**MHC binding:**

1. What is the minimal and maximal number of different HLA class I molecules a cell can express?
2. What two subunits form the HLA class I molecule?
3. Which of the two HLA class I subunits interact with the peptide?
4. What two subunits form the HLA class II molecule?
5. Which of the two HLA class II subunits interact with the peptide?
6. What is the most common length of peptides that bind to HLA class I?
7. What is the most common length of peptides that bind to HLA class II?
8. What is an anchor position in an HLA binding motif?
9. Which peptide positions are most frequent anchors in HLA class I binding motifs?
10. When predicting peptide binding to HLA, should you focus on HLA anchor positions, or non-anchor positions?
11. What does NetMHC predict?
12. For which MHC class I molecules can NetMHC be used to make predictions?
13. Which tool(s) can be used for MHC class I molecule not covered by NetMHC?
14. As a rule of thumb, how large a proportion of the peptides derived from a given pathogen, does an MHC class I molecule bind?
15. Why are artificial neural network methods proposed to be better than linear methods for predicting peptide-HLA binding?
Antigen processing and presentation

1. What is the role of the proteasome in antigen processing?
2. What is the role of TAP in antigen processing?
3. What does the NetCTLpan tool predict?
4. What does NetChop predict?
5. What does NetTepi predict?
6. Does antigen presentation distinguish between self and none-self?
7. For CD8 T cells, which peptide positions interact most frequently with the TCR?
8. Where in the antigen presentation pathway does the immune-system distinguish between self and none-self?