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## Isolation and Screening of Antifungal Activity from Sediment Soil in the Ansan Industrial Estate

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About 120 samples were collected from the sediment soil in the Ansan industrial estate. These strains, BCNU 316, BCNU 317, BCNU 318, BCNU 319 and BCNU 320 were isolated significant antifungal activities microorganisms for use in the treatment of human fungal pathogens such as *Candida albicans, Microsporum gypseum* and *Epidermophyton floccosum* and phytopathogenic fungi such as *Rhizotonia solani, Aspergillus niger, Fusarium oxysporium and Sclerotinia sclerotiorum.* Antibacterial activities were evaluated against to Gram-positive bacteria (4 species; *Bacillus cereus, Clavibacter michiganensis, Micrococcus luteus and Staphylococcus aureus*), Gram-negative bacteria (8 species; *Acinebacter calcoacetius, Citrobacter freundii, Escherichia coli, Pseudomonas aeruginosa, Proteus mirabillis, Proteus vulgaris, Shigella sonnei*, and *Salmonella typhimurium*). In the screening for antifungal activities, these strains showed the greatest activities for *Rhizoctonia solan*i, and BCNU 317 showed inhibitory activity against mycelial growth of human fungal pathogen such as *E. floccosum* and plant pathogenic fungi such as *Rh. solani, A. niger, S. sclerotiorum* and *F. oxysporium*. showed mostly activities for fungal pathogens. But these strains did not showed any antibacterial activity.

**Key words:** antifugal activity, isolation

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## Designing a Surface Comparison Method on Protein Active Site

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Problems in a living body have been arisen if there are any changes in the protein structure because structure and function are strongly related. Protein structure study is an essential element to learn for revealing the biological function and process of lives. The best functional match does not always have the best overall structural similarity. Cases are known in which protein sharing similar for and/or sequence have completely different function. Thus protein functions can be determined by highly conserved particular substructure such as active site. We need to predict the function and classify proteins by an active site analysis in stead of whole structure analysis.

This paper uses the three-dimension protein structure expressed by the smallest geometry, that is, a triangle. The coordinate of side chain on surface is essentially needed to compare active site because side chain determines shape of surface toward the outside. We define a particular substructure set as the triangle which consists of lengths among the Ca and side chain of amino acid residue. Distance matrix is established with a substructure set and uses RMSD in order to compare the place around active site. Distance based matrix is generated to compare detailed shapes of active site. This approach uses active site and its substructure in stead of whole protein structure and sequence in order to effectively compare the active site of protein.

**Key word:** Active site, substructure, distance matrix