

**Bioinformatic analysis in oncogenic proteins network between cervical cancer cells based on gene ontology**

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After high risk HPV infection, two viral oncogenic proteins, E6 and E7 play a critical role in inducing cervical cancers by interacting with p53 and pRB for inactivation of these cellular regulatory proteins, respectively. Large-scale genetic technologies are producing sets of genes and proteins that are differentially regulated under varying conditions. The functional data that can be associated with each gene is quite complex. Here, to quantitatively understand possible multiple relationships between differentially expressed profiles of gene and cervical cancer-specific pathway, the annotation project directed by the Gene Ontology (GO) Consortium was used. In this study, we constructed a recombinant *E. coli* and produced oncoproteins to investigate the molecular pathway of tumor suppression effect with a protein chip.

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