

A FAMILY OF PHYLOGENETICALLY RELATED TRANSCRIPTIONAL ACTIVATION DOMAINS

Tech ID: 33374 / UC Case 2024-061-0

PATENT STATUS

Patent Pending

BRIEF DESCRIPTION

Eukaryotic transcription factors (TFs) control transcription with DNA binding domains and effector domains (DBDs). TFs contain long intrinsically disordered regions (IDRs) that do not fold into a single 3D structure and inhabit a dynamic ensemble of conformations. The IDRs of TFs contain effector domains like repression domains that bind to co-repressor complexes and activation domains (ADs) that bind to coactivator complexes. ADs are difficult to predict from protein sequence because they are poorly conserved and intrinsically disordered.

UC Berkeley Researchers have developed an Acidic Exposure Model motivated a mechanistic, composition-based predictor that accurately identified known and new human ADs. The evolution of ADs remains largely unstudied and mysterious. In multiple sequence alignments ADs show much lower conservation than DBDs. In an aspect we disclose 673 highly active short transcriptional activation domains. These sequences are all phylogenetically related.

SUGGESTED USES

- » Used for synthetic biology in yeast and in other eukaryotes
- » CRISPR-activation assays and for over expression systems for biosynthesis

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OTHER INFORMATION

CATEGORIZED AS

- » **Agriculture & Animal Science**
- » Transgenics
- » **Biotechnology**
- » Genomics
- » **Veterinary**
- » Therapeutics

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