RECENT PATENTS ON BIOINFORMATICS IN DRUG RESEARCH

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DETECTION METHOD OF DISULFIDE BOND CONNECTIVITY BY PRINCIPAL COMPONENT ANALYSIS (PCA)-BASED DIMENSIONALITY REDUCTION TECHNIQUE.

Patent No.:CN 101477113;
Publication Date: 15-01-2009

Abstract
The invention falls into the field of bioinformatics and relates to a detection method of disulfide bond connectivity by principal component anal. (PCA)-based dimensionality redn. technique. The method involves extg. multiple sequence feature vectors and secondary structure vectors detected by PSIPRED protein structure prediction server from the Protein Data Bank (PDB), wherein the vectors in total include 623 dimensionalities; reducing the 623 dimensionalities of the vectors to 300 dimensionalities by PCA method; and inputting the vectors of 300 dimensionalities to a support vector regression (SVR) classifier and predicting to give results. The invention increases the effective features of the protein feature vectors inputted to the SVR classifier, so as to improve the detection accuracy of disulfide bond connectivity. The invention also increases the detection speed and reduces the information redundancy through reducing the dimensionalities of the vectors.

APPARATUS, METHOD, AND COMPUTER PROGRAM FOR IDENTIFICATION OF PROTEIN FUNCTIONS BY BIOINFORMATICS.

Patent No.: JP 2009151406
Publication Date: 07-09-2009

Abstract
The app., method, and computer program are used for identification of the functions of proteins with unknown functions on the basis of 3-dimensional structures of proteins with known functions and those of proteins with unknown functions. The app. has a memory part for storing 3-dimensional structures of 2 receptors as proteins with known functions, a memory part for storing 3-dimensional structures of 2 ligands, a training data prodn. part for calcg. shape complementarity evaluation values of each receptor with known functions when it docks with ligands on the basis of 3-dimensional structures and for calcg. charge information of each receptor, a part for inputting 3-dimensional structures of proteins with unknown functions, an identification input data prodn. part for calcg. shape complementarity evaluation values of proteins known functions when they dock with ligands on the basis of 3-dimensional structures and for calcg. charge information of the proteins, and a learning-identification part for learning the training data and identifying the functions of the proteins. The functions of the proteins are identified by detg. the functions of receptors whose shape complementarity evaluation values and charge information are similar to those of the proteins, on the basis of similarities of shape complementarity evaluation values and charge information of docking of 2 receptors with common functions to 2 ligands. Protein interactions are considered in the protein function identification.
GENE SYNTHESIS SOFTWARE

Patent No: US 7,587,284
Publication Date: September 8, 2009

Abstract:
Pieces of software and databases are used to facilitate the design and synthesis of genes. The synthesis techniques allow identification, quantification, transcription, translation, and manipulation of portions of the gene sequence represented as 0's and 1's in a computing system. These pieces of software and databases compile constraint information provided by a user to create synthetic genes to express proteins lacking disordered or variable regions and containing surface mutations that promote solubility and/or crystallization. Regions of the gene sequence that do not form stable structures can be removed and replaced by a short biological linker to improve crystallization of proteins.

DRUG SELECTION FOR BREAST CANCER THERAPY USING ANTIBODY-BASED ARRAYS

Pub. No.: WO/2009/108637
Publication Date: 03.09.2009

Abstract:
The present invention provides compositions and methods for detecting the activation states of components of signal transduction pathways in tumor cells. Information on the activation states of components of signal transduction pathways derived from use of the invention can be used for cancer diagnosis, prognosis, and in the design of cancer treatment.

MICROARRAY FOR PREDICTING THE PROGNOSIS OF NEUROBLASTOMA
AND METHOD FOR PREDICTING THE PROGNOSIS OF NEUROBLASTOMA

Abstract
A microarray for predicting the prognosis of neuroblastoma, wherein the microarray has 25 to 45 probes related to good prognosis, which are hybridized to a gene transcript whose expression is increased in a good prognosis patient with neuroblastoma and are selected from 96 polynucleotides consisting of the nucleotide sequences of SEQ. ID NOs. 1, 5, 6, 14, 16, 17, 19, 22-24, 28, 29, 31, 37, 39, 40, 43, 44, 47-52, 54, 57-60, 62, 64, 65, 67, 68, 72-75, 77, 78, 80-82, 84, 87, 89-91, 94, 100, 103, 112, 113, 118, 120, 129, 130, 132, 136, 138, 142, 144, 145, 148, 150-153, 155, 158-160, 163-165, 169-171, 173, 174, 177, 178, 180-182, 184, 186, 187, 189, 191, 192, 194, 195, 198-200 or their partial continuous sequences or their complementary strands, and 25 to 45 probes related to poor prognosis, which are hybridized to a gene transcript whose expression is increased in a poor prognosis patient with neuroblastoma and are selected from 104 polynucleotides consisting of the nucleotide sequences of SEQ. ID NOs. 2-4, 7-13, 15, 18, 20, 21, 25-27, 30, 32-36, 38, 41, 42, 45, 46, 53, 55, 56, 61, 63, 64, 66, 69-71, 76, 79, 83, 85, 86, 88, 92, 93, 95-99, 101, 102, 104-111, 114-117, 119, 121-128, 131, 133-135, 137, 139-141, 143, 146, 147, 149, 154, 156, 157, 161, 162, 166-168, 172, 175, 176, 179, 183, 185, 188, 190, 193, 196, 197 or their partial continuous sequences or their complementary strands.

STRUCTURE OF THE HEPATITIS C VIRUS NS2 PROTEIN

Abstract:
The present invention provides a crystallized C-terminal domain of an NS2 protein of hepatitis C virus, methods of producing the same and methods of use thereof. The present invention also relates to structural elements of the C-terminal domain of hepatitis C virus NS2 protein, and methods of inhibiting hepatitis C virus infection, replication and/or pathogenesis, by interacting with the same.
METHODS AND COMPOSITIONS FOR DIAGNOSIS AND MONITORING AUTO IMMUNE AND CHRONIC INFLAMMATORY DISEASES

Publication Date: October 20, 2009

Abstract:
Methods of diagnosing or monitoring auto immune and chronic inflammatory diseases, particularly systemic lupus erythematosis and rheumatoid arthritis, in a patient by detecting the expression level of one or more genes in a patient, are described. Diagnostic oligonucleotides for diagnosing or monitoring auto immune and chronic inflammatory diseases, particularly systemic lupus erythematosis and rheumatoid arthritis and kits or systems containing the same are also described.

STRUCTURE OF A PROTEIN PHOSPHATASE 2A HOLOENZYME: INSIGHTS INTO TAU DEPHOSPHORYLATION

Publication number: US2009233858
Publication date: 2009-09-17
Abstract;
Embodiments of the present invention relate to crystals and atomic coordinates for PP2A, as well as methods for using these atomic coordinates to prepare modulators of PP2A and inhibitors prepared using such methods. Further embodiments relate to biochemical analyses of the interactions of PP2A alone or in complex with Tau. Further embodiments relate to compositions including mimetics and small molecules, optionally, secondary agents, which may be used to treat disorders in which PP2A activity and/or Tau plays a contributing role.

Reagent sets and gene signatures for renal tubule injury

Patent No.: US7,588,892
Abstract:
The invention discloses reagent sets and gene signatures for predicting onset of renal tubule injury in a subject. The invention also provides a necessary set of 186 genes useful for generating signatures of varying size and performance capable of predicting onset of renal tubule injury. The invention also provides methods, apparatuses and reagents useful for predicting future renal tubule injury based on expression levels of genes in the signatures. In one particular embodiment the invention provides a method for predict whether a compound will induce renal tubule injury using gene expression data from sub-acute treatments.

Identification of a gene expression profile that differentiates ischemic and nonischemic cardiomyopathy

 Patent No.: US 7,592,138
Publication Date: September 22, 2009

Abstract:
A method of preparing a gene expression prediction profile for distinguishing ischemic and nonischemic cardiomyopathy comprises the steps of obtaining clinical specimens from patients suffering from ischemic or nonischemic cardiomyopathy, isolating nucleic acid sequences from at least a plurality of said specimens, obtaining a gene expression level corresponding to each individual of said nucleic acid sequence by a gene expression profiling method, identifying genes having differences in gene expression by comparing the gene expression level of an ischemic specimen with the gene expression level of a nonischemic specimen, and identifying a gene expression prediction profile comprises genes identified as having differences in gene expression so that said prediction profile distinguishes ischemic and nonischemic cardiomyopathy.

Genomic data mining using clustering logic and filtering criteria
Abstract:
A method for automatic analysis of genomic information in order to determine relationships among genes allows one to determine complex relationships among genes. First a clustering algorithm is chosen and is applied to the table, obtaining sub-tables of data relative to groups of genes that satisfy the chosen clustering criterion. Therefore, all possible combinations of pair of sub-tables are generated and characteristic parameters are calculated for genes contained in these sub-tables. Finally, for each combination a characteristic value is calculated with a decision algorithm defined in function of these parameters, by considering the genes of the combination as constituting a "Gene Network" if this characteristic value exceeds a pre-defined threshold. The method is preferably is implemented by a relative system of identification of groups of co-expressed and co-regulated genes comprising an intelligent fuzzy sub-system trained off-line identified by a neural network.
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