Structural and functional characterisation of clusterin

Lipi Das¹, Ashok Varma¹

¹Varma Lab, ACTREC, Tata Memorial Center, Navi Mumbai, India
E-mail: daslipi1292@gmail.com

Head and neck squamous cell carcinoma (HNSCC) is the sixth most common form of cancer worldwide and the most prevalent in the Indian male population. Despite many advancements made in the past decades in the development of novel treatment modalities, the five-year survival rates for HNSCC patients has remained below 60% [1]. In this study we have used a proteomics based approach to identify differentially expressed proteins. Our study reveals clusterin as one of the proteins which may be used to assess response to treatment. Clusterin is a highly conserved secreted glycoprotein that is expressed in a wide variety of tissues [2]. The protein is synthesized as a 449 amino acid polypeptide, which is post-translationally cleaved to give rise to the functionally active form of the protein. The functionally active form of the protein consists of two chains, designated as alpha and beta, connected via multiple disulphide bridges [2]. It has been observed that protein exhibits 49.1% helicity, 47.1% random coil nature, and 3.8% strand-like structure. The protein is known to possess many glycosylation sites which allow the protein to also function as a molecular chaperone under conditions of stress [2]. It has been reported that clusterin positive laryngeal tumors are more aggressive in nature [3] and hence it would be of interest to study the structure and folding pattern of clusterin.


Keywords: Clusterin, secondary structure, chaperone