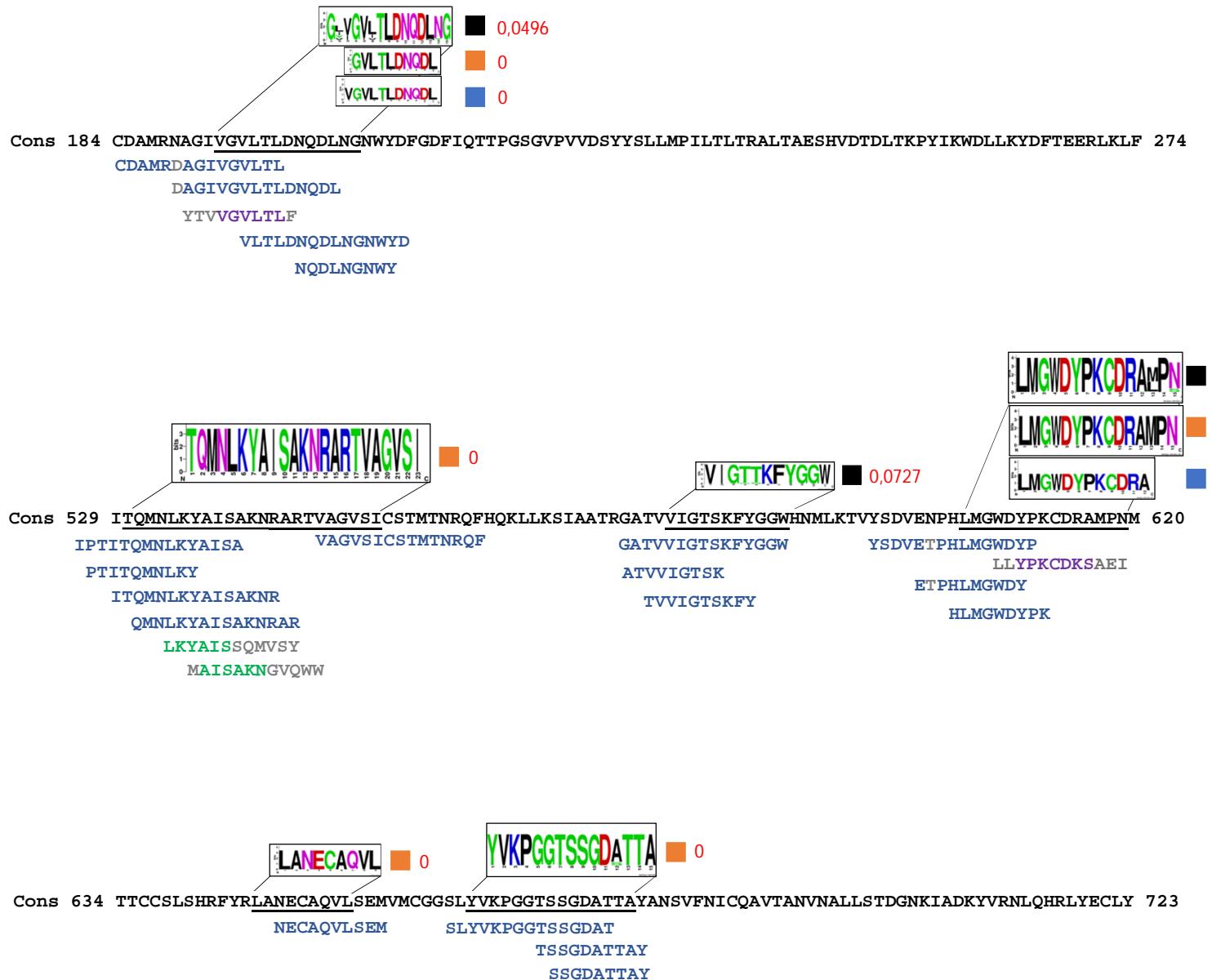
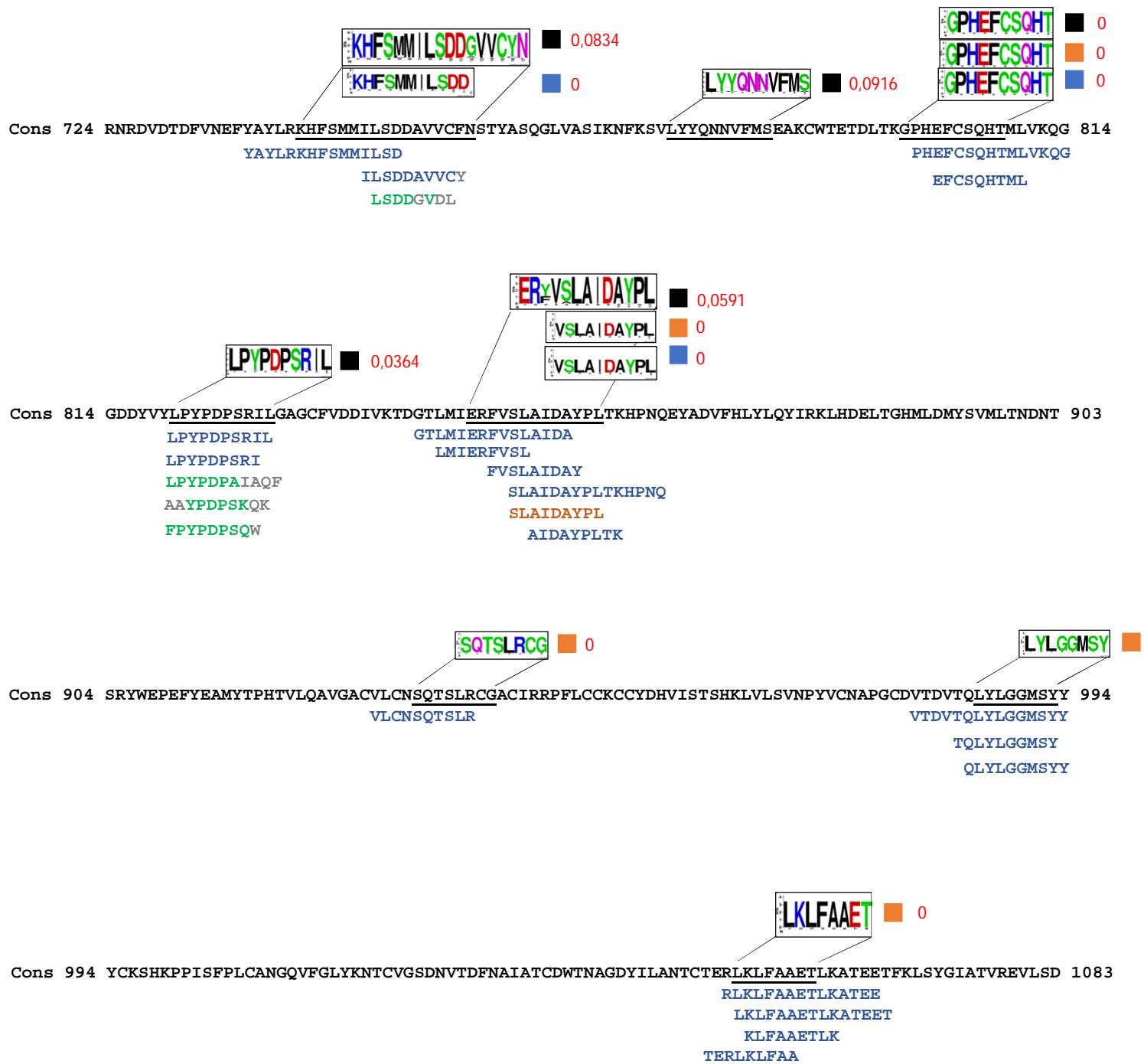


## ORF1ab



## ORF1ab



### Color map

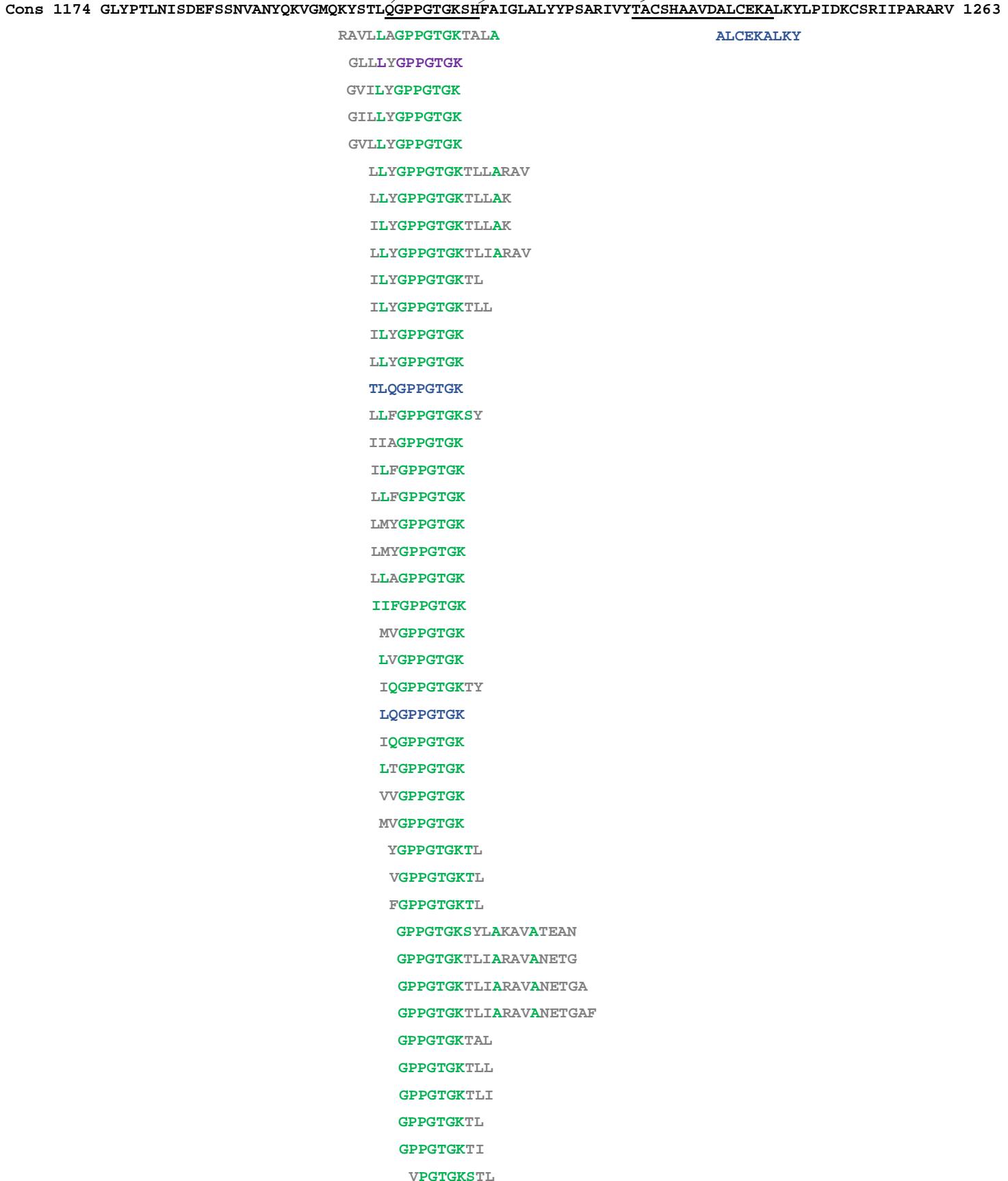
- Unknown
- SARS-CoV
- Human
- Other Coronavirus
- Amino acid mismatch
- Consensus conserved region

### Symbols

- Pan-coronavirus conservation
- Betacoronavirus conservation
- Human coronavirus conservation

Average entropy

## ORF1ab



## ORF1ab



### Color map

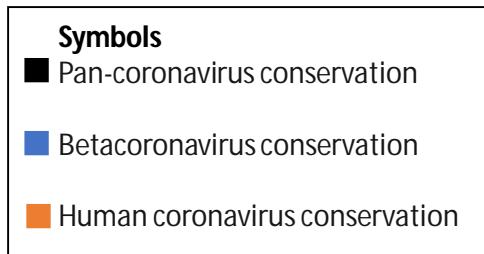
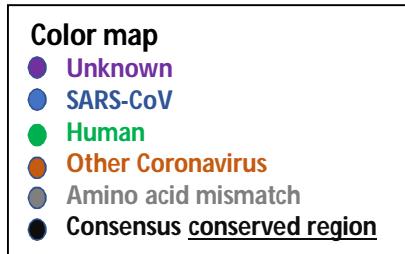
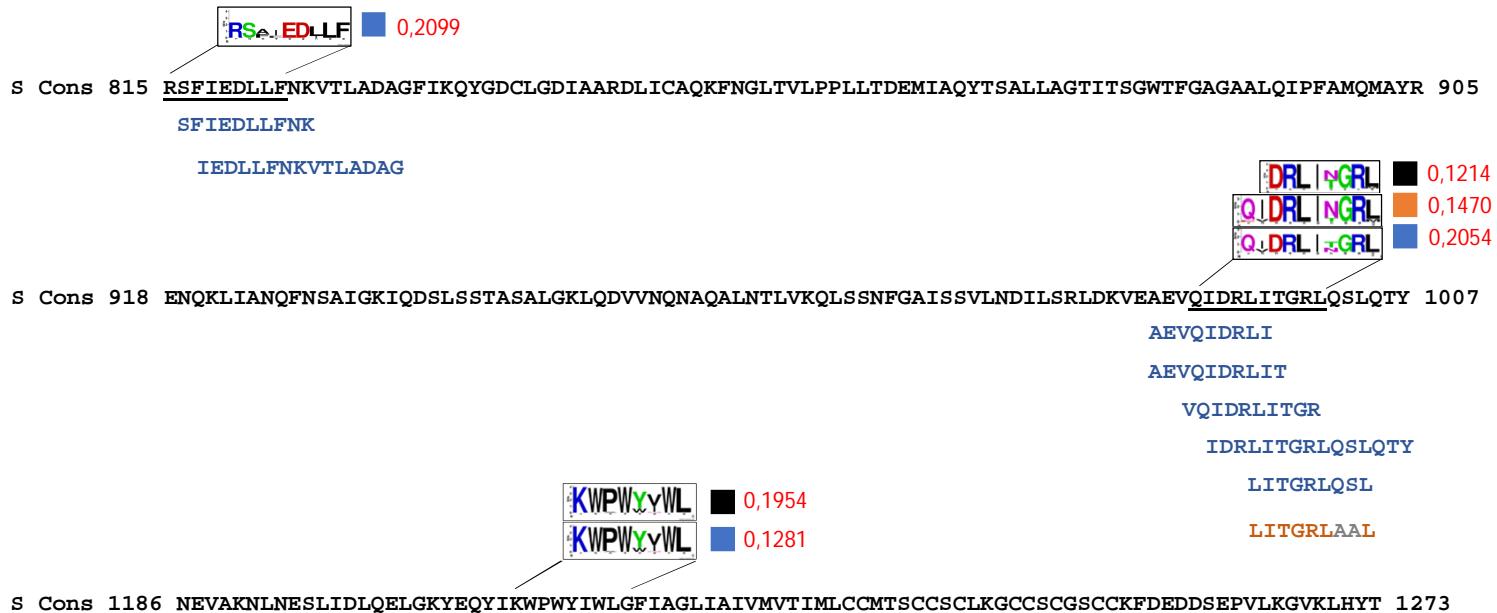
- Unknown
- SARS-CoV
- Human
- Other Coronavirus
- Amino acid mismatch
- Consensus conserved region

### Symbols

- Pan-coronavirus conservation
- Betacoronavirus conservation
- Human coronavirus conservation

Average entropy

## Spike

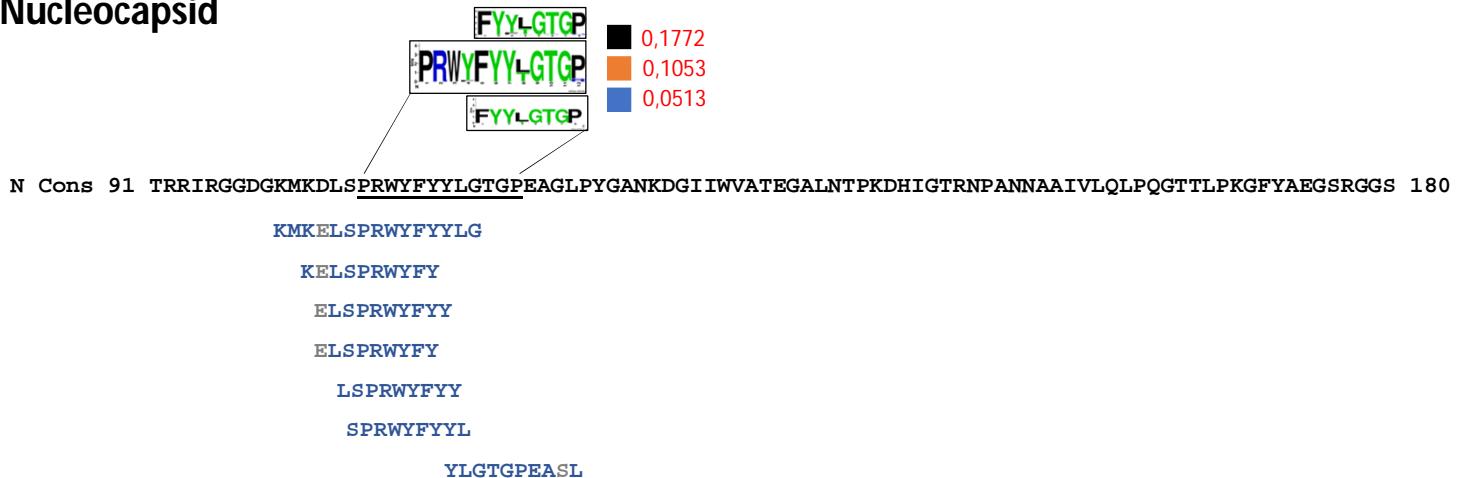


Average entropy

## Membrane



## Nucleocapsid



### Color map

- Unknown
- SARS-CoV
- Human
- Other Coronavirus
- Amino acid mismatch
- Consensus conserved region

### Symbols

- Pan-coronavirus conservation
- Betacoronavirus conservation
- Human coronavirus conservation

Average entropy

**Supplementary Figure S2.** SARS-CoV-2 ORF fragments containing conserved regions in Human, Betacoronavirus or Pan-coronavirus alignments are shown. Epitope description was carried out based on experimentally described epitopes from the Immune Epitope Database (IEDB, [www.iedb.org](http://www.iedb.org)). Species were the epitope was described are indicated by sequence color. Logos of conserved sequences along the three alignments (Pan-coronavirus, Betacoronavirus or Human coronavirus) were included. The alignment where the conserved regions were identified is indicated by color squares