METHODS AND COMPOSITIONS FOR CONTROLLING GENE EXPRESSION BY RNA PROCESSING

Tech ID: 22273 / UC Case 2012-055-0

PATENT STATUS

<table>
<thead>
<tr>
<th>Country</th>
<th>Type</th>
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<td>European Patent Office</td>
<td>Issued Patent</td>
<td>2880171</td>
<td>10/03/2018</td>
<td>2012-055</td>
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<tr>
<td>United States Of America</td>
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<td>9,745,610</td>
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BRIEF DESCRIPTION

Genetic systems often behave unpredictably due to structural interactions between DNA, RNA and protein components as well as functional interactions with host factors and metabolites. Due to these complexities, the ability to program gene expression quantitatively based on the characteristics of individual components is very limited. In nature, the control of the activity of an RNA transcript is crucial to its function. For example, the transcription, translation, and degradation of an mRNA is crucial to any gene expression event, and all three processes are controlled by a combination of elements including promoters, ribosome binding sites (RBSs), and cis-regulatory signals encoded in untranslated regions (UTRs). Methods and/or tools to facilitate the combination of various regulatory elements originating from various different sources to predictably control the activity of any desired RNA would be beneficial for numerous biotechnology applications. However, regulatory elements can unpredictably interact with each other through the formation of RNA structures and the recruitment of factors that affect global transcript accessibility and stability.

UC Berkeley researchers have developed methods and compositions for identifying appropriate combinations of regulatory elements simply and quickly. The invention allows for the combination of multiple regulatory elements in a fashion that predictably affects RNA activity.

SUGGESTED USES

» A synthetic RNA-processing platform (e.g., assembly of promoters, ribosome binding sites, cis-regulatory elements and riboregulators into single- and multigene operons)

PUBLICATION

RNA processing enables predictable programming of gene expression

ADDITIONAL TECHNOLOGIES BY THESE INVENTORS

» Methods and Compositions for Using Argonaute to Modify a Single-Stranded Target Nucleic Acid
» COMPOSITIONS AND METHODS FOR IDENTIFYING HOST CELL TARGET PROTEINS FOR TREATING RNA VIRUS INFECTIONS
» Cas9 Variants With Altered DNA Cleaving Activity
» Cas12-mediated DNA Detection Reporter Molecules
» Cas13a/C2c2 - A Dual Function Programmable RNA Endonuclease
» Methods For High Signal-To-Noise Imaging Of Chromosomal Loci In Cells Using Fluorescent Cas9
» A Dual-RNA Guided CasZ Gene Editing Technology
» CRISPR-CAS EFFECTOR POLYPEPTIDES AND METHODS OF USE THEREOF (“Cas-VariPhi”)
» A Protein Inhibitor Of Cas9
» Small Cas9 Protein Inhibitor
» Split-Cas9 For Regulatable Genome Engineering
» Decorating Chromatin for Precise Genome Editing Using CRISPR
» CRISPR-CAS EFFECTOR POLYPEPTIDES AND METHODS OF USE THEREOF (“Cas-Theta”)
COMPOSITIONS AND METHODS FOR INCREASING HOMOLOGY-DIRECTED REPAIR

Single Conjugative Vector for Genome Editing by RNA-guided Transposition

Improved Cas12a Proteins for Accurate and Efficient Genome Editing

CRISPR-CAS EFFECTOR POLYPEPTIDES AND METHODS OF USE THEREOF ("Cas-Omega")

CRISPR-CAS EFFECTOR POLYPEPTIDES AND METHODS OF USE THEREOF

Type V CRISPR/Cas Effector Proteins for Cleaving ssDNA and Detecting Target DNA

THERMOSTABLE RNA-GUIDED ENDONUCLEASES AND METHODS OF USE THEREOF (GeoCas9)

Structure-Guided Methods Of Cas9-Mediated Genome Engineering

Endonucleases For RNA Detection And Analysis

Efficient Site-Specific Integration Of New Genetic Information Into Human Cells

CRISPR-CAS EFFECTOR POLYPEPTIDES AND METHODS OF USE THEREOF (CasGamma)

Improved gRNA and Protein Design for CasX-based Gene Editing Platform

Class 2 CRISPR/Cas COMPOSITIONS AND METHODS OF USE

Compositions and Methods of Use for Variant Csy4 Endonucleases

Identification Of Sites For Internal Insertions Into Cas9

Chimeric Cas9 Variants With Novel Engineered Enzymatic Activities

Small Molecule Assisted Cell Penetrating Cas9 RNP Delivery