



Computational and experimental approaches to determine the immunopeptidome landscape on cancer cells.

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The mobilization of the immune system has become a promising approach to help fight cancers. Tumour cells express mutated gene products and it is expected that these should generate non-tolerant neoantigens that when presented on MHC class I molecules will stimulate an immune response that will eliminate the tumour cells. This notion has been supported by experimental data and forms the basis for various approaches to exploit the immune system for novel cancer therapeutics such as vaccines or activation of the immune synapse. An important aspect of these strategies is to better understand and predict what neoantigens are presented on different types of cancers. The ICCVS is contributing to these efforts by developing novel new bioinformatics platforms that will allow us to predict the neopeptidome based on the genetic information. We are also interested to understand the source of antigen peptide material for the MHC class I pathway and how this is regulated in cells under various conditions and how we can interfere with these processes to make cancer cells more immunogenic. Finally, we are developing techniques to follow the dynamics of antigens presented on single cancer cells.

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