



## MARINE-EXPRES

Post-genomic validation of marine genomics through the development of medium throughput tools for expression, crystallization and functional screening of target genes

Partners:

- 1) **SBR**, Roscoff, France, UMR7139, CNRSUPMC, microbial, algal node partner 2 together with **MPI-MM**, Bremen, Germany, microbial node partner 5
- 2) **SZN**, Naples, Italy, EDD node partner 22
- 3) **IFREMER**, IFREMER-CNRS-UBO, UMR 6197, microbial node partner 3
- 4) **CCMAR**, Faro, Portugal, Fish and Shellfish node partner 21
- 5) **OBS-Banyuls**, CNRSUPMC, UMR 7628, algal node partner 2
- 6) **MBA**, Plymouth, UK, algal node partner 16

After the success of a large number of genomic projects the different research labs are now confronted with numerous putative genes and those of unknown function. The upcoming challenge is therefore to go beyond the bioinformatic data in order to assess post-genomic validation. To understand the precise biological function of a single gene, the biochemical and physiological characterization of its product is essential and this is often greatly aided by the availability of 3-D structural information. When aiming at the 3D-structure of a protein, a second bottleneck is encountered at the step of crystallization of these proteins.

The scope of this project is to get around the bottle necks of soluble protein expression and crystallization and to develop enabling technologies applicable to proteins that come from various marine organisms. More precisely, we are setting up medium throughput strategies adapted to marine organisms for the production, expression and, eventually, the crystallization of proteins from marine bacteria and eukaryotes. The strategies developed for bacteria, macro and micro algae, ascidia and teleost fish in the first place, may well be extended in the future to other models such as oyster, fish or other marine vertebrates.

### Milestones

- Select and precisely analyze the target genes with respect to modularity, transmembrane regions, etc. using bioinformatics.
- Retrieve full length cDNA for the eukaryotic genes of interest
- Develop a strategy for the cloning, transformation and expression with various tags in a medium/high throughput manner a) for different *E.coli* strains, b) in *Pichia pastoris*
- Develop strategies for refolding if no soluble product is obtained in any of the expression systems
- Purify the soluble proteins and validate their function by activity tests
- Develop a medium/high throughput screening of crystallization conditions for recombinant proteins