

LERU STudent REseArch Mobility Programme (STREAM)  
Project proposal



**Host University:**  
Università degli studi di Milano



**Field:**  
Biology/chemistry

**Specified field, subject:**  
Biochemistry, molecular biology

**Research project title:**  
Structural Bases of human pathologies



Possible starting month(s):

Sep	Oct	Nov	Dec	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug
				x							



Possible duration in months:

1	2	3	4	5	6
			x	x	x



**Suitable for students in:** 2<sup>nd</sup> cycle (Master students)

**Prerequisites:** A sound background in basic biochemistry and molecular biology

**Restrictions:** none



**Description:**

The proposed experimental activity relies on the application of the X-ray crystallographic methods to the study of protein structures. The analysis of protein 3D-structures has been providing crucial information for almost any branch of biochemistry and molecular biology in the last thirty years. Knowledge of 3D structures is the requisite for studying in detail the molecular mechanisms of action in enzymes, to target the protein-protein or protein-drug recognition principles, for a rational approach to drug design, and for innumerable macromolecular simulation techniques, paving the way to biomed/biotech applications. In summary the main experimental approaches of the proposed project are distributed as follows: 1. Protein/construct expression and purification; 2. Protein crystal growth; 3. X-ray protein crystal diffraction (data collected at the European synchrotron facilities); 4. Bio-crystallographic analysis and in silico modeling; 5. Bioinformatics analysis; 6. Biophysical characterization of proteins in vitro. The proposed project will allow the candidate to learn the bases of the X-ray crystallography methods and to apply them to one of the following research themes (at choice): 1. Antifreeze proteins: structure determination of proteins able to interfere with ice crystal formation and structural-based site-directed mutagenesis to improve their antifreeze performance for biotech applications; 2. Structural vaccinology: 3D structure analyses of protein antigens from human pathogens



as a pre-requisite for in silico epitope predictions and subsequent antigen/epitope engineering and testing. Toxic protein aggregation: proteins aggregate in vivo leading to several severe disorders such Alzheimer and Parkinson diseases. In order to understand the molecular bases of such aggregation the protein structures and their fold stability are investigated.

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