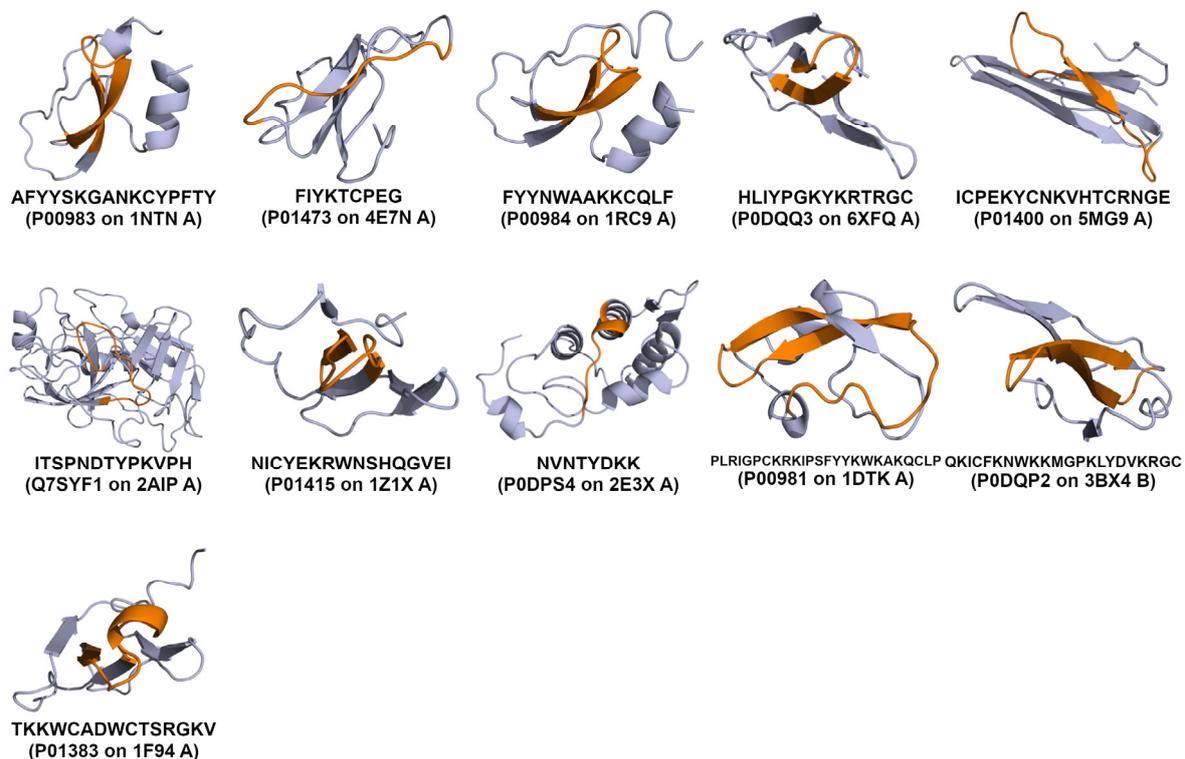


**Figure S1.** Mapping of selected epitopes from PDB. Epitope location is highlighted in orange. PDB structures in parenthesis.



**Figure S2.** Mapping of selected epitopes from models. Epitope location is highlighted in orange. Reference sequence accession number and PDB structures in parenthesis.

```

M Y H L W I K C L A
- - H L W I - C L A
M Y H L W - K C L A
- Y H L W I K C - -
M Y H X W I K C L A

```

**Figure S3.** Illustration of an example alignment depicting which residues were accounted for the entropy calculation. In blue, positions that are taken into consideration. In orange, not considered positions.

```

MESG**DYEVVYP*SALPKGQVQNVLHLERE*KGLFSEDTET*YSPDG
MESG  DYEVVYP  SALPKGQVQNVLHLERE  KGLFSEDTET  YSPDG

          SALPKGQVQ          KGLFSEDT
            ALPKGQVN          GLFSEDT
            -----          LFSEDT
          SALPKGQVQ          FSEDTET
                               -----
                               KGLFSEDTET

          LPKGQVN
          PKGQVN
          KGQVNLH
          GQVNLHL
          VQVNLHL
          QVNLHLER
          NVLHLERE
          -----
          KGQVNLHLER

```

**Figure S4.** Illustration of epitope prediction. Sequences are broken into conserved fragments (asterisks indicate non-conserved residues), and each fragment is considered separately and analyzed 8-mer by 8-mer. Overlapping 8-mers are incorporated into the final epitopes if they fulfill any tier criteria. Struckthrough peptides represent discarded fragments due to their short length. In grey, 8-mers discarded for not fulfilling any tier criteria, or having a high blast identity. Bold peptides indicate the final predicted epitopes.