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CIC biomaGUNE
MEMBER OF BASQUE RESEARCH & TECHNOLOGY ALLIANCE

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# Protein Libraries: Creation, Screening and Sorting

**Wednesday, 12th November**
**12.00 p.m.**

CIC biomaGUNE - Seminar Room

Protein libraries provide a way to probe and identify new amino acid sequences of interest. A library of protein sequences can be created by randomizing certain amino acids, while maintaining specific residues in strategic positions. These libraries can then be screened and sorted according to their characteristics. In this seminar, two protein libraries are going to be discussed: (1) the epitope library and (2) the adeno associated virus (AAV) library.

Epitopes are small protein regions in antigens recognized by antibodies. Predicting which antigenic sequences will bind to specific antibodies is a challenging yet an essential task for developing new vaccines and in vitro antibody testing. By creating epitope libraries one can understand and predict these recognition patterns. In this project we explore the use of microfluidics as a high-throughput method for screening and selection of a created epitope library.

AAV are virus with great promise for gene therapy, since they lack pathogenicity, infect non-dividing cells and can integrate well into the host genome. The goal of creating a AAV library is to increase the tropism of this virus, that is its ability to infect tissues. VP3 is the protein of AVV that contains all surface-exposed residues of the viral capsid that contribute to its tropism. In this project, we randomized the variable regions of the VP3 sequence, through quantum algorithms and by taking into consideration insights from computational protein design.

The methods developed in these projects can be applied for numerous types of protein libraries, demonstrating the importance of these libraries as tools in protein engineering, understanding protein-protein interaction and ultimately in the development of new therapeutics.