**Computational Chemistry: New Approaches to the Old C60 Story**

**Jerzy Leszczynski**

*Department of Chemistry and Biochemistry Jackson State University,*

# Jackson, MS, USA

 There are not too many cases when a discovery of a single compound had been recognized by the Nobel Committee. Fullerene represents such an outstanding example. The original paper describing this unique compound was published in 1985 and the Nobel Prize follows in 1996. Such noble recognition had raised many expectations associated with a new carbon form. They were not limited just to its basic chemistry but also include possible applications of C60. Sorry to say but such expectations have not entirely materialized and two other members of the carbon family – carbon nanotubes and graphene have been significantly more utilized.

 By now one recognizes that pristine (i.e. non-functionalized) C60 fullerene has very limited possible applications. In contrast, fullerene’s derivatives with various functional groups are promising candidates for medicinal applications since properly designed functional groups facilitate solubility in water and assure interactions with only targeted protein. In addition, the way such a group is constructed allows maximizing desired interactions. Recently, the progress with a functionalizing of C60 provides a pool of fullerene derivatives that due to a new set of characteristics could find a potential application in medicine.

As always, a prediction of possible effects of newly studied species on biological targets should precede their commercial applications. The talk summarizes the results of recently performed comprehensive computational study of interactions between a large set of fullerene nanoparticle derivatives (169 functionalized, C60, C70 and C80 compounds) with the group of almost 1200 proteins that are responsible for various diseases. The study has been carried out using innovative approach that combines various complementary computational techniques such as a high-throughput virtual screening (virtual HTS) supported by comprehensive protein-ligand docking studies and cheminformatics techniques to assure reliability of obtained data. Several significant relationships between structural characteristics and biological activities are noticed that could be revealed only by investigating a sizable set of fullerenes together with a large set of proteins. Importantly, we determined a set of fullerene derivatives which are most likely to be very potent against some target proteins. This conclusion is augmented by a list of fullerene derivatives that could be potentially toxic because of low selectivity and high binding activity for a number of target proteins.