Sujet de stage de M2
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Bioinformatics analysis of caveolin proteins

Caveolae (little caves) are small vesicular invaginations (50 to 100 nm), of the cell membrane, structurally and biochemically specialized membrane microdomains. Caveolae presence on the surface of the cell membrane greatly increases this surface and this observation, added to the presence of many types of proteins, may be related to their involvement in a great diversity of physiological functions: pynocitosis, transcytosis, endocytosis, membrane traffic, cholesterol homeostasis, signal transduction and lipids recycling.

Caveolins are a family of small (3kDa smaller in size) integral membrane proteins, assuming a hairpin-like structure within the membrane with both N- and C-terminal facing to cytoplasm and it has three members in vertebrates: caveolin-1 (CAV-1), caveolin-2 (CAV-2) and caveolin-3 (CAV-3) which is specific for muscle cells. Caveolins form oligomers and associate to cholesterol and spingholipids being the principal components of caveolae and participating in many important cellular processes, such as vesicular transport, signal transduction, cholesterol homeostasis and tumor suppression. They act as scaffolding proteins in caveolae concentrating various signalling molecules.

There are not yet structural data concerning caveolin proteins and the characterisation of their interactions is challenging. We propose a bioinformatics analysis of caveolin proteins in order to predict their structural and functional properties and to analyze their interactions with membrane environments. This analysis assumes the use of sequence based prediction tools in order to identify hydrophobic regions, disordered regions, domains and analysis of molecular dynamics simulation of the interactions between some regions of caveolin proteins and membrane systems. Interactions of caveolins with cholesterol can also be studied.