

# Method for Identifying Drug Targets Using Sequence Data

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## Technology description

### Description

Horizontal gene transfer is defined as the movement of genetic material between phylogenetically unrelated organisms by mechanisms other than parent to progeny inheritance. Any biological advantage provided to the recipient organism by the transferred DNA creates selective pressure for its retention in the host genome. Horizontal transmission is now considered a major factor in the process of environmental adaptation, for both individual species and entire microbial populations. These adaptations can include acquisition of new metabolic competencies, allowing survival under extreme conditions, resistance to drugs or environmental pollutants, defenses against external predators, and resistance to internal parasites. Horizontal transfer has also been proposed to play a role in the emergence of novel human diseases, as well as determining their virulence. The dynamics of horizontal gene transfer in pathogenic organisms may prove particularly useful in identifying novel targets for therapeutic agents, predicting the phylogenetic specificity of these agents, and estimating the likelihood of resistance development.

Scientists at UCSD have discovered a computer algorithm for the identification of genes that have been acquired by lateral gene transfer, rather than normal inheritance. The user inputs a file of protein sequence data from each of several test organisms, and receives as output a ranked list of genes with statistical data describing their likelihood of horizontal transfer. Genes that have been laterally acquired by more than one member of a group of pathogens can be used for identifying potential drug targets that would disrupt survival of an entire group of pathogenic organisms sharing a particular habitat.

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