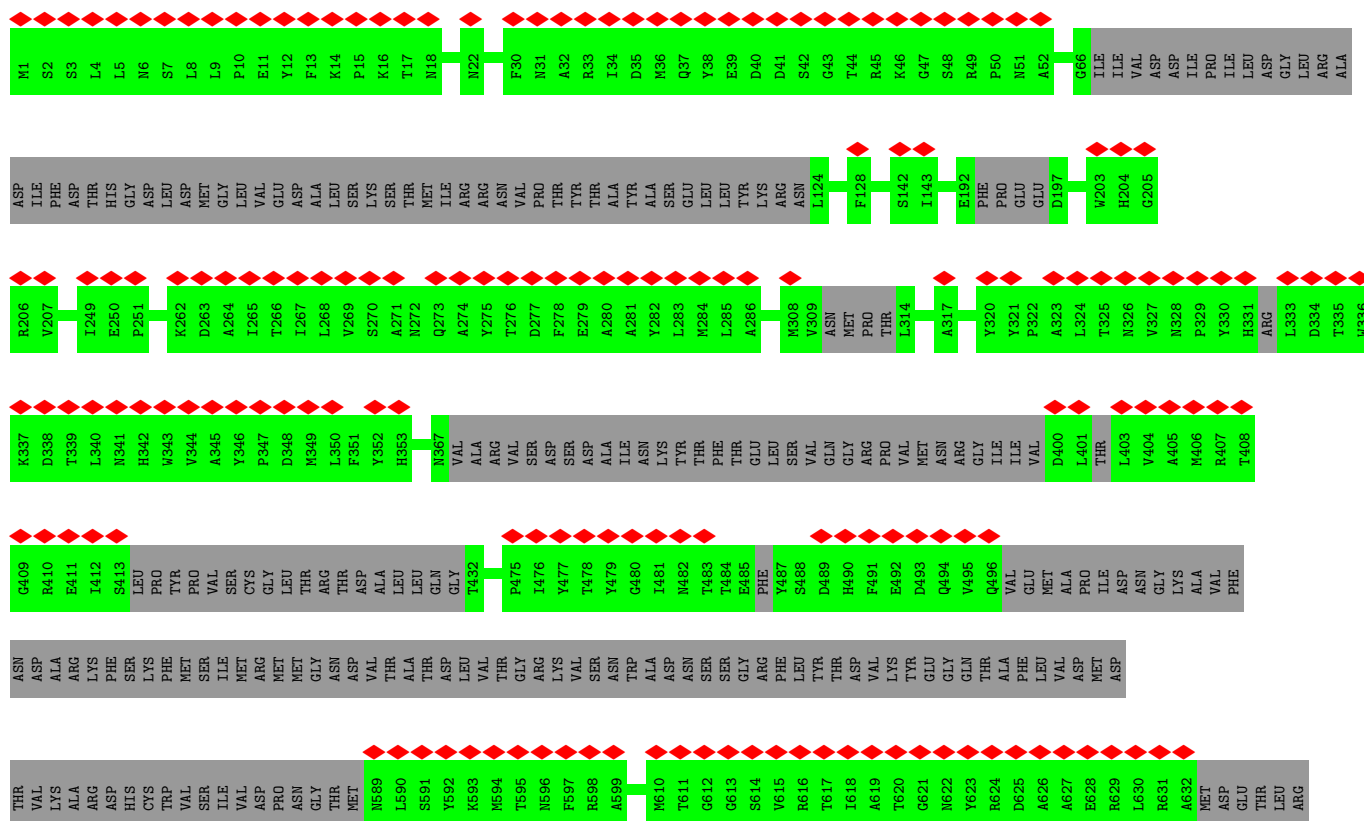
- Molecule 1: Major capsid protein

Chain AT:  60% 85% 15%





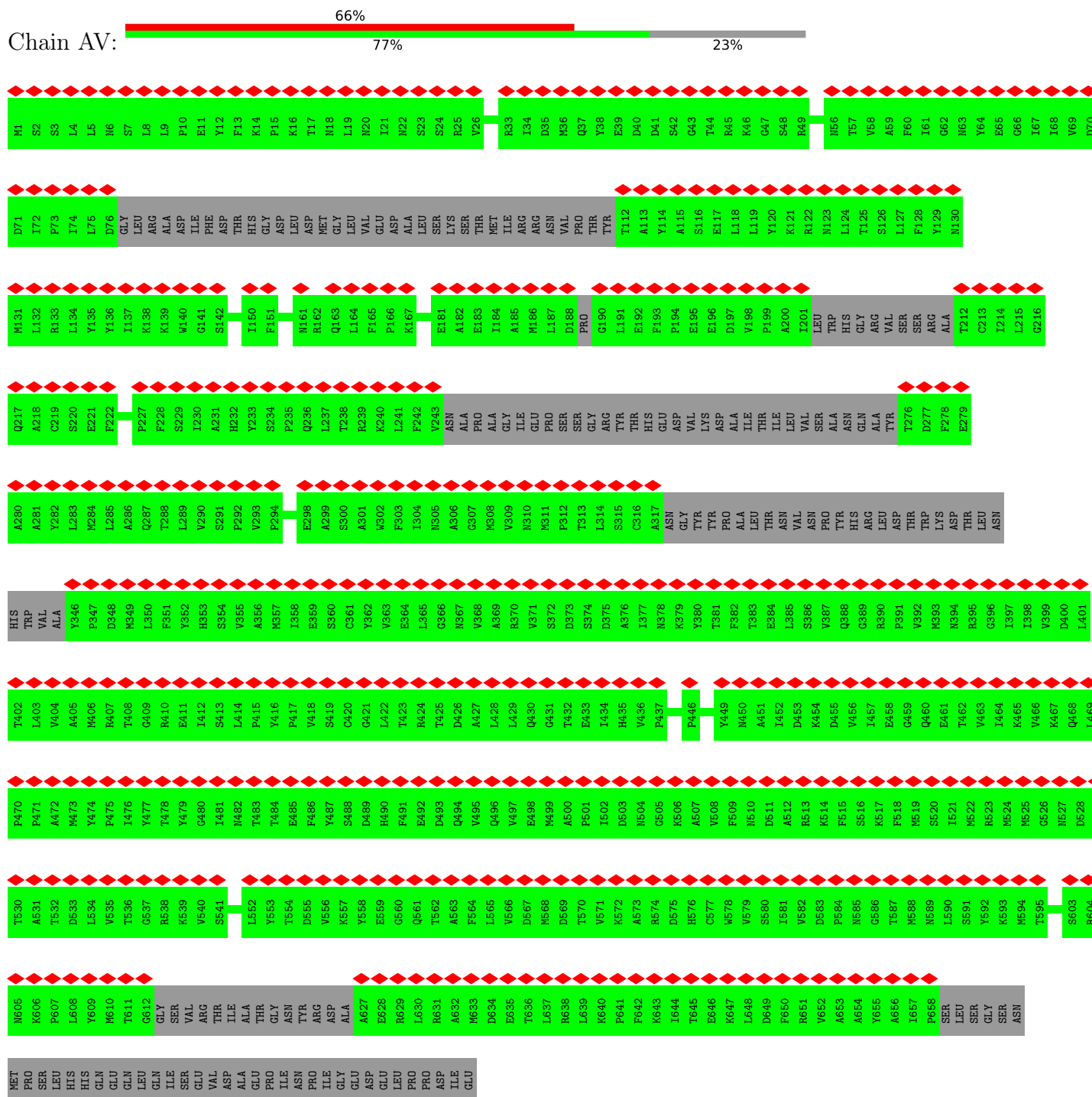
• Molecule 1: Major capsid protein



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

• Molecule 1: Major capsid protein

Chain AV:

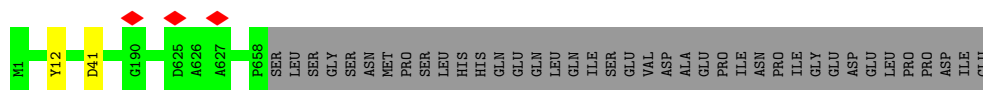


• Molecule 1: Major capsid protein

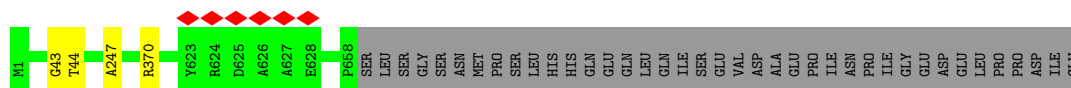
Chain AW:

94%

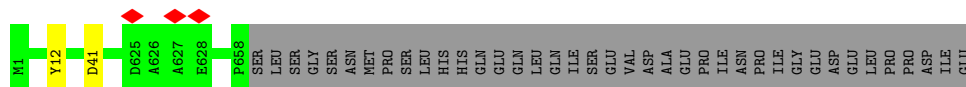
6%



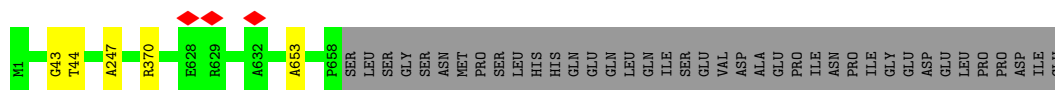
- Molecule 1: Major capsid protein



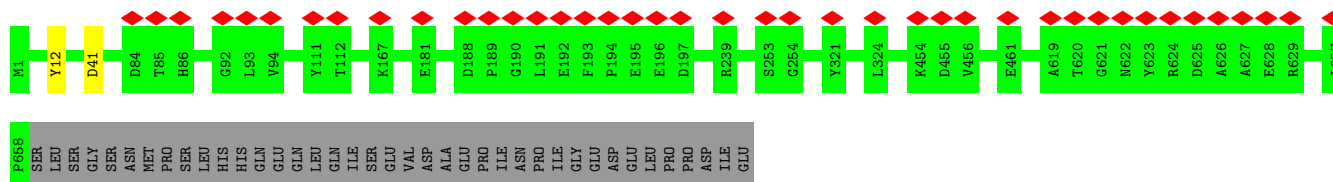
- Molecule 1: Major capsid protein



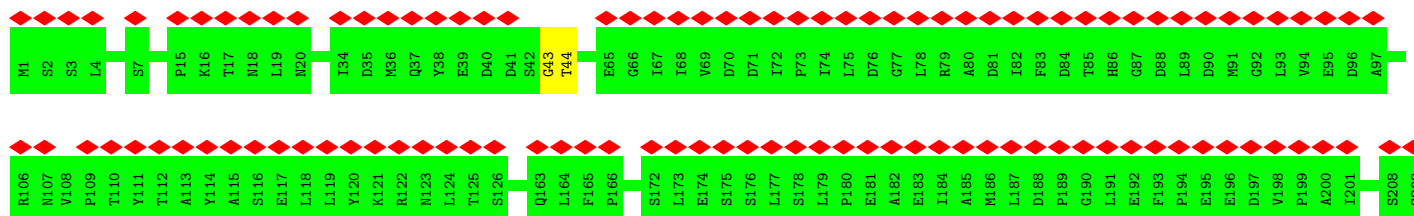
- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein



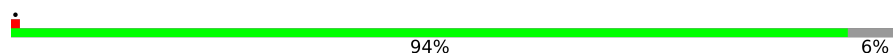
- Molecule 1: Major capsid protein





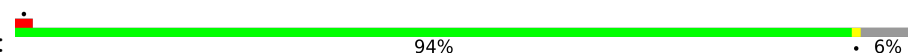
ILE  
SER  
GLU  
VAL  
ASP  
ALA  
GLU  
PRO  
ILE  
ASN  
PRO  
ILE  
GLY  
GLU  
ASP  
GLU  
LEU  
PRO  
PRO  
ASP  
ILE  
GLU

- Molecule 1: Major capsid protein

Chain BF:  94% 6%

W1 Y12 D41 G190 D625 A626 A627 E628 R629 P658  
SER LEU SER GLY SER ASN MET PRO SER LEU HIS HIS GLN GLU LEU LEU ILE SER GLU VAL ASP ALA GLU PRO ILE ILE GLY ASP GLU LEU PRO PRO ASP ILE GLU

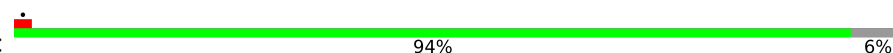
- Molecule 1: Major capsid protein

Chain BG:  94% 6%

W1 G43 T44 A247 D334 R370 A619 T620 G621 R624 D625 A626 A627 E628 R629 L630 R631 A632 M633 T645 E646 K647 A653 P658  
SER LEU SER GLY SER ASN MET PRO SER LEU HIS HIS GLN GLU LEU LEU ILE ILE SER SER VAL ASP ALA GLU PRO PRO ILE ILE ASN

PRO  
ILE  
GLU  
GLU  
ASP  
GLU  
LEU  
PRO  
ASP  
ILE  
GLU

- Molecule 1: Major capsid protein

Chain BH:  94% 6%

W1 Y12 D41 T85 S142 D188 P189 G190 I457 E458 G459 Q460 N622 Y623 R624 D625 A626 A627 E628 R629 P658  
SER LEU SER GLY SER ASN MET PRO SER LEU HIS HIS GLN GLN GLN ILE SER GLU VAL ASP ALA GLU PRO PRO ILE ILE GLY GLU

ASP  
GLU  
LEU  
PRO  
PRO  
ASP  
ILE  
GLU

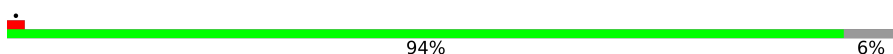
- Molecule 1: Major capsid protein

Chain BI:  94% 6%

W1 G43 T44 T85 K100 S175 A247 S253 G254 R370 G459 T536 G537 G621 N622 Y623 R624 D625 A626 A627 E628 R629 L630 R631 A632 M633 D634 K647 L648 A653 P658  
SER LEU SER GLY SER ASN MET PRO SER LEU HIS HIS GLN GLN GLN ILE SER LEU GLY SER ASP ALA GLU PRO PRO ILE ILE GLN GLN LEU

GLN  
ILE  
SER  
GLU  
VAL  
ASP  
ALA  
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GLY  
ASP  
GLU  
LEU  
PRO  
ASP  
ILE  
GLU

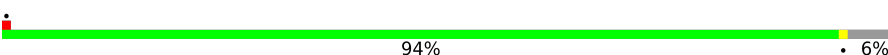
- Molecule 1: Major capsid protein

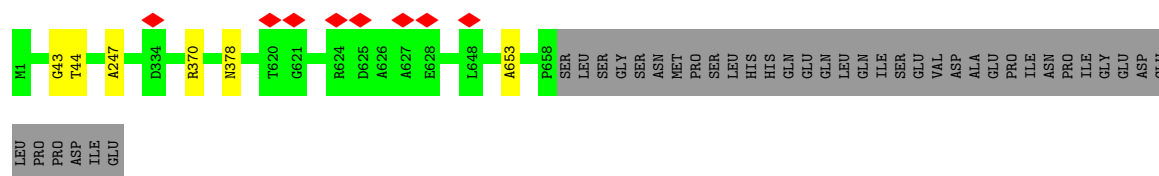
Chain BJ:  94% 6%

W1 E11 Y12 D41 S142 D148 E174 S175 T443 T457 E458 T570 D625 A626 A627 E628 P658  
SER LEU SER GLY SER ASN MET PRO SER LEU HIS HIS GLN GLN GLN ILE SER LEU VAL ASP ALA GLU PRO ILE ILE ASN PRO ILE ILE GLY GLU ASP

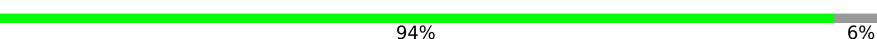
GLU  
LEU  
PRO  
PRO  
ASP  
ILE  
GLU

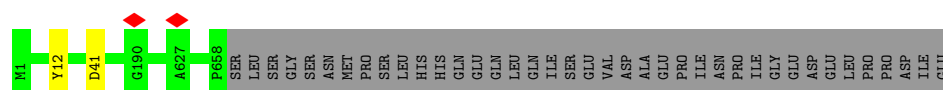
- Molecule 1: Major capsid protein

Chain BK:  94% 6%

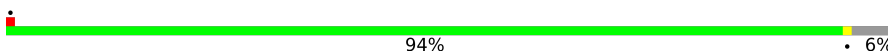


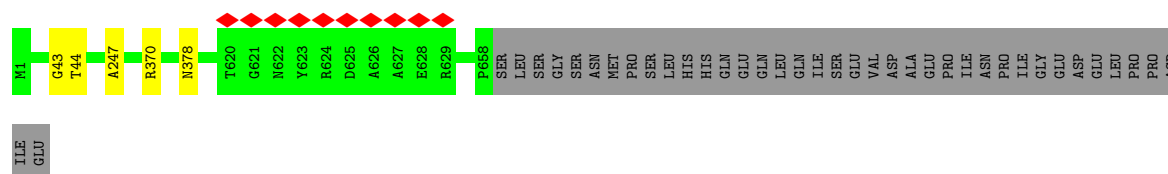
- Molecule 1: Major capsid protein

Chain BL:  94% 6%

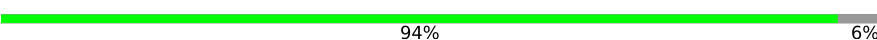


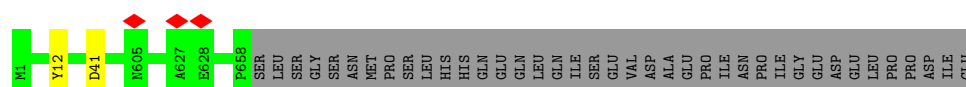
- Molecule 1: Major capsid protein

Chain BM:  94% 6%

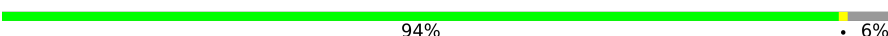


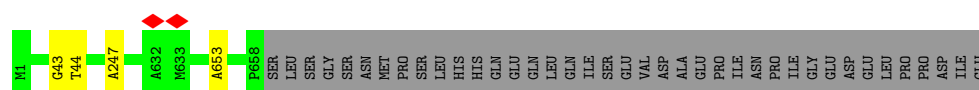
- Molecule 1: Major capsid protein

Chain BN:  94% 6%



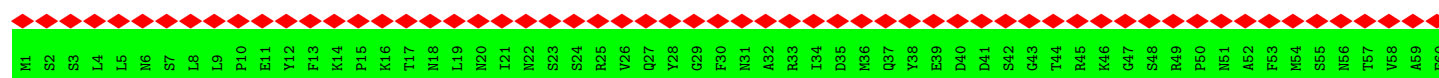
- Molecule 1: Major capsid protein

Chain BO:  94% 6%



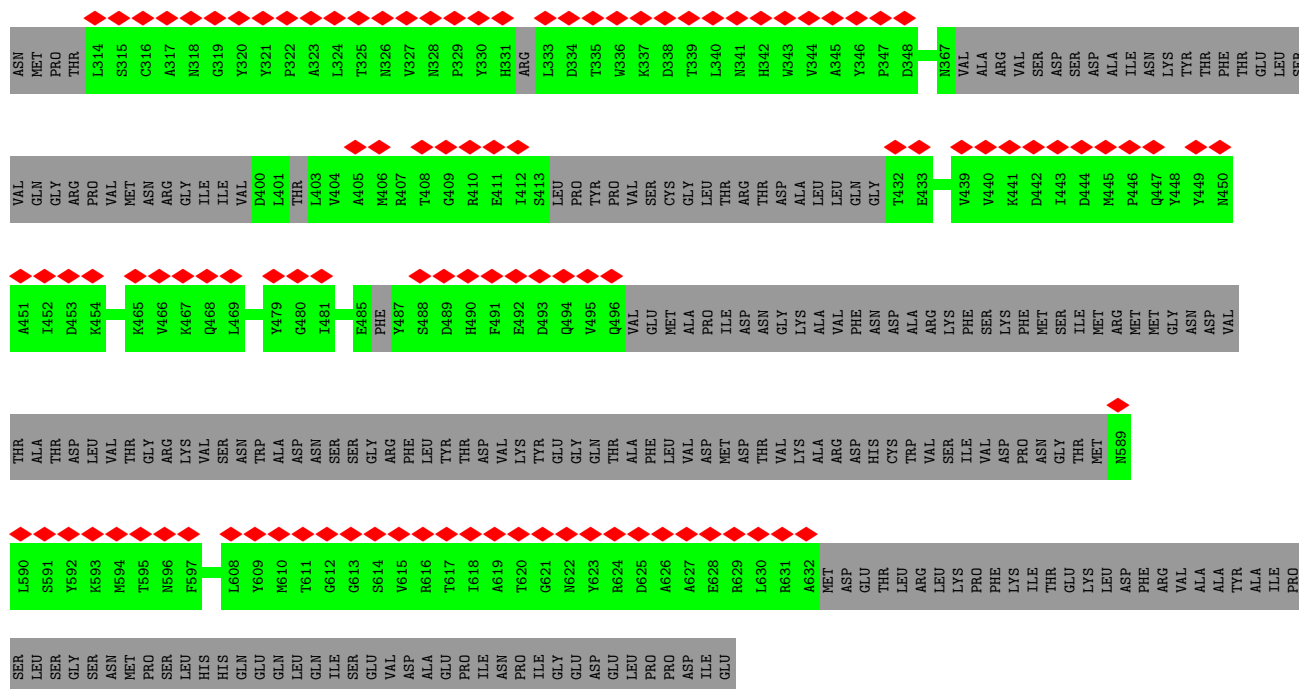
- Molecule 1: Major capsid protein

Chain BP:  77% 85% 15%

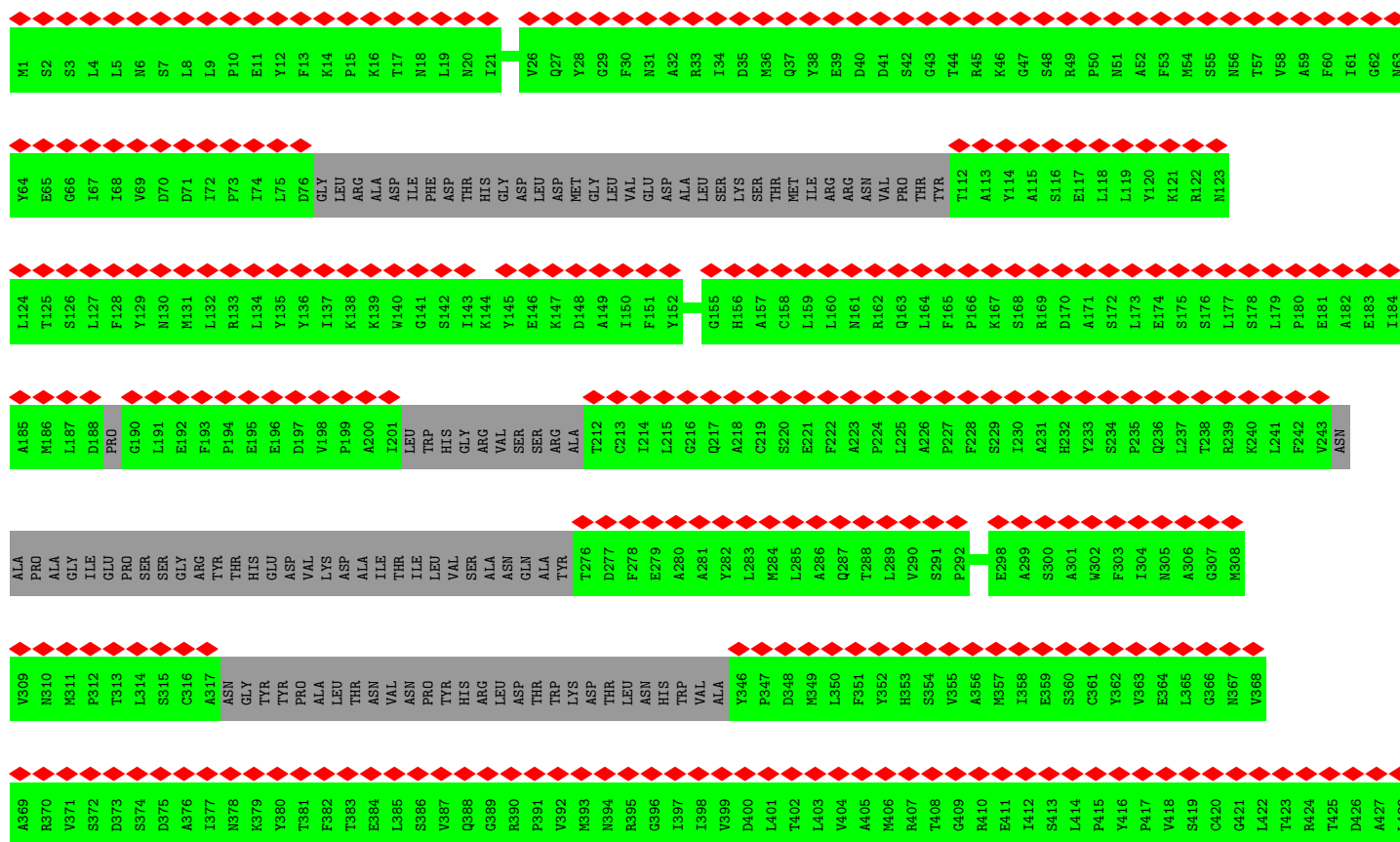
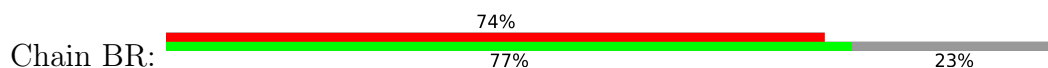


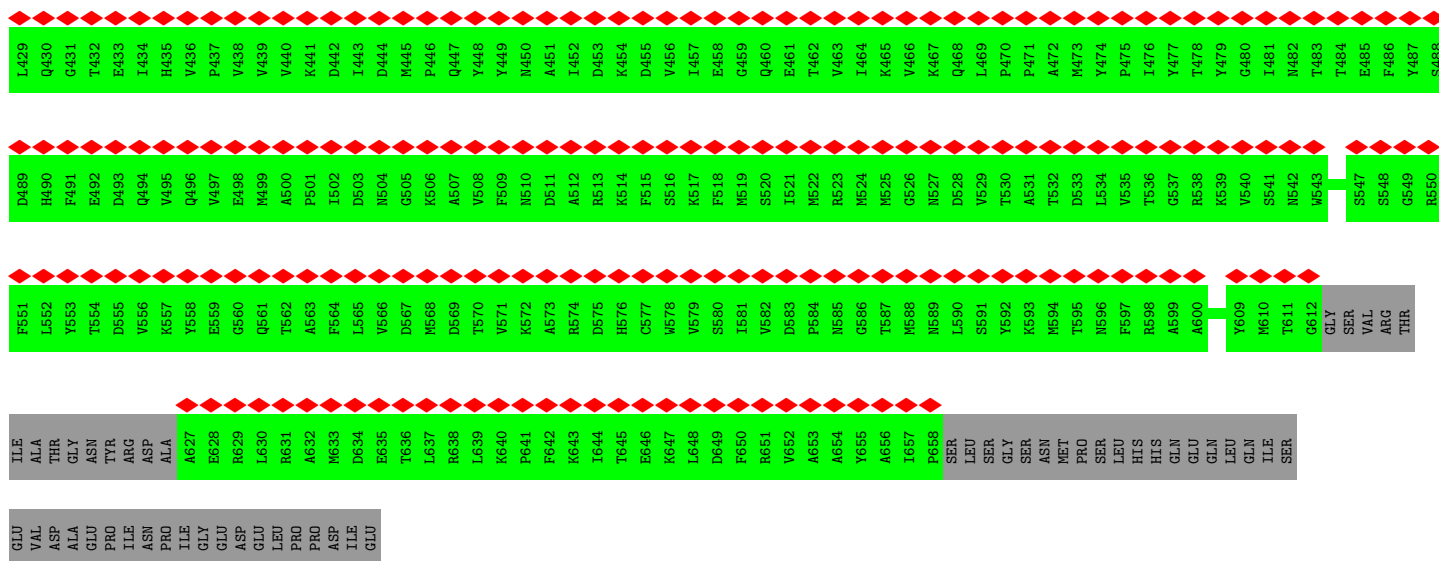




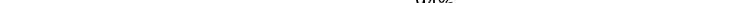


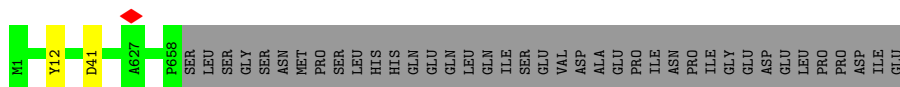
• Molecule 1: Major capsid protein



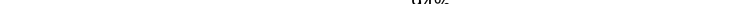


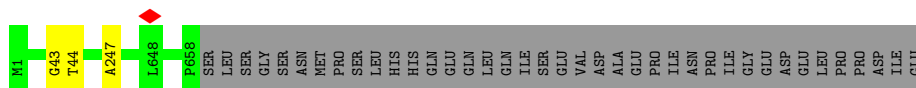
- Molecule 1: Major capsid protein

Chain BS:  94% 6%

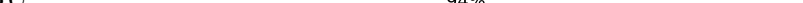


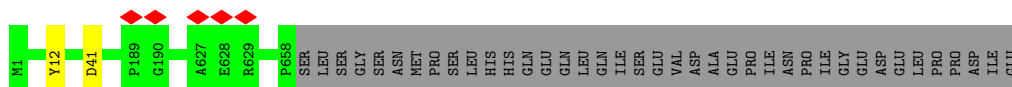
- Molecule 1: Major capsid protein

Chain BT:  94% 6%

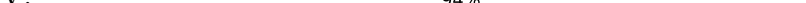


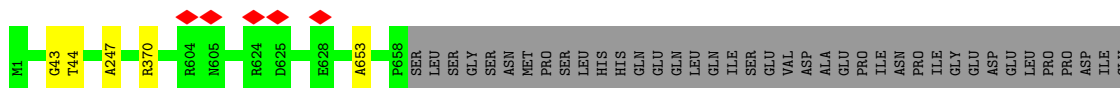
- Molecule 1: Major capsid protein

Chain BU:  94% 6%

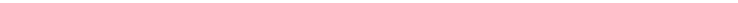


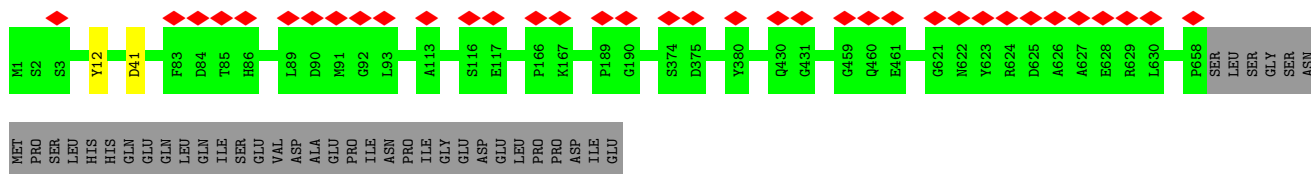
- Molecule 1: Major capsid protein

Chain BV:  94% • 6%

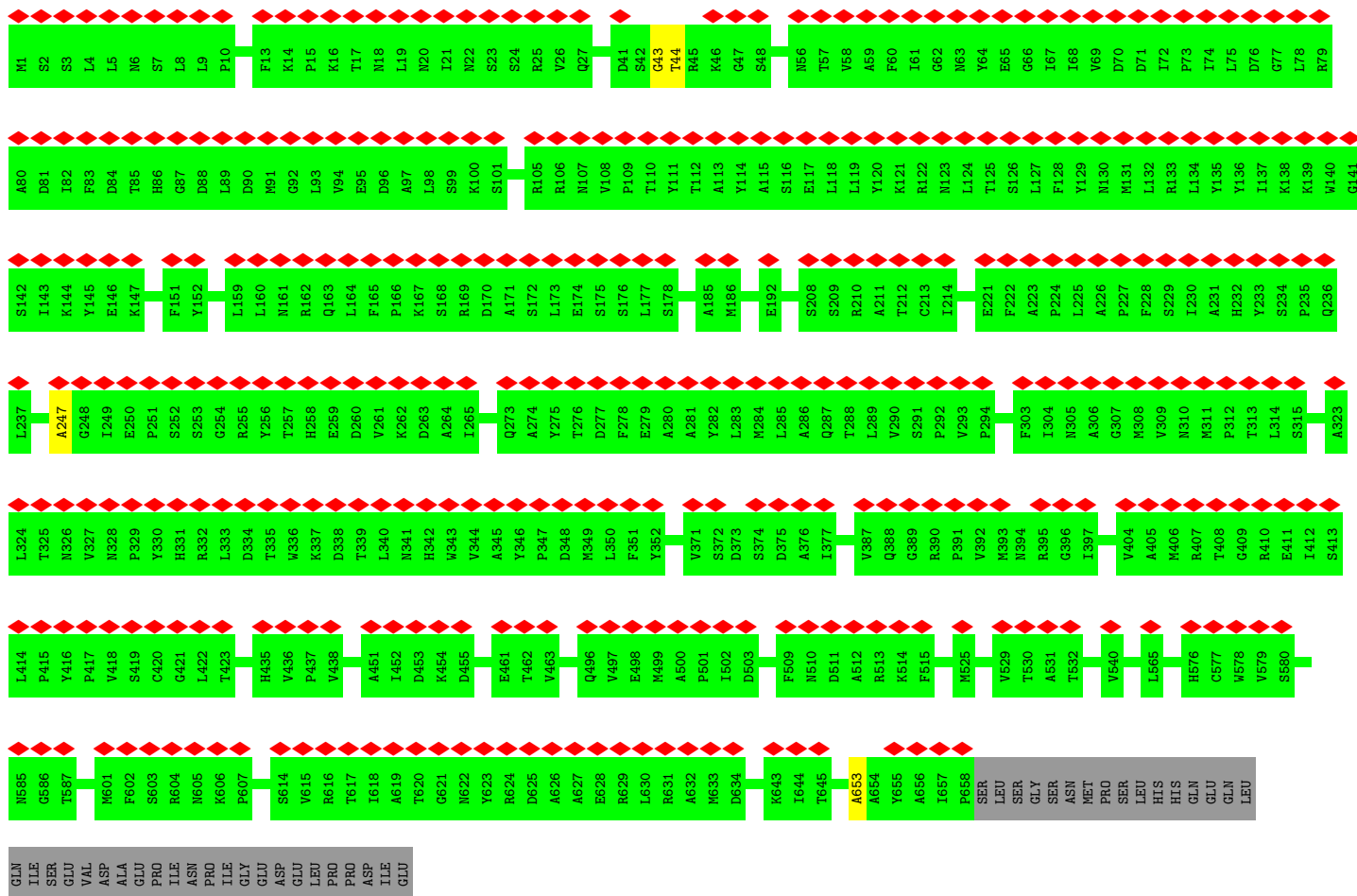


- Molecule 1: Major capsid protein

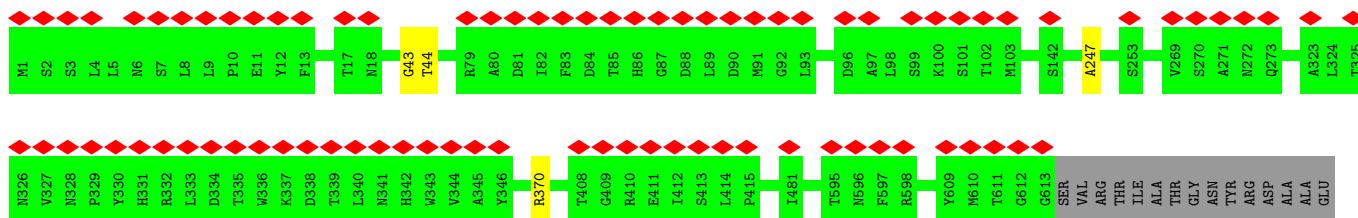
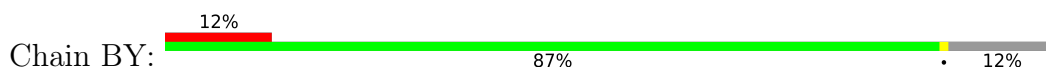
Chain BW: 

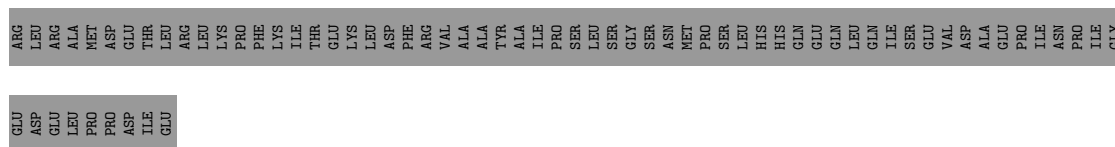


• Molecule 1: Major capsid protein

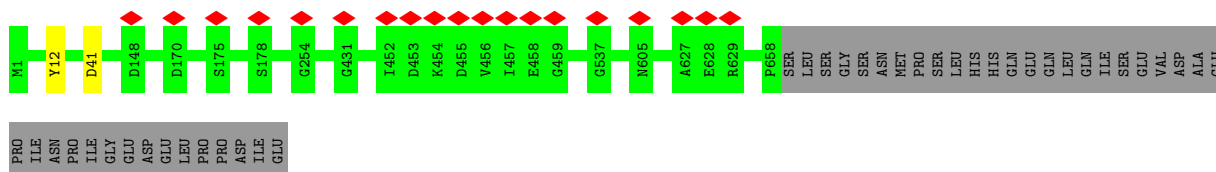


• Molecule 1: Major capsid protein

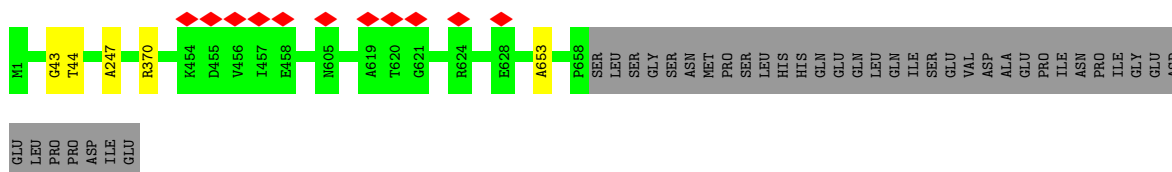




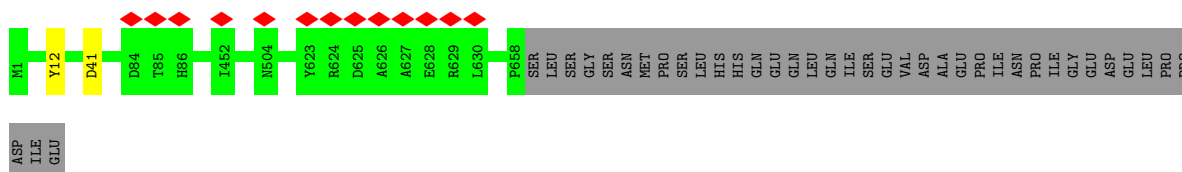
- Molecule 1: Major capsid protein



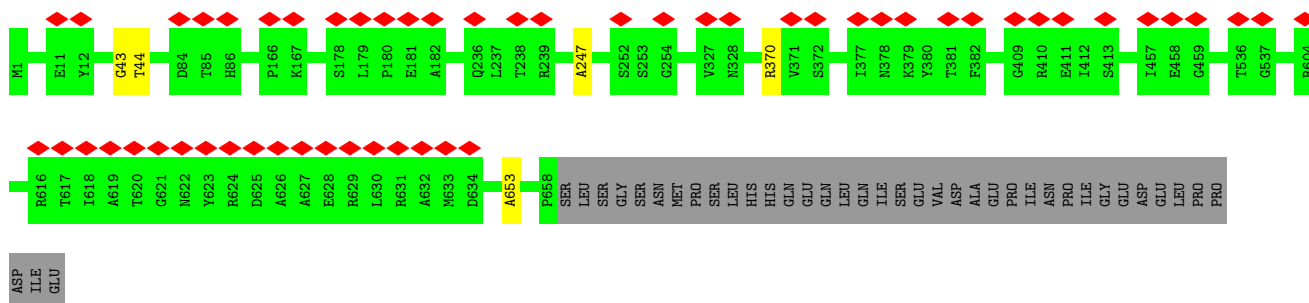
- Molecule 1: Major capsid protein



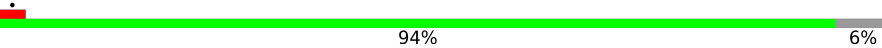
- Molecule 1: Major capsid protein

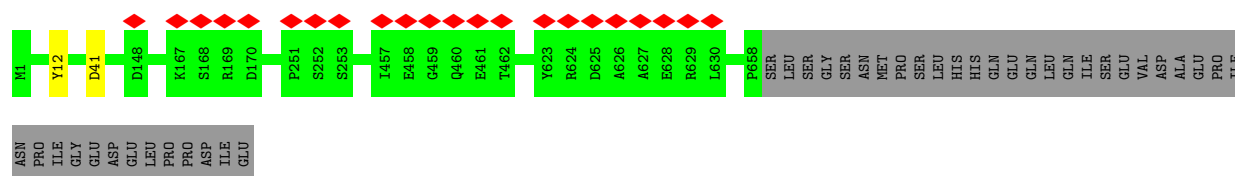


- Molecule 1: Major capsid protein

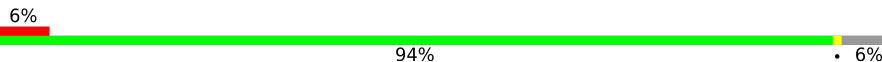


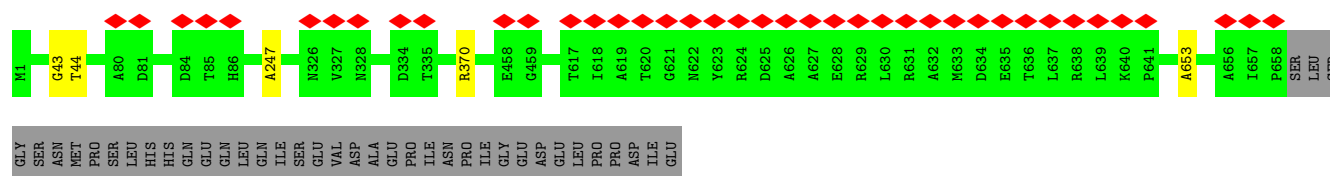
- Molecule 1: Major capsid protein

Chain CD:  94% 6%

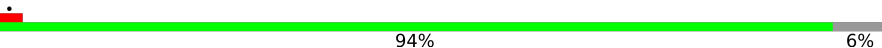


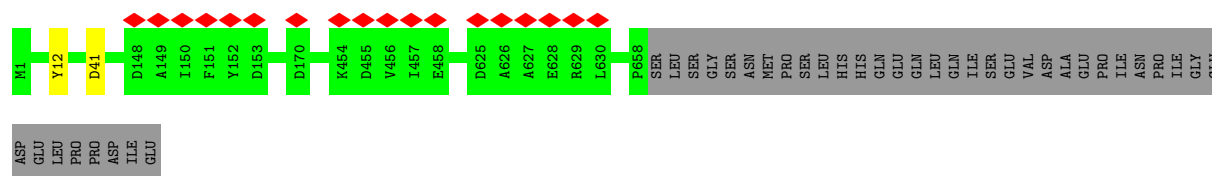
- Molecule 1: Major capsid protein

Chain CE:  94% 6%

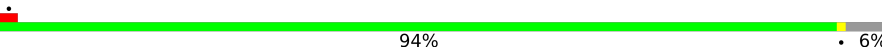


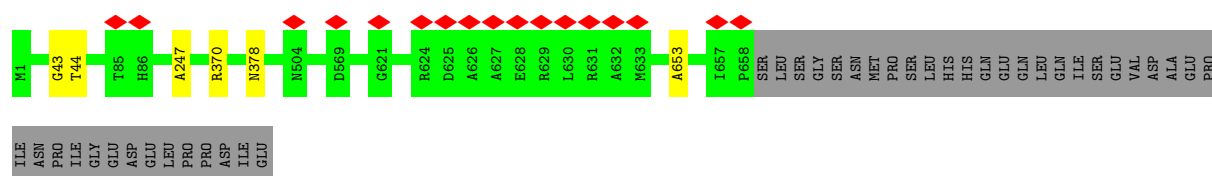
- Molecule 1: Major capsid protein

Chain CF:  94% 6%

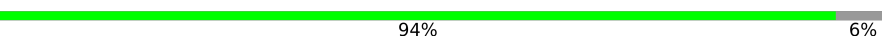


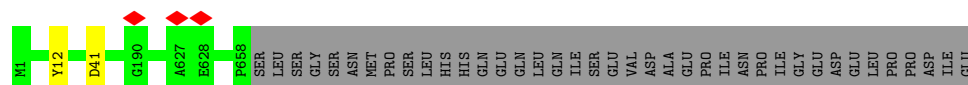
- Molecule 1: Major capsid protein

Chain CG:  94% 6%



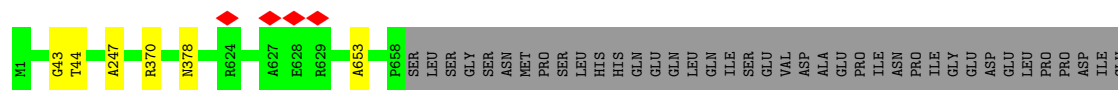
- Molecule 1: Major capsid protein

Chain CH:  94% 6%

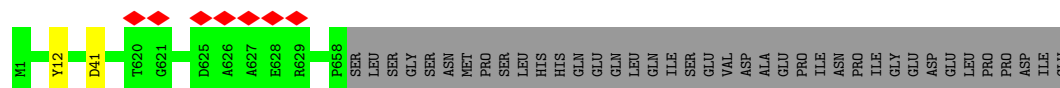


- Molecule 1: Major capsid protein

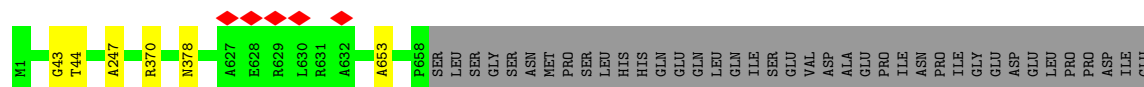
Chain CI:  94% 6%



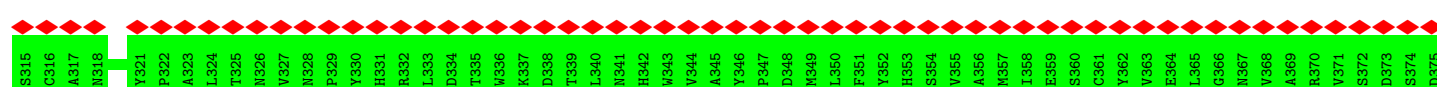
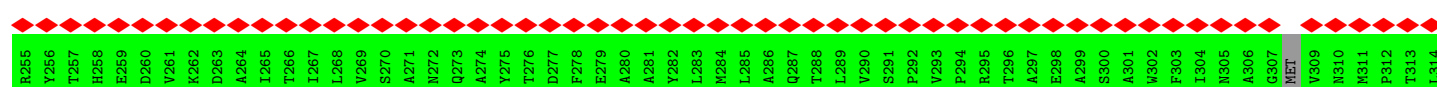
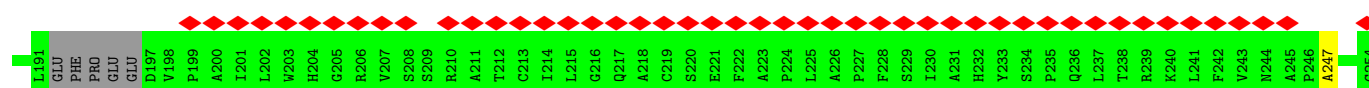
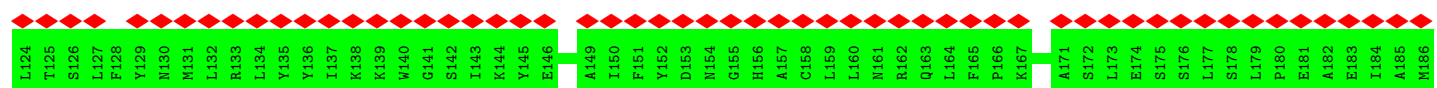
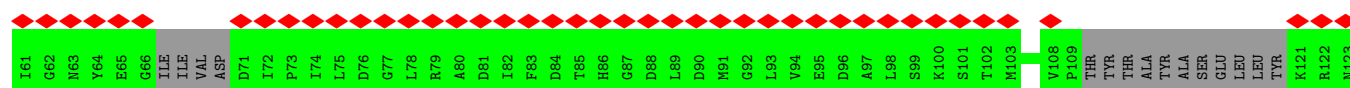
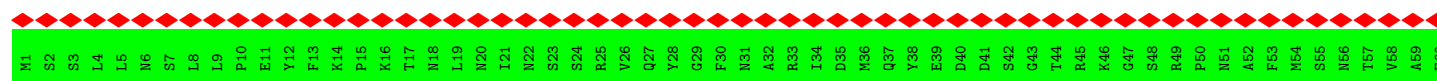
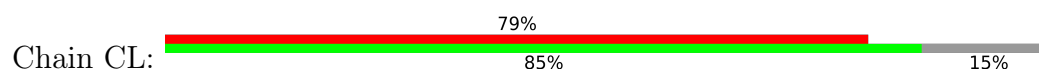
- Molecule 1: Major capsid protein

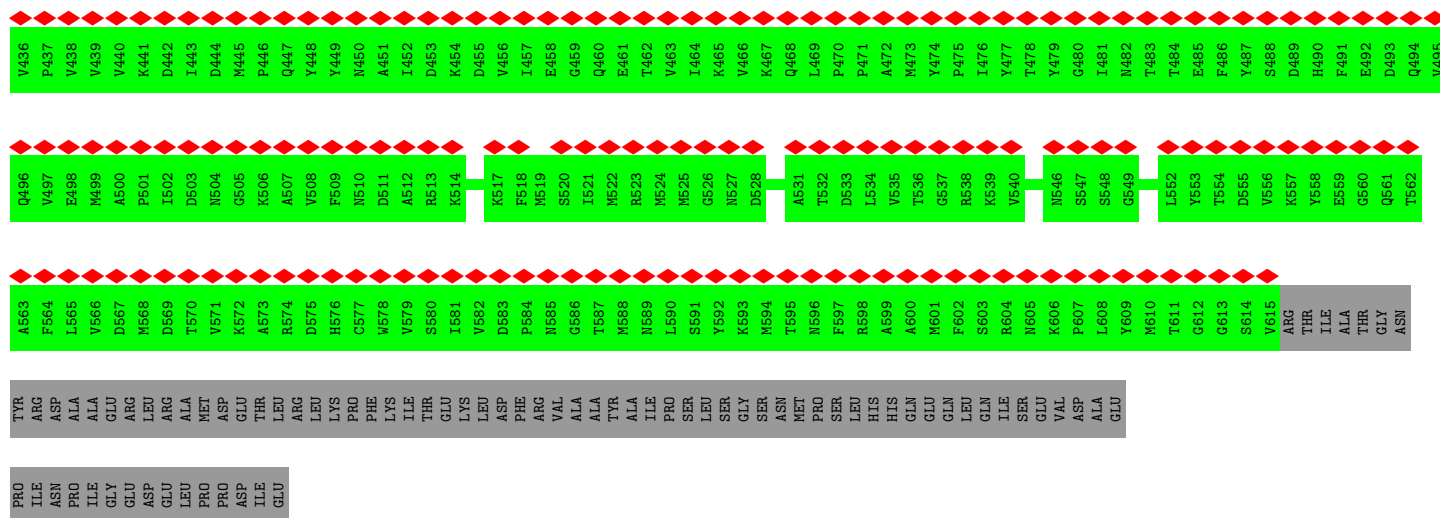


- Molecule 1: Major capsid protein

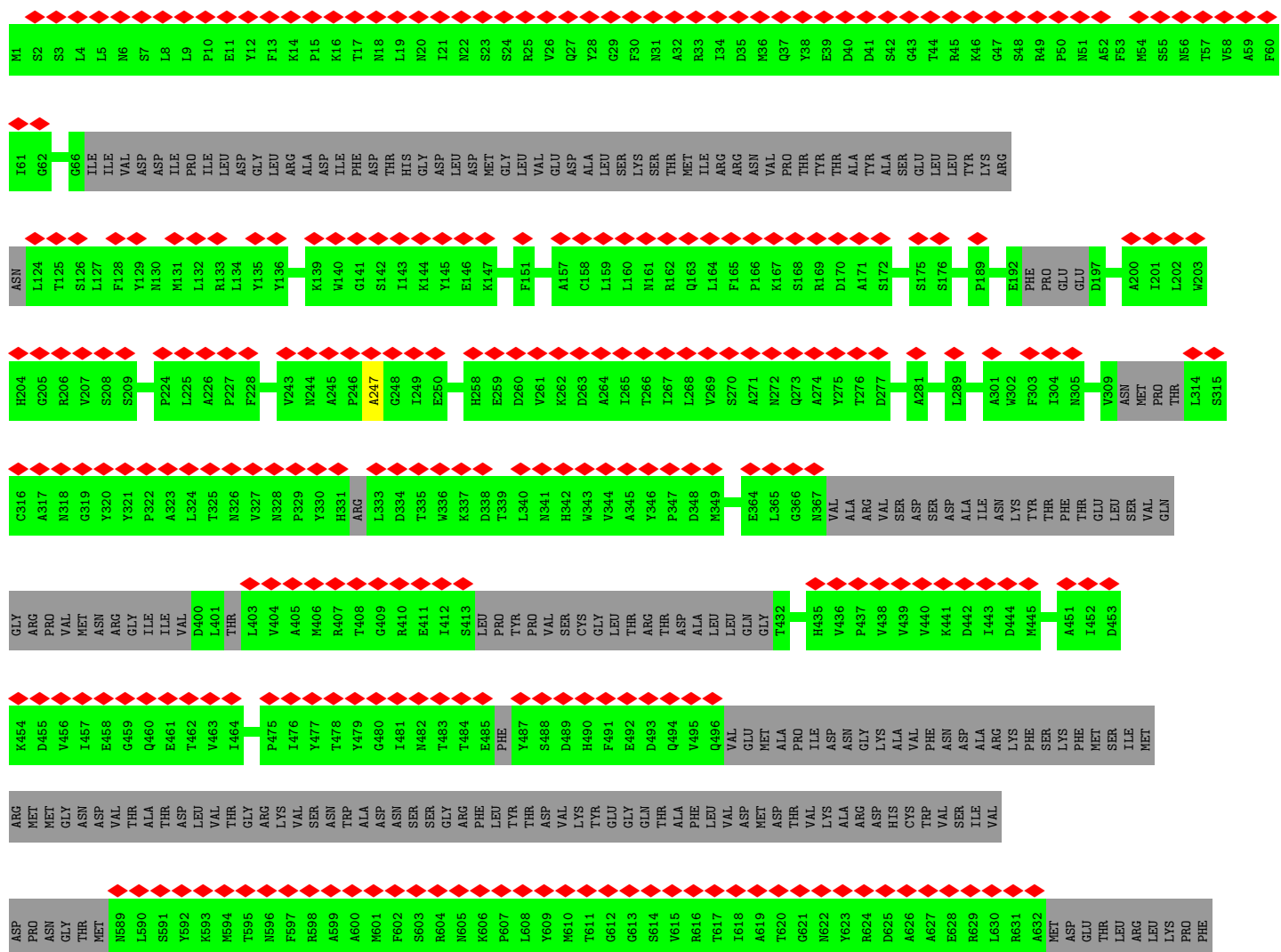
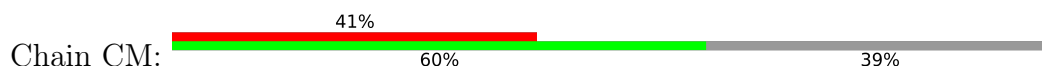


- Molecule 1: Major capsid protein



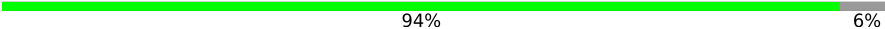


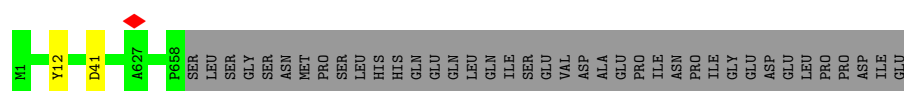
• Molecule 1: Major capsid protein



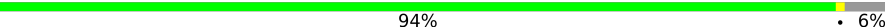
- Molecule 1: Major capsid protein

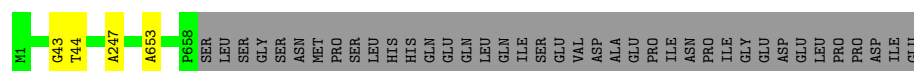


Chain CO:  94% 6%

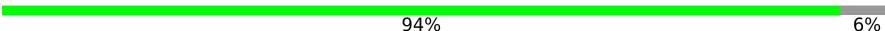


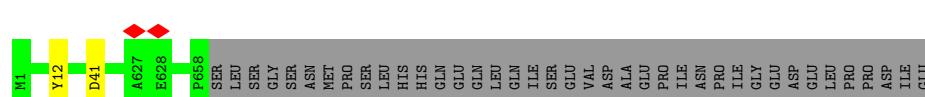
- Molecule 1: Major capsid protein

Chain CP:  94% 6%

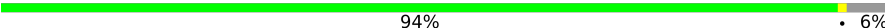


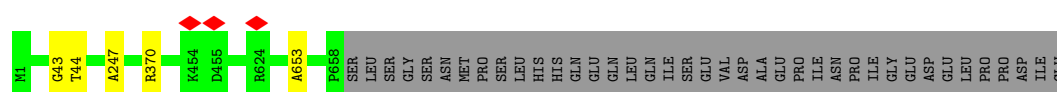
- Molecule 1: Major capsid protein

Chain CQ:  94% 6%



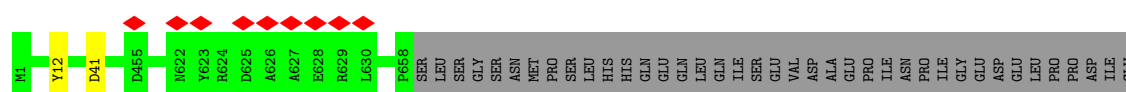
- Molecule 1: Major capsid protein

Chain CR:  94% 6%

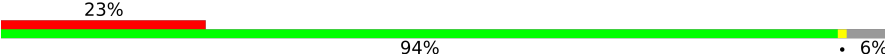


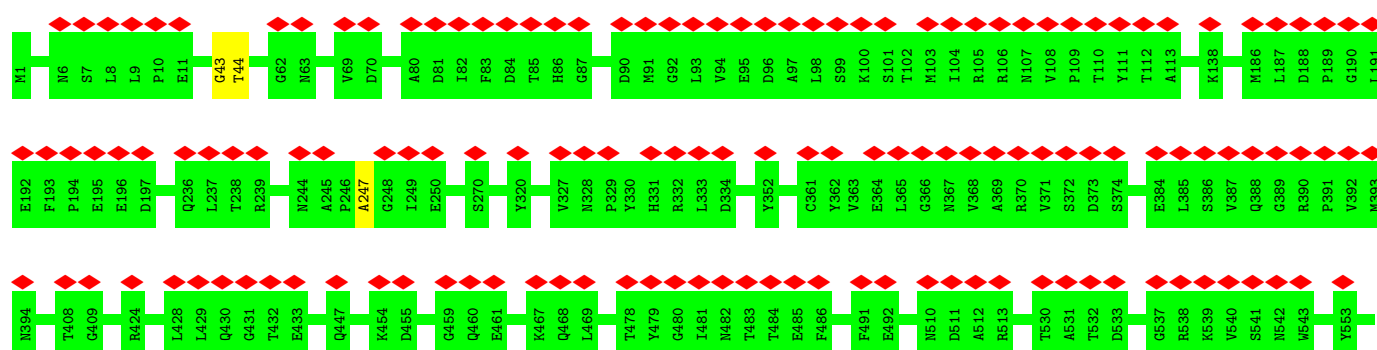
- Molecule 1: Major capsid protein

Chain CS:  94% 6%



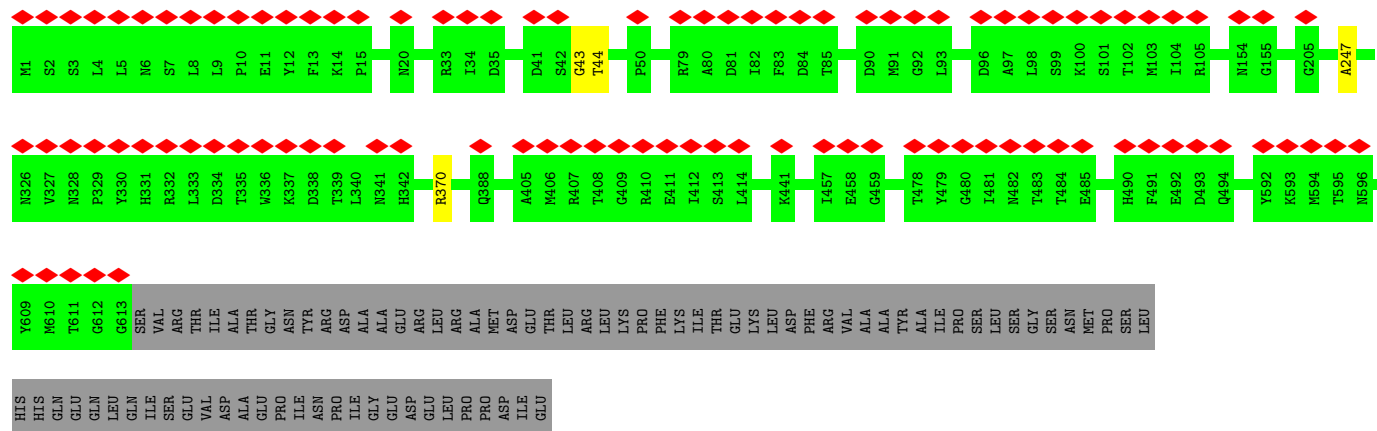
- Molecule 1: Major capsid protein

Chain CT:  23% 94% 6%

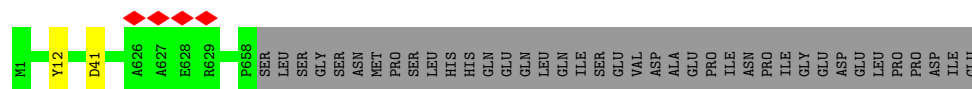




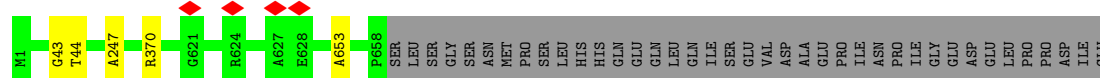
- Molecule 1: Major capsid protein



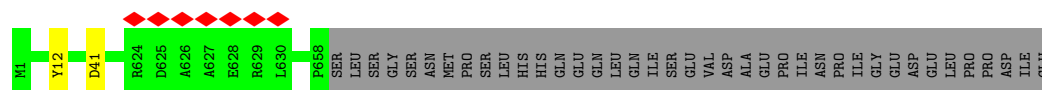
- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein



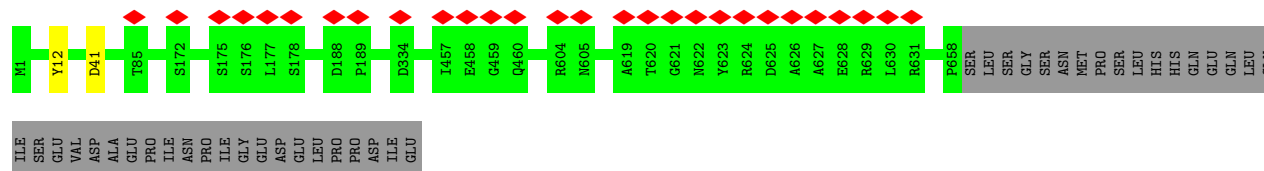
- Molecule 1: Major capsid protein





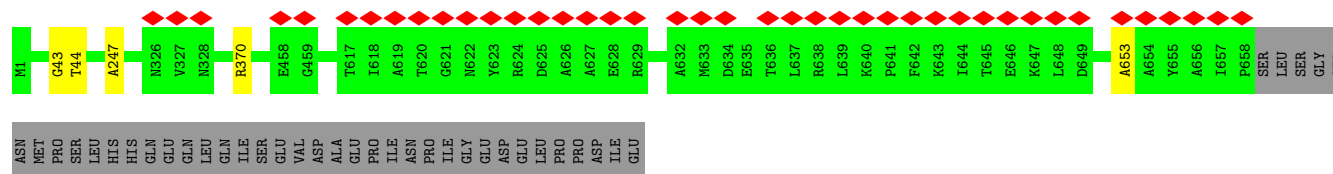
- Molecule 1: Major capsid protein

Chain CZ:   
94% 6%



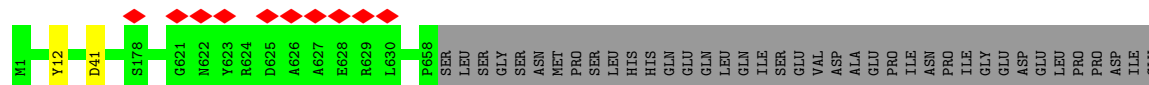
- Molecule 1: Major capsid protein

Chain DA:   
94% 6%



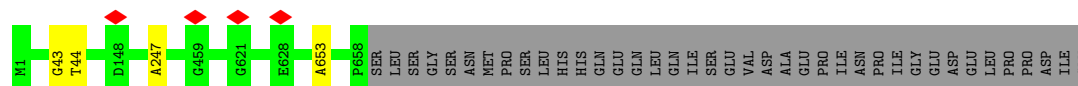
- Molecule 1: Major capsid protein

Chain DB:   
94% 6%



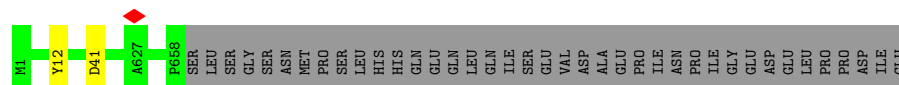
- Molecule 1: Major capsid protein

Chain DC:   
94% 6%



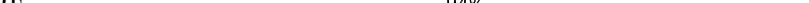
- Molecule 1: Major capsid protein

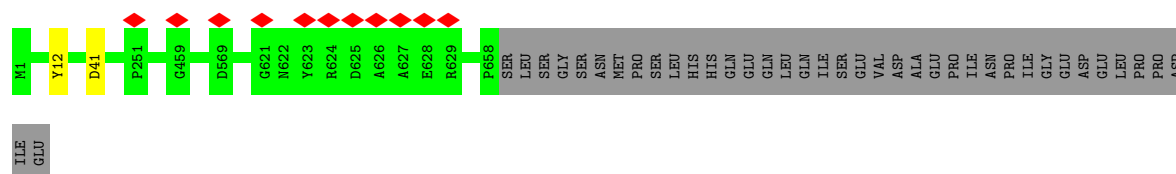
Chain DD:   
94% 6%

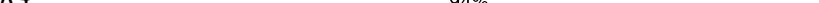


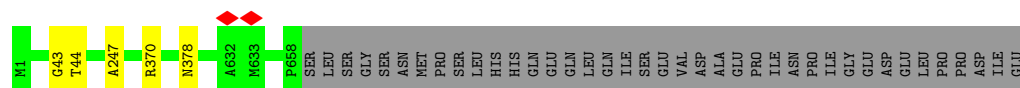
- Molecule 1: Major capsid protein

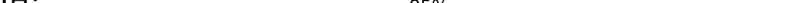
| Position | Residue | Conservation | Charge | Hydrophobicity | Size | Flexibility | Order |
|----------|---------|--------------|--------|----------------|------|-------------|-------|
| 1        | M1      | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 1     |
| 2        | G43     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 2     |
| 3        | T44     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 3     |
| 4        | A247    | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 4     |
| 5        | R370    | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 5     |
| 6        | N378    | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 6     |
| 7        | E628    | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 7     |
| 8        | A653    | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 8     |
| 9        | P658    | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 9     |
| 10       | SER     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 10    |
| 11       | LEU     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 11    |
| 12       | SER     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 12    |
| 13       | SER     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 13    |
| 14       | GLY     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 14    |
| 15       | SER     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 15    |
| 16       | SER     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 16    |
| 17       | ASN     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 17    |
| 18       | MET     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 18    |
| 19       | PRO     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 19    |
| 20       | SER     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 20    |
| 21       | SER     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 21    |
| 22       | HIS     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 22    |
| 23       | LEU     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 23    |
| 24       | GLN     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 24    |
| 25       | GLN     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 25    |
| 26       | GLU     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 26    |
| 27       | GLN     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 27    |
| 28       | LEU     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 28    |
| 29       | LEU     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 29    |
| 30       | GLN     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 30    |
| 31       | ILE     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 31    |
| 32       | SER     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 32    |
| 33       | GLU     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 33    |
| 34       | VAL     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 34    |
| 35       | ASP     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 35    |
| 36       | ALA     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 36    |
| 37       | GLU     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 37    |
| 38       | PRO     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 38    |
| 39       | ILE     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 39    |
| 40       | ASN     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 40    |
| 41       | PRO     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 41    |
| 42       | ILE     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 42    |
| 43       | GLY     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 43    |
| 44       | GLU     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 44    |
| 45       | ASP     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 45    |
| 46       | GLU     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 46    |
| 47       | LEU     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 47    |
| 48       | PRO     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 48    |
| 49       | PRO     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 49    |
| 50       | ASP     | 0.00         | 0.00   | 0.00           | 0.00 | 0.00        | 50    |

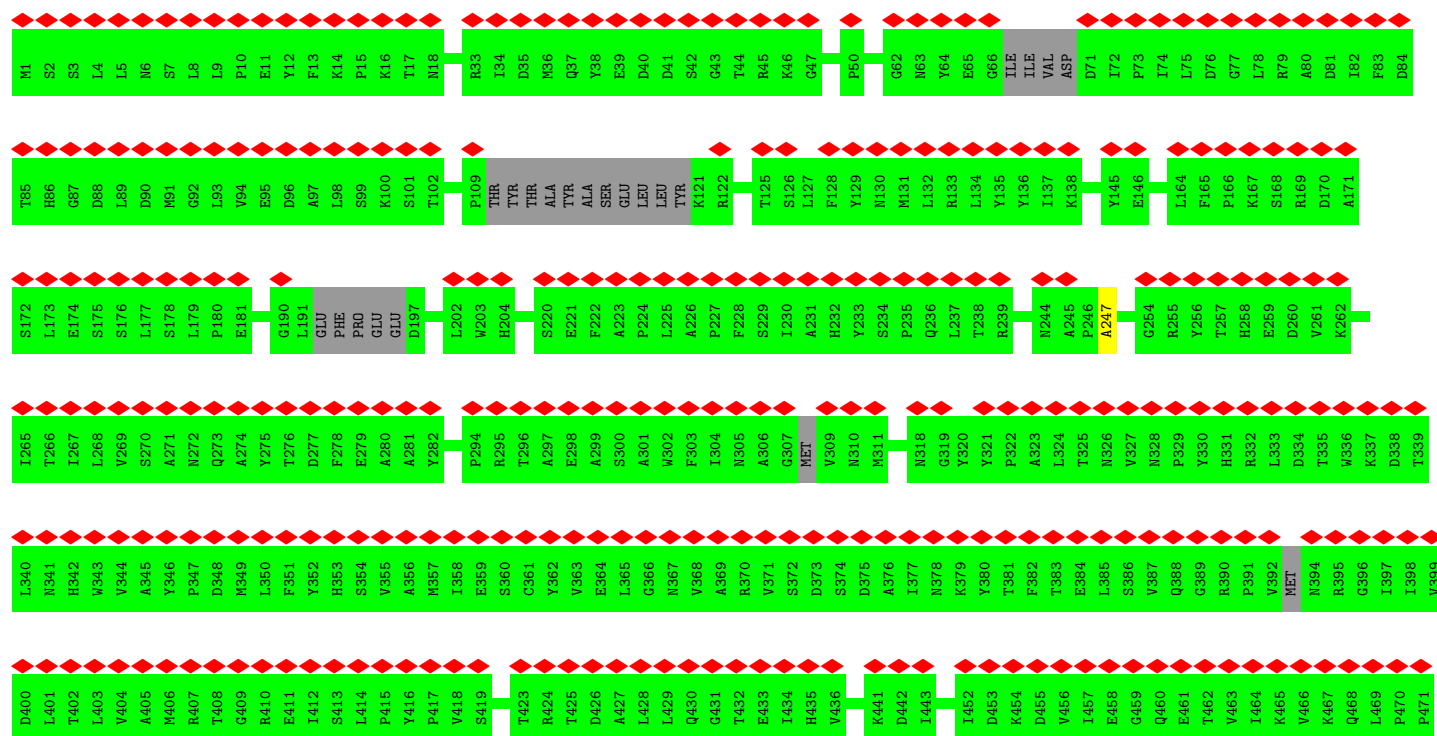
- Chain DF:  94% 6%

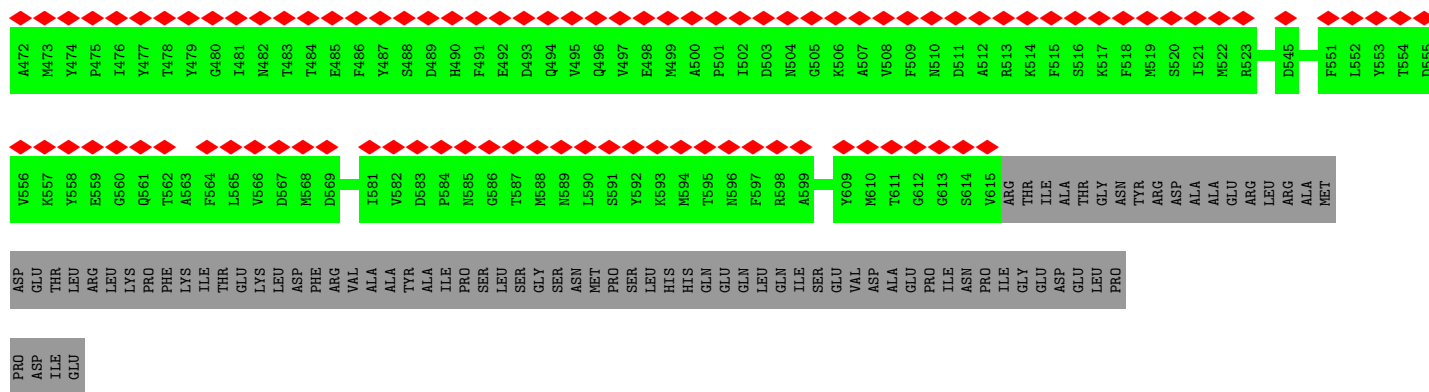


- Chain DG:  94% • 6%

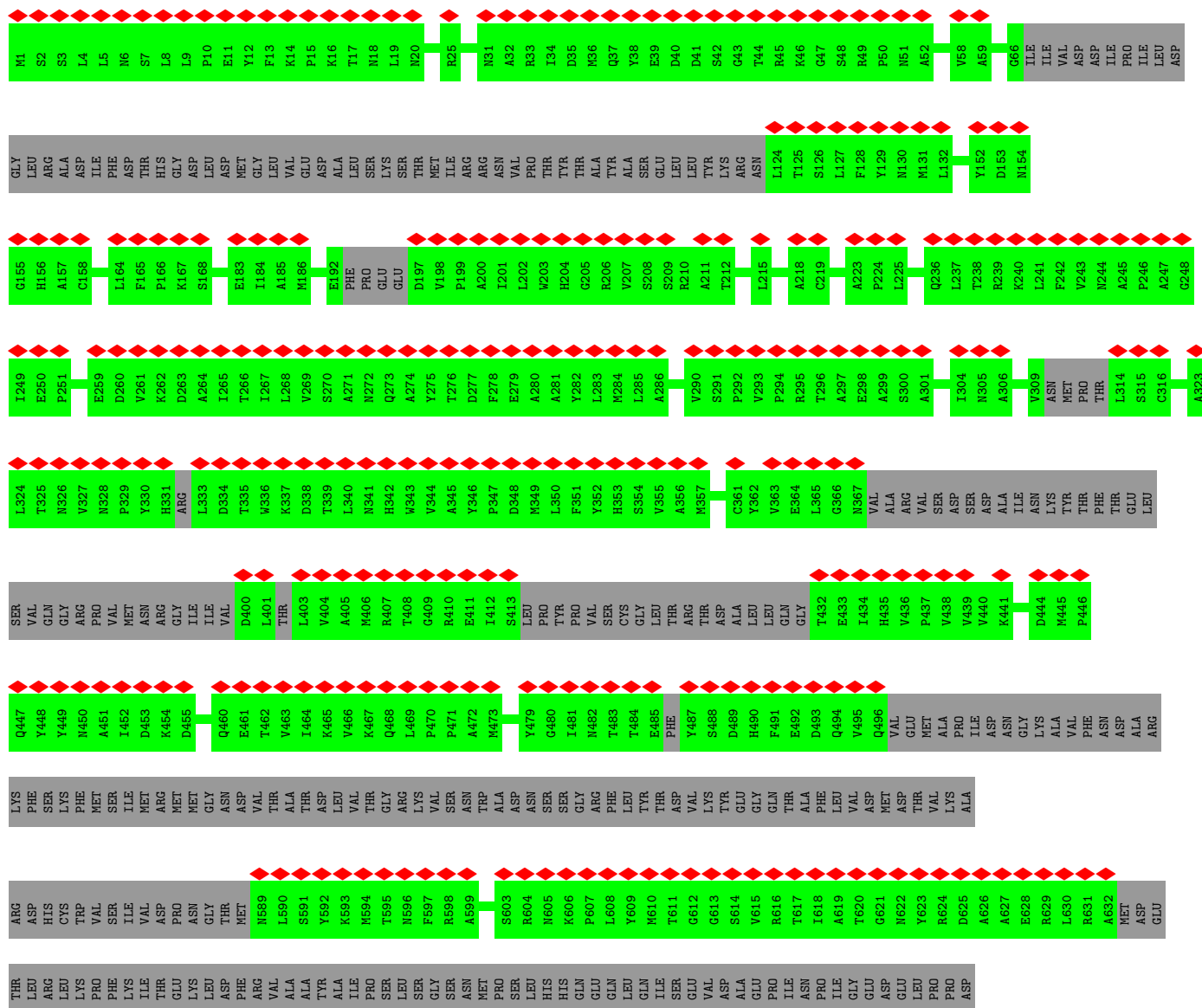


- Chain DH:  59% 85% 15%



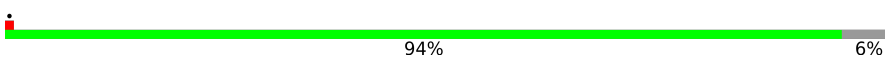


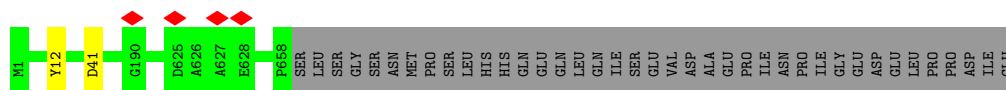
● Molecule 1: Major capsid protein



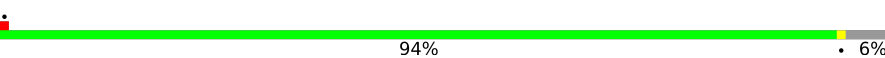


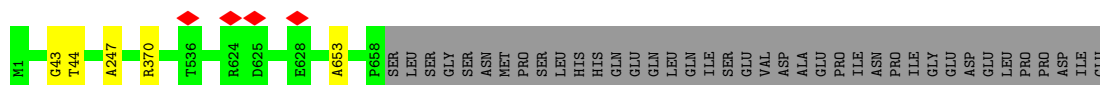
- Molecule 1: Major capsid protein

Chain DM:  94% 6%

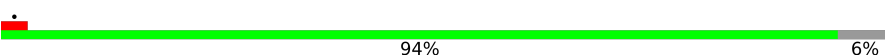


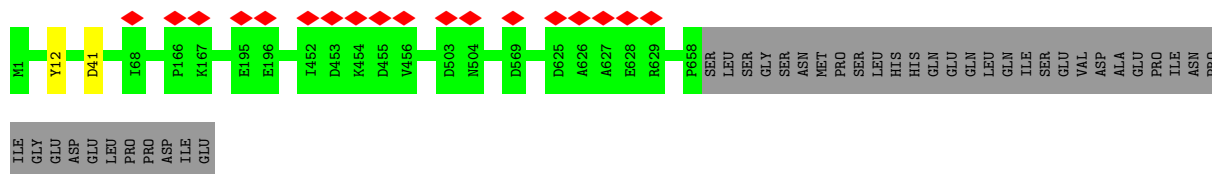
- Molecule 1: Major capsid protein

Chain DN:  94% 6%

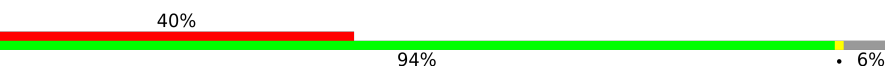


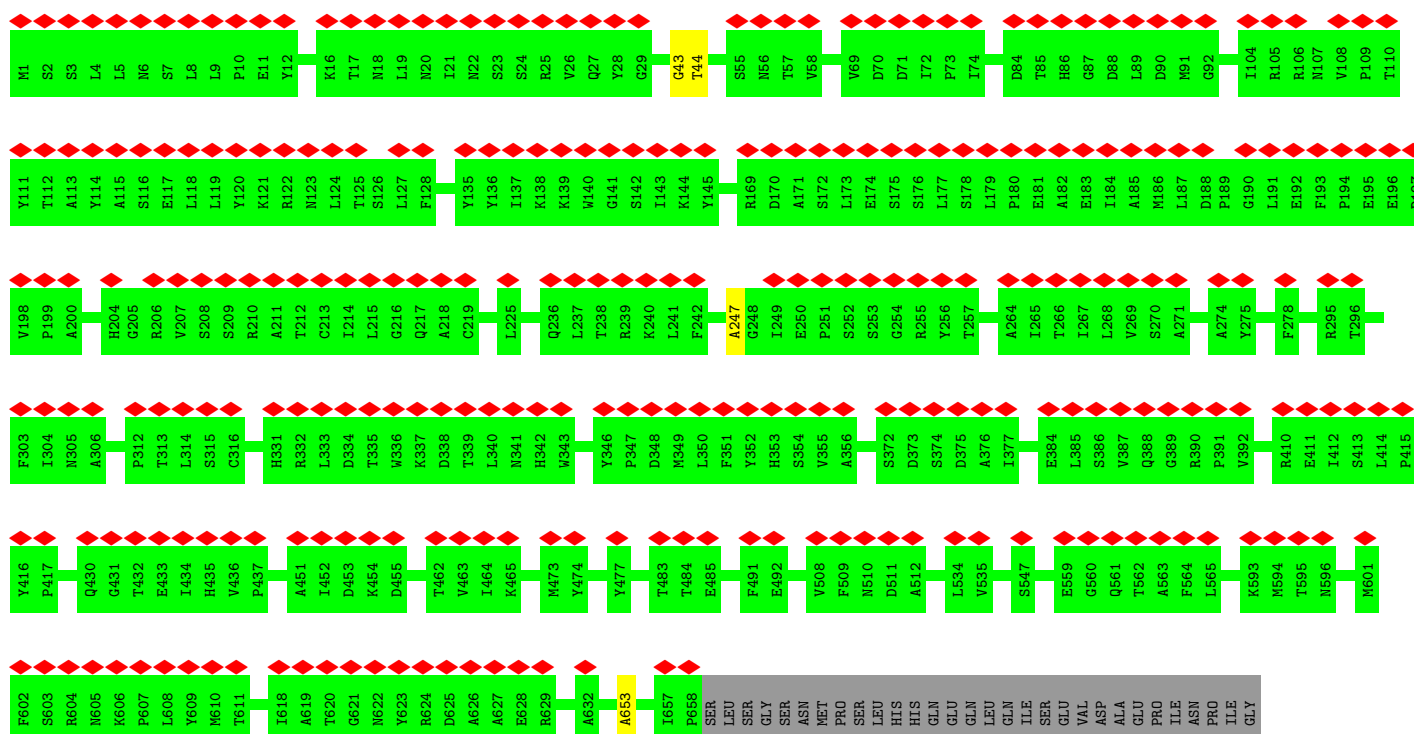
- Molecule 1: Major capsid protein

Chain DO:  94% 6%



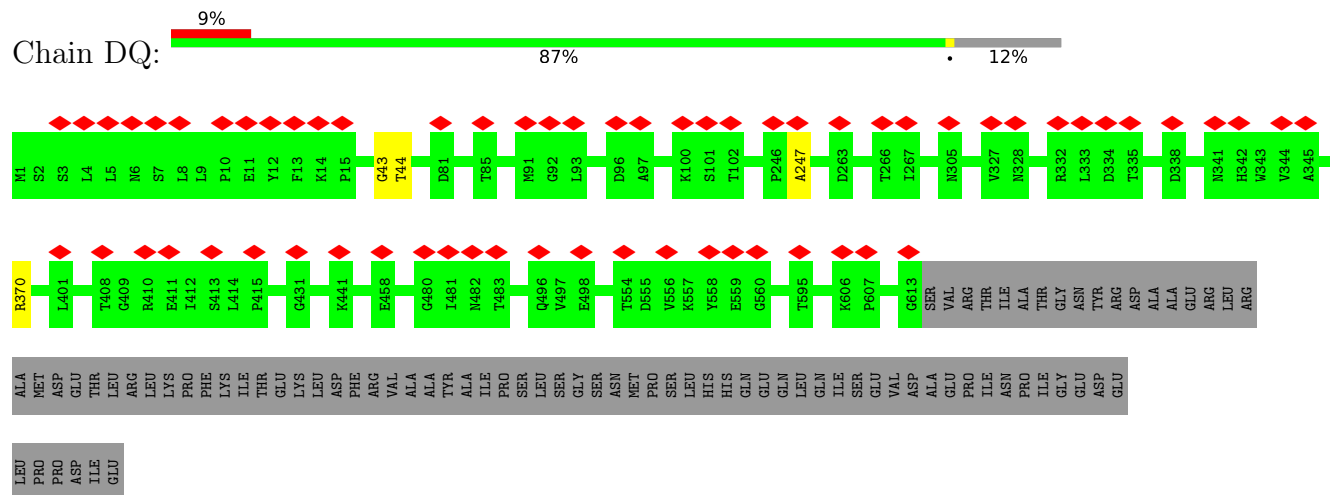
- Molecule 1: Major capsid protein

Chain DP:  40% 94% 6%

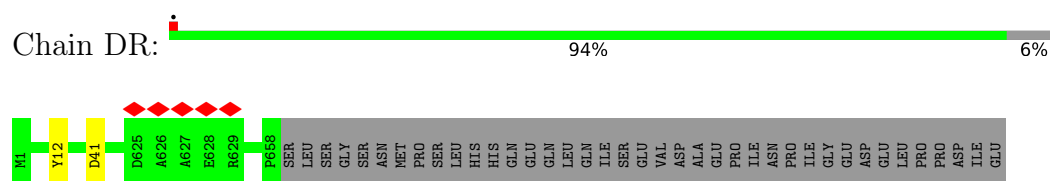


GLU  
ASP  
GLU  
LEU  
PRO  
PRO  
ASP  
ILE  
GLU

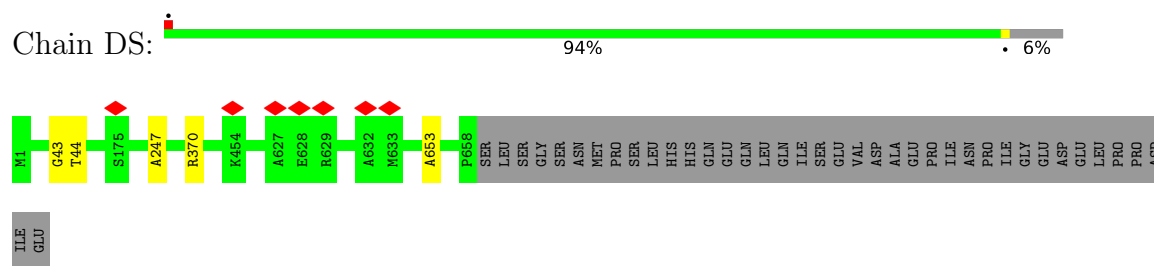
- Molecule 1: Major capsid protein



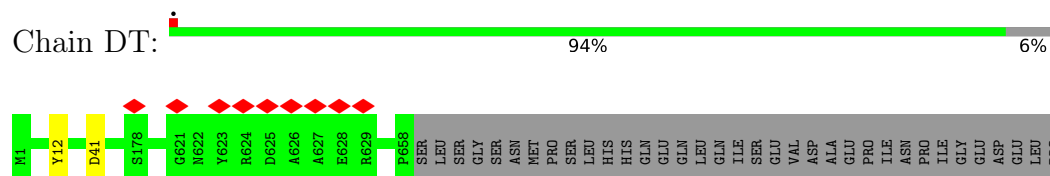
- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein

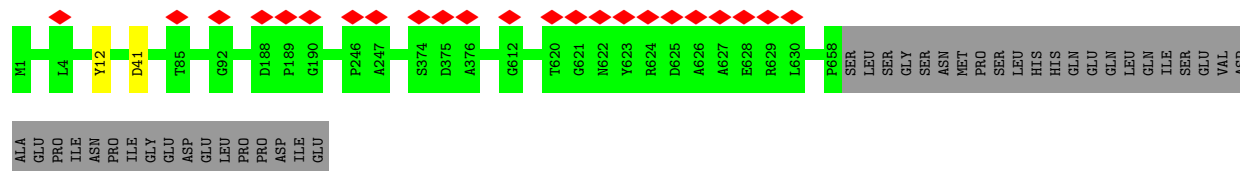






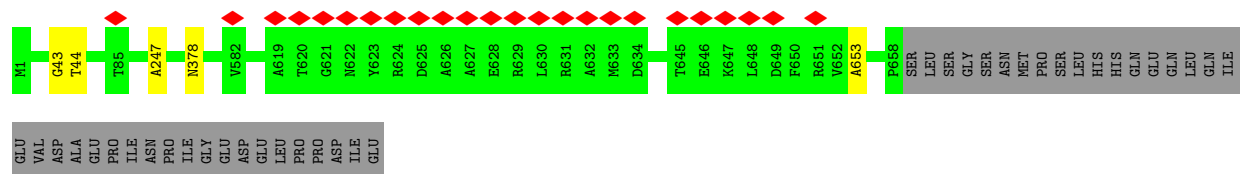
- Molecule 1: Major capsid protein

Chain DV: 94% 6%



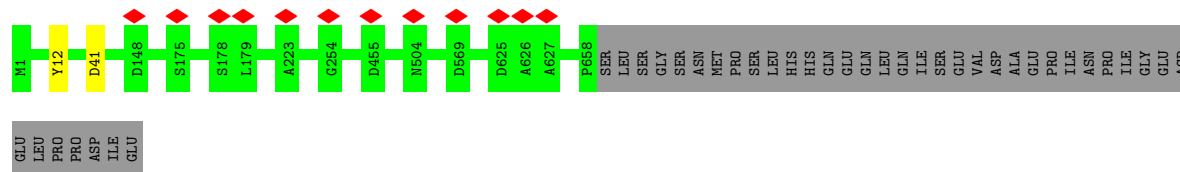
- Molecule 1: Major capsid protein

Chain DW: 94% 6%



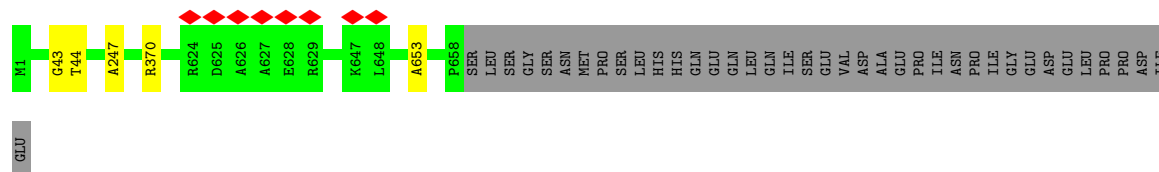
- Molecule 1: Major capsid protein

Chain DX: 94% 6%



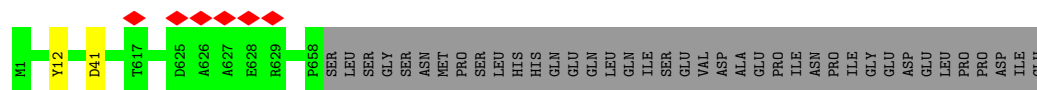
- Molecule 1: Major capsid protein

Chain DY: 94% 6%

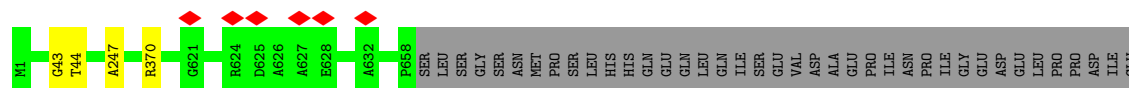


- Molecule 1: Major capsid protein

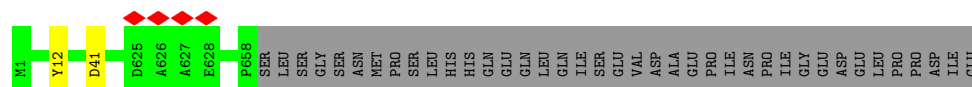
Chain DZ: 94% 6%



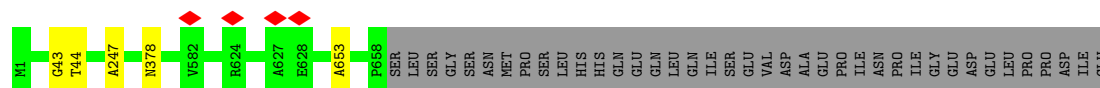
- Molecule 1: Major capsid protein



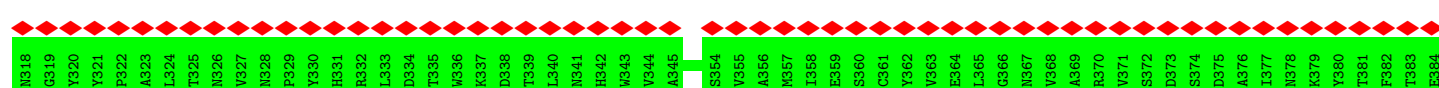
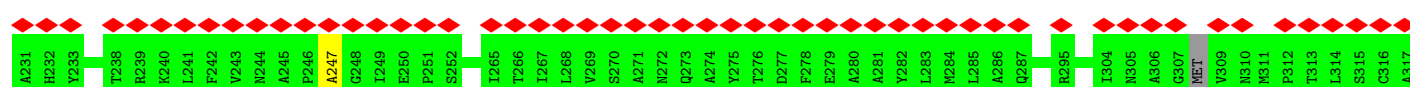
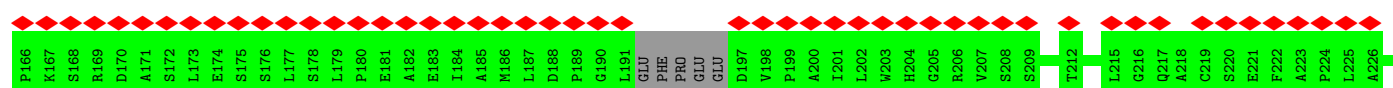
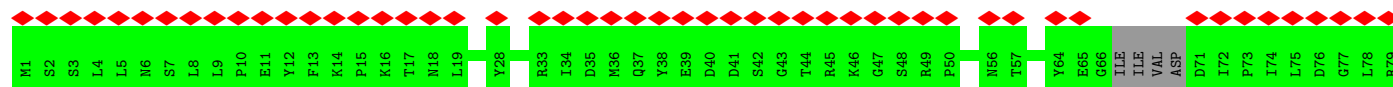
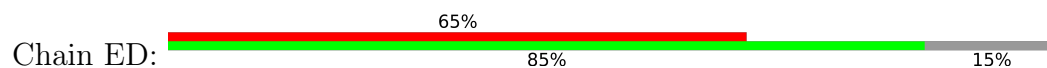
- Molecule 1: Major capsid protein

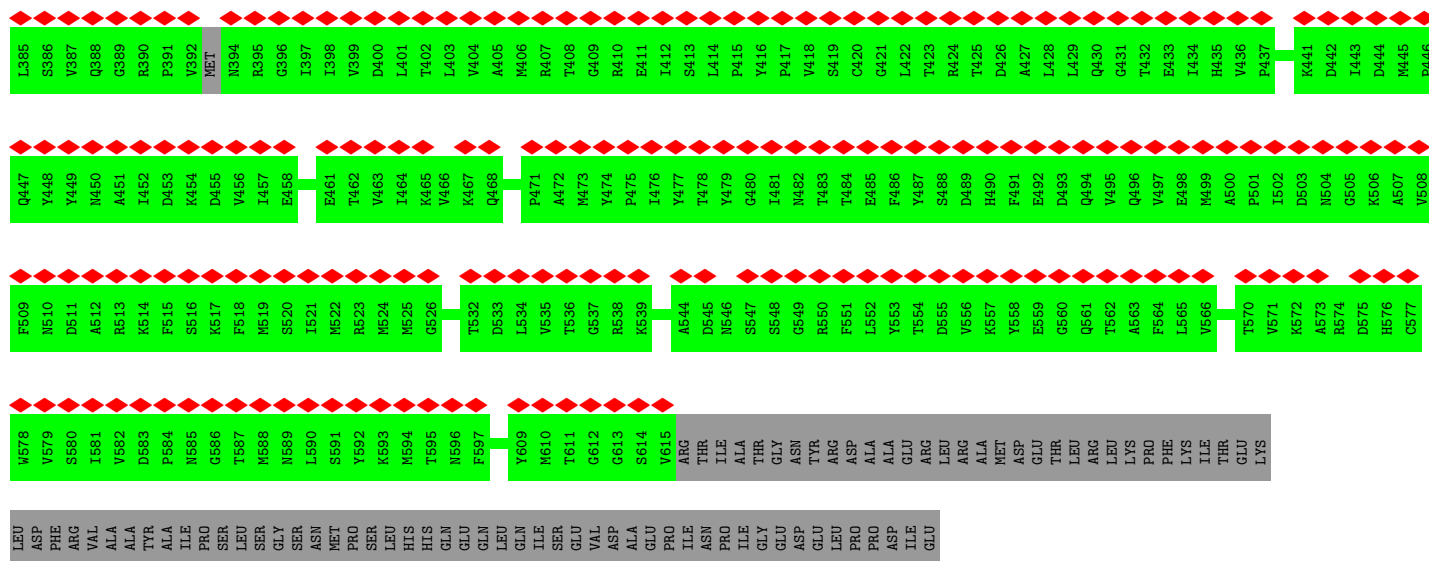


- Molecule 1: Major capsid protein

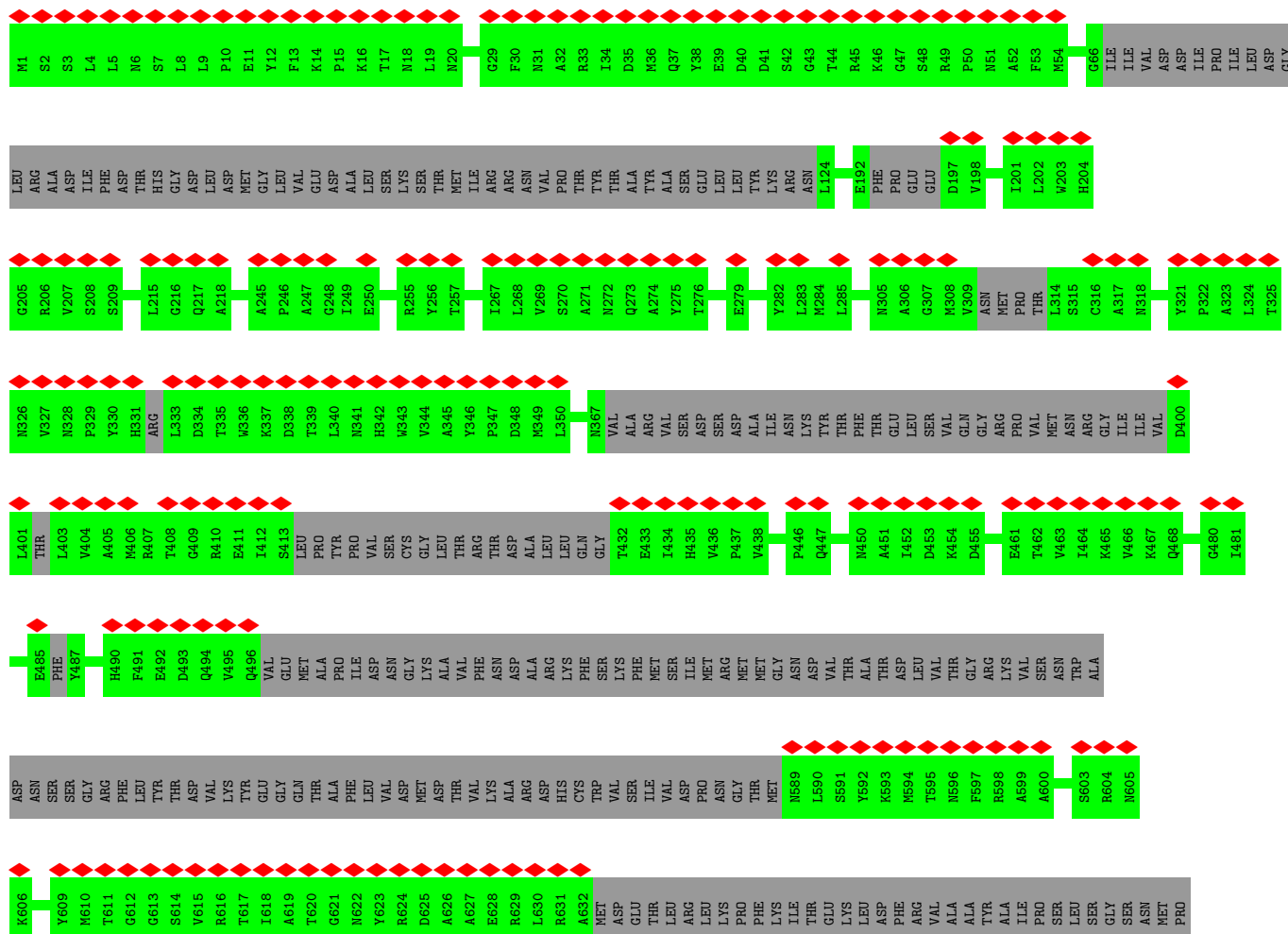


- Molecule 1: Major capsid protein





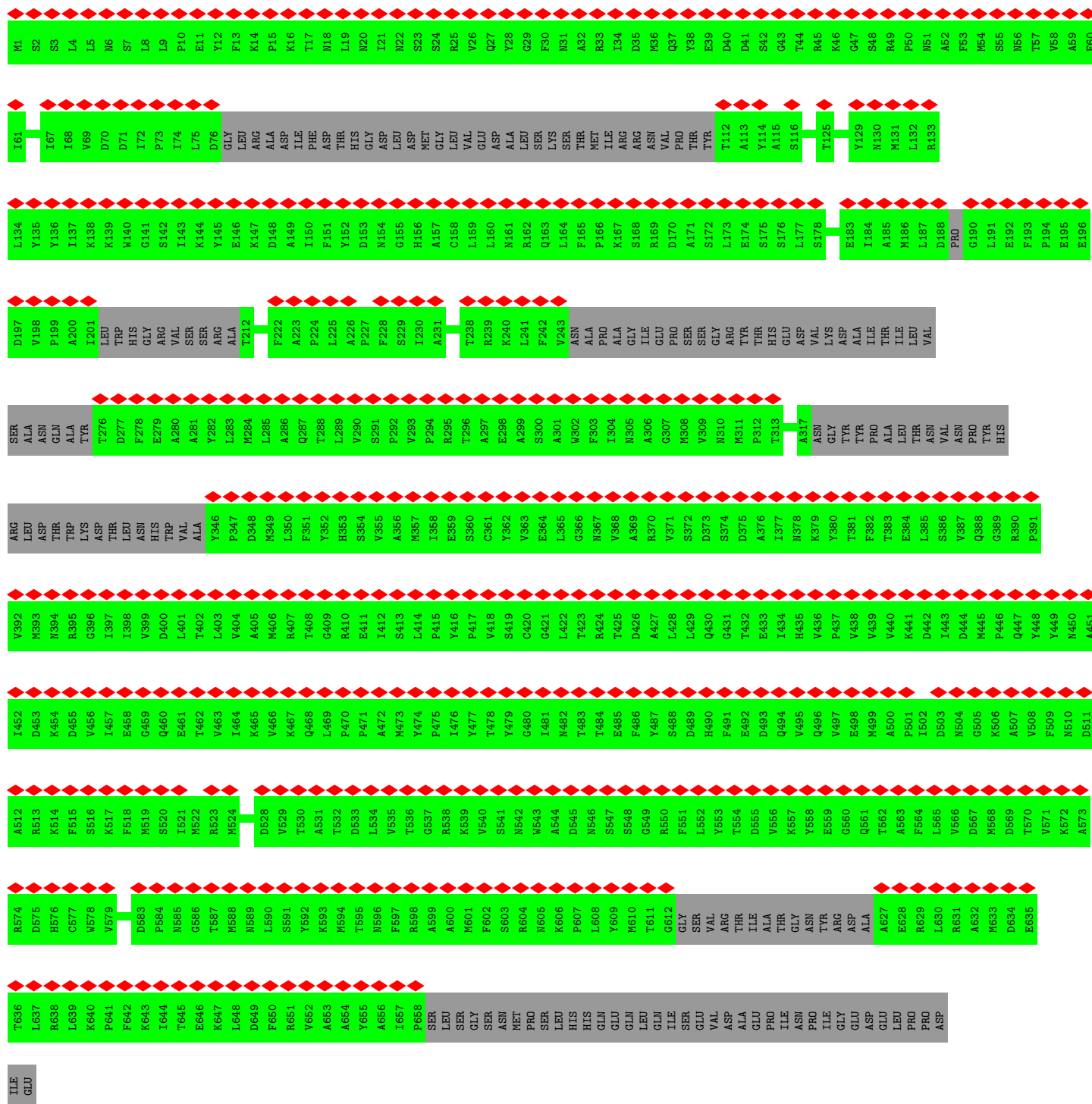
### • Molecule 1: Major capsid protein



SER LEU HIS HIS GLN GLN LEU LEU SER SER GLU VAL ASP ALA GLU PRO PRO ASN PRO ILE ILE GLY GLY ASP GLU LEU PRO PRO ILE ILE GLU

● Molecule 1: Major capsid protein

Chain EF: 



## 4 Experimental information

| Property                             | Value                                   | Source    |
|--------------------------------------|-----------------------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE                         | Depositor |
| Imposed symmetry                     | POINT, Not provided                     |           |
| Number of particles used             | 1120                                    | Depositor |
| Resolution determination method      | FSC 0.143 CUT-OFF                       | Depositor |
| CTF correction method                | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope                           | FEI TITAN KRIOS                         | Depositor |
| Voltage (kV)                         | 300                                     | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 36                                      | Depositor |
| Minimum defocus (nm)                 | 700                                     | Depositor |
| Maximum defocus (nm)                 | 1700                                    | Depositor |
| Magnification                        | 130000                                  | Depositor |
| Image detector                       | GATAN K2 SUMMIT (4k x 4k)               | Depositor |
| Maximum map value                    | 8.764                                   | Depositor |
| Minimum map value                    | -3.432                                  | Depositor |
| Average map value                    | -0.238                                  | Depositor |
| Map value standard deviation         | 1.000                                   | Depositor |
| Recommended contour level            | 1                                       | Depositor |
| Map size (Å)                         | 603.97125, 603.97125, 603.97125         | wwPDB     |
| Map dimensions                       | 560, 560, 560                           | wwPDB     |
| Map angles (°)                       | 90.0, 90.0, 90.0                        | wwPDB     |
| Pixel spacing (Å)                    | 1.07852, 1.07852, 1.07852               | Depositor |

## 5 Model quality

### 5.1 Standard geometry

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

| Mol | Chain | Bond lengths |         | Bond angles |               |
|-----|-------|--------------|---------|-------------|---------------|
|     |       | RMSZ         | # Z  >5 | RMSZ        | # Z  >5       |
| 1   | AA    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | AB    | 1.46         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | AC    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | AD    | 1.47         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | AE    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | AF    | 1.47         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | AG    | 1.46         | 0/2451  | 1.99        | 2/3062 (0.1%) |
| 1   | AH    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | AI    | 1.47         | 0/2631  | 1.99        | 4/3287 (0.1%) |
| 1   | AJ    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | AK    | 1.47         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | AL    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | AM    | 1.46         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | AN    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | AO    | 1.47         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | AP    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | AQ    | 1.47         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | AR    | 1.46         | 0/2635  | 2.00        | 0/3292        |
| 1   | AS    | 1.47         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | AT    | 1.46         | 0/2366  | 1.98        | 4/2947 (0.1%) |
| 1   | AU    | 1.44         | 0/1682  | 2.00        | 0/2085        |
| 1   | AV    | 1.46         | 0/2145  | 1.96        | 0/2669        |
| 1   | AW    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | AX    | 1.46         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | AY    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | AZ    | 1.47         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | BA    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | BB    | 1.47         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | BC    | 1.47         | 0/2451  | 1.99        | 2/3062 (0.1%) |
| 1   | BD    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | BE    | 1.47         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | BF    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | BG    | 1.47         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | BH    | 1.47         | 0/2635  | 2.00        | 0/3292        |

| Mol | Chain | Bond lengths |         | Bond angles |               |
|-----|-------|--------------|---------|-------------|---------------|
|     |       | RMSZ         | # Z  >5 | RMSZ        | # Z  >5       |
| 1   | BI    | 1.46         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | BJ    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | BK    | 1.47         | 0/2631  | 1.99        | 4/3287 (0.1%) |
| 1   | BL    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | BM    | 1.47         | 0/2631  | 1.99        | 4/3287 (0.1%) |
| 1   | BN    | 1.46         | 0/2635  | 2.00        | 0/3292        |
| 1   | BO    | 1.47         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | BP    | 1.46         | 0/2366  | 1.98        | 4/2947 (0.1%) |
| 1   | BQ    | 1.45         | 0/1682  | 2.00        | 0/2085        |
| 1   | BR    | 1.46         | 0/2145  | 1.96        | 0/2669        |
| 1   | BS    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | BT    | 1.47         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | BU    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | BV    | 1.47         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | BW    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | BX    | 1.47         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | BY    | 1.47         | 0/2451  | 1.99        | 2/3062 (0.1%) |
| 1   | BZ    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | CA    | 1.47         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | CB    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | CC    | 1.47         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | CD    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | CE    | 1.46         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | CF    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | CG    | 1.47         | 0/2631  | 1.99        | 4/3287 (0.1%) |
| 1   | CH    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | CI    | 1.47         | 0/2631  | 1.99        | 4/3287 (0.1%) |
| 1   | CJ    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | CK    | 1.47         | 0/2631  | 1.99        | 4/3287 (0.1%) |
| 1   | CL    | 1.46         | 0/2366  | 1.98        | 4/2947 (0.1%) |
| 1   | CM    | 1.45         | 0/1682  | 2.00        | 2/2085 (0.1%) |
| 1   | CN    | 1.46         | 0/2145  | 1.96        | 0/2669        |
| 1   | CO    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | CP    | 1.46         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | CQ    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | CR    | 1.47         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | CS    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | CT    | 1.47         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | CU    | 1.47         | 0/2451  | 1.99        | 2/3062 (0.1%) |
| 1   | CV    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | CW    | 1.47         | 0/2631  | 1.99        | 2/3287 (0.1%) |
| 1   | CX    | 1.47         | 0/2635  | 2.00        | 0/3292        |
| 1   | CY    | 1.47         | 0/2631  | 1.99        | 2/3287 (0.1%) |

| Mol | Chain | Bond lengths |          | Bond angles |                   |
|-----|-------|--------------|----------|-------------|-------------------|
|     |       | RMSZ         | # Z  >5  | RMSZ        | # Z  >5           |
| 1   | CZ    | 1.47         | 0/2635   | 2.00        | 0/3292            |
| 1   | DA    | 1.46         | 0/2631   | 1.99        | 2/3287 (0.1%)     |
| 1   | DB    | 1.47         | 0/2635   | 2.00        | 0/3292            |
| 1   | DC    | 1.47         | 0/2631   | 1.99        | 2/3287 (0.1%)     |
| 1   | DD    | 1.47         | 0/2635   | 2.00        | 0/3292            |
| 1   | DE    | 1.47         | 0/2631   | 1.99        | 4/3287 (0.1%)     |
| 1   | DF    | 1.47         | 0/2635   | 2.00        | 0/3292            |
| 1   | DG    | 1.47         | 0/2631   | 1.99        | 4/3287 (0.1%)     |
| 1   | DH    | 1.46         | 0/2366   | 1.98        | 2/2947 (0.1%)     |
| 1   | DI    | 1.45         | 0/1682   | 2.00        | 0/2085            |
| 1   | DJ    | 1.46         | 0/2145   | 1.96        | 0/2669            |
| 1   | DK    | 1.46         | 0/2635   | 2.00        | 0/3292            |
| 1   | DL    | 1.46         | 0/2631   | 1.99        | 4/3287 (0.1%)     |
| 1   | DM    | 1.47         | 0/2635   | 2.00        | 0/3292            |
| 1   | DN    | 1.47         | 0/2631   | 1.99        | 2/3287 (0.1%)     |
| 1   | DO    | 1.47         | 0/2635   | 2.00        | 0/3292            |
| 1   | DP    | 1.47         | 0/2631   | 1.99        | 2/3287 (0.1%)     |
| 1   | DQ    | 1.47         | 0/2451   | 1.99        | 2/3062 (0.1%)     |
| 1   | DR    | 1.47         | 0/2635   | 2.00        | 0/3292            |
| 1   | DS    | 1.47         | 0/2631   | 1.99        | 2/3287 (0.1%)     |
| 1   | DT    | 1.47         | 0/2635   | 2.00        | 0/3292            |
| 1   | DU    | 1.47         | 0/2631   | 1.99        | 2/3287 (0.1%)     |
| 1   | DV    | 1.47         | 0/2635   | 2.00        | 0/3292            |
| 1   | DW    | 1.46         | 0/2631   | 1.99        | 4/3287 (0.1%)     |
| 1   | DX    | 1.47         | 0/2635   | 2.00        | 0/3292            |
| 1   | DY    | 1.47         | 0/2631   | 1.99        | 2/3287 (0.1%)     |
| 1   | DZ    | 1.47         | 0/2635   | 2.00        | 0/3292            |
| 1   | EA    | 1.47         | 0/2631   | 1.99        | 2/3287 (0.1%)     |
| 1   | EB    | 1.46         | 0/2635   | 2.00        | 0/3292            |
| 1   | EC    | 1.46         | 0/2631   | 1.99        | 4/3287 (0.1%)     |
| 1   | ED    | 1.46         | 0/2366   | 1.98        | 2/2947 (0.1%)     |
| 1   | EE    | 1.45         | 0/1682   | 2.00        | 0/2085            |
| 1   | EF    | 1.46         | 0/2145   | 1.96        | 0/2669            |
| All | All   | 1.47         | 0/280190 | 1.99        | 140/349870 (0.0%) |

There are no bond length outliers.

The worst 5 of 140 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms  | Z    | Observed(°) | Ideal(°) |
|-----|-------|-----|------|--------|------|-------------|----------|
| 1   | BG    | 247 | ALA  | CA-C-N | 5.54 | 125.36      | 120.10   |
| 1   | BG    | 247 | ALA  | C-N-CA | 5.54 | 125.36      | 120.10   |
| 1   | CC    | 247 | ALA  | CA-C-N | 5.53 | 125.35      | 120.10   |

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| Mol | Chain | Res | Type | Atoms  | Z    | Observed(°) | Ideal(°) |
|-----|-------|-----|------|--------|------|-------------|----------|
| 1   | CC    | 247 | ALA  | C-N-CA | 5.53 | 125.35      | 120.10   |
| 1   | CR    | 247 | ALA  | CA-C-N | 5.53 | 125.35      | 120.10   |

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

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

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1   | AA    | 2636  | 0        | 696      | 2       | 0            |
| 1   | AB    | 2632  | 0        | 694      | 4       | 0            |
| 1   | AC    | 2636  | 0        | 696      | 2       | 0            |
| 1   | AD    | 2632  | 0        | 694      | 4       | 0            |
| 1   | AE    | 2636  | 0        | 696      | 2       | 0            |
| 1   | AF    | 2632  | 0        | 694      | 3       | 0            |
| 1   | AG    | 2452  | 0        | 649      | 2       | 0            |
| 1   | AH    | 2636  | 0        | 696      | 2       | 0            |
| 1   | AI    | 2632  | 0        | 694      | 4       | 0            |
| 1   | AJ    | 2636  | 0        | 696      | 2       | 0            |
| 1   | AK    | 2632  | 0        | 694      | 4       | 0            |
| 1   | AL    | 2636  | 0        | 696      | 2       | 0            |
| 1   | AM    | 2632  | 0        | 694      | 3       | 0            |
| 1   | AN    | 2636  | 0        | 696      | 2       | 0            |
| 1   | AO    | 2632  | 0        | 694      | 4       | 0            |
| 1   | AP    | 2636  | 0        | 696      | 2       | 0            |
| 1   | AQ    | 2632  | 0        | 694      | 4       | 0            |
| 1   | AR    | 2636  | 0        | 696      | 2       | 0            |
| 1   | AS    | 2632  | 0        | 694      | 4       | 0            |
| 1   | AT    | 2372  | 0        | 625      | 0       | 0            |
| 1   | AU    | 1692  | 0        | 436      | 0       | 0            |
| 1   | AV    | 2152  | 0        | 556      | 0       | 0            |
| 1   | AW    | 2636  | 0        | 696      | 2       | 0            |
| 1   | AX    | 2632  | 0        | 694      | 3       | 0            |
| 1   | AY    | 2636  | 0        | 696      | 2       | 0            |
| 1   | AZ    | 2632  | 0        | 694      | 4       | 0            |
| 1   | BA    | 2636  | 0        | 696      | 2       | 0            |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1   | BB    | 2632  | 0        | 694      | 3       | 0            |
| 1   | BC    | 2452  | 0        | 649      | 3       | 0            |
| 1   | BD    | 2636  | 0        | 696      | 2       | 0            |
| 1   | BE    | 2632  | 0        | 694      | 4       | 0            |
| 1   | BF    | 2636  | 0        | 696      | 2       | 0            |
| 1   | BG    | 2632  | 0        | 694      | 4       | 0            |
| 1   | BH    | 2636  | 0        | 696      | 2       | 0            |
| 1   | BI    | 2632  | 0        | 694      | 4       | 0            |
| 1   | BJ    | 2636  | 0        | 696      | 2       | 0            |
| 1   | BK    | 2632  | 0        | 694      | 4       | 0            |
| 1   | BL    | 2636  | 0        | 696      | 2       | 0            |
| 1   | BM    | 2632  | 0        | 694      | 3       | 0            |
| 1   | BN    | 2636  | 0        | 696      | 2       | 0            |
| 1   | BO    | 2632  | 0        | 694      | 3       | 0            |
| 1   | BP    | 2372  | 0        | 625      | 0       | 0            |
| 1   | BQ    | 1692  | 0        | 436      | 0       | 0            |
| 1   | BR    | 2152  | 0        | 556      | 0       | 0            |
| 1   | BS    | 2636  | 0        | 696      | 2       | 0            |
| 1   | BT    | 2632  | 0        | 694      | 2       | 0            |
| 1   | BU    | 2636  | 0        | 696      | 2       | 0            |
| 1   | BV    | 2632  | 0        | 694      | 4       | 0            |
| 1   | BW    | 2636  | 0        | 696      | 2       | 0            |
| 1   | BX    | 2632  | 0        | 694      | 3       | 0            |
| 1   | BY    | 2452  | 0        | 649      | 3       | 0            |
| 1   | BZ    | 2636  | 0        | 696      | 2       | 0            |
| 1   | CA    | 2632  | 0        | 694      | 4       | 0            |
| 1   | CB    | 2636  | 0        | 696      | 2       | 0            |
| 1   | CC    | 2632  | 0        | 694      | 4       | 0            |
| 1   | CD    | 2636  | 0        | 696      | 2       | 0            |
| 1   | CE    | 2632  | 0        | 694      | 4       | 0            |
| 1   | CF    | 2636  | 0        | 696      | 2       | 0            |
| 1   | CG    | 2632  | 0        | 694      | 4       | 0            |
| 1   | CH    | 2636  | 0        | 696      | 2       | 0            |
| 1   | CI    | 2632  | 0        | 694      | 4       | 0            |
| 1   | CJ    | 2636  | 0        | 696      | 2       | 0            |
| 1   | CK    | 2632  | 0        | 694      | 4       | 0            |
| 1   | CL    | 2372  | 0        | 625      | 0       | 0            |
| 1   | CM    | 1692  | 0        | 436      | 0       | 0            |
| 1   | CN    | 2152  | 0        | 556      | 0       | 0            |
| 1   | CO    | 2636  | 0        | 696      | 2       | 0            |
| 1   | CP    | 2632  | 0        | 694      | 3       | 0            |
| 1   | CQ    | 2636  | 0        | 696      | 2       | 0            |

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| Mol | Chain | Non-H  | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|--------|----------|----------|---------|--------------|
| 1   | CR    | 2632   | 0        | 694      | 4       | 0            |
| 1   | CS    | 2636   | 0        | 696      | 2       | 0            |
| 1   | CT    | 2632   | 0        | 694      | 3       | 0            |
| 1   | CU    | 2452   | 0        | 649      | 3       | 0            |
| 1   | CV    | 2636   | 0        | 696      | 2       | 0            |
| 1   | CW    | 2632   | 0        | 694      | 4       | 0            |
| 1   | CX    | 2636   | 0        | 696      | 2       | 0            |
| 1   | CY    | 2632   | 0        | 694      | 4       | 0            |
| 1   | CZ    | 2636   | 0        | 696      | 2       | 0            |
| 1   | DA    | 2632   | 0        | 694      | 4       | 0            |
| 1   | DB    | 2636   | 0        | 696      | 2       | 0            |
| 1   | DC    | 2632   | 0        | 694      | 3       | 0            |
| 1   | DD    | 2636   | 0        | 696      | 2       | 0            |
| 1   | DE    | 2632   | 0        | 694      | 4       | 0            |
| 1   | DF    | 2636   | 0        | 696      | 2       | 0            |
| 1   | DG    | 2632   | 0        | 694      | 3       | 0            |
| 1   | DH    | 2372   | 0        | 625      | 0       | 0            |
| 1   | DI    | 1692   | 0        | 436      | 0       | 0            |
| 1   | DJ    | 2152   | 0        | 556      | 0       | 0            |
| 1   | DK    | 2636   | 0        | 696      | 2       | 0            |
| 1   | DL    | 2632   | 0        | 694      | 4       | 0            |
| 1   | DM    | 2636   | 0        | 696      | 2       | 0            |
| 1   | DN    | 2632   | 0        | 694      | 4       | 0            |
| 1   | DO    | 2636   | 0        | 696      | 2       | 0            |
| 1   | DP    | 2632   | 0        | 694      | 3       | 0            |
| 1   | DQ    | 2452   | 0        | 649      | 3       | 0            |
| 1   | DR    | 2636   | 0        | 696      | 2       | 0            |
| 1   | DS    | 2632   | 0        | 694      | 4       | 0            |
| 1   | DT    | 2636   | 0        | 696      | 2       | 0            |
| 1   | DU    | 2632   | 0        | 694      | 3       | 0            |
| 1   | DV    | 2636   | 0        | 696      | 2       | 0            |
| 1   | DW    | 2632   | 0        | 694      | 3       | 0            |
| 1   | DX    | 2636   | 0        | 696      | 2       | 0            |
| 1   | DY    | 2632   | 0        | 694      | 4       | 0            |
| 1   | DZ    | 2636   | 0        | 696      | 2       | 0            |
| 1   | EA    | 2632   | 0        | 694      | 3       | 0            |
| 1   | EB    | 2636   | 0        | 696      | 2       | 0            |
| 1   | EC    | 2632   | 0        | 694      | 3       | 0            |
| 1   | ED    | 2372   | 0        | 625      | 0       | 0            |
| 1   | EE    | 1692   | 0        | 436      | 0       | 0            |
| 1   | EF    | 2152   | 0        | 556      | 0       | 0            |
| All | All   | 280400 | 0        | 73880    | 133     | 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 0.

The worst 5 of 133 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) |
|-----------------|-----------------|--------------------------|-------------------|
| 1:AZ:43:GLY:HA3 | 1:CK:44:THR:O   | 2.04                     | 0.58              |
| 1:AK:43:GLY:HA3 | 1:AO:44:THR:O   | 2.04                     | 0.57              |
| 1:AS:44:THR:O   | 1:CR:43:GLY:HA3 | 2.04                     | 0.57              |
| 1:BC:43:GLY:HA3 | 1:DP:44:THR:O   | 2.04                     | 0.57              |
| 1:DL:43:GLY:HA3 | 1:EA:44:THR:O   | 2.04                     | 0.57              |

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   | AA    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | AB    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | AC    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | AD    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | AE    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | AF    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | AG    | 611/697 (88%) | 566 (93%) | 45 (7%) | 0        | 100         | 100 |
| 1   | AH    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | AI    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | AJ    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | AK    | 656/697 (94%) | 604 (92%) | 52 (8%) | 0        | 100         | 100 |
| 1   | AL    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |

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| Mol | Chain | Analysed      | Favoured  | Allowed | Outliers | Percentiles |     |
|-----|-------|---------------|-----------|---------|----------|-------------|-----|
| 1   | AM    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | AN    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | AO    | 656/697 (94%) | 604 (92%) | 52 (8%) | 0        | 100         | 100 |
| 1   | AP    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | AQ    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | AR    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | AS    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | AT    | 581/697 (83%) | 538 (93%) | 43 (7%) | 0        | 100         | 100 |
| 1   | AU    | 403/697 (58%) | 376 (93%) | 27 (7%) | 0        | 100         | 100 |
| 1   | AV    | 524/697 (75%) | 489 (93%) | 35 (7%) | 0        | 100         | 100 |
| 1   | AW    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | AX    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | AY    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | AZ    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | BA    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | BB    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | BC    | 611/697 (88%) | 566 (93%) | 45 (7%) | 0        | 100         | 100 |
| 1   | BD    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | BE    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | BF    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | BG    | 656/697 (94%) | 604 (92%) | 52 (8%) | 0        | 100         | 100 |
| 1   | BH    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | BI    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | BJ    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | BK    | 656/697 (94%) | 604 (92%) | 52 (8%) | 0        | 100         | 100 |
| 1   | BL    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | BM    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | BN    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | BO    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | BP    | 581/697 (83%) | 538 (93%) | 43 (7%) | 0        | 100         | 100 |
| 1   | BQ    | 403/697 (58%) | 376 (93%) | 27 (7%) | 0        | 100         | 100 |

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| Mol | Chain | Analysed      | Favoured  | Allowed | Outliers | Percentiles |     |
|-----|-------|---------------|-----------|---------|----------|-------------|-----|
| 1   | BR    | 524/697 (75%) | 489 (93%) | 35 (7%) | 0        | 100         | 100 |
| 1   | BS    | 657/697 (94%) | 613 (93%) | 44 (7%) | 0        | 100         | 100 |
| 1   | BT    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | BU    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | BV    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | BW    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | BX    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | BY    | 611/697 (88%) | 566 (93%) | 45 (7%) | 0        | 100         | 100 |
| 1   | BZ    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | CA    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | CB    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | CC    | 656/697 (94%) | 604 (92%) | 52 (8%) | 0        | 100         | 100 |
| 1   | CD    | 657/697 (94%) | 613 (93%) | 44 (7%) | 0        | 100         | 100 |
| 1   | CE    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | CF    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | CG    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | CH    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | CI    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | CJ    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | CK    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | CL    | 581/697 (83%) | 538 (93%) | 43 (7%) | 0        | 100         | 100 |
| 1   | CM    | 403/697 (58%) | 376 (93%) | 27 (7%) | 0        | 100         | 100 |
| 1   | CN    | 524/697 (75%) | 489 (93%) | 35 (7%) | 0        | 100         | 100 |
| 1   | CO    | 657/697 (94%) | 613 (93%) | 44 (7%) | 0        | 100         | 100 |
| 1   | CP    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | CQ    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | CR    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | CS    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | CT    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | CU    | 611/697 (88%) | 566 (93%) | 45 (7%) | 0        | 100         | 100 |
| 1   | CV    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |

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| Mol | Chain | Analysed      | Favoured  | Allowed | Outliers | Percentiles |     |
|-----|-------|---------------|-----------|---------|----------|-------------|-----|
| 1   | CW    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | CX    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | CY    | 656/697 (94%) | 604 (92%) | 52 (8%) | 0        | 100         | 100 |
| 1   | CZ    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | DA    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | DB    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | DC    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | DD    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | DE    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | DF    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | DG    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | DH    | 581/697 (83%) | 538 (93%) | 43 (7%) | 0        | 100         | 100 |
| 1   | DI    | 403/697 (58%) | 376 (93%) | 27 (7%) | 0        | 100         | 100 |
| 1   | DJ    | 524/697 (75%) | 489 (93%) | 35 (7%) | 0        | 100         | 100 |
| 1   | DK    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | DL    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | DM    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | DN    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | DO    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | DP    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | DQ    | 611/697 (88%) | 566 (93%) | 45 (7%) | 0        | 100         | 100 |
| 1   | DR    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | DS    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | DT    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | DU    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |
| 1   | DV    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | DW    | 656/697 (94%) | 604 (92%) | 52 (8%) | 0        | 100         | 100 |
| 1   | DX    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | DY    | 656/697 (94%) | 604 (92%) | 52 (8%) | 0        | 100         | 100 |
| 1   | DZ    | 657/697 (94%) | 614 (94%) | 43 (6%) | 0        | 100         | 100 |
| 1   | EA    | 656/697 (94%) | 603 (92%) | 53 (8%) | 0        | 100         | 100 |

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| Mol | Chain | Analysed          | Favoured    | Allowed   | Outliers | Percentiles |     |
|-----|-------|-------------------|-------------|-----------|----------|-------------|-----|
| 1   | EB    | 657/697 (94%)     | 614 (94%)   | 43 (6%)   | 0        | 100         | 100 |
| 1   | EC    | 656/697 (94%)     | 603 (92%)   | 53 (8%)   | 0        | 100         | 100 |
| 1   | ED    | 581/697 (83%)     | 538 (93%)   | 43 (7%)   | 0        | 100         | 100 |
| 1   | EE    | 403/697 (58%)     | 376 (93%)   | 27 (7%)   | 0        | 100         | 100 |
| 1   | EF    | 524/697 (75%)     | 489 (93%)   | 35 (7%)   | 0        | 100         | 100 |
| All | All   | 69680/76670 (91%) | 64615 (93%) | 5065 (7%) | 0        | 100         | 100 |

There are no Ramachandran outliers to report.

### 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](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.



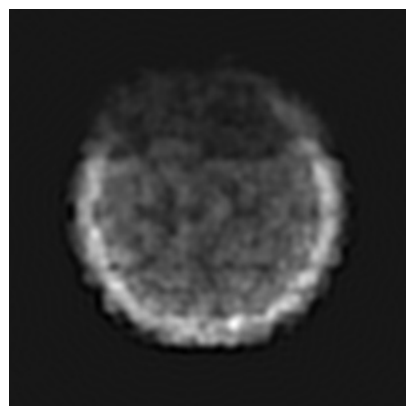
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14963. These allow visual inspection of the internal detail of the map and identification of artifacts.

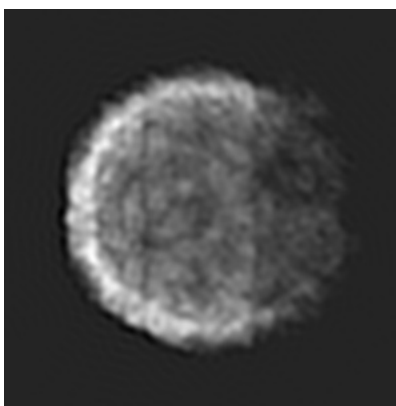
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

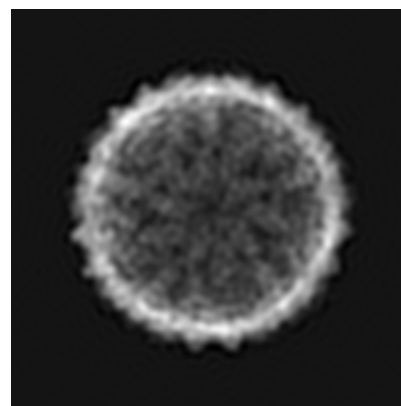
#### 6.1.1 Primary map



X

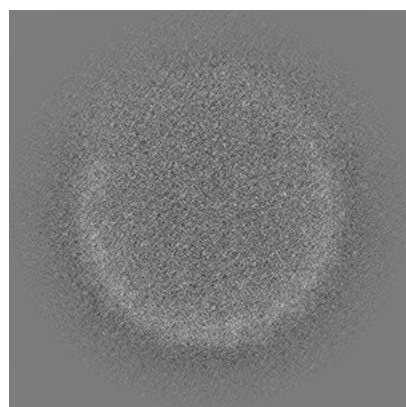


Y

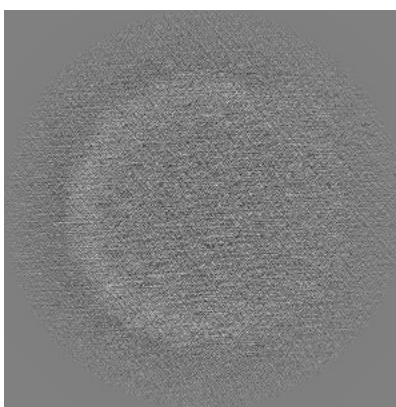


Z

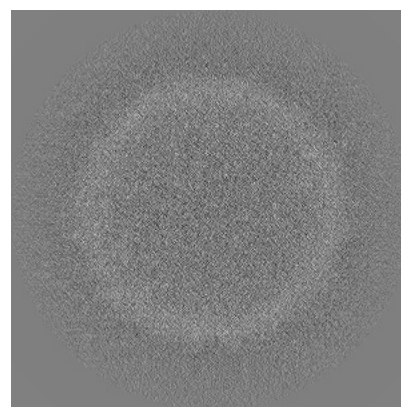
#### 6.1.2 Raw map



X



Y



Z

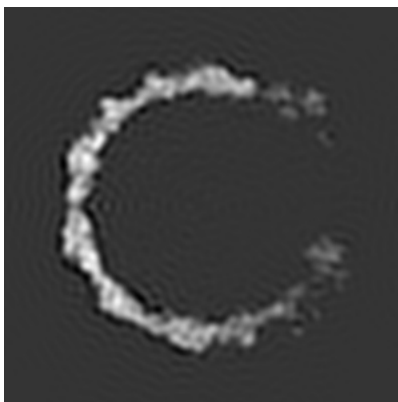
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

### 6.2.1 Primary map



X Index: 280

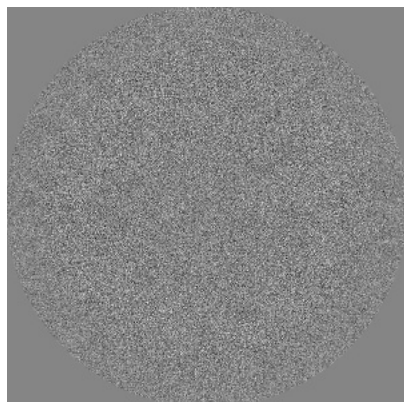


Y Index: 280

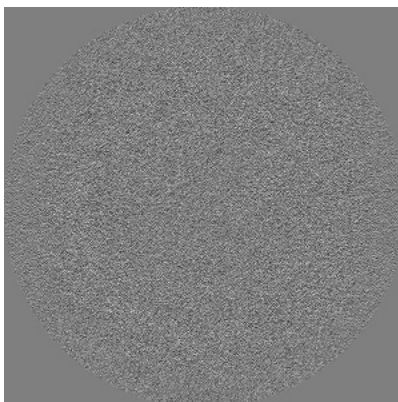


Z Index: 280

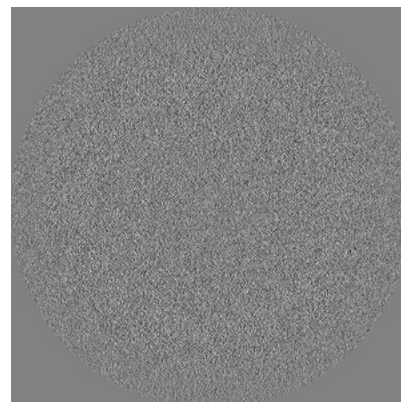
### 6.2.2 Raw map



X Index: 280



Y Index: 280

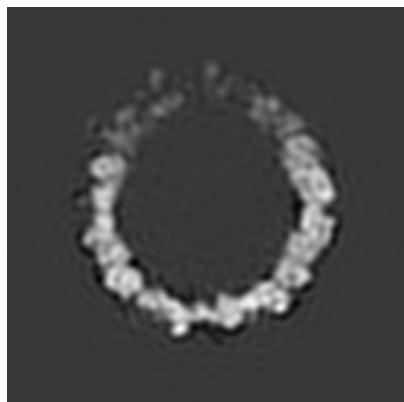


Z Index: 280

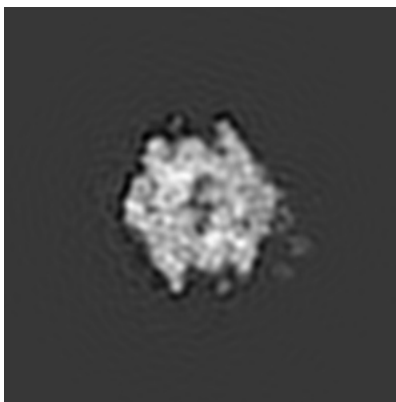
The images above show central slices of the map in three orthogonal directions.

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

### 6.3.1 Primary map



X Index: 185

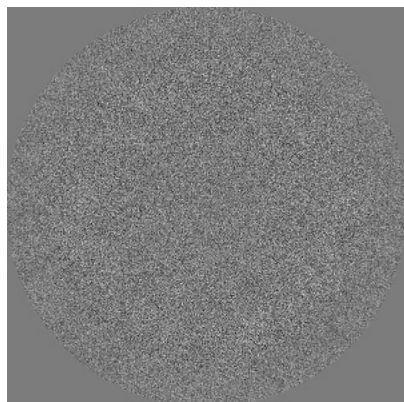


Y Index: 116

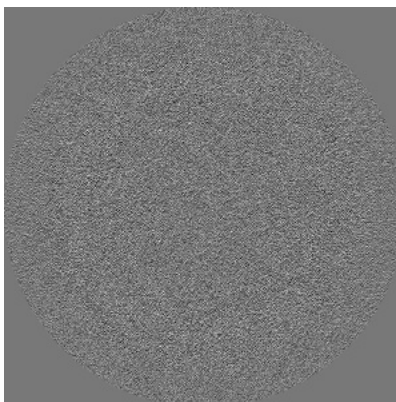


Z Index: 144

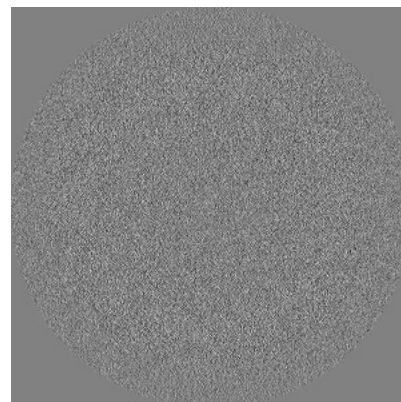
### 6.3.2 Raw map



X Index: 300



Y Index: 272



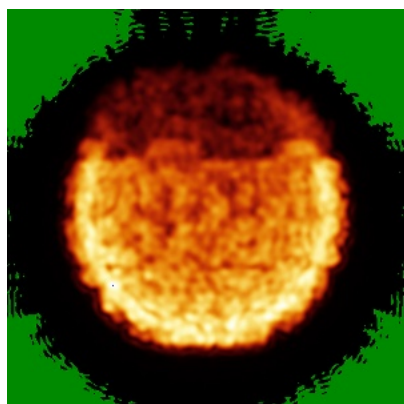
Z Index: 280

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

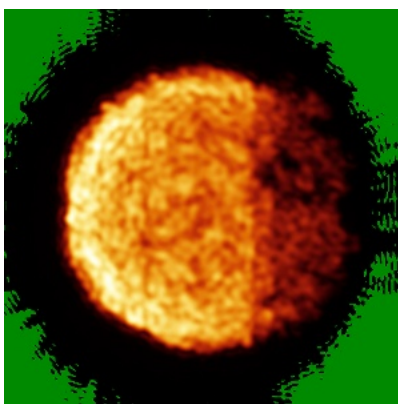


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

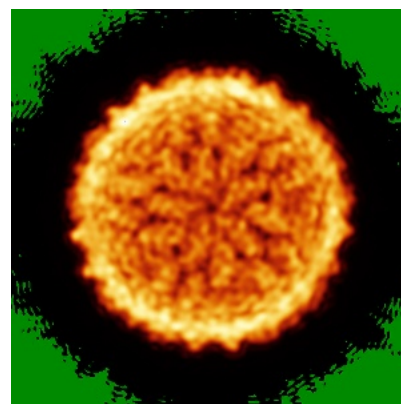
### 6.4.1 Primary map



X

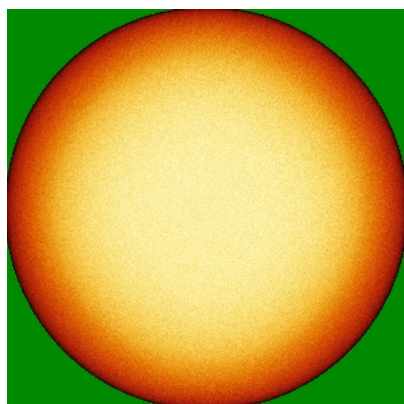


Y

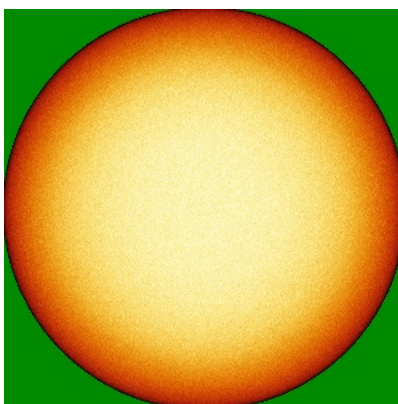


Z

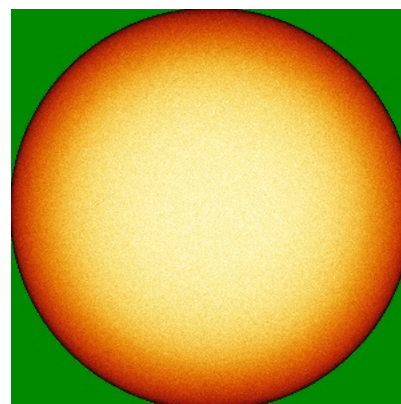
### 6.4.2 Raw map



X



Y

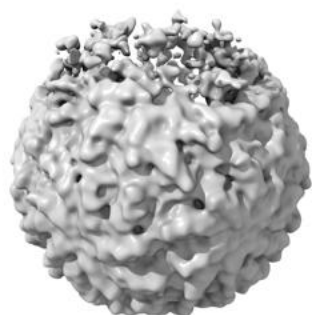


Z

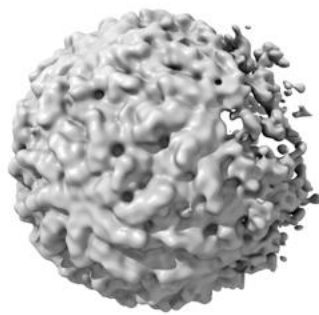
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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

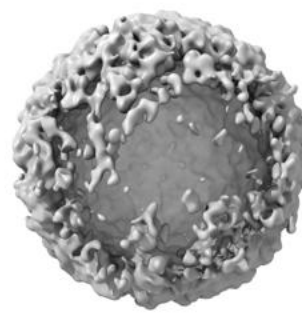
### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

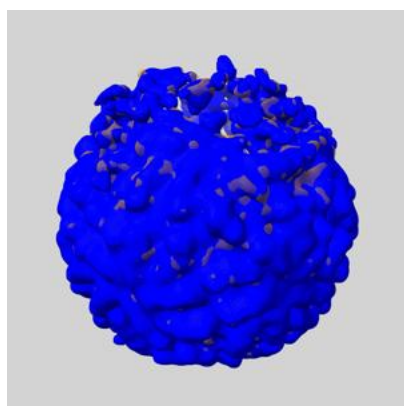
## 6.6 Mask visualisation [i](#)

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

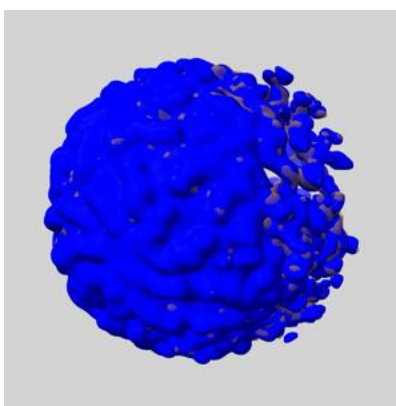
A mask typically either:

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

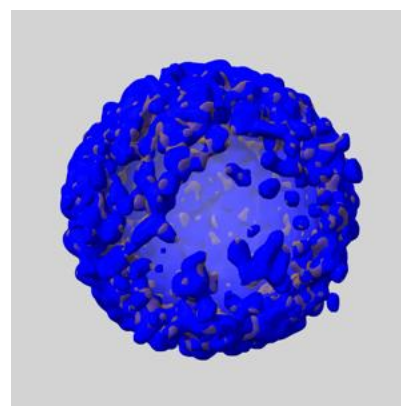
### 6.6.1 emd\_14963\_msk\_1.map [i](#)



X



Y

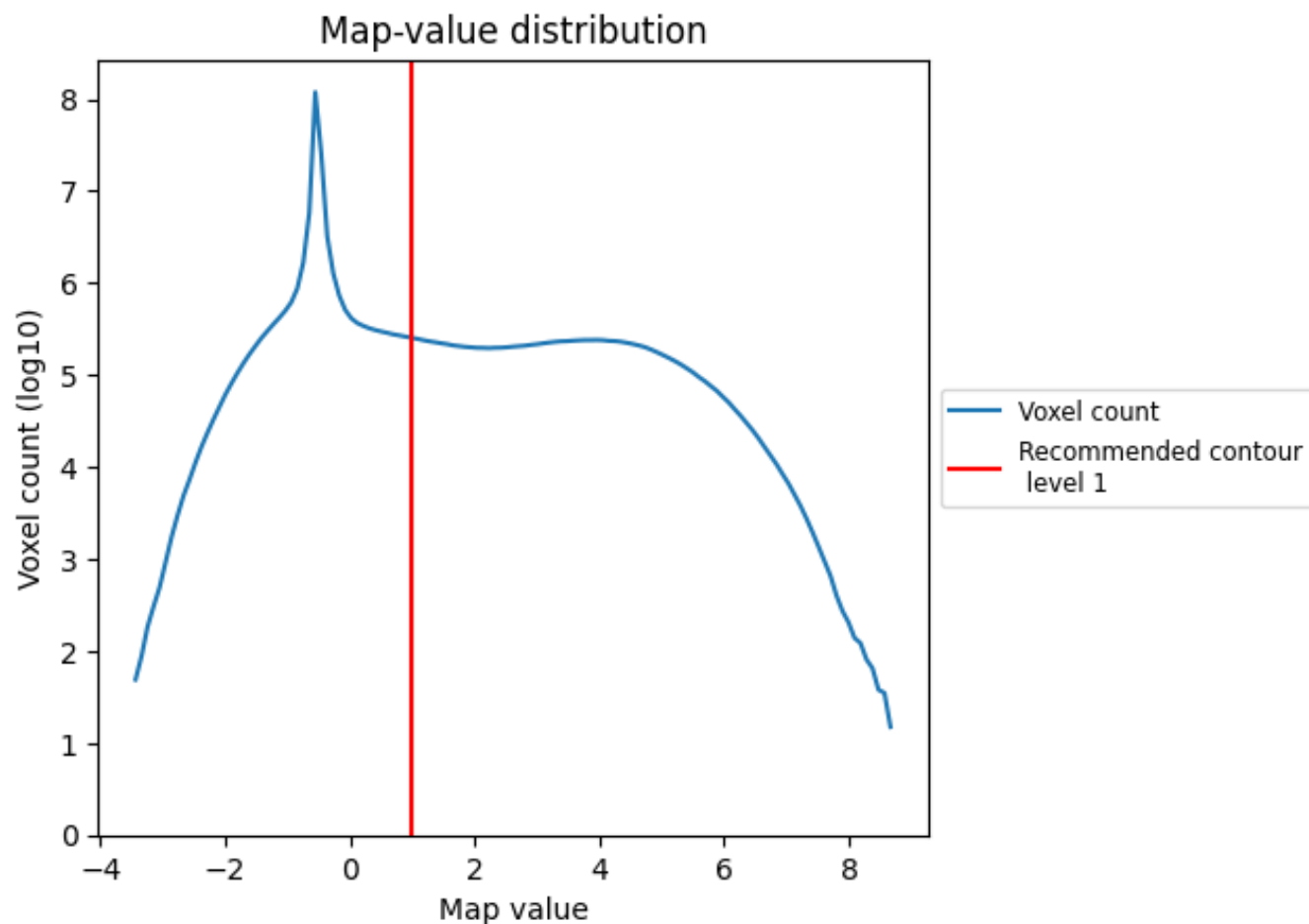


Z

## 7 Map analysis [i](#)

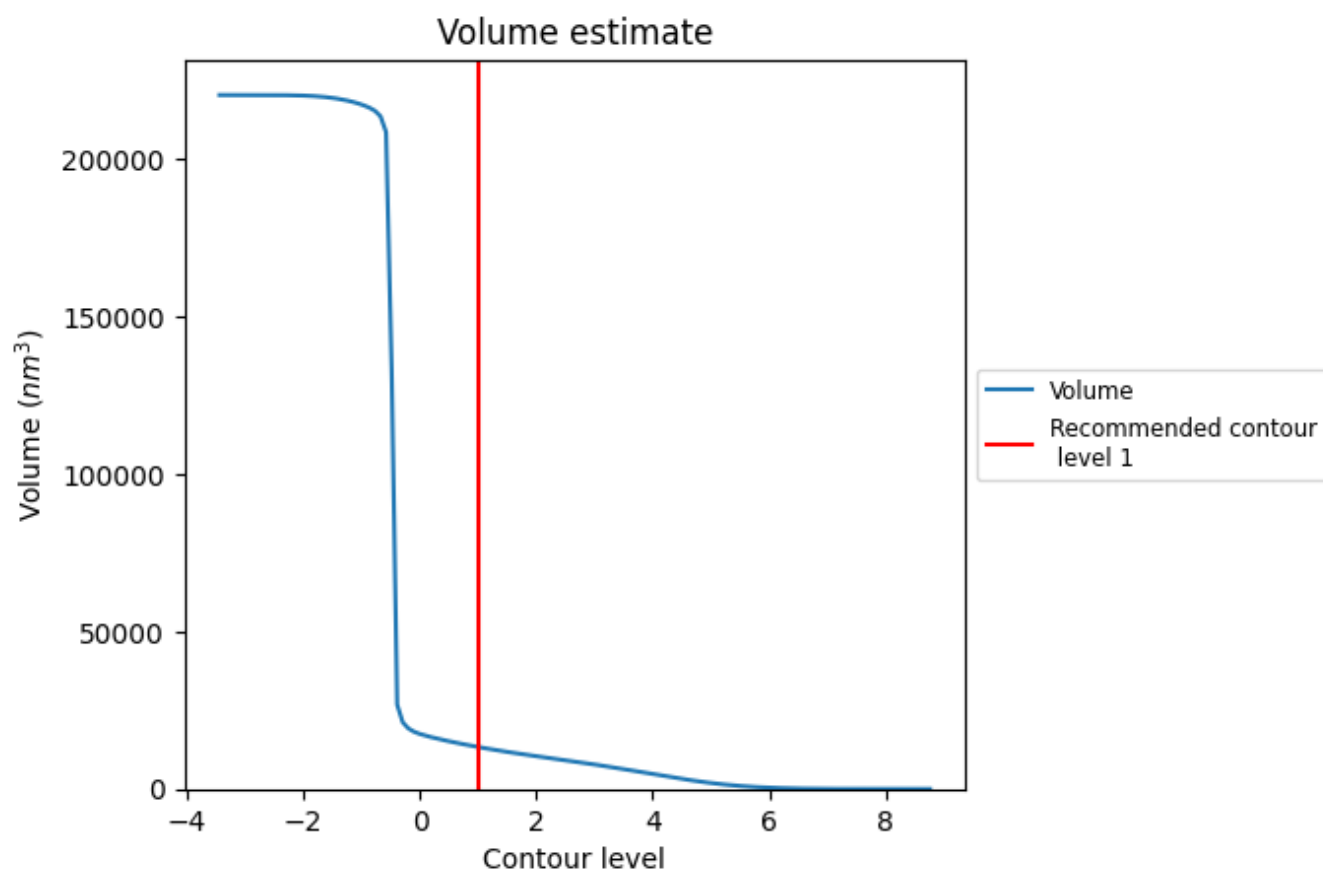
This section contains the results of statistical analysis of the map.

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



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

## 7.2 Volume estimate [i](#)

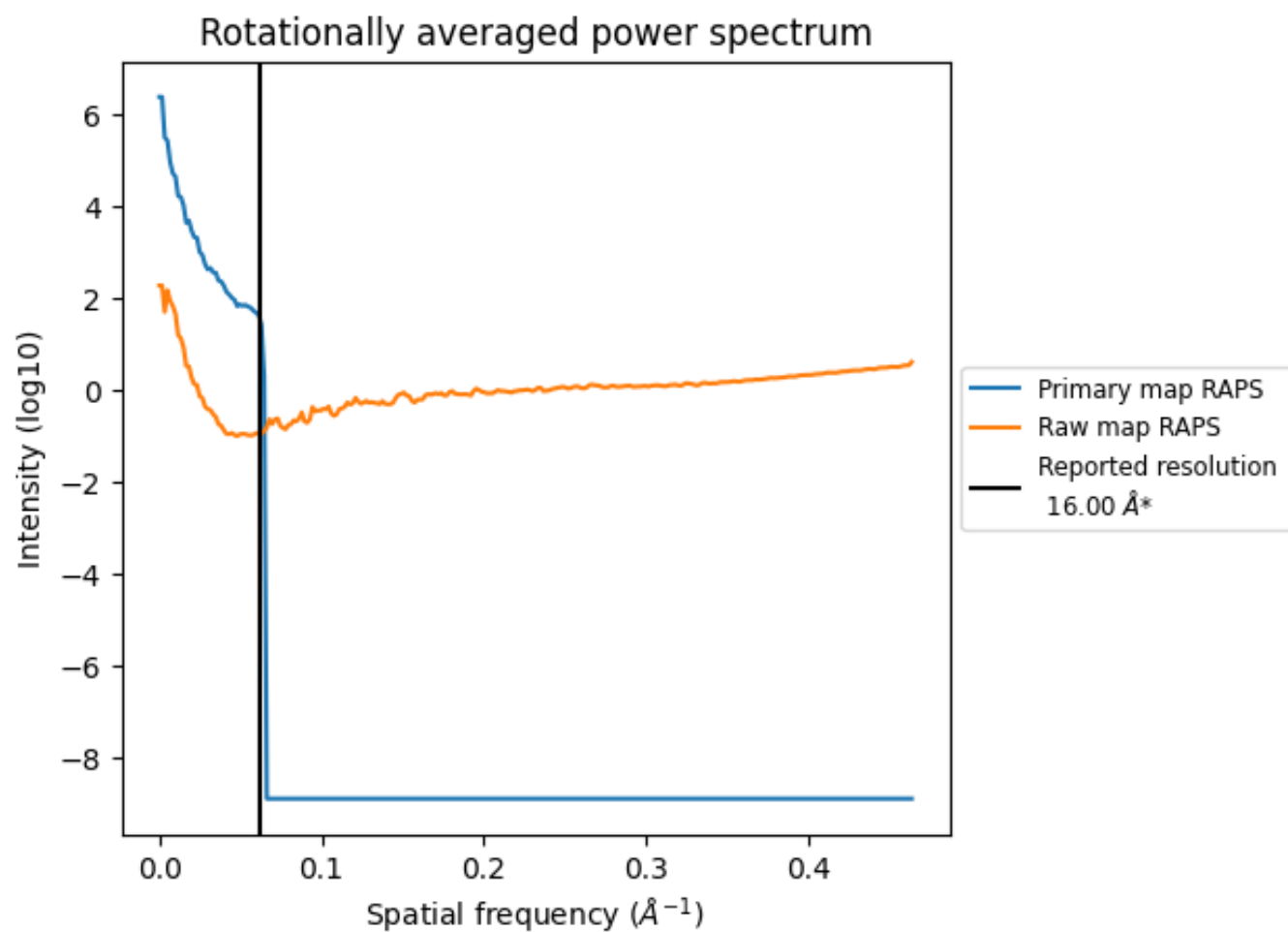


The volume at the recommended contour level is 13348 nm<sup>3</sup>; this corresponds to an approximate mass of 12058 kDa.

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



### 7.3 Rotationally averaged power spectrum ⓘ

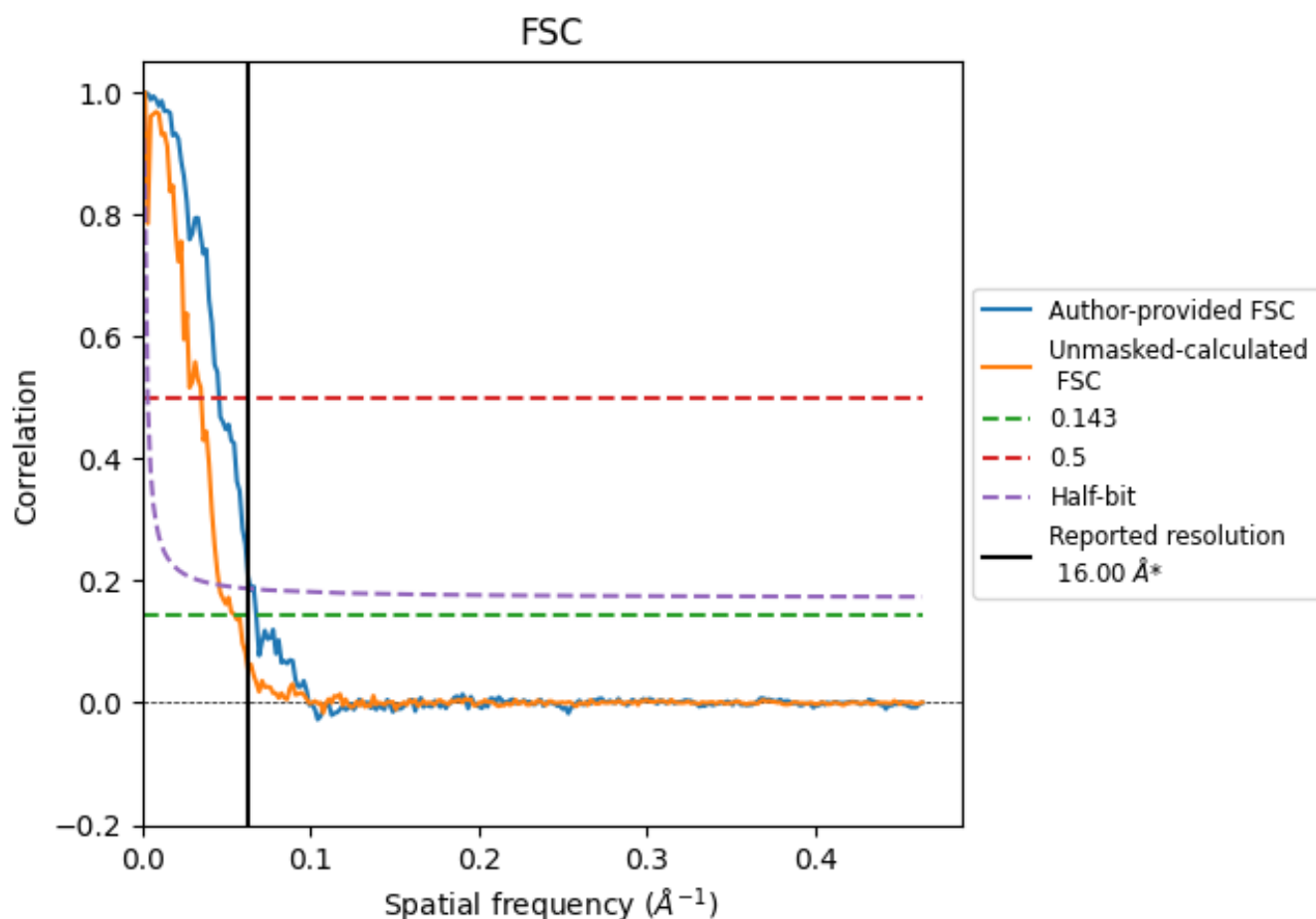


\*Reported resolution corresponds to spatial frequency of 0.062  $\text{\AA}^{-1}$

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

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.062 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

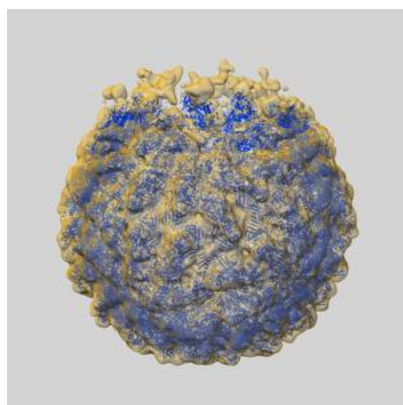
| Resolution estimate (Å)   | Estimation criterion (FSC cut-off) |       |          |
|---------------------------|------------------------------------|-------|----------|
|                           | 0.143                              | 0.5   | Half-bit |
| Reported by author        | 16.00                              | -     | -        |
| Author-provided FSC curve | 14.75                              | 21.93 | 15.53    |
| Unmasked-calculated*      | 18.18                              | 28.49 | 21.88    |

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 18.18 differs from the reported value 16.0 by more than 10 %

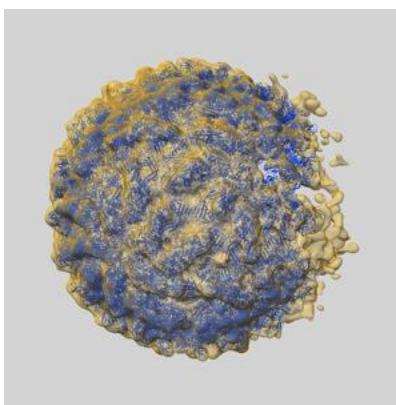
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14963 and PDB model 7ZTS. Per-residue inclusion information can be found in section [3](#) on page [14](#).

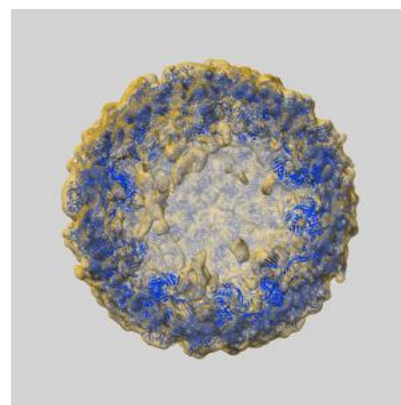
### 9.1 Map-model overlay [i](#)



X



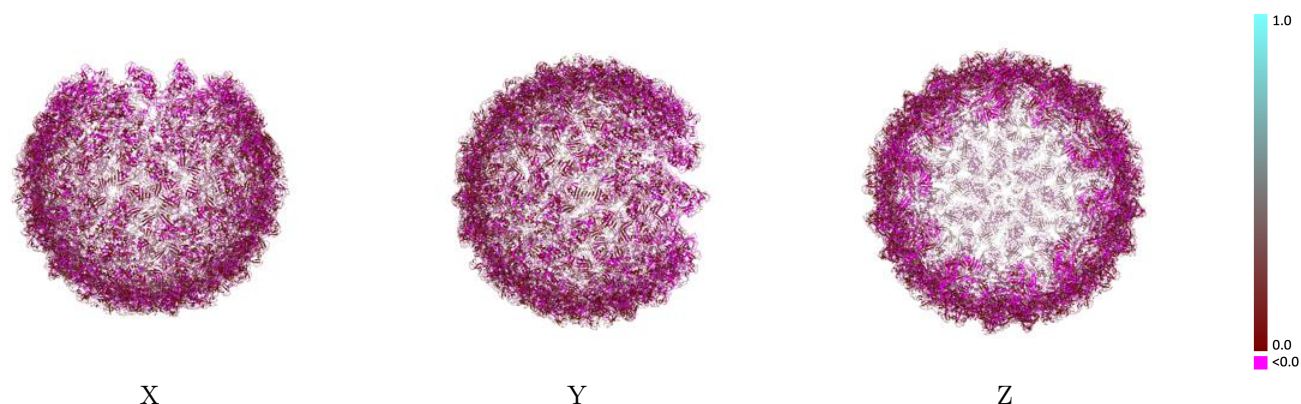
Y



Z

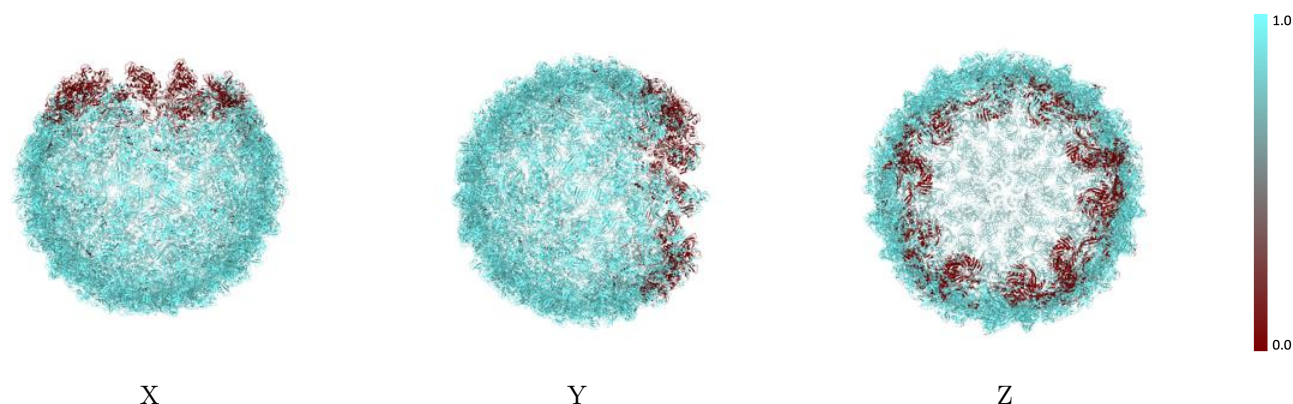
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



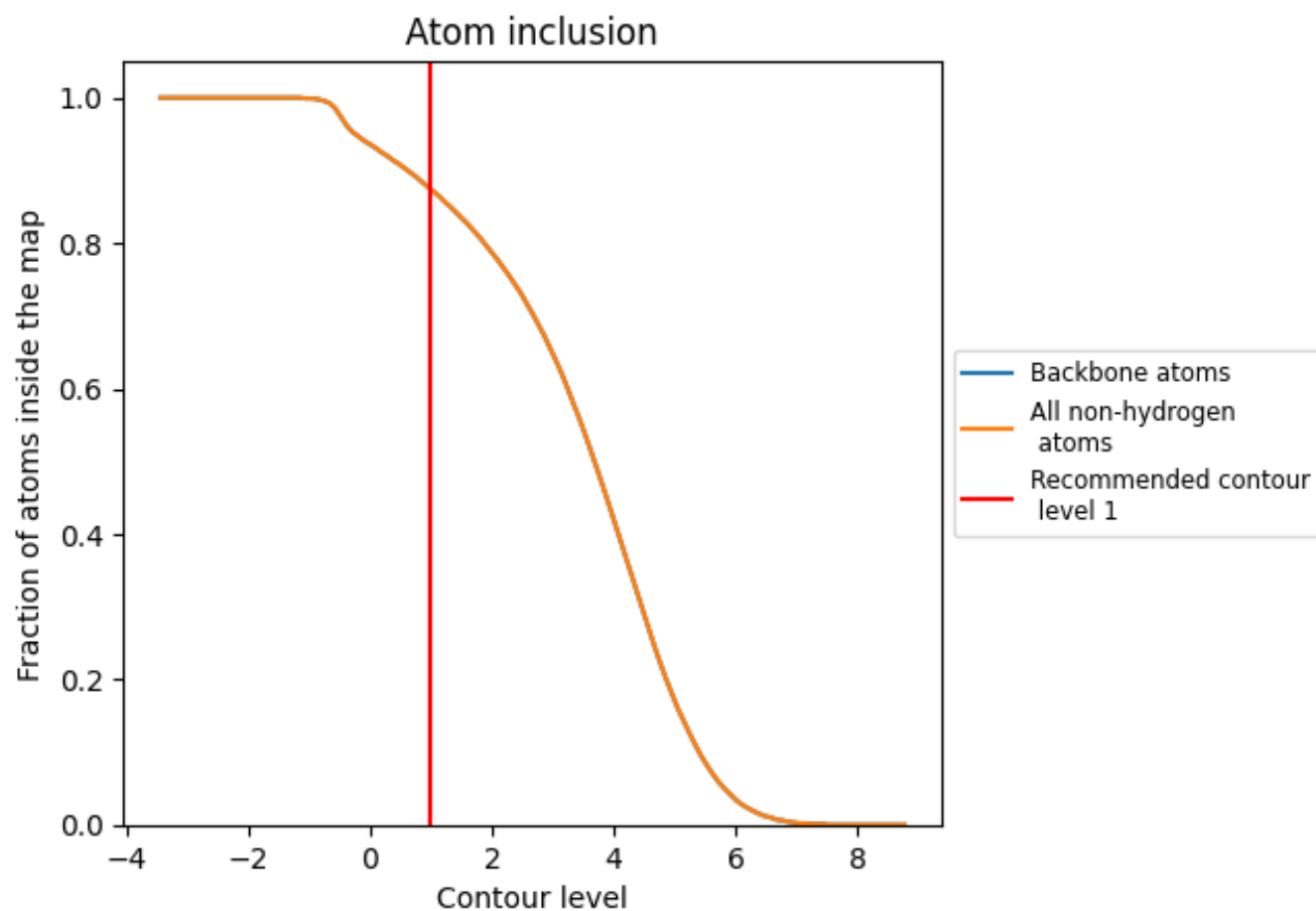
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 87% 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 (1) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion                                                                             | Q-score                                                                                     |
|-------|--------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------|
| All   |  0.8740   |  0.0510    |
| AA    |  0.9900   |  0.0730    |
| AB    |  0.9880   |  0.0650    |
| AC    |  0.9900   |  0.0690    |
| AD    |  0.9950   |  0.0690    |
| AE    |  0.9580   |  0.0620    |
| AF    |  0.5660   |  0.0250    |
| AG    |  0.9580   |  0.0540    |
| AH    |  0.9920   |  0.0690    |
| AI    |  0.9930   |  0.0550    |
| AJ    |  0.9850   |  0.0620    |
| AK    |  0.9760   |  0.0520    |
| AL    |  0.9820   |  0.0540    |
| AM    |  0.9680   |  0.0550    |
| AN    |  0.9880  |  0.0590   |
| AO    |  0.9920 |  0.0580  |
| AP    |  0.9930 |  0.0740  |
| AQ    |  0.9900 |  0.0640  |
| AR    |  0.9970 |  0.0670  |
| AS    |  0.9960 |  0.0660  |
| AT    |  0.2820 |  0.0010  |
| AU    |  0.5750 |  0.0060  |
| AV    |  0.1310 |  -0.0140 |
| AW    |  0.9940 |  0.0630  |
| AX    |  0.9880 |  0.0600  |
| AY    |  0.9940 |  0.0650  |
| AZ    |  0.9940 |  0.0580  |
| BA    |  0.9240 |  0.0520  |
| BB    |  0.4040 |  0.0220  |
| BC    |  0.9630 |  0.0480  |
| BD    |  0.9770 |  0.0520  |
| BE    |  0.9590 |  0.0600  |
| BF    |  0.9880 |  0.0610  |
| BG    |  0.9750 |  0.0490  |
| BH    |  0.9680 |  0.0590  |



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| Chain | Atom inclusion                                                                             | Q-score                                                                                     |
|-------|--------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------|
| BI    |  0.9590   |  0.0480    |
| BJ    |  0.9730   |  0.0600    |
| BK    |  0.9840   |  0.0530    |
| BL    |  0.9950   |  0.0620    |
| BM    |  0.9840   |  0.0660    |
| BN    |  0.9940   |  0.0660    |
| BO    |  0.9960   |  0.0590    |
| BP    |  0.0900   |  -0.0120   |
| BQ    |  0.4760   |  -0.0080   |
| BR    |  0.0400   |  -0.0050   |
| BS    |  0.9970   |  0.0620    |
| BT    |  0.9960   |  0.0620    |
| BU    |  0.9910   |  0.0640    |
| BV    |  0.9880   |  0.0540    |
| BW    |  0.9320   |  0.0460    |
| BX    |  0.4290   |  0.0190    |
| BY    |  0.8510   |  0.0390    |
| BZ    |  0.9640  |  0.0610   |
| CA    |  0.9720 |  0.0500  |
| CB    |  0.9760 |  0.0560  |
| CC    |  0.8990 |  0.0460  |
| CD    |  0.9570 |  0.0480  |
| CE    |  0.9310 |  0.0570  |
| CF    |  0.9650 |  0.0620  |
| CG    |  0.9710 |  0.0450  |
| CH    |  0.9940 |  0.0660  |
| CI    |  0.9920 |  0.0570  |
| CJ    |  0.9810 |  0.0590  |
| CK    |  0.9880 |  0.0610  |
| CL    |  0.0620 |  -0.0090 |
| CM    |  0.3090 |  0.0010  |
| CN    |  0.0600 |  0.0030  |
| CO    |  0.9950 |  0.0690  |
| CP    |  0.9990 |  0.0700  |
| CQ    |  0.9920 |  0.0670  |
| CR    |  0.9910 |  0.0560  |
| CS    |  0.9820 |  0.0540  |
| CT    |  0.7330 |  0.0260  |
| CU    |  0.8270 |  0.0360  |
| CV    |  0.9930 |  0.0600  |
| CW    |  0.9910 |  0.0630  |
| CX    |  0.9860 |  0.0590  |

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| Chain | Atom inclusion                                                                             | Q-score                                                                                    |
|-------|--------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|
| CY    |  0.9770   |  0.0530   |
| CZ    |  0.9500   |  0.0560   |
| DA    |  0.9300   |  0.0450   |
| DB    |  0.9820   |  0.0540   |
| DC    |  0.9930   |  0.0560   |
| DD    |  0.9960   |  0.0680   |
| DE    |  0.9970   |  0.0690   |
| DF    |  0.9790   |  0.0610   |
| DG    |  0.9960   |  0.0670   |
| DH    |  0.2900   |  0.0100   |
| DI    |  0.2650   |  0.0130   |
| DJ    |  0.4750   |  -0.0070  |
| DK    |  0.9920   |  0.0670   |
| DL    |  0.9960   |  0.0690   |
| DM    |  0.9910   |  0.0750   |
| DN    |  0.9920   |  0.0650   |
| DO    |  0.9720   |  0.0670   |
| DP    |  0.5430   |  0.0300   |
| DQ    |  0.8780   |  0.0400   |
| DR    |  0.9900  |  0.0630  |
| DS    |  0.9850 |  0.0590 |
| DT    |  0.9830 |  0.0700 |
| DU    |  0.9790 |  0.0520 |
| DV    |  0.9610 |  0.0490 |
| DW    |  0.9620 |  0.0580 |
| DX    |  0.9740 |  0.0580 |
| DY    |  0.9840 |  0.0530 |
| DZ    |  0.9880 |  0.0720 |
| EA    |  0.9900 |  0.0630 |
| EB    |  0.9920 |  0.0620 |
| EC    |  0.9910 |  0.0650 |
| ED    |  0.2210 |  0.0030 |
| EE    |  0.4950 |  0.0160 |
| EF    |  0.0890 |  0.0020 |