Selection of Highly Expressed Gene Variants in Escherichia coli Using Translationally Coupled Antibiotic Selection Markers

Strategies to select highly expressed variants of a protein coding sequence are usually based on trial-and-error approaches, which are time-consuming and expensive. We address this problem using translationally coupled antibiotic resistance markers. The system requires that the target gene can be fused at the 3'-end with a translational coupling element and an antibiotic resistance gene. Highly expressed target genes can then be selected using a fast and simple whole cell survival assay in the presence of high antibiotic concentrations. Herein we show that the system can be used to select highly expressing clones from libraries sampling translation initiation sites.

General information
State: Published
Organisations: Novo Nordisk Foundation Center for Biosustainability, Research Groups, Microbial Evolution and Synthetic Biology, Stockholm University
Contributors: Rennig, M., Daley, D. O., Nørholm, M. H. H.
Pages: 259-268
Publication date: 2018

Host publication information
Title of host publication: Synthetic Metabolic Pathways
Volume: 1671
ISBN (Print): 978-1-4939-7294-4
ISBN (Electronic): 978-1-4939-7295-1
(Keywords: Antibiotic resistance, Gene expression, Library screening, Protein production optimization, Selection, Translational coupling
DOIs: 10.1007/978-1-4939-7295-1_16
Source: FindIt
Source-ID: 2393668049
Research output: Research - peer-review › Book chapter – Annual report year: 2018