Mining microbial genomes for biologically active compounds

Most microbes of importance to human and environmental health are not amenable to experimentation. As a result, we do not know what molecules these microbes use to manipulate their environment- many of which are likely to be of high commercial value because of their application in medicine and biotechnology. We developed a method termed Mutational Enrichment Analysis post Phenotypic Selection (MEAPS) to mine any microbial genome for genes required for activities of interest. We envision that this experimental/bioinformatic platform will reveal many commercially important biologicals from microbial communities associated with humans, livestock and industrial settings.





Duke File (IDF) #

T-004851



Inventor(s)

- Valdivia, Raphael
- Bae, Sena



m College

School of Medicine (SOM)

For more information please contact

Thomas, Dennis 919-681-7580 dennis.thomas@duke.edu