

Recent patents in computational biology

Patent number	Description	Assignee	Inventor	Date
US 10,025,900	Computational methods for engineering, selecting, and/or identifying proteins with a desired activity. Also, automated computational design and screening methods to engineer proteins with desired functional activities including, but not limited to, ligand binding, catalytic activity, substrate specificity, regioselectivity and/or stereoselectivity.	Arzeda (Seattle)	Zanghellini A, Ban Y-EA, Althoff EA, Grabs D, Azoitei ML	7/17/2018
US 10,007,662	A biologically inspired model for sequence representation, method of construction and application of such models, and systems incorporating same that captures the statistical nature of sequences and uses that for sequence encoding, recognition, and recall. The model can be trained in real time, has few tunable parameters, and is highly parallelizable, which ensures that it can scale up to very large problems.	Iowa State University Research Foundation (Ames, IA, USA)	Stoytchev A, Sukhoy V	6/26/2018
US 9,965,597	Methods and systems for drug discovery collaboration, providing collaborative drug discovery electronic workplaces simultaneously accessible by multiple user computing devices. Each workplace includes an indication of one or more items, such as compounds, and data pertaining to such items, such as computational and experimental data. Updates to a workplace made by one user may be saved to the workplace definition and propagated and displayed to other users. New items of interest may be added to a workplace. A new item added to a workplace may also be saved to the database and registered with the system for use by other users and in connection with other workplaces.	Schrodinger (New York)	Becker S, Schoolman B, Jordan WC, Murcko M, Friesner RC	5/8/2018
US 9,938,532	An aptamer whose structure comprises at least one nucleotide sequence 5'-GGCA(A/G)GGA-3', that can specifically bind to the poly(A) hairpin of the 5'UTR region of the genome of the human immunodeficiency virus type 1 (HIV-1), providing the method for producing aptamers with said sequence by means of a combination of experimental techniques of <i>in vitro</i> selection of nucleic acids with computational techniques of sequence optimization. Also, a DNA gene structure for synthesizing said aptamers, preferably RNA.	Spanish National Research Council (Madrid), National Institute of Aerospace Technology (Madrid)	Berzal Herranz A, Briones Llorente C, Sanchez-Luque FJ, Cuevas Manrubia S, Stich M	4/10/2018
US 9,922,164	Methods and computational tools based, at least in part, on computer simulations that identify macromolecule binding regions and aggregation prone regions of a protein. Substitutions may then be made in these aggregation prone regions to engineer proteins with enhanced stability and/or a reduced propensity for aggregation. Similarly, substitutions may then be made in these macromolecule binding regions to engineer proteins with altered binding affinity for the macromolecule.	Novartis (Basel, Switzerland), Massachusetts Institute of Technology (Cambridge, MA, USA)	Chennamsetty N, Helk B, Trout B, Kayser V, Voynov V	3/20/2018
US 9,890,368	Polypeptide fragments comprising an amino-terminal fragment of the polymerase acidic (PA) subunit of a viral RNA-dependent RNA polymerase or variants thereof possessing endonuclease activity, wherein said PA subunit is from a virus belonging to the Orthomyxoviridae family. Also, (i) crystals of the polypeptide fragments which are suitable for structure determination of said polypeptide fragments using X-ray crystallography and (ii) computational methods using the structural coordinates of said polypeptide to screen for and design compounds that modulate, preferably inhibit the endonucleolytically active site within the polypeptide fragment.	European Molecular Biology Laboratory (Heidelberg, Germany), French National Center for Scientific Research (Paris), Université Grenoble Alpes (Saint Martin d'Heres, France)	Bouvier D, Crepin T, Ruigrok R, Dias A, Cusack S	2/13/2018
US 9,848,760	Systems and methods for the continual modification of intestinal microbes, including sampling devices, analysis devices, computational devices and user interface devices as well as methods for the use of such devices in combination.	Gearbox LLC (Bellevue, WA, USA)	Bangera M, Boyden ES, Hyde RA, Kare JT, Leuthardt EC, Rivet DJ, Wood Jr. LL	12/26/2017
US 9,798,751	A method and apparatus for constructing a neuroscience-inspired dynamic architecture (NIDA) for an artificial neural network, comprising the construction of an artificial neural network embodiment in a multi-dimensional space in memory such that a neuron is connected by a synapse to another neuron. The neuron and the synapse each have parameters and have features of long-term potentiation and long-term depression. Furthermore, crossover and mutation are employed to select children of parents. Through learning, an initial network may evolve into a different network when NIDA is applied to solve different problems of control, anomaly detection and classification over selected time units.	University of Tennessee Research Foundation (Knoxville, TN, USA)	Birdwell JD, Schuman C	10/24/2017
US 9,797,013	Devices and methods for detecting and controlling an individual polymer in a mixture when acted upon by another compound, for example, an enzyme, in a nanopore. The devices and methods also determine the nucleotide base sequence of a polynucleotide under feedback control or using signals generated by the interactions between the polynucleotide and the nanopore. Of particular use in the fields of molecular biology, structural biology, cell biology, molecular switches, molecular circuits, and molecular computational devices, and the manufacture thereof.	The Regents of the University of California (Oakland, CA, USA)	Akeson MA, Deamer DW, Chen RJA	10/24/2017

Source: United States Patent and Trademark Office (<http://www.uspto.gov>).