Journal of Nanomedicine & Biotherapeutic

Extended Abstract

Design of aggregation resistant protein biotherapeutics

Salvador Ventura

Abstract

Protein biotherapeuticshas emerged as promising new drugs for human disorders. However, they are extremely sensitive to stress, a major problem being the formation of aggregates during production and delivery, which impact the product quality and produce adverse immunogenic reactions. Here the author introduces A3D, an evolution of the AGGRESCAN algorithm, a new tool able to predict and assist the redesign of aggregation propensity in protein 3D-structures.

Biography

Salvador Ventura is Full Professor at the Department of Biochemistry and Molecular Biology and leader of the Protein Folding and Conformational Diseases group at the Institute of Biotechnology and Biomedicine, Autonomous University of Barcelona (UAB). He has authored more than 110 peer-reviewed research and review papers on protein folding and proteomics, apart from several book chapters and patents. He got his PhD in Biology at the UAB in 1998 and worked as postdoctoral fellow (1999-2001) at EMBL-Heidelberg. He has been researcher at Harvard Medical School (USA) and KarolinskaInstitutet (Sweden) among other centres. He rejoined UAB as a Ramon y Cajal researcher in 2003. He received the UAB 2008 Excellence Research Award and in 2009 the ICREA-Academia Award on Biological and Medical Sciences.

Salvador Ventura

This work is previously presented on
5th World Congress on Biotechnology

Volume 10•Issue 2