

# Biophysical principles of intra- and inter-molecular recognition in protein folding and interactions involving disordered proteins

<https://neurodegenerationresearch.eu/survey/biophysical-principles-of-intra-and-inter-molecular-recognition-in-protein-folding-and-interactions-involving-disordered-proteins/>

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### Country

Canada

## Title of project or programme

Biophysical principles of intra- and inter-molecular recognition in protein folding and interactions involving disordered proteins

## Source of funding information

CIHR

## Total sum awarded (Euro)

€ 503,575

## Start date of award

01/10/2012

## Total duration of award in years

5.0

## The project/programme is most relevant to:

Neurodegenerative disease in general

## Keywords

### Research Abstract

Advances in modern biomedical research depend on a knowledge of the molecular basis of life. Proteins are a diverse class of biomolecules performing various vital functions in all living things.

The three dimensional shape — or shapes — of a protein is encoded by its specific sequence of amino acids, and this sequence is in turn encoded by a gene. For some proteins, folding into a highly ordered globular shape is essential for function, whereas misfolding can lead to diseases such as Alzheimer's and Parkinson's. In this context, switch-like folding is important for avoiding undesirable, disease-causing aggregation. For other proteins, however, a disordered form is necessary for them to function. Therefore, developing a fundamental understanding of how proteins fold and unfold is of great intellectual and technological significance, and will benefit all areas of biomedical research. Ultimately, this knowledge should be deducible from chemistry and physics. Currently, however, it is not yet feasible in most cases to predict a protein's folding and dynamic behaviours from its amino acid sequence because no one understands well enough the intricate forces that guide some proteins to fold while the same set of basic forces can lead other proteins to adopt a fuzzy collection of disordered shapes. Current knowledge is also limited as to the forces that lead proteins to recognize their specific partners, a process that is crucial for biological function. Taking clues from available data and working closely with experimentalists, we will develop computational models toward systematically unraveling the workings of these forces.

### **Lay Summary**

**Further information available at:**

#### **Types:**

Investments > €500k

#### **Member States:**

Canada

#### **Diseases:**

Neurodegenerative disease in general

#### **Years:**

2016

#### **Database Categories:**

N/A

#### **Database Tags:**

N/A