Title (en)

METHODS AND SYSTEMS FOR THE IDENTIFICATION OF COMPONENTS OF MAMMALIAN BIOCHEMICAL NETWORKS AS TARGETS FOR THERAPEUTIC AGENTS

Title (de)

VERFAHREN UND SYSTEME ZUM IDENTIFIZIEREN VON KOMPONENTEN VON BIOCHEMISCHEN NETZWERKEN FÜR SÄUGETIERE ALS TARGETS FÜR THERAPEUTISCHE MITTEL

Title (fr)

PROCEDES ET SYSTEMES PERMETTANT D'IDENTIFIER DES COMPOSANTS DE RESEAUX BIOCHIMIQUES MAMMALIENS COMME ETANT DES CIBLES D'AGENTS THERAPEUTIQUES

Publication

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Application

EP 02773968 A 20021104

Priority

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Abstract (en)

[origin: WO03040992A1] Systems and methods for modeling the interactions of the several genes, proteins and other components of a cell, employing mathematical techniques to represent the interrelationships between the cell components and the manipulation of the dynamics of the cell to determine which components of a cell may be targets for interaction with therapeutic agents. A first such method is based on a cell simulation approach in which a cellular biochemical network intrinsic to a phenotype of the cell is simulated by specifying its components and their interrelationships. The various interrelationships are represented with one or more mathematical equations which are solved to simulate a first state of the cell. The simulated network is then perturbed by deleting one or more components, changing the concentration of one or more components, or modifying one or more mathematical equations representing the interrelationships between one or more of the components. The equations representing the perturbed network are solved to simulate a second state of the cell which is compared to the first state to identify the effect of the perturbation on the state of the network, thereby identifying one or more components as targets. A second method for identifying components of a cell as targets for interaction with therapeutic agents is based upon an analytical approach, in which a stable phenotype of a cell is specified and correlated to the state of the cell and the role of that cellular state to its operation. A cellular biochemical network believed to be intrinsic to that phenotype is then specified by identifying its components and their interrelationships and representing those interrelationships in one or more mathematical equations. The network is then perturbed and the equations representing the perturbed network are solved to determine whether the perturbation is likely to cause the transition of the cell from one phenotype to another, thereby identifying one or more components as targets.

IPC 1-7

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IPC 8 full level

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CPC (source: EP US)

G01N 33/5091 (2013.01 - EP); **G16B 5/00** (2019.01 - EP); **G16B 5/30** (2019.01 - EP US); G01N 2333/4739 (2013.01 - EP); G01N 2800/52 (2013.01 - EP); G16B 5/10 (2019.01 - EP US); G16B 5/20 (2019.01 - EP US)

Citation (search report)

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