EDITORIAL

Studies on protein have been far in advance today. The mechanism of protein function has been disclosed. Proteins synthesized in a cell undertake several post-translational modifications that are essential in their functional regulation. By the completion of a rough draft of the human genome, the way genes and protein interact in forming other protein can now be investigated. The diversity of protein has been found to increase, which is likely resulting from alternative splicing and post-translational modification of proteins. An organism has different protein expression in different parts of the body, in different stages of life cycle and in different environmental conditions. There is a difference in the protein compliment of the cell. Different proteins are present in different cells, and at different amount, and even the activity of the proteins can also be different. This increasing protein diversity cannot be characterized by gene expression analysis only. A small protein is needed as molecular chaperones. The change of the latter may result in unfolded protein or the discrepancy of protein function. A remarkable number of protein unfolded clusters may impede signaling function which is often found in the diseases among elderly, such as in major neurodegenerative disorders, e.g. Alzheimer's disease, Parkinson's disease, and dementia. It is currently found that most of stress proteins have a function as molecular chaperones. Those findings obviously pave more ways to the research of protein, either for diagnostic or therapeutic purposes.

The Editors