Human Epidermal growth factor Receptor 2: in silico docking simulation

Diana Sousa, Débora Ferreira, Andrea Silva, Leon Kluskens and Ligia Rodrigues (CEB-UMInho)

Breast cancer is the most frequently diagnosed cancer and the leading cause of cancer death among females, accounting for 23% of the total cancer cases and 14% of the cancer deaths.1 Human Epidermal growth factor Receptor 2 (HER2) is a protein that is overexpressed in 25-30% of breast cancers and is involved in cell growth regulation, survival and differentiation.2 Aptamers generated from Systematic Evolution of Ligands by EXponential Enrichment (SELEX) emerged as a potential new tool for the development of targeted cancer therapies due to their three-dimensional structures that specifically recognize cell surface receptors, such as HER2.3 In this study, HER2-aptamers were screened and identified using SELEX. To design an approach for computational analysis of the isolated aptamers, their structures were modelled by mfold4, a web-based methodology for DNA structure prediction and hybridization software. The HER2 protein structure was obtained from Protein Data Bank (PDB) and using ZDOCK server5, the aptamer-target interactions were predicted through a combination of shape complementarity and statistical potential terms for scoring. Finally, the interactions scores were compared with the experimental results. In silico interaction scores and the experimental outcomes suggest that the best docking results are obtained for the lower

binding energy constants. The good agreement between in silico and experimental results highlight the reliability of this new approach. Also, the results provide valuable guidelines for the application of docking simulations for the prediction of aptamer-ligand structures, as well as for the design of novel features of ligand-aptamer complexes.

Universidade do Minho
Escola de Engenharia

2017

Bioinformatics Open Days (BOD)

Book Conference

22-02-2017 to 24-02-2017