Efficacy of Rapid Construction of Protein Structural Variants for Proteomic Analysis

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In the era of post human genome project, it suggests that twenty thousand genes and their products work as the maintenance of homeostasis and/or crisis and exacerbation of diseases. Because the function of genes is embodied of expressing proteins which is the last product of central dogma , it is essential for development of novel proteomic drugs to elucidate the relationship between “structure of protein and functional pattern of receptor-ligand binding” and “emergence of existence and affection”. From this point of view, it is important that structural and/or functional analysis of structural variant proteins (for example, which have specific binding capacity to objective receptor) should be examined, however, there is no high through-put method to make enormous functional proteins. Recently, we developed novel phage display method, which express and analyze over 10 million different types of mutant proteins by our original strategies. In this presentation, we introduce this novel method and a part of the analytical studies using proteomics concept for development of protein interaction study and disease proteomics.