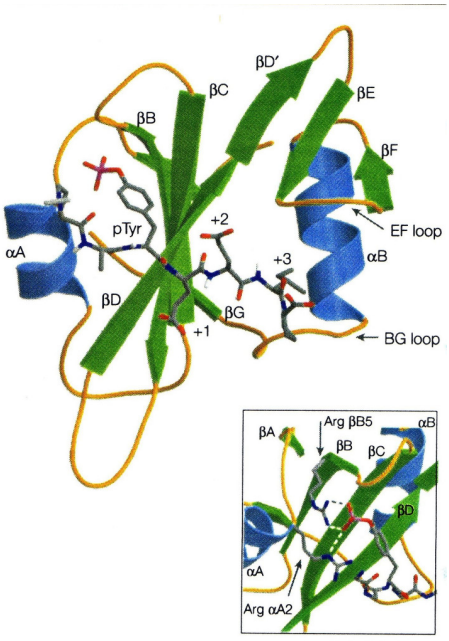
Título prospectivo da dissertação de mestrado

Peptidomimetics for phosphoproteome analysis

Resumo prospectivo do plano de trabalho da dissertação de mestrado

The phosphoproteome consists of the entire complement of phosphorylated proteins (p-Pr) in cells. Phosphoproteomics may prove to be valuable in unravelling p-Pr as markers that are potential drug targets or of predictive value in disease therapeutics. As the stoichiometry of phosphorylation is very low and the event is highly dynamic, phosphoproteome analysis usually comprises a first step of enrichment. Despite progress on the development of enrichment methods, IMAC (Immobilized Metal Affinity Chromatography) using Fe3+, Zr4+ or Ti4+ remains the commonest method with its associated low selectivity. The need of proteomic methods compatible with large-scale analysis is a trigger for the development of selective and robust p-Pr binding molecules.

Peptidomimetics are peptide-based structures that can be designed and engineered to target specific molecules. The proposed Master research programme will involve the design and synthesis of peptidomimetics with potential to bind to phosphorylated proteins.



The work will involve:
(i) In silico studies of the specific interactions with phosphorylated proteins and design of biomimetic structures binding to phosphorylated moieties (molecular modelling)
(ii) Solid-phase synthesis of peptidomimetics using standard Fmoc solid-phase chemistry and characterization by mass spectroscopy (ESI-MS) and circular dichroism spectroscopy (CD).
(iii) Preliminary screening of the interactions between the peptidomimetics and phosphorylated proteins (protein quantification methods; fluorescence microscopy; multiplate reader; high-throughput screening methods)

Supervisors: Dr. Olga Iranzo (oiranzo@itqb.unl.pt) and Dr. Ana Cecília Roque (cecilia.roque@dq.fct.unl.pt). Local de realização: ITQB and REQUIMTE