DETERMINATION OF NATIVELY UNFOLDED REGIONS OF SUPEROXIDE DISMUTASE FROM *PACIFASTACUS LENIUSCULUS*

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The roles of natively unfolded proteins in some important biological functions such as transcriptional regulation, translation and cellular signal transduction have been shown in many papers. According to the results of these papers on unfolded regions of proteins, having unfolded regions provides proteins better flexibility and also better interaction ability with their ligand or binding sites. Superoxide dismutase (SOD) is a house-keeping enzyme that protects cells from harmful effects of superoxide radical anion. SOD catalyses the dismutation reaction of superoxide radical anion to hydrogen peroxide. In the present study, unfolded regions of a novel cell surface SOD that has been found in *Pacifastacus leniusculus* were analysed by a newly developed bioinformatic tool called RONN. Amino acid composition and some physicochemical parameters of SOD from *Pacifastacus leniusculus* such as pI, negatively and positively charged residues, aliphatic index and grand average of hydropathicity were also investigated in the present study. Although there are technically three unfolded regions (at residues 88–92, 153–174 and 183–217) in SOD from *Pacifastacus leniusculus*, probability of disorder of the last region was higher than those of other unfolded regions. One of the possible property of unfolded regions in proteins is to provide better interaction with their binding sites. Inasmuch as cell surface SOD from *Pacifastacus leniusculus* is a binding protein for a cell adhesive peroxidase in crayfish, having unfolded regions provides SOD to bind effectively cell adhesive peroxidase. Algorithms developed in bioinformatics for prediction for unfolded region in proteins might provide a different view of point for evaluation of structure-activity relationships.