

Rodrigo Gallardo

VIB Switch Laboratory
Department of Cellular and Molecular Medicine
Katholieke Universiteit Leuven



BSc Natural and Exact Science, University of Chile, Chile 2000
Lic Molec. Biotechnology Engineering, University of Chile, Chile 2004
PreDoc. license in Biomedical Sciences, K.U.Leuven, Belgium 2008
PhD Bioengineering, Free Universiteit Brussel, Belgium 2012

Current Position

Postdoctoral scientist VIB Switch Laboratory at K.U.Leuven

E-mail: rodrigo.gallardo@switch.vib-kuleuven.be

Phone: +32 16 377367

Current Project Members

Research Technician: Meine Ramakers, MSc

Keywords

Protein aggregation - Amyloidosis - APR- Peptide synthesis - Biophysics - Protein Peptide interactions - Protein structure

Science

Protein aggregation is the process by which proteins lose their solubility and structure, and therefore their function. It has been documented that protein aggregation is at the root of wide spectrum diseases, ranging from neurodegeneration to cancer. A currently debated hypothesis is that protein aggregation is caused by partial exposure of Aggregation Prone Regions (APR) that, under normal conditions, are usually "protected" into the protein hydrophobic core. Once APRs are exposed they engage into auto and hetero-interactions that drive the harbouring protein into aggregation. My research focuses on understanding from a biophysical point of view why only some APRs drive protein aggregation while others not. To solve this question I first use Solid Phase Peptide Synthesis and HPLC techniques to produce sufficient amounts of APRs as short peptides. Then I apply a set of chemical techniques to stabilize the APR preparations. Finally I apply a set of physicochemical techniques to determine intrinsic parameters of APR aggregation. By combining all these techniques in a systematic high throughput-sampling pipeline we will build a set of rules that, once implemented in a computational algorithm will allow prediction of aggregation-functional APRs.

The results can be directly applied not only to the basic understanding of protein aggregation and the diseases it causes, but also to several fields. For instance, identification of functional APRs can be applied to reverse-engineer proteins to avoid aggregation which is a bottleneck to the use of peptides in the pharmaceutical industry.

Recent Research Projects

IWT 'Strategisch Basis Onderzoek'

Period: 02.2012-09.2014

Title: Healthcare Applications of Targeted Protein Aggregation

Role: PostDoc

Recent Fellowships

Vrije Universiteit Brussel - PhD fellowship

Period: 01.05.2008 – 28.02.2012

Title: 'Simultaneous peptide and lipid binding controls membrane recruitment of the scaffolding protein syntenin'

Role: PhD student

Selected Publications

Gallardo R, Ramakers M, De Smet F, Couceiro JR, Schymkowitz J and Rousseau F. (In preparation) A synthetic biology approach to dissect toxicity from function on amyloid diseases.

Bednarska N, Van Eldere J, Ganesan A, **Gallardo R**, Vogel I, Baatsen P, Goethals M, Hammarström, Nilsson P, Gevaert K, Schymkowitz F and Rousseau F. (2014) Induction of protein aggregation as a novel antibiotic mechanism. *Nature Biotechnology*. (In revision)

Esselens C, Sannerud R, **Gallardo R**, Baert V, Kaden D, Serneels L, De Strooper B, Rousseau F, Multhaup G, Schymkowitz J, Langedijk JP, Annaert W. (2012) Peptides based on the presenilin-APP binding domain inhibit APP processing and ABeta production through interfering with the APP transmembrane domain. *FASEB J*.

Xu J, Reumers J, Couceiro JR, De Smet F, **Gallardo R**, Rudyak S, Cornelis A, Rozenski J, Zwolinska A, Marine JC, Lambrechts D, Suh YA, Rousseau F, Schymkowitz J. (2011) Gain of function of mutant p53 by coaggregation with multiple tumor suppressors. *Nat Chem Biol*.

Gallardo R, Ivarsson Y, Schymkowitz J, Rousseau F, Zimmermann P. (2010) Structural diversity of PDZ-lipid interactions. *Chembiochem*.