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Ricerca

# Ricerca partner FAFB-EU-LCP-3 BIO-INFORMATICS

*01 dicembre 2017*

Oggetto: Ricerca Partner FAFB-EU-LCP-3 BIO-INFORMATICS

Richiesta di partner da parte di un Istituto di ricerca Lituano di Microbiologia e Biotecnologie, interessato a coinvolgere ricercatori italiani in un progetto relativo al Topic:

KBBE-2007-3-2-08: BIO-INFORMATICS - Microbial genomics and bio-informatics

Di seguito una breve descrizione del progetto e le caratteristiche del partner richiesto.

Chi fosse interessato al progetto, può contattare:

Federica Prete
APRE - Agenzia per la promozione della ricerca europea
Piazza G. Marconi, 25 - 00144 Roma
Italy
Tel. +39 06 5911817 Fax. +39 06 5911908
E-mail prete@apre.it

facendo riferimento al codice PARTNER SEARCH FAFB-EU-LCP-3

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<Reference n.: FAFB-EU-LCP-3>
<Deadline: 31/08/2007>
<Programme: FAFB>
<Project Title: Topology and compositional determinants of secretion signals as potent classifiers for non-classically secreted proteins.>
<Financial Scheme: Large Collaborative Project>
<Description: Topic : KBBE-2007-3-2-08: BIO-INFORMATICS - Microbial genomics and bio-

informatics

Background information:
Increasing amount of large scale date from genomic research determines urgent need to specify the proteome, including the secretome, i.e., the part of proteins secreted form the cell.
Capability of bacteria to release particular proteins into the extracellular medium by means of different secretion pathways are processes of basic importance for bacterial life as well as provides diverse biotechnological applications.
A number of prediction and classification tools have been developed to predict adequate protein cell localization and signal peptide cleavage sites in proteins secreted by 'classical', i.e., signal peptide - dependent pathways. However approximately 25 per cents of known extracellular proteins are classified as 'non-classically' secreted proteins lacking cleavable signal peptides. At present only one prediction method Secretome P can be used for this purpose [1, 2], which nevertheless does not specify any definite secretion type (type III or type I) possibly involved in non-classical protein secretion.

Several compositional and structural features at the termini of sequences have been proposed as specific unprocessed secretion signals of 'non-classically' secreted proteins. However, definite sizes, location and composition of secretion signals remain obscure, possibly due to the fact that studies in the field are mostly focused on some functionally related protein groups from a limited number of organisms and, as a consequence, fundamentals of secretion processes remain to be elucidated and fully understood.

Objectives and expected results:
Our recent studies revealed definite amino acid frequencies of occurrence [3] and selected variables from periodicity patterns of aromatic and aliphatic amino acid residues [4] as the reliable predictors to discriminate between type III and type I secreted proteins, however further investigations in the field could provide substantially stronger set of predictors.
The goal of this research project is to define more precisely the composition, size and location of possible secretion signal for substrates of 'non-classical' secretion (type III and type I) pathways to provide strongly improved tool for identification of secretome proteins from genomic sequences of bacteria (proteobacteria and, possibly, firmicutes [4]).
The tool for identification and classification of secretome proteins could verify the compatibility between various secretion substrates (recombinant heterologous proteins such as vaccines, etc.) and secretion machinery (of potent carrier strain) in order to predict overall efficiency of the process. Achieved prediction and classification algorithms could provide a basis for implementation of prediction and classification tool.

<excerpt>
<Organisation Type: Centro di Ricerca>
<Partner Sought: Research organizations interested in Protein subcellular location prediction, Microbial proteomics or Software development>