Molecular Modelling of Elastin-Like Polypeptides

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Elastin is a cross-linked protein responsible for elasticity to many tissues and organs. Therefore, elastin is most abundant in organs where elasticity is of major importance, like in blood vessels which stretch and relax more than a billion times during life, in elastic ligaments, in lung and in skin[1]. It is an insoluble, hydrophobic and extensively cross-linked protein forming fibers which are present in variable amounts depending on the tissue. Although it has been involved in numerous biological activities, elastin's function is restricted to elasticity.

Elastin-like poly peptides (ELPs) are a family of polypeptides derived from a portion of the primary sequence of elastin, VPGXG, where V:valine, P:proline, G:glycine, and X: any aminoacid except proline. Several studies have explored the effect of substituting different amino acids in the fourth position of the sequence on thermally responsive behaviour. ELPs and their derivatives have been used for a number of applications, including drug delivery, protein purification, and tissue engineering. For example, Chilkoti and co-workers have evaluated temperature-responsive ELPs for potential applications in cancer therapy[2,3]. VPGVG is the most abundant repeating peptide in elastin.

This talk focuses on our study of the physical basis of elastin's conformational properties and mostly associated physical terms; heat capacity, total energy, radius of gyration, end-to-end distance and helicity. Instead of X in VPGXG sequence, valine(val), lysine(lys), glutamine(gln), tryptophan(trp), glutamic acid(glu), histidine(his) have been used. Simulations have carried on an open-source with free code software package called SMMP (Simple Molecular Mechanics for Proteins)[4]. It contains a number of modern Monte Carlo algorithms for simulation of proteins in generalized ensembles with ECEPP/2, ECEPP/3 and the FLEX optional potentials. Six different elastin sequences are simulated in vacuum and, then to examine the effect of protein–solvent interactions by means of solvent-accessible surface method all of them are simulated in OONS [5] parameter set. Plots related to above physical parameters have been performed. In vacuum, transition temperatures are confined in an interval between 320-340 K, on the other hand, in aqueous solution a shift takes place towards 200-230 K approximately. Although the minimum conformational energies in vacuum are between -10 and -17 kcal/mol, they vary between -21 and -35 kcal/mol in aqueous solution. In addition to this, the minimum conformational energy (VPGVG)