



S&T IN-DEPTH

THE LATEST IN SCIENCE AND TECHNOLOGY RESEARCH LITERATURE

FEATURE TOPIC: SYNTHETIC BIOLOGY

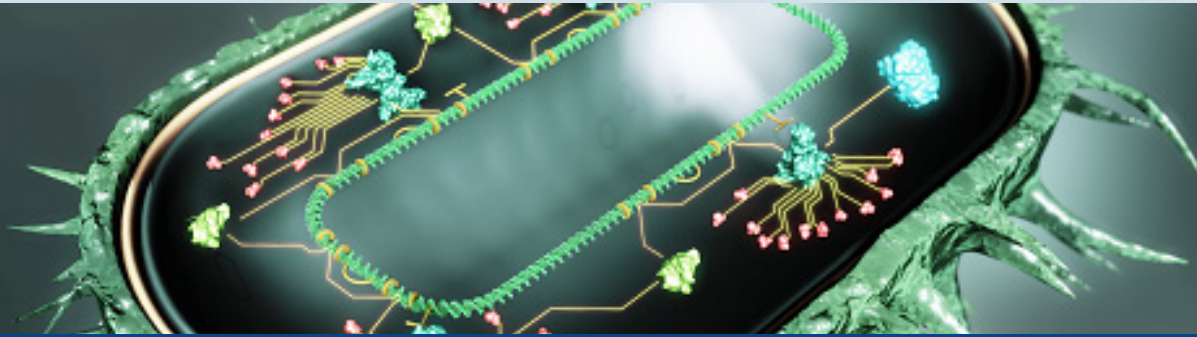


TABLE OF CONTENTS

REVIEW ARTICLES

- Aims and methods of biosteganography (Canada) 2016
- The emerging age of cell-free synthetic biology (USA) 2014
- Engineering for the 21st Century: Synthetic Biology (USA) 2013
- Foundations and Emerging Paradigms for Computing in Living Cells (USA) 2016
- Large-scale de novo DNA synthesis: technologies and applications (USA) 2014
- The next generation mass storage devices - Physical principles and current status (China) 2014
- Parallel Networks: Synthetic Biology and Artificial Intelligence (USA) 2014
- Rapid prototyping of microbial cell factories via genome-scale engineering (USA) 2015
- Towards practical, high-capacity, low-maintenance information storage in synthesized DNA (England) 2013

APPLICATIONS - BIOWEAPONS

- Assessing and Managing the Risks of Potential Pandemic Pathogen Research (USA) 2015
- An Avian H7N1 Gain-of-Function Experiment of Great Concern (France) 2014
- Biosecurity and Open-Source Biology: The Promise and Peril of Distributed Synthetic Biological Technologies (USA) 2015
- Construction of a synthetic infectious cDNA clone of Grapevine Algerian latent virus (GALV-Nf) and its biological activity in *Nicotiana benthamiana* and grapevine plants (Italy) 2014
- Dual-use research and the H5N1 bird flu: Is restricting publication the solution to biosecurity issues? (Switzerland) 2014

- The ethics of biosafety considerations in gain-of-function research resulting in the creation of potential pandemic pathogens (USA) 2015
- Infectious Diseases Society of America and Gain-of-Function Experiments With Pathogens Having Pandemic Potential (USA) 2016
- Moving beyond metagenomics to find the next pandemic virus (USA) 2016
- A New Synthesis for Dual Use Research of Concern (USA) 2015
- Security Vulnerabilities and Countermeasures for Target Localization in Bio-NanoThings Communication Networks (Italy) 2016
- Synonymous Virus Genome Recoding as a Tool to Impact Viral Fitness (Spain) 2016
- Synthetic biology: from mainstream to counterculture (Ireland) 2016
- Synthetic Biology: A Utilitarian Perspective (Scotland) 2013
- Synthetic virus seeds for improved vaccine safety: Genetic reconstruction of poliovirus seeds for a PER-C6 (R) cell based inactivated poliovirus vaccine (three Netherlands) 2015

APPLICATIONS - CRYPTOGRAPHY/INFORMATION SECURITY

- Binary DNA Nanostructures for Data Encryption (USA) 2012
- BioCode: Two biologically compatible Algorithms for embedding data in non-coding and coding regions of DNA (Ireland) 2013
- Chaos-based image encryption scheme combining DNA coding and entropy (China) 2016
- Color image encryption scheme using CML and DNA sequence operations (China) 2016
- Design and synthesis of digitally encoded polymers

- that can be decoded and erased (France) 2015
- DNA-LCEB: a high-capacity and mutation-resistant DNA data-hiding approach by employing encryption, error correcting codes, and hybrid twofold and fourfold codon-based strategy for synonymous substitution in amino acids (Finland) 2014
 - An efficient and noise resistive selective image encryption scheme for gray images based on chaotic maps and DNA complementary rules (China) 2016
 - An Encryption Scheme Based on DNA Microdots Technology (China) 2015
 - Hiding message into DNA sequence through DNA coding and chaotic maps (China) 2014
 - Image watermarking using chaotic map and DNA coding (China) 2015
 - An improved color image encryption based on multiple DNA sequence operations with DNA synthetic image and chaos (India) 2015
 - An Improved Encryption Scheme Based on DNA Sequence (China) 2015
 - An Improved Level of Security for DNA Steganography Using Hyperelliptic Curve Cryptography (India) 2016
 - Information Hiding in Noncoding DNA for DNA Steganography (South Korea) 2015
 - Message in a molecule (Israel) 2016
 - A new RGB image encryption algorithm based on DNA encoding and elliptic curve Diffie-Hellman cryptography (India) 2016
 - A novel chaos-based image encryption using DNA sequence operation and Secure Hash Algorithm SHA-2 (Tunisia) 2016
 - A novel text and image encryption method based on chaos theory and DNA computing (Iran) 2013
 - A Resettable and Reprogrammable DNA-Based Security System To Identify Multiple Users with Hierarchy (China) 2014
 - A robust image encryption algorithm resistant to attacks using DNA and chaotic logistic maps (India) 2016
 - A survey on reversible watermarking techniques for relational databases (Pakistan) 2015
 - Trichocyanines: a Red-Hair-Inspired Modular Platform for Dye-Based One-Time-Pad Molecular Cryptography (Italy) 2015
 - 'Yeast Mail' : A Novel Saccharomyces Application (NSA) to Encrypt Messages (Germany) 2014
 - Cellular and molecular engineering of yeast *Saccharomyces cerevisiae* for advanced biobutanol production (Japan) 2016
 - Computational Approaches for Microalgal Biofuel Optimization: A Review (United Arab Emirates) 2014
 - Cyanobacterial chassis engineering for enhancing production of biofuels and chemicals (China) 2016
 - Decoupling production from growth by magnesium sulfate limitation boosts de novo limonene production (Germany) 2016
 - Engineering biofuel tolerance in non-native producing microorganisms (China) 2014
 - From cyanochemicals to cyanofactories: a review and perspective (China) 2016
 - Frontiers in microbial 1-butanol and isobutanol production (USA) 2016
 - Genetic resources for advanced biofuel production described with the Gene Ontology (USA) 2014
 - Microalgal bioengineering for sustainable energy development: Recent transgenesis and metabolic engineering strategies (India) 2016
 - Modular and selective biosynthesis of gasoline-range alkanes (USA) 2016
 - Rationally Engineered Synthetic Coculture for Improved Biomass and Product Formation (Finland) 2014
 - Recent advances and challenges of the use of cyanobacteria towards the production of biofuels (France) 2016
 - Recent Progress on Systems and Synthetic Biology Approaches to Engineer Fungi As Microbial Cell Factories (Brazil) 2016
 - Synthetic biology for microbial production of lipid-based biofuels (USA) 2015
 - Synthetic methylotrophy: engineering the production of biofuels and chemicals based on the biology of aerobic methanol utilization (USA) 2015
 - Transforming exoelectrogens for biotechnology using synthetic biology (USA) 2016
 - Yeast synthetic biology toolbox and applications for biofuel production (USA) 2015

APPLICATIONS - ENERGY

- 2,3 Butanediol production in an obligate photoautotrophic cyanobacterium in dark conditions via diverse sugar consumption (USA) 2016
- Advances in bioprocessing for efficient bio-manufacture (China) 2015
- Better together: engineering and application of microbial symbioses (USA) 2015
- Biotechnological and bioinformatics approaches for augmentation of biohydrogen production: A review (India) 2016

APPLICATIONS - INFORMATION STORAGE

- Codes for DNA Sequence Profiles (Singapore) 2016
- Coding Macromolecules: Inputting Information in Polymers Using Monomer-Based Alphabets (France) 2015
- Configuration Synthesis for Programmable Analog Devices with Arco (USA) 2016
- A Cytomorphic Chip for Quantitative Modeling of Fundamental Bio-Molecular Circuits (USA) 2015
- A DNA-Based Archival Storage System (USA) 2016
- DNA nanotechnology: new adventures for an old warhorse (USA) 2015
- Empirical Laws and Foreseeing the Future of Technological Progress (Portugal) 2016

- Feasibility study of molecular memory device based on DNA using methylation to store information (Australia) 2016
- Information-containing macromolecules (England) 2014
- Molecular computing: paths to chemical Turing machines (the Netherlands) 2015
- Molecular logic gates based on DNA tweezers responsive to multiplex restriction endonucleases (China) 2016
- Molecules with a sense of logic: a progress report (Sweden) 2015
- Multiple types of logic gates based on a single G-quadruplex DNA strand (China) 2014
- Multiplexed Sequence Encoding: A Framework for DNA Communication (USA) 2016
- Nucleic Acid Based Logical Systems (USA) 2014
- Nucleic acid memory (USA) 2016
- Particles with an identity: Tracking and tracing in commodity products (Switzerland) 2016
- Programmable DNA-Mediated Multitasking Processor (Singapore) 2015
- Reading Polymers: Sequencing of Natural and Synthetic Macromolecules (France) 2014
- A Rewritable, Random-Access DNA-Based Storage System (USA) 2015
- Robust Chemical Preservation of Digital Information on DNA in Silica with Error-Correcting Codes (Switzerland) 2015
- Synthetic DNA The next generation of big data storage (Ireland) 2013

APPLICATIONS - MATERIALS

- Adding Functions to Biomaterial Surfaces through Protein Incorporation (Ireland) 2016
- Advanced Biotechnology: Metabolically Engineered Cells for the Bio-Based Production of Chemicals and Fuels, Materials, and Health-Care Products (Germany) 2015
- Bioengineering microbial communities: Their potential to help, hinder and disgust (Australia) 2016
- Bioengineering Virus-Like Particles as Vaccines (Australia) 2014
- Bridging the gap between systems biology and synthetic biology (USA) 2013
- Chemically Modifying Viruses for Diverse Applications (USA) 2016
- Creating biological nanomaterials using synthetic biology (USA) 2014
- Designing Synthetic Biology (USA) 2014
- DNA Nanostructures on Membranes as Tools for Synthetic Biology (Poland) 2016
- Engineering control of bacterial cellulose production using a genetic toolkit and a new cellulose-producing strain (England) 2016
- Engineering microbial cell factories: Metabolic engineering of *Corynebacterium glutamicum* with a focus on non-natural products (Germany) 2015

- Exploring the potential of metallic nanoparticles within synthetic biology (Scotland) 2014
- Integrated Micro/Nanoengineered Functional Biomaterials for Cell Mechanics and Mechanobiology: A Materials Perspective (USA) 2014
- Modern approaches to the creation of industrial microorganism strains (Russia) 2015
- Novel theranostic agents for next-generation personalized medicine: small molecules, nanoparticles, and engineered mammalian cells (Switzerland) 2015
- Opportunities in plant synthetic biology (England) 2014
- A survey of enabling technologies in synthetic biology
- Synthetic biology to access and expand nature's chemical diversity (USA) 2016
- Synthetic biology for mammalian cell technology and materials sciences (Germany) 2013
- Viruses, Artificial Viruses and Virus-Based Structures for Biomedical Applications (the Netherlands) 2016

APPLICATIONS - SENSORS/SENSING

- Application of genetically engineered microbial whole-cell biosensors for combined chemosensing (China) 2016
- Approaches towards molecular amplification for sensing (England) 2016
- Development of a highly specific and sensitive cadmium and lead microbial biosensor using synthetic CadC-T7 genetic circuitry (South Korea) 2016
- DNA nanotechnology-enabled biosensors (China) 2016
- Environmental Sensing of Heavy Metals Through Whole Cell Microbial Biosensors: A Synthetic Biology Approach (Australia) 2015
- Enzyme-driven i-motif DNA folding for logic operations and fluorescent biosensing (China) 2015
- Fluigi: Microfluidic Device Synthesis for Synthetic Biology (USA) 2014
- Global transcriptomic responses of *Escherichia coli* K-12 to volatile organic compounds (Singapore) 2016
- Initiator-catalyzed self-assembly of duplex-looped DNA hairpin motif based on strand displacement reaction for logic operations and amplified biosensing (China) 2016
- Synthetic biology and biomimetic chemistry as converging technologies fostering a new generation of smart biosensors (Italy) 2015
- Synthetic Biology and Microdevices: A Powerful Combination (Belgium) 2013
- A tutorial review for employing enzymes for the construction of G-quadruplex-based sensing platforms (China) 2016
- Ultraspecific electrochemical DNA biosensor by coupling spontaneous cascade DNA branch migration and dual-signaling sensing strategy (China) 2016
- Understanding and exploiting feedback in synthetic biology (USA) 2013

Review Articles

[Aims and methods of biosteganography \(Canada\) 2016](#)

Author(s): Brunet, TDP (Brunet, Tyler D. P.)

Source: JOURNAL OF BIOTECHNOLOGY Volume: 226 Pages: 56-64 DOI: 10.1016/j.jbiotec.2016.03.044 Published: MAY 20 2016

ABSTRACT: Applications of biotechnology to information security are now possible and have potentially far reaching political and technological implications. This change in information security practices, initiated by advancements in molecular biological and biotechnology, warrants reasonable and widespread consideration by biologists, biotechnologists and philosophers. I offer an explication of the landmark contributions, developments and current possibilities of biosteganography the process of transmitting secure messages via biological mediums. I address, (i) how information can be stored and encoded in biological mediums, (ii) how biological mediums (e.g. DNA, RNA, protein) and storage systems (e.g. cells, biofilms, organisms) influence the nature of information security, and (iii) what constitutes a viable application of such biotechnologies. (C) 2016 Elsevier B.V. All rights reserved.

Author(s) affiliation: [Brunet, Tyler D. P.] Dalhousie Univ, Computat Biol & Bioinformat, 6050 Univ Ave, Halifax, NS B3H 1W5, Canada.

Reprint Address: Brunet, TDP (reprint author), Dalhousie Univ, Computat Biol & Bioinformat, 6050 Univ Ave, Halifax, NS B3H 1W5, Canada.

E-mail Author(s) affiliation: tyler.brunet@dal.ca

Times Cited: 0

Number of references: 60

Tags: Review article, Applications - Cryptography/Information security, Synthetic biology

[The emerging age of cell-free synthetic biology \(USA\) 2014](#)

Author(s): Smith, MT (Smith, Mark Thomas); Wilding, KM (Wilding, Kristen M.); Hunt, JM (Hunt, Jeremy M.); Bennett, AM (Bennett, Anthony M.); Bundy, BC (Bundy, Bradley C.)

Source: FEBS LETTERS Volume: 588 Issue: 17 Pages: 2755-2761 DOI: 10.1016/j.febslet.2014.05.062 Published: AUG 25 2014

ABSTRACT: The engineering of and mastery over biological parts has catalyzed the emergence of synthetic biology. This field has grown exponentially in the past decade. As increasingly more applications of synthetic biology are pursued, more challenges are encountered, such as delivering genetic material into cells and optimizing genetic circuits in vivo. An in vitro or cell-free approach to synthetic biology simplifies and avoids many of the pitfalls of in vivo synthetic biology. In this review, we describe some of the innate features that make cell-free systems compelling platforms for synthetic biology and discuss emerging improvements of cell-free technologies. We also select and highlight recent and emerging applications of cell-free synthetic biology. (C) 2014 Federation of European Biochemical Societies. Published by Elsevier B.V. All rights reserved.

Author(s) affiliation: [Smith, Mark Thomas; Wilding, Kristen M.; Hunt, Jeremy M.; Bennett, Anthony M.; Bundy, Bradley C.] Brigham Young Univ, Dept Chem Engr, Provo, UT 84602 USA.

Reprint Address: Bundy, BC (reprint author), Brigham Young Univ, Dept Chem Engr, 350 Clyde Bldg, Provo, UT 84602 USA.

E-mail Author(s) affiliation: bundy@byu.edu

Times cited: 14

Number of references: 115

Tags: Review article, Applications - Materials, Synthetic biology

[Engineering for the 21st Century: Synthetic Biology \(USA\) 2013](#)

Author(s): Munnelly, K (Munnelly, Kevin)

Source: ACS SYNTHETIC BIOLOGY Volume: 2 Issue: 5 Pages: 213-215 DOI: 10.1021/sb400039g Published: MAY 2013

ABSTRACT: For years, scientists have hoped that biology would find its engineering counterpart - a series of principles that could be used as reliably as chemical engineering is for chemistry. Thanks to major advances in synthetic biology, those hopes may soon be realized.

Author(s) affiliation: Gen9 Inc, Cambridge, MA 02139 USA.

Reprint Address: Munnelly, K (reprint author), Gen9 Inc, 500 Technol Sq, Cambridge, MA 02139 USA.

E-mail Author(s) affiliation: kmunnelly@gen9bio.com

Times Cited: 3

Number of references: 4

Tags: Review article, Synthetic biology

Foundations and Emerging Paradigms for Computing in Living Cells (USA) 2016

Author(s): Ma, KC (Ma, Kevin C.); Perli, SD (Perli, Samuel D.); Lu, TK (Lu, Timothy K.)

Source: JOURNAL OF MOLECULAR BIOLOGY Volume: 428 Issue: 5 Special Issue: SI Pages: 893-915 DOI: 10.1016/j.jmb.2016.02.018 Part: B Published: FEB 27 2016

ABSTRACT: Genetic circuits, composed of complex networks of interacting molecular machines, enable living systems to sense their dynamic environments, perform computation on the inputs, and formulate appropriate outputs. By rewiring and expanding these circuits with novel parts and modules, synthetic biologists have adapted living systems into vibrant substrates for engineering. Diverse paradigms have emerged for designing, modeling, constructing, and characterizing such artificial genetic systems. In this paper, we first provide an overview of recent advances in the development of genetic parts and highlight key engineering approaches. We then review the assembly of these parts into synthetic circuits from the perspectives of digital and analog logic, systems biology, and metabolic engineering, three areas of particular theoretical and practical interest. Finally, we discuss notable challenges that the field of synthetic biology still faces in achieving reliable and predictable forward-engineering of artificial biological circuits. (C) 2016 Published by Elsevier Ltd.

Author(s) affiliation: [Ma, Kevin C.; Perli, Samuel D.; Lu, Timothy K.] MIT, Dept Biol Engr & Elect Engr & Comp Sci, Elect Res Lab, Synthet Biol Grp, Cambridge, MA 02142 USA.

Reprint Address: Lu, TK (reprint author), MIT, Dept Biol Engr & Elect Engr & Comp Sci, Elect Res Lab, Synthet Biol Grp, Cambridge, MA 02142 USA.

E-mail Author(s) affiliation: timlu@mit.edu

Times Cited: 1

Number of references: 300

Tags: Review article, Synthetic biology

Large-scale de novo DNA synthesis: technologies and applications (USA) 2014

Author(s): Kosuri, S (Kosuri, Sriram); Church, GM (Church, George M.)

Source: NATURE METHODS Volume: 11 Issue: 5 Pages: 499-507 DOI: 10.1038/NMETH.2918 Published: MAY 2014

ABSTRACT: For over 60 years, the synthetic production of new DNA sequences has helped researchers understand and engineer biology. Here we summarize methods and caveats for the de novo synthesis of DNA, with particular emphasis on recent technologies that allow for large-scale and low-cost production. In addition, we discuss emerging applications enabled by large-scale de novo DNA constructs, as well as the challenges and opportunities that lie ahead.

Author(s) affiliation: [Kosuri, Sriram] Calif State Univ Los Angeles, Dept Chem & Biochem, Los Angeles, CA 90032 USA.

[Church, George M.] Wyss Inst Biol Inspired Engr, Boston, MA USA.

[Church, George M.] Harvard Univ, Sch Med, Dept Genet, Boston, MA USA.

Reprint Address: Kosuri, S (reprint author), Calif State Univ Los Angeles, Dept Chem & Biochem, Los Angeles, CA 90032 USA.

E-mail Author(s) affiliation: sri@ucla.edu

Times Cited: 58

Number of references: 137

Tags: Review article, Applications - Bioweapons, Synthetic biology

The next generation mass storage devices - Physical principles and current status (China) 2014

Author(s): Wang, L (Wang, L.); Gai, S (Gai, S.)

Source: CONTEMPORARY PHYSICS Volume: 55 Issue: 2 Pages: 75-93 DOI: 10.1080/00107514.2013.878565 Published: APR 3 2014

ABSTRACT: The amount of digital data today has been increasing at a phenomenal rate due to the widespread digitalisation service in almost every industry. The need to store such ever-increasing data aggressively triggers the requirement to augment the storage capacity of the conventional storage technologies. Unfortunately, the physical limitations that conventional forms face have severely handicapped their potential to meet the storage need from both consumer and industry point of view. The focus has therefore been switched into the development of the innovative data storage technologies such as scanning probe memory, nanocrystal memory, carbon nanotube memory, DNA memory, and organic memory. In this paper, we review the physical principles of these emerging storage technologies and their superiorities as the next generation data storage device, as well as their respective technical challenges on further enhancing the storage capacity. We also compare these novel technologies with the mainstream data storage means according to the technology roadmap on areal density.

Author(s) affiliation: [Wang, L.; Gai, S.] Nanchang HangKong Univ, Sch Informat Engr, Nanchang 330063, Peoples R China.

Reprint Address: Wang, L (reprint author), Nanchang HangKong Univ, Sch Informat Engr, Nanchang 330063, Peoples R China.

E-mail Author(s) affiliation: LeiWang@nchu.edu.cn

Times Cited: 3

Number of references: 188

Tags: Review article, Synthetic biology

Parallel Networks: Synthetic Biology and Artificial Intelligence (USA) 2014

Author(s): Deans, TL (Deans, Tara L.)

Source: ACM JOURNAL ON EMERGING TECHNOLOGIES IN COMPUTING SYSTEMS Volume: 11 Issue: 3 Special Issue: SI Article Number: 21 DOI: 10.1145/2667229 Published: DEC 2014

ABSTRACT: Synthetic biology has emerged as an important technology for engineering cells to behave in controllable and predictable ways. The promise of this modern technology is dependent on our understanding of cellular complexity to allow us to engineer cells with novel function. In this regard, the fields of computer science and synthetic biology are critical for accelerating both our understanding of biological systems, and our ability to quantitatively engineer cells. Thus, advances in biology and biotechnology are arising at the intersection of computer science and synthetic biology approaches. This review seeks to introduce the field of synthetic biology to the computer science community, and to ignite a curiosity and interest in fostering a unique synergy for possible collaborations between synthetic biologists and computer scientists.

Author(s) affiliation: Univ Utah, Dept Bioengn, Salt Lake City, UT 84112 USA.

Reprint Address: Deans, TL (reprint author), Univ Utah, Dept Bioengn, Biopolymers Res Bldg, 20 South 2030 East, Salt Lake City, UT 84112 USA.

E-mail Author(s) affiliation: tara.deans@utah.edu

Times Cited: 0

Number of references: 179

Tags: Review article, Applications - Bioweapons, Synthetic biology

Rapid prototyping of microbial cell factories via genome-scale engineering (USA) 2015

Author(s): Si, T (Si, Tong); Xiao, H (Xiao, Han); Zhao, HM (Zhao, Huimin)

Source: BIOTECHNOLOGY ADVANCES Volume: 33 Issue: 7 Special Issue: SI Pages: 1420-1432 DOI: 10.1016/j.biotechadv.2014.11.007 Published: NOV 15 2015

ABSTRACT: Advances in reading, writing and editing genetic materials have greatly expanded our ability to reprogram biological systems at the resolution of a single nucleotide and on the scale of a whole genome. Such capacity has greatly accelerated the cycles of design, build and test to engineer microbes for efficient synthesis of fuels, chemicals and drugs. In this review, we summarize the emerging technologies that have been applied, or are potentially useful for genome-scale engineering in microbial systems. We will focus on the development of high-throughput methodologies, which may accelerate the prototyping of microbial cell factories. (C) 2014 Elsevier Inc. All rights reserved.

Author(s) affiliation: [Si, Tong; Xiao, Han; Zhao, Huimin] Univ Illinois, Dept Chem & Biomol Engr, Urbana, IL 61801 USA.

Reprint Address: Zhao, HM (reprint author), Univ Illinois, Dept Chem & Biomol Engr, Urbana, IL 61801 USA.

E-mail Author(s) affiliation: zhao5@illinois.edu

Times Cited: 4

Number of references: 194

Tags: Review article, Applications - Bioweapons, Synthetic biology

Towards practical, high-capacity, low-maintenance information storage in synthesized DNA (England) 2013

Author(s): Goldman, N (Goldman, Nick); Bertone, P (Bertone, Paul); Chen, SY (Chen, Siyuan); Dessimoz, C (Dessimoz, Christophe); LeProust, EM (LeProust, Emily M.); Sipos, B (Sipos, Botond); Birney, E (Birney, Ewan)

Source: NATURE Volume: 494 Issue: 7435 Pages: 77-80 DOI: 10.1038/nature11875 Published: FEB 7 2013

ABSTRACT: Digital production, transmission and storage have revolutionized how we access and use information but have also made archiving an increasingly complex task that requires active, continuing maintenance of digital media. This challenge has focused some interest on DNA as an attractive target for information storage(1) because of its capacity for high-density information encoding, longevity under easily achieved conditions(2-4) and proven track record as an information bearer. Previous DNA-based information storage approaches have encoded only trivial amounts of information(5-7) or were not amenable to scaling-up(8), and used no robust error-correction and lacked examination of their cost-efficiency for large-scale information archival(9). Here we describe a scalable method that can reliably store more information than has been handled before. We encoded computer files totalling 739 kilobytes of hard-disk storage and with an estimated Shannon information(10) of 5.2×10^6 bits into a DNA code, synthesized this DNA, sequenced it and reconstructed the original files with 100% accuracy. Theoretical analysis indicates that our DNA-based storage scheme could be scaled far beyond current global information volumes and offers a realistic technology for large-scale, long-term and infrequently accessed digital archiving. In fact, current trends in technological advances are reducing DNA synthesis costs at a pace that should make our scheme cost-effective for sub-50-year archiving within a decade.

Author(s) affiliation: [Goldman, Nick; Bertone, Paul; Dessimoz, Christophe; Sipos, Botond; Birney, Ewan] European Bioinformat Inst, Hinxton CB10 1SD, England.

[Chen, Siyuan; LeProust, Emily M.] Genom LSSU, Agilent Technol, Santa Clara, CA 95051 USA.

Reprint Address: Goldman, N (reprint author), European Bioinformat Inst, Wellcome Trust Genome Campus, Hinxton CB10 1SD, England.

E-mail Author(s) affiliation: goldman@ebi.ac.uk

Times Cited: 60

Number of references: 28

Tags: Review article, Applications - Information storage, Synthetic biology

Applications - Bioweapons

Assessing and Managing the Risks of Potential Pandemic Pathogen Research (USA) 2015

Author(s): Rozell, DJ (Rozell, Daniel J.)

Source: MBIO Volume: 6 Issue: 4 Article Number: e01075-15 DOI: 10.1128/mBio.01075-15 Published: JUL-AUG 2015

Author(s) affiliation: SUNY Stony Brook, Dept Technol & Soc, Stony Brook, NY 11794 USA.

Reprint Address: Rozell, DJ (reprint author), SUNY Stony Brook, Dept Technol & Soc, Stony Brook, NY 11794 USA.

Times Cited: 0

Number of references: 46

Tags: Applications - Bioweapons, Synthetic biology

An Avian H7N1 Gain-of-Function Experiment of Great Concern (France) 2014

Author(s): Wain-Hobson, S (Wain-Hobson, Simon)

Source: MBIO Volume: 5 Issue: 5 Article Number: e01882-14 DOI: 10.1128/mBio.01882-14 Published: SEP-OCT 2014

ABSTRACT: Inappropriately named gain-of-function influenza research seeks to confer airborne transmission on avian influenza A viruses that otherwise cause only dead-end infections in humans. A recent study has succeeded in doing this with a highly pathogenic ostrich H7N1 virus in a ferret model without loss of virulence. If transposable to humans, this would constitute a novel virus with a case fatality rate similar to 30 greater than that of Spanish flu. A commentary from three distinguished virologists considered the benefits of this work to outweigh potential risks. I beg to disagree with conclusions in both papers, for the underlying science is not as strong as it appears.

Author(s) affiliation: [Wain-Hobson, Simon] Inst Pasteur, Paris, France.

Reprint Address: Wain-Hobson, S (reprint author), Inst Pasteur, Paris, France.

E-mail Author(s) affiliation: simon@pasteur.fr

Times Cited: 3

Number of references: 19

Tags: Applications - Bioweapons, Synthetic biology

Biosecurity and Open-Source Biology: The Promise and Peril of Distributed Synthetic Biological Technologies (USA) 2015

Author(s): Evans, NG (Evans, Nicholas G.); Selgelid, MJ (Selgelid, Michael J.)

Source: SCIENCE AND ENGINEERING ETHICS Volume: 21 Issue: 4 Pages: 1065-1083 DOI: 10.1007/s11948-014-9591-3

Published: AUG 2015

ABSTRACT: In this article, we raise ethical concerns about the potential misuse of open-source biology (OSB): biological research and development that progresses through an organisational model of radical openness, deskilling, and innovation. We compare this organisational structure to that of the open-source software model, and detail salient ethical implications of this model. We demonstrate that OSB, in virtue of its commitment to openness, may be resistant to governance attempts.

Author(s) affiliation: [Evans, Nicholas G.] Univ Penn, Dept Med Eth & Hlth Policy, Philadelphia, PA 19104 USA.

[Selgelid, Michael J.] Monash Univ, Ctr Human Bioeth, Melbourne, Vic 3800, Australia.

Reprint Address: Evans, NG (reprint author), Univ Penn, Dept Med Eth & Hlth Policy, Suite 320,3401 Market St, Philadelphia, PA 19104 USA.

E-mail Author(s) affiliation: neva9257@gmail.com; michael.selgelid@monash.edu

Times Cited: 1

Number of references: 54

Tags: Applications - Bioweapons, Synthetic biology

Construction of a synthetic infectious cDNA clone of Grapevine Algerian latent virus (GALV-Nf) and its biological activity in Nicotiana benthamiana and grapevine plants (Italy) 2014

Author(s): Lovato, A (Lovato, Arianna); Faoro, F (Faoro, Franco); Gambino, G (Gambino, Giorgio); Maffi, D (Maffi, Dario); Bracale, M (Bracale, Marcella); Polverari, A (Polverari, Annalisa); Santi, L (Santi, Luca)

Source: VIROLOGY JOURNAL Volume: 11 Article Number: 186 DOI: 10.1186/1743-422X-11-186 Published: NOV 3 2014

ABSTRACT: We developed and tested a synthetic GALV construct for the inoculation of Nicotiana benthamiana plants and different grapevine genotypes to investigate the ability of this virus to infect and spread systemically in different hosts. Sequence analysis

showed that the GALV coat protein is highly conserved among diverse isolates. The first epidemiological survey of cDNAs collected from 152 grapevine plants with virus-like symptoms did not reveal the presence of GALV in any of the samples. This is the first report describing the development of a synthetic GALV-Nf cDNA clone, its artificial transmission to grapevine plants and the resulting symptoms and cytopathological alterations.

Author(s) affiliation: [Lovato, Arianna; Polverari, Annalisa] Univ Verona, Dept Biotechnol, I-37134 Verona, Italy.

[Faoro, Franco; Maffi, Dario] Univ Milan, Dept Agr & Environm Sci DiSAA, I-20133 Milan, Italy.

[Faoro, Franco; Gambino, Giorgio] CNR, Inst Sustainable Plant Protect, Grugliasco Unit, I-10095 Grugliasco, TO, Italy.

[Bracale, Marcella] Univ Insubria, Dept Environm Hlth & Safety, I-21100 Varese, Italy.

[Santi, Luca] Univ Tuscia, Dept Sci & Technol Agr Forestry Nat & Energy DAFN, I-01100 Viterbo, Italy.

Reprint Address: Polverari, A (reprint author), Univ Verona, Dept Biotechnol, Str Grazie 15, I-37134 Verona, Italy.

E-mail Author(s) affiliation: annalisa.polverari@univr.it

Times Cited: 2

Number of references: 53

Tags: Applications - Bioweapons, Synthetic biology

[Dual-use research and the H5N1 bird flu: Is restricting publication the solution to biosecurity issues? \(Switzerland\) 2014](#)

Author(s): Engel-Glatte, S (Engel-Glatte, Sabrina)

Source: SCIENCE AND PUBLIC POLICY Volume: 41 Issue: 3 Pages: 370-383 DOI: 10.1093/scipol/sct064 Published: JUN 2014

ABSTRACT: Recent studies altering the host range of the H5N1 bird flu virus have refueled intense debates over the potential misuse of academic life science research. To curtail the bioterrorism threat, it has been suggested that dissemination of the research results and methodology should be restricted. However, doubts have been raised over the suitability and effectiveness of this measure. Using the H5N1 studies as an example, this paper summarizes the main arguments of the debate. Particular attention is paid to the issue of the tacit knowledge required to replicate published life science research results, which has so far received limited attention. Taking into account the importance of tacit knowledge for life science research, it is argued that preventing publication of the methodology does not decrease the threat of bioterrorism.

Author(s) affiliation: Univ Basel, Inst Biomed Eth, CH-4055 Basel, Switzerland.

Reprint Address: Engel-Glatte, S (reprint author), Univ Basel, Inst Biomed Eth, Bernoullistr 28, CH-4055 Basel, Switzerland.

E-mail Author(s) affiliation: sabrina.engel@unibas.ch

Times Cited: 0

Number of references: 89

Tags: Applications - Bioweapons, Synthetic biology

[The ethics of biosafety considerations in gain-of-function research resulting in the creation of potential pandemic pathogens \(USA\) 2015](#)

Author(s): Evans, NG (Evans, Nicholas Greig); Lipsitch, M (Lipsitch, Marc); Levinson, M (Levinson, Meira)

Source: JOURNAL OF MEDICAL ETHICS Volume: 41 Issue: 11 Pages: 901-908 DOI: 10.1136/medethics-2014-102619 Published: NOV 2015

ABSTRACT: This paper proposes an ethical framework for evaluating biosafety risks of gain-of-function (GOF) experiments that create novel strains of influenza expected to be virulent and transmissible in humans, so-called potential pandemic pathogens (PPPs). Such research raises ethical concerns because of the risk that accidental release from a laboratory could lead to extensive or even global spread of a virulent pathogen. Biomedical research ethics has focused largely on human subjects research, while biosafety concerns about accidental infections, seen largely as a problem of occupational health, have been ignored.

Author(s) affiliation: [Evans, Nicholas Greig] Univ Penn, Dept Med Eth & Hlth Policy, Perelman Sch Med, Philadelphia, PA 19104 USA.

[Lipsitch, Marc] Harvard TH Chan Sch Publ Hlth, Ctr Communicable Dis Dynam, Dept Epidemiol, Boston, MA USA.

[Levinson, Meira] Harvard Univ, Grad Sch Educ, Cambridge, MA 02138 USA.

Reprint Address: Evans, NG (reprint author), Univ Penn, Dept Med Eth & Hlth Policy, Philadelphia, PA 19104 USA.

E-mail Author(s) affiliation: evann@mail.med.upenn.edu

Times Cited: 0

Number of references: 57

Tags: Applications - Bioweapons, Synthetic biology

[Infectious Diseases Society of America and Gain-of-Function Experiments With Pathogens Having Pandemic Potential \(USA\) 2016](#)

Author(s): Frank, GM (Frank, Gregory M.); Adalja, A (Adalja, Amesh); Barbour, A (Barbour, Alan) et al

Source: JOURNAL OF INFECTIOUS DISEASES Volume: 213 Issue: 9 Pages: 1359-1361 DOI: 10.1093/infdis/jiv474 Published: MAY 1 2016

Author(s) affiliation: [Frank, Gregory M.] Infect Dis Soc Amer, 1300 Wilson Blvd, Arlington, VA 22209 USA.

[Hayden, Frederick G.] Univ Virginia, Sch Med, Charlottesville, VA 22908 USA.

[Adalja, Amesh] Univ Pittsburgh, Med Ctr, Ctr Hlth Secur, Pittsburgh, PA 15260 USA.

[Barbour, Alan] Univ Calif Irvine, Dept Med, Irvine, CA 92717 USA.

Reprint Address: Frank, GM (reprint author), Infect Dis Soc Amer, 1300 Wilson Blvd, Arlington, VA 22209 USA.

E-mail Author(s) affiliation: gfrank@idsociety.org

Times Cited: 2

Number of references: 10

Tags: Applications - Bioweapons, Synthetic biology

Moving beyond metagenomics to find the next pandemic virus (USA) 2016

Author(s): Racaniello, V (Racaniello, Vincent)

Source: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA Volume: 113 Issue: 11 Pages: 2812-2814 DOI: 10.1073/pnas.1601512113 Published: MAR 15 2016

Author(s) affiliation: [Racaniello, Vincent] Columbia Univ, Med Ctr, Dept Microbiol & Immunol, New York, NY 10032 USA.

Reprint Address: Racaniello, V (reprint author), Columbia Univ, Med Ctr, Dept Microbiol & Immunol, New York, NY 10032 USA.

E-mail Author(s) affiliation: vrr1@columbia.edu

Times Cited: 0

Number of references: 10

Tags: Applications - Bioweapons, Synthetic biology

A New Synthesis for Dual Use Research of Concern (USA) 2015

Author(s): Imperiale, MJ (Imperiale, Michael J.); Casadevall, A (Casadevall, Arturo)

Source: PLOS MEDICINE Volume: 12 Issue: 4 Article Number: e1001813 DOI: 10.1371/journal.pmed.1001813 Published: APR 2015

Author(s) affiliation: [Imperiale, Michael J.] Univ Michigan, Dept Microbiol & Immunol, Ann Arbor, MI 48109 USA.

[Casadevall, Arturo] Johns Hopkins Bloomberg Sch Publ Hlth, Dept Mol Microbiol & Immunol, Baltimore, MD USA.

Reprint Address: Imperiale, MJ (reprint author), Univ Michigan, Dept Microbiol & Immunol, Ann Arbor, MI 48109 USA.

E-mail Author(s) affiliation: imperial@umich.edu

Times Cited: 1

Number of references: 28

Tags: Applications - Bioweapons, Synthetic biology

Security Vulnerabilities and Countermeasures for Target Localization in Bio-NanoThings Communication Networks (Italy) 2016

Author(s): Giaretta, A (Giaretta, Alberto); Balasubramaniam, S (Balasubramaniam, Sasitharan); Conti, M (Conti, Mauro)

Source: IEEE TRANSACTIONS ON INFORMATION FORENSICS AND SECURITY Volume: 11 Issue: 4 Pages: 665-676 DOI: 10.1109/TIFS.2015.2505632 Published: APR 2016

ABSTRACT: In this paper, we focus on specific Bio-NanoThings, i.e., bacteria, where engineering their ability to emit or sense molecules can result in functionalities, such as cooperative target localization. Although this opens opportunities, e.g., for novel healthcare applications of the future, this can also lead to new problems, such as a new form of bioterrorism. In this paper, we investigate the disruptions that malicious Bio-NanoThings (M-BNTs) can create for molecular nanonetworks. In particular, we introduce two types of attacks: 1) blackhole and 2) sentry attacks. In blackhole attack M-BNTs emit attractant chemicals to draw-in the legitimate Bio-NanoThings (L-BNTs) from searching for their target, while in the sentry attack, the M-BNTs emit repellents to disperse the L-BNTs from reaching their target. We also present a countermeasure that L-BNTs can take to be resilient to the attacks, where we consider two forms of decision processes that includes Bayes' rule as well as a simple threshold approach. We run a thorough set of simulations to assess the effectiveness of the proposed attacks as well as the proposed countermeasure. Our results show that the attacks can significantly hinder the regular behavior of Bio-NanoThings, while the countermeasures are effective for protecting against such attacks.

Author(s) affiliation: [Giaretta, Alberto; Conti, Mauro] Univ Padua, Dept Math, I-35122 Padua, Italy.

[Balasubramaniam, Sasitharan] Tampere Univ Technol, Dept Elect & Commun Engr, Nano Commun Ctr, Tampere 33720, Finland.

Reprint Address: Giaretta, A; Conti, M (reprint author), Univ Padua, Dept Math, I-35122 Padua, Italy.

Balasubramaniam, S (reprint author), Tampere Univ Technol, Dept Elect & Commun Engr, Nano Commun Ctr, Tampere 33720, Finland.

E-mail Author(s) affiliation: giaretta.alberto@gmail.com; sasi.bala@tut.fi; conti@math.unipd.it

Times Cited: 0

Number of references: 37

Tags: Applications - Bioweapons, Synthetic biology

Synonymous Virus Genome Recoding as a Tool to Impact Viral Fitness (Spain) 2016

Author(s): Martinez, MA (Angel Martinez, Miguel); Jordan-Paiz, A (Jordan-Paiz, Ana); Franco, S (Franco, Sandra); Nevot, M (Nevot, Maria)

Source: TRENDS IN MICROBIOLOGY Volume: 24 Issue: 2 Pages: 134-147 DOI: 10.1016/j.tim.2015.11.002 Published: FEB 2016

ABSTRACT: Synthetic genome recoding is a novel method of generating viruses with altered phenotypes, whereby many synonymous mutations are introduced into the protein coding region of the virus genome without altering the encoded proteins. Virus genome recoding with large numbers of slightly deleterious mutations has produced attenuated forms of several RNA viruses. Virus genome recoding can also aid in investigating virus interactions with innate immune responses, identifying functional virus genome structures, strategically ameliorating cis-inhibitory signaling sequences related to complex viral functions, to unravel the relevance of codon usage for the temporal regulation of viral gene expression and improving our knowledge of virus mutational robustness and adaptability. The present review discusses the impacts of synonymous genome recoding with regard to expanding our comprehension of virus biology, and the development of new and better therapeutic strategies.

Author(s) affiliation: [Angel Martinez, Miguel; Jordan-Paiz, Ana; Franco, Sandra; Nevot, Maria] Univ Autonoma Barcelona, Hosp Univ Germans Trias & Pujol, IrsiCaixa, Badalona, Spain.

Reprint Address: Martinez, MA (reprint author), Univ Autonoma Barcelona, Hosp Univ Germans Trias & Pujol, IrsiCaixa, Badalona, Spain.

E-mail Author(s) affiliation: mmartinez@irsicaixa.es

Times Cited: 0

Number of references: 74

Tags: Applications - Bioweapons, Synthetic biology

Synthetic biology: from mainstream to counterculture (Ireland) 2016

Author(s): Sleator, RD (Sleator, Roy D.)

Source: ARCHIVES OF MICROBIOLOGY Volume: 198 Issue: 7 Pages: 711-713 DOI: 10.1007/s00203-016-1257-x Published: SEP 2016

ABSTRACT: Existing at the interface of science and engineering, synthetic biology represents a new and emerging field of mainstream biology. However, there also exists a counterculture of Do-It-Yourself biologists, citizen scientists, who have made significant inroads, particularly in the design and development of new tools and techniques. Herein, I review the development and convergence of synthetic biology's mainstream and countercultures.

Author(s) affiliation: [Sleator, Roy D.] Cork Inst Technol, Dept Biol Sci, Cork, Ireland.

Reprint Address: Sleator, RD (reprint author), Cork Inst Technol, Dept Biol Sci, Cork, Ireland.

E-mail Author(s) affiliation: roy.sleator@cit.ie

Times Cited: 0

Number of references: 30

Tags: Applications - Bioweapons, Synthetic biology

Synthetic Biology: A Utilitarian Perspective (Scotland) 2013

Author(s): Smith, K (Smith, Kevin)

Source: BIOETHICS Volume: 27 Issue: 8 Special Issue: SI Pages: 453-463 DOI: 10.1111/bioe.12050 Published: OCT 2013

ABSTRACT: I examine the positive and negative features of synthetic biology (SynBio') from a utilitarian ethical perspective. The potential beneficial outcomes from SynBio in the context of medicine are substantial; however it is not presently possible to predict precise outcomes due to the nascent state of the field. Potential negative outcomes from SynBio also exist, including iatrogenesis and bioterrorism; however it is not yet possible to quantify these risks. I argue that the application of a precautionary' approach to SynBio is ethically fraught, as is the notion that SynBio-associated knowledge ought to be restricted. I conclude that utilitarians ought to support a broadly laissez-faire stance in respect of SynBio.

Author(s) affiliation: [Smith, Kevin] Abertay Univ, Dundee, Scotland.

Reprint Address: Smith, K (reprint author), Abertay Univ Contemporary Sci, Baxter Bldg Monifieth, Dundee DD1 1HG, Tayside, Scotland.

E-mail Author(s) affiliation: K.Smith@abertay.ac.uk

Times Cited: 4

Number of references: 45

Tags: Applications - Bioweapons, Synthetic biology

[Synthetic virus seeds for improved vaccine safety: Genetic reconstruction of poliovirus seeds for a PER.C6 \(R\) cell based inactivated poliovirus vaccine \(the Netherlands\) 2015](#)

Author(s): Sanders, BP (Sanders, Barbara P.); Edo-Matas, D (Edo-Matas, Diana); Papic, N (Papic, Natasa); Schuitemaker, H (Schuitemaker, Hanneke); Custers, JHHV (Custers, Jerome H. H. V.)

Source: VACCINE Volume: 33 Issue: 42 Pages: 5498-5502 DOI: 10.1016/j.vaccine.2015.08.081 Published: OCT 13 2015

ABSTRACT: Safety of vaccines can be compromised by contamination with adventitious agents. One potential source of adventitious agents is a vaccine seed, typically derived from historic clinical isolates with poorly defined origins. Here we generated synthetic poliovirus seeds derived from chemically synthesized DNA plasmids encoding the sequence of wild-type poliovirus strains used in marketed inactivated poliovirus vaccines. The synthetic strains were phenotypically identical to wild-type polioviruses as shown by equivalent infectious titers in culture supernatant and antigenic content, even when infection cultures are scaled up to 10-25 L bioreactors. Moreover, the synthetic seeds were genetically stable upon extended passaging on the PER.C6 (R) cell culture platform. Use of synthetic seeds produced on the serum-free PER.C6 (R) cell platform ensures a perfectly documented seed history and maximum control over starting materials. It provides an opportunity to maximize vaccine safety which increases the prospect of a vaccine end product that is free from adventitious agents. (C) 2015 Elsevier Ltd. All rights reserved.

Author(s) affiliation: [Sanders, Barbara P.; Edo-Matas, Diana; Papic, Natasa; Schuitemaker, Hanneke; Custers, Jerome H. H. V.] Janssen Infect Dis & Vaccines, NL-2333 CN Leiden, Netherlands.

Reprint Address: Sanders, BP (reprint author), Janssen Infect Dis & Vaccines, Archimedesweg 4, NL-2333 CN Leiden, Netherlands.

E-mail Author(s) affiliation: bsander2@its.jnj.com

Times Cited: 0

Number of references: 22

Tags: Applications - Bioweapons, Synthetic biology

Applications - Cryptography/Information Security

[Binary DNA Nanostructures for Data Encryption \(USA\) 2012](#)

Author(s): Halvorsen, K (Halvorsen, Ken); Wong, WP (Wong, Wesley P.)

Source: PLOS ONE Volume: 7 Issue: 9 Article Number: e44212 DOI: 10.1371/journal.pone.0044212 Published: SEP 11 2012

ABSTRACT: We present a simple and secure system for encrypting and decrypting information using DNA self-assembly. Binary data is encoded in the geometry of DNA nanostructures with two distinct conformations. Removing or leaving out a single component reduces these structures to an encrypted solution of ssDNA, whereas adding back this missing "decryption key" causes the spontaneous formation of the message through self-assembly, enabling rapid read out via gel electrophoresis. Applications include authentication, secure messaging, and barcoding.

Author(s) affiliation: [Halvorsen, Ken; Wong, Wesley P.] Harvard Univ, Sch Med, Immune Dis Inst, Program Cellular & Mol Med, Boston, MA 02114 USA.

[Halvorsen, Ken; Wong, Wesley P.] Childrens Hosp, Boston, MA 02115 USA.

Reprint Address: Halvorsen, K (reprint author), Harvard Univ, Sch Med, Immune Dis Inst, Program Cellular & Mol Med, Boston, MA 02114 USA.

E-mail Author(s) affiliation: wong@idi.harvard.edu

Times Cited: 6

Number of references: 29

Tags: Applications - Cryptography/Information security, Synthetic biology

[BioCode: Two biologically compatible Algorithms for embedding data in non-coding and coding regions of DNA \(Ireland\) 2013](#)

Author(s): Haughton, D (Haughton, David); Balado, F (Balado, Felix)

Source: BMC BIOINFORMATICS Volume: 14 Article Number: 121 DOI: 10.1186/1471-2105-14-121 Published: APR 9 2013

ABSTRACT: The algorithms encode information in near optimal ways from a coding point of view, as we demonstrate by means of theoretical and empirical (in silico) analyses. Also, they are shown to encode information in a robust way, such that mutations have isolated effects. Furthermore, the preservation of codon statistics, while achieving a near-optimum embedding rate, implies that BioCode pcDNA is also a near-optimum first-order steganographic method.

Author(s) affiliation: [Haughton, David; Balado, Felix] Univ Coll Dublin, Sch Comp Sci & Informat, Belfield, Dublin, Ireland.

Reprint Address: Haughton, D (reprint author), Univ Coll Dublin, Sch Comp Sci & Informat, Belfield, Dublin, Ireland.

E-mail Author(s) affiliation: david.haughton@ucdconnect.ie

Times Cited: 7

Number of references: 29

Tags: Applications - Cryptography/Information security, Synthetic biology

continued

Chaos-based image encryption scheme combining DNA coding and entropy (China) 2016

Author(s): Zhen, P (Zhen, Ping); Zhao, G (Zhao, Geng); Min, LQ (Min, Lequan); Jin, X (Jin, Xin)

Source: MULTIMEDIA TOOLS AND APPLICATIONS Volume: 75 Issue: 11 Pages: 6303-6319 DOI: 10.1007/s11042-015-2573-x Published: JUN 2016

ABSTRACT: Information security has become more and more important issue in modern society, one of which is the digital image protection. In this paper, a secure image encryption scheme based on logistic and spatiotemporal chaotic systems is proposed. The extreme sensitivity of chaotic system can greatly increase the complexity of the proposed scheme. Further more, the scheme also takes advantage of DNA coding and eight DNA coding rules are mixed to enhance the efficiency of image confusion and diffusion. To resist the chosen-plaintext attack, information entropy of DNA coded image is modulated as the parameter of spatiotemporal chaotic system, which can also guarantee the sensitivity of plain image in the encryption process. So even a slight change in plain image can cause the complete change in cipher image. The experimental analysis shows that it can resistant different attacks, such as the brute-force attack, statistical attack and differential attack. What's more, The image encryption scheme can be easily implemented by software and is promising in practical application.

Author(s) affiliation: [Zhen, Ping; Min, Lequan] Univ Sci & Technol Beijing, Sch Automat & Elect Engn, Beijing 100083, Peoples R China.

[Zhao, Geng; Jin, Xin] Beijing Elect Sci & Technol Inst, Beijing 100070, Peoples R China.

Reprint Address: Zhen, P (reprint author), Univ Sci & Technol Beijing, Sch Automat & Elect Engn, Beijing 100083, Peoples R China.

Jin, X (reprint author), Beijing Elect Sci & Technol Inst, Beijing 100070, Peoples R China.

E-mail Author(s) affiliation: zhenping1989@126.com; zg@besti.edu.cn; minlequan@sina.com; jinxin@besti.edu.cn

Times Cited: 1

Number of references: 22

Tags: Applications - Cryptography/Information security, Synthetic biology

Color image encryption scheme using CML and DNA sequence operations (China) 2016

Author(s): Wang, XY (Wang, Xing-yuan); Zhang, HL (Zhang, Hui-li); Bao, XM (Bao, Xue-mei)

Source: BIOSYSTEMS Volume: 144 Pages: 18-26 DOI: 10.1016/j.biosystems.2016.03.011 Published: JUN 2016

ABSTRACT: In this paper, an encryption algorithm for color images using chaotic system and DNA (Deoxyribonucleic acid) sequence operations is proposed. Three components for the color plain image is employed to construct a matrix, then perform confusion operation on the pixels matrix generated by the spatiotemporal chaos system, i.e., CML (coupled map lattice). DNA encoding rules, and decoding rules are introduced in the permutation phase. The extended Hamming distance is proposed to generate new initial values for CML iteration combining color plain image. Permute the rows and columns of the DNA matrix and then get the color cipher image from this matrix. Theoretical analysis and experimental results prove the cryptosystem secure and practical, and it is suitable for encrypting color images of any size. (C) 2016 Elsevier Ireland Ltd. All rights reserved.

Author(s) affiliation: [Wang, Xing-yuan; Zhang, Hui-li; Bao, Xue-mei] Dalian Univ Technol, Fac Elect Informat & Elect Engn, Dalian 116024, Peoples R China.

Reprint Address: Wang, XY (reprint author), Dalian Univ Technol, Fac Elect Informat & Elect Engn, Dalian 116024, Peoples R China.

E-mail Author(s) affiliation: wangxy@dlut.edu.cn; zhanghui7873@foxmail.com; baoxueimei1989@163.com

Source Item Page Count: 9

Times Cited: 0

Number of references: 33

Tags: Applications - Cryptography/Information security, Synthetic biology

Design and synthesis of digitally encoded polymers that can be decoded and erased (France) 2015

Author(s): Roy, RK (Roy, Raj Kumar); Meszynska, A (Meszynska, Anna); Laure, C (Laure, Chloe); Charles, L (Charles, Laurence); Verchin, C (Verchin, Claire); Lutz, JF (Lutz, Jean-Francois)

Source: NATURE COMMUNICATIONS Volume: 6 Article Number: 7237 DOI: 10.1038/ncomms8237 Published: MAY 2015

ABSTRACT: Biopolymers such as DNA store information in their chains using controlled sequences of monomers. Here we describe a non-natural information-containing macromolecule that can store and retrieve digital information. Monodisperse sequence-encoded poly(alkoxyamine amide)s were synthesized using an iterative strategy employing two chemoselective steps: the reaction of a primary amine with an acid anhydride and the radical coupling of a carbon-centred radical with a nitroxide. A binary code was implemented in the polymer chains using three monomers: one nitroxide spacer and two interchangeable anhydrides defined as 0-bit and 1-bit. This methodology allows encryption of any desired sequence in the chains. Moreover, the formed sequences are easy to decode using tandem mass spectrometry. Indeed, these polymers follow predictable fragmentation pathways that can be easily deciphered. Moreover, poly(alkoxyamine amide) s are thermolabile. Thus, the digital information encrypted in the chains can be erased by heating the polymers in the solid state or in solution.

Author(s) affiliation: [Roy, Raj Kumar; Meszynska, Anna; Laure, Chloe; Verchin, Claire; Lutz, Jean-Francois] CNRS, Inst Charles Sadron, Precis Macromol Chem, UPR22, F-67034 Strasbourg 2, France.

[Charles, Laurence] Aix Marseille Univ, CNRS, Inst Rad Chem, UMR 7273, F-13397 Marseille 20, France.

Reprint Address: Lutz, JF (reprint author), CNRS, Inst Charles Sadron, Precis Macromol Chem, UPR22, BP84047,23 Rue Loess, F-67034 Strasbourg 2, France.

E-mail Author(s) affiliation: jflutz@unistra.fr

Times Cited: 29

Number of references: 41

Tags: Applications - Cryptography/Information security, Synthetic biology

DNA-LCEB: a high-capacity and mutation-resistant DNA data-hiding approach by employing encryption, error correcting codes, and hybrid twofold and fourfold codon-based strategy for synonymous substitution in amino acids (Finland) 2014

Author(s): Hafeez, I (Hafeez, Ibbad); Khan, A (Khan, Asifullah); Qadir, A (Qadir, Abdul)

Source: MEDICAL & BIOLOGICAL ENGINEERING & COMPUTING Volume: 52 Issue: 11 Pages: 945-961 DOI: 10.1007/s11517-014-1194-2 Published: NOV 2014

ABSTRACT: Data-hiding in deoxyribonucleic acid (DNA) sequences can be used to develop an organic memory and to track parent genes in an offspring as well as in genetically modified organism. However, the main concerns regarding data-hiding in DNA sequences are the survival of organism and successful extraction of watermark from DNA. This implies that the organism should live and reproduce without any functional disorder even in the presence of the embedded data. Consequently, performing synonymous substitution in amino acids for watermarking becomes a primary option. In this regard, a hybrid watermark embedding strategy that employs synonymous substitution in both twofold and fourfold codons of amino acids is proposed. This work thus presents a high-capacity and mutation-resistant watermarking technique, DNA-LCEB, for hiding secret information in DNA of living organisms. By employing the different types of synonymous codons of amino acids, the data storage capacity has been significantly increased. It is further observed that the proposed DNA-LCEB employing a combination of synonymous substitution, lossless compression, encryption, and Bose-Chaudary-Hocquenghem coding is secure and performs better in terms of both capacity and robustness compared to existing DNA data-hiding schemes. The proposed DNA-LCEB is tested against different mutations, including silent, miss-sense, and non-sense mutations, and provides substantial improvement in terms of mutation detection/correction rate and bits per nucleotide. A web application for DNA-LCEB is available at <http://111.68.99.218/DNA-LCEB>.

Author(s) affiliation: [Hafeez, Ibbad] Univ Helsinki, Dept Comp Sci, SF-00510 Helsinki, Finland.

[Hafeez, Ibbad; Khan, Asifullah; Qadir, Abdul] PIEAS, Dept Comp & Informat Sci, Islamabad, Pakistan.

Reprint Address: Khan, A (reprint author), PIEAS, Dept Comp & Informat Sci, Islamabad, Pakistan.

E-mail Author(s) affiliation: asif@pieas.edu.pk

Source Item Page Count: 17

Times Cited: 0

Number of references: 35

Tags: Applications - Cryptography/Information security, Synthetic biology

An efficient and noise resistive selective image encryption scheme for gray images based on chaotic maps and DNA complementary rules (China) 2016

Author(s): Kulsoom, A (Kulsoom, Ayesha); Xiao, D (Xiao, Di); Aqeel-Ur-Rehman (Aqeel-Ur-Rehman); Abbas, SA (Abbas, Syed Ali)

Source: MULTIMEDIA TOOLS AND APPLICATIONS Volume: 75 Issue: 1 Pages: 1-23 DOI: 10.1007/s11042-014-2221-x Published: JAN 2016

ABSTRACT: A novel image encryption algorithm in streaming mode is proposed which exhaustively employs an entire set of DNA complementary rules alongwith one dimensional chaotic maps. The proposed algorithm is highly efficient due to encrypting the subset of digital image which contains 92.125 % of information. DNA addition operation is carried out on this MSB part. The core idea of the proposed scheme is to scramble the whole image by means of piecewise linear chaotic map (PWLCM) followed by decomposition of image into most significant bits (MSB) and least significant bits (LSB). The logistic sequence is XORed with the decoded MSB and LSB parts separately and finally these two parts are combined to get the ciphered image. The parameters for PWLCM, logistic map and selection of different DNA rules for encoding and decoding of both parts of an image are derived from 128-bit MD5 hash of the plain image. Simulated experimental results in terms of quantitative and qualitative ways prove the encryption quality. Efficiency and robustness against different noises make the proposed cipher a good candidate for real time applications.

Author(s) affiliation: [Kulsoom, Ayesha; Xiao, Di; Aqeel-Ur-Rehman; Abbas, Syed Ali] Chongqing Univ, Coll Comp Sci & Engr, Chongqing 630044, Peoples R China.

Reprint Address: Kulsoom, A (reprint author), Chongqing Univ, Coll Comp Sci & Engr, Chongqing 630044, Peoples R China.

E-mail Author(s) affiliation: ayeshakhattak1@yahoo.com

Source Item Page Count: 23

Times Cited: 3

Number of references: 42

Tags: Applications - Cryptography/Information security, Synthetic biology

An Encryption Scheme Based on DNA Microdots Technology (China) 2015

Author(s): Cui, GZ (Cui, Guangzhao); Wang, Y (Wang, Yan); Han, D (Han, Dong); Wang, YF (Wang, Yanfeng); Wang, ZC (Wang, Zicheng); Wu, YM (Wu, Yanmin)

Source: JOURNAL OF COMPUTATIONAL AND THEORETICAL NANOSCIENCE Volume: 12 Issue: 7 Special Issue: SI Pages: 1434-1439 DOI: 10.1166/jctn.2015.3909 Published: JUL 2015

ABSTRACT: As a new research area of information security, DNA cryptography has achieved rapid advancements over recent years. It has been demonstrated that data hiding and encryption can be realized based on DNA digital encoding and microdots steganographic techniques. Here we present a more secure encryption scheme utilizing DNA microdots. It is noteworthy that the scheme achieves double concealing, which combines the properties of traditional cryptography and DNA microdots. The security of the scheme is analyzed from several aspects as well. Finally, the simulation proved a strong confidentiality of the encryption scheme.

Author(s) affiliation: [Cui, Guangzhao; Wang, Yan; Han, Dong; Wang, Yanfeng; Wang, Zicheng; Wu, Yanmin] Zhengzhou Univ Light Ind, Coll Elect & Informat Engn, Zhengzhou 450002, Henan, Peoples R China.

[Cui, Guangzhao; Wang, Zicheng] Zhengzhou Univ Light Ind, Henan Key Lab Informat Based Elect Appliances, Zhengzhou 450002, Henan, Peoples R China.

Reprint Address: Wang, ZC (reprint author), Zhengzhou Univ Light Ind, Coll Elect & Informat Engn, Zhengzhou 450002, Henan, Peoples R China.

Times Cited: 0

Number of references: 25

Tags: Applications - Cryptography/Information security, Synthetic biology

Hiding message into DNA sequence through DNA coding and chaotic maps (China) 2014

Author(s): Liu, GY (Liu, Guoyan); Liu, HJ (Liu, Hongjun); Kadir, A (Kadir, Abdurahman)

Source: MEDICAL & BIOLOGICAL ENGINEERING & COMPUTING Volume: 52 Issue: 9 Pages: 741-747 DOI: 10.1007/s11517-014-1177-3 Published: SEP 2014

ABSTRACT: The paper proposes an improved reversible substitution method to hide data into deoxyribonucleic acid (DNA) sequence, and four measures have been taken to enhance the robustness and enlarge the hiding capacity, such as encode the secret message by DNA coding, encrypt it by pseudo-random sequence, generate the relative hiding locations by piecewise linear chaotic map, and embed the encoded and encrypted message into a randomly selected DNA sequence using the complementary rule. The key space and the hiding capacity are analyzed. Experimental results indicate that the proposed method has a better performance compared with the competing methods with respect to robustness and capacity.

Author(s) affiliation: [Liu, Guoyan] Weifang Med Univ, Affiliated Hosp, Dept Dermatol, Weifang 261031, Peoples R China.

[Liu, Hongjun] Weifang Vocat Coll, Sch Informat Engn, Weifang 261041, Peoples R China.

[Kadir, Abdurahman] Xinjiang Univ Finance & Econ, Sch Comp Sci & Engn, Urumqi 830012, Peoples R China.

Reprint Address: Liu, HJ (reprint author), Weifang Vocat Coll, Sch Informat Engn, Weifang 261041, Peoples R China.

E-mail Author(s) affiliation: smithliu@126.com

Times Cited: 1

Number of references: 14

Tags: Applications - Cryptography/Information security, Synthetic biology

Image watermarking using chaotic map and DNA coding (China) 2015

Author(s): Wang, B (Wang, Bin); Zhou, SH (Zhou, Shihua); Zheng, XD (Zheng, Xuedong); Zhou, CJ (Zhou, Changjun); Dong, J (Dong, Jing); Zhao, LB (Zhao, Libo)

Source: OPTIK Volume: 126 Issue: 24 Pages: 4846-4851 DOI: 10.1016/j.ijleo.2015.09.217 Published: 2015

ABSTRACT: In this work, we propose a novel architecture of image watermarking using chaotic map and DNA coding. Firstly, two logistic chaotic maps are used to structure a secure architecture with embedding watermarking into the LSB (least significant bit) of cover image. Analyzing numerical experimental results and comparing with previous works show that the proposed architecture possesses higher security than previous works. Then the method of DNA coding is jointed into the architecture to improve the ER (embedding rate). It not only significantly increases the ER, but also accelerates the development of DNA-based watermarking. The improved architecture is suitable for protecting the copyright of cover image in DNA-based information security. (C) 2015 Elsevier GmbH. All rights reserved.

Author(s) affiliation: [Wang, Bin; Zhou, Shihua; Zheng, Xuedong; Zhou, Changjun; Dong, Jing; Zhao, Libo] Dalian Univ, Minist Educ,

Key Lab Adv Design & Intelligent Comp, Dalian 116622, Peoples R China.

Reprint Address: Wang, B (reprint author), Dalian Univ, Minist Educ, Key Lab Adv Design & Intelligent Comp, Dalian 116622, Peoples R China.

E-mail Author(s) affiliation: wangbinpaper@gmail.com

Times Cited: 0

Number of references: 40

Tags: Applications - Cryptography/Information security, Synthetic biology

An improved color image encryption based on multiple DNA sequence operations with DNA synthetic image and chaos (India) 2015

Author(s): Kalpana, J (Kalpana, J.); Murali, P (Murali, P.)

Source: OPTIK Volume: 126 Issue: 24 Pages: 5703-5709 DOI: 10.1016/j.ijleo.2015.09.091 Published: 2015

ABSTRACT: Image encryption is a useful solution to achieve confidentiality while transmitting digital images over unsecure public networks. Among recently proposed encryption schemes, a DNA-based approach Wei et al. (J. Syst. Softw. 85 (2012) 299) with good encryption effect has been reported. An effort has been made in this paper to improve its performance, by infusing more pseudo randomness into this algorithm. For this, three modifications have been suggested: (1) For each pixel of the color image, adoption of multiple DNA encoding rules as against a single rule in Wei et al. a. Syst. Softw. 85 (2012) 299); (2) multiple DNA operations instead of a single DNA operation as in [17] for diffusion of pixels and (3) combination of the image to be encrypted with another synthetic image as against combination with itself as in [17]. Here, the choice of DNA encoding rule, DNA operation and DNA synthetic image creation are all done based on the outcome of various chaotic maps and systems. The simulation results and security analysis show that our algorithm not only has a better encryption effect but also has a better ability of resisting statistical and differential attacks on comparison with the original proposal. (C) 2015 Elsevier GmbH. All rights reserved.

Author(s) affiliation: [Kalpana, J.; Murali, P.] JR Polytech Coll, Tiruchchirappalli, Tamil Nadu, India.

[Murali, P.] Anna Univ, Dept Comp Sci & Engn, Vis Lab, Tiruchchirappalli, Tamil Nadu, India.

Reprint Address: Kalpana, J (reprint author), JR Polytech Coll, Tiruchchirappalli, Tamil Nadu, India.

E-mail Author(s) affiliation: kalpanalak@gmail.com; pmurali_me@rediffmail.com

Times Cited: 0

Number of references: 28

Tags: Applications - Cryptography/Information security, Synthetic biology

An Improved Encryption Scheme Based on DNA Sequence (China) 2015

Author(s): Cui, GZ (Cui, Guangzhao); Han, D (Han, Dong); Wang, Y (Wang, Yan); Zhang, XC (Zhang, Xuncai); Wang, YF (Wang, Yanfeng); Wang, ZC (Wang, Zicheng)

Source: JOURNAL OF COMPUTATIONAL AND THEORETICAL NANOSCIENCE Volume: 12 Issue: 7 Special Issue: SI Pages: 1368-1372 DOI: 10.1166/jctn.2015.3899 Published: JUL 2015

ABSTRACT: A scheme utilizing DNA technology for the purposes of DNA cryptography has been developed. To enhance the security of DNA cryptosystem, we used DNA digital encoding, complementary rules and biotechnological methods in this scheme. The experimental result showed that the scheme is feasible and the security analysis indicated that the scheme has a strong confidentiality.

Author(s) affiliation: [Cui, Guangzhao; Han, Dong; Wang, Yan; Zhang, Xuncai; Wang, Yanfeng; Wang, Zicheng] Zhengzhou Univ Light Ind, Coll Elect & Informat Engn, Zhengzhou 450002, Henan, Peoples R China.

[Cui, Guangzhao; Zhang, Xuncai; Wang, Yanfeng; Wang, Zicheng] Zhengzhou Univ Light Ind, Henan Key Lab Informat Based Elect Appliances, Zhengzhou 450002, Henan, Peoples R China.

Reprint Address: Wang, ZC (reprint author), Zhengzhou Univ Light Ind, Coll Elect & Informat Engn, Zhengzhou 450002, Henan, Peoples R China.

Times Cited: 0

Number of references: 25

Tags: Applications - Cryptography/Information security, Synthetic biology

An Improved Level of Security for DNA Steganography Using Hyperelliptic Curve Cryptography (India) 2016

Author(s): Vijayakumar, P (Vijayakumar, P.); Vijayalakshmi, V (Vijayalakshmi, V.); Zayaraz, G (Zayaraz, G.)

Source: WIRELESS PERSONAL COMMUNICATIONS Volume: 89 Issue: 4 Pages: 1221-1242 DOI: 10.1007/s11277-016-3313-x Published: AUG 2016

ABSTRACT: This paper describes about existing steganographic based hiding methods using LSB techniques, RSA algorithm, DNA cryptography and DNA steganography, which is used to prevent copying, forgery and unauthorized access of videos, audios and images. Existing hiding methods had demerit of increased key size, computational cost, speed and size of the input. Thus the DNA steganography based Hyperelliptic Curve Cryptography (HECC) is proposed which provides a higher level of security to image file

and also assure the digital media security. The proposed HECC based DNA steganography is compared with traditional cryptographic techniques results in 30 and 42 % increased processing time for encryption process and decryption process respectively. Finally, the proposed scheme is compared with other traditional steganographic technique in terms of Mean Square Error, Peak Signal to Noise Ratio (PSNR), embedding capacity. From the simulation results, it is inferred that, the proposed steganographic method has, the less embedding capacity, high MSR and PSNR value compared with other steganographic methods.

Author(s) affiliation: [Vijayakumar, P; Vijayalakshmi, V] Pondicherry Engn Coll, Dept ECE, Pondicherry, India.

[Zayaraz, G.] Pondicherry Engn Coll, Dept CSE, Pondicherry, India.

Reprint Address: Vijayakumar, P (reprint author), Pondicherry Engn Coll, Dept ECE, Pondicherry, India.

E-mail Author(s) affiliation: Vijayrgcet@gmail.com; vvijizai@pec.edu; gzayaraz@pec.edu

Times Cited: 0

Number of references: 17

Tags: Applications - Cryptography/Information security, Synthetic biology

Information Hiding in Noncoding DNA for DNA Steganography (South Korea) 2015

Author(s): Santoso, KN (Santoso, Kevin Nathanael); Lee, SH (Lee, Suk-Hwan); Hwang, WJ (Hwang, Won-Joo); Kwon, KR (Kwon, Ki-Ryong)

Source: IEICE TRANSACTIONS ON FUNDAMENTALS OF ELECTRONICS COMMUNICATIONS AND COMPUTER SCIENCES Volume: E98A Issue: 7 Pages: 1529-1536 DOI: 10.1587/transfun.E98.A.1529 Published: JUL 2015

ABSTRACT: This paper presents an information hiding method for DNA steganography with which a massive amount of data can be hidden in a noncoding strand. Our method maps the encrypted data to the DNA sequence using a numerical mapping table, before concealing it in the noncoding sequence using a secret key comprising sector length and the random number generator's seed. Our encoding algorithm is sector-based and reference dependent. Using modular arithmetic, we created a unique binary-base translation for every sector. By conducting a simulation study, we showed that our method could preserve amino acid information, extract hidden data without reference to the host DNA sequence, and detect the position of mutation error. Experimental results verified that our method produced higher data capacity than conventional methods, with a bpn (bitper-nucleotide) value that ranged from approximately 1-2, depending on the selected sector length. Additionally, our novel method detected the positions of mutation errors by the presence of a parity base in each sector.

Author(s) affiliation: [Santoso, Kevin Nathanael; Kwon, Ki-Ryong] Pukyong Natl Univ, Dept IT Convergence & Applicat Engn, Seoul, South Korea.

[Lee, Suk-Hwan] Tongmyong Univ, Dept Informat Secur, Busan, South Korea.

[Hwang, Won-Joo] Inje Univ, Dept Informat & Commun Engn, Gimhae Si, South Korea.

Reprint Address: Kwon, KR (reprint author), Pukyong Natl Univ, Dept IT Convergence & Applicat Engn, Seoul, South Korea.

E-mail Author(s) affiliation: kev_nathanael@yahoo.com; skylee@tu.ac.kr; ichwang@inje.ac.kr; krkwon@pknu.ac.kr

Times Cited: 0

Number of references: 24

Tags: Applications - Cryptography/Information security, Synthetic biology

Message in a molecule (Israel) 2016

Author(s): Sarkar, T (Sarkar, Tanmay); Selvakumar, K (Selvakumar, Karuthapandi); Motiei, L (Motiei, Leila); Margulies, D (Margulies, David)

Source: NATURE COMMUNICATIONS Volume: 7 Article Number: 11374 DOI: 10.1038/ncomms11374 Published: MAY 2016

ABSTRACT: Since ancient times, steganography, the art of concealing information, has largely relied on secret inks as a tool for hiding messages. However, as the methods for detecting these inks improved, the use of simple and accessible chemicals as a means to secure communication was practically abolished. Here, we describe a method that enables one to conceal multiple different messages within the emission spectra of a unimolecular fluorescent sensor. Similar to secret inks, this molecular-scale messaging sensor (m-SMS) can be hidden on regular paper and the messages can be encoded or decoded within seconds using common chemicals, including commercial ingredients that can be obtained in grocery stores or pharmacies. Unlike with invisible inks, however, uncovering these messages by an unauthorized user is almost impossible because they are protected by three different defence mechanisms: steganography, cryptography and by entering a password, which are used to hide, encrypt or prevent access to the information, respectively.

Author(s) affiliation: [Sarkar, Tanmay; Selvakumar, Karuthapandi; Motiei, Leila; Margulies, David] Weizmann Inst Sci, Dept Organ Chem, IL-7610001 Rehovot, Israel.

Reprint Address: Margulies, D (reprint author), Weizmann Inst Sci, Dept Organ Chem, IL-7610001 Rehovot, Israel.

E-mail Author(s) affiliation: david.margulies@weizmann.ac.il

Times Cited: 0

Number of references: 64

Tags: Applications - Cryptography/Information security, Synthetic biology

Multiplexed Sequence Encoding: A Framework for DNA Communication (USA) 2016

Author(s): Zakeri, B (Zakeri, Bijan); Carr, PA (Carr, Peter A.); Lu, TK (Lu, Timothy K.)

Source: PLOS ONE Volume: 11 Issue: 4 Article Number: e0152774 DOI: 10.1371/journal.pone.0152774 Published: APR 6 2016

ABSTRACT: Synthetic DNA has great propensity for efficiently and stably storing non-biological information. With DNA writing and reading technologies rapidly advancing, new applications for synthetic DNA are emerging in data storage and communication. Traditionally, DNA communication has focused on the encoding and transfer of complete sets of information. Here, we explore the use of DNA for the communication of short messages that are fragmented across multiple distinct DNA molecules. We identified three pivotal points in a communication-data encoding, data transfer & data extraction-and developed novel tools to enable communication via molecules of DNA. To address data encoding, we designed DNA-based individualized keyboards (iKeys) to convert plaintext into DNA, while reducing the occurrence of DNA homopolymers to improve synthesis and sequencing processes. To address data transfer, we implemented a secret-sharing system-Multiplexed Sequence Encoding (MuSE)-that conceals messages between multiple distinct DNA molecules, requiring a combination key to reveal messages. To address data extraction, we achieved the first instance of chromatogram patterning through multiplexed sequencing, thereby enabling a new method for data extraction. We envision these approaches will enable more widespread communication of information via DNA.

Author(s) affiliation: [Zakeri, Bijan; Lu, Timothy K.] MIT, Dept Elect Engn & Comp Sci, Dept Biol Engn, Elect Res Lab, 77 Massachusetts Ave, Cambridge, MA 02139 USA.

[Carr, Peter A.] MIT, Lincoln Lab, 244 Wood St, Lexington, MA 02420 USA.

Reprint Address: Zakeri, B (reprint author), MIT, Dept Elect Engn & Comp Sci, Dept Biol Engn, Elect Res Lab, 77 Massachusetts Ave, Cambridge, MA 02139 USA.

Zakeri, B; Carr, PA (reprint author), MIT, Synthet Biol Ctr, 500 Technol Sq, Cambridge, MA 02139 USA.

Carr, PA (reprint author), MIT, Lincoln Lab, 244 Wood St, Lexington, MA 02420 USA.

E-mail Author(s) affiliation: bijan.zakeri@oxfordalumni.org; carr@ll.mit.edu

Times Cited: 0

Number of references: 24

Tags: Applications - Cryptography/Information security, Synthetic biology

A new RGB image encryption algorithm based on DNA encoding and elliptic curve Diffie-Hellman cryptography (India) 2016

Author(s): Kumar, M (Kumar, Manish); Iqbal, A (Iqbal, Akhlag); Kumar, P (Kumar, Pranjal)

Source: SIGNAL PROCESSING Volume: 125 Pages: 187-202 DOI: 10.1016/j.sigpro.2016.01.017 Published: AUG 2016

ABSTRACT: With the increasing use of media in communications, there is a need for image encryption for security against attacks. In this paper, we have proposed a new algorithm for image security using Elliptic Curve Cryptography (ECC) diversified with DNA encoding. The algorithm first encodes the RGB image using DNA encoding followed by asymmetric encryption based on Elliptic Curve Diffie-Hellman Encryption (ECDHE). The proposed algorithm is applied on standard test images for analysis. The analysis is performed on key spaces, key sensitivity, and statistical analysis. The results of the analysis conclude that the proposed algorithm can resist exhaustive attacks and is apt for practical applications. (C) 2016 Elsevier B.V. All rights reserved.

Author(s) affiliation: [Kumar, Manish; Kumar, Pranjal] Birla Inst Technol & Sci Pilani, Dept Math, Hyderabad Campus, Hyderabad 500078, Telangana, India.

[Iqbal, Akhlag] Cent Univ Punjab, Sch Basic & Appl Sci, Ctr Math & Stat, Bathinda 151001, Punjab, India.

Reprint Address: Kumar, M (reprint author), Birla Inst Technol & Sci Pilani, Dept Math, Hyderabad Campus, Hyderabad 500078, Telangana, India.

E-mail Author(s) affiliation: manish.math.bhu@gmail.com

Times Cited: 0

Number of references: 33

Tags: Applications - Cryptography/Information security, Synthetic biology

A novel chaos-based image encryption using DNA sequence operation and Secure Hash Algorithm SHA-2 (Tunisia) 2016

Author(s): Guesmi, R (Guesmi, R.); Farah, MAB (Farah, M. A. B.); Kachouri, A (Kachouri, A.); Samet, M (Samet, M.)

Source: NONLINEAR DYNAMICS Volume: 83 Issue: 3 Pages: 1123-1136 DOI: 10.1007/s11071-015-2392-7 Published: FEB 2016

ABSTRACT: In this paper, we propose a novel image encryption algorithm based on a hybrid model of deoxyribonucleic acid (DNA) masking, a Secure Hash Algorithm SHA-2 and the Lorenz system. Our study uses DNA sequences and operations and the chaotic Lorenz system to strengthen the cryptosystem. The significant advantages of this approach are improving the information entropy which is the most important feature of randomness, resisting against various typical attacks and getting good experimental results.

The theoretical analysis and experimental results show that the algorithm improves the encoding efficiency, enhances the security of the ciphertext and has a large key space and a high key sensitivity, and it is able to resist against the statistical and exhaustive attacks.

Author(s) affiliation: [Guesmi, R.; Farah, M. A. B.; Kachouri, A.; Samet, M.] Sfax Univ, Natl Engr Sch Sfax, Lab Elect & Informat Technol, BPW 3038, Sfax, Tunisia.

Reprint Address: Guesmi, R (reprint author), Sfax Univ, Natl Engr Sch Sfax, Lab Elect & Informat Technol, BPW 3038, Sfax, Tunisia.

E-mail Author(s) affiliation: ramzi.guesmi@gmail.com; med.farah@yahoo.fr; abdennaceur.kachouri@enis.rnu.tn; mounir.samet@enis.rnu.tn

Times Cited: 1

Number of references: 41

Tags: Applications - Cryptography/Information security, Synthetic biology

A novel text and image encryption method based on chaos theory and DNA computing (Iran) 2013

Author(s): Babaei, M (Babaei, Majid)

Source: NATURAL COMPUTING Volume: 12 Issue: 1 Special Issue: SI Pages: 101-107 DOI: 10.1007/s11047-012-9334-9

Published: MAR 2013

ABSTRACT: In today's world, the security of information is associated with valid and reliable encryption algorithms that we have used in our systems. Today, the latest methods for data encryption are based on DNA computing. In this paper, we consider a reliable data encryption algorithm (OTP) which is theoretically unbreakable, but it experiences some disadvantages in its algorithm. These drawbacks have prevented the common use of its scheme in modern cryptosystems. In this research, we include a logistic chaotic map as an input of OTP algorithm. So, the obtained result of 'Matlab Simulation' could prove the efficiency of proposed algorithm in image encryption. In addition to the cryptography of text files, we can propose an interesting encryption algorithm based on a chaotic selection between original message DNA strands and OTP DNA strands. Finally, the empirical results of our proposed algorithm will be compared with AES Open SSI algorithm.

Author(s) affiliation: Shahrood Univ Technol, Dept Comp Engr, Shahrood, Iran.

Reprint Address: Babaei, M (reprint author), Shahrood Univ Technol, Dept Comp Engr, Shahrood, Iran.

E-mail Author(s) affiliation: babae.majid@gmail.com

Times Cited: 12

Number of references: 19

Tags: Applications - Cryptography/Information security, Synthetic biology

A Resettable and Reprogrammable DNA-Based Security System To Identify Multiple Users with Hierarchy (China) 2014

Author(s): Li, HL (Li, Hailong); Hong, W (Hong, Wei); Dong, SJ (Dong, Shaojun); Liu, YQ (Liu, Yaqing); Wang, EK (Wang, Erkang)

Source: ACS NANO Volume: 8 Issue: 3 Pages: 2796-2803 DOI: 10.1021/nn406523y Published: MAR 2014

ABSTRACT: Molecular-level security devices have raised ever-increasing interest in recent years to protect data and information from illegal invasion. Prior molecular keypad locks have an output signal dependent upon not only the appropriate combination but also the exact sequence of inputs, but it cannot be reset or reprogrammed. Here, a DNA-based security system with reset and never-reported reprogram function is successfully developed in proof-of-principle, with which one can change the password in case that the system is cracked. The previous password becomes invalid in the reprogrammed security system. Interestingly, more than one password is designed to permit multiple users to access. By harnessing the intrinsic merit of the different passwords, the system can distinguish different user who is endowed with prior authority. The intelligent device is addressed on solid support and facilitates electronic processes, avoiding chemical accumulation in the system by simple removal of the electrode from the input solution and indicating a main avenue for its further development.

Author(s) affiliation: [Liu, Yaqing] Changchun Inst Appl Chem, State Key Lab Electroanalyt Chem, Changchun 130022, Peoples R China.

Chinese Acad Sci, Grad Sch, Beijing 100039, Peoples R China.

Reprint Address: Liu, YQ (reprint author), Changchun Inst Appl Chem, State Key Lab Electroanalyt Chem, Changchun 130022, Peoples R China.

E-mail Author(s) affiliation: yaqingliu@ciac.jl.cn; ekwang@ciac.jl.cn

Times Cited: 11

Number of references: 17

Tags: Applications - Cryptography/Information security, Synthetic biology

[A robust image encryption algorithm resistant to attacks using DNA and chaotic logistic maps \(India\) 2016](#)

Author(s): Jain, A (Jain, Anchal); Rajpal, N (Rajpal, Navin)

Source: MULTIMEDIA TOOLS AND APPLICATIONS Volume: 75 Issue: 10 Pages: 5455-5472 DOI: 10.1007/s11042-015-2515-7
Published: MAY 2016

ABSTRACT: An image encryption technique using DNA (Deoxyribonucleic acid) operations and chaotic maps has been proposed in this paper. Firstly, the input image is DNA encoded and a mask is generated by using 1D chaotic map. This mask is added with the DNA encoded image using DNA addition. Intermediate result is DNA complemented with the help of a complement matrix produced by two 1D chaotic maps. Finally, the resultant matrix is permuted using 2D chaotic map followed by DNA decoding to get the cipher image. Proposed technique is totally invertible and it can resist known plain text attack, statistical attacks and differential attacks.

Author(s) affiliation: [Jain, Anchal] Inderprastha Engn Coll, Dept Comp Sci & Engn, Ghaziabad, India.

[Rajpal, Navin] GGSIP Univ, Univ Sch Informat & Commun Technol, Delhi, India.

Reprint Address: Jain, A (reprint author), Inderprastha Engn Coll, Dept Comp Sci & Engn, Ghaziabad, India.

E-mail Author(s) affiliation: anchalresearch10@gmail.com; navin_rajpal@yahoo.com

Times Cited: 2

Number of references: 24

Tags: Applications - Cryptography/Information security, Synthetic biology

[A survey on reversible watermarking techniques for relational databases \(Pakistan\) 2015](#)

Author(s): Iftikhar, S (Iftikhar, Saman); Kamran, M (Kamran, M.); Anwar, Z (Anwar, Zahid)

Source: SECURITY AND COMMUNICATION NETWORKS Volume: 8 Issue: 15 Pages: 2580-2603 DOI: 10.1002/sec.1196
Published: OCT 2015

ABSTRACT: Over the past few years, reversible watermarking techniques for relational databases have been proposed to provide protection of ownership rights, data tempering, and data integrity. Mainly, these techniques ensure original data recovery from watermarked data, whereas irreversible watermarking schemes only protect ownership rights. This characteristic of reversible watermarking has emerged as a candidate solution for the protection of ownership rights of data, intolerable to modifications such as medical data, genetic data, credit card, and bank account data. The main objective of this paper is to make an extensive survey of the state-of-the-art in reversible watermarking techniques for relational databases to reflect recent research progress and to point out the key issues for future research. In order to analyze these techniques, a classification has been performed on the basis of (i) the extent of modifications introduced by the watermarking scheme in the underlying data and (ii) the robustness of the embedded watermark against malicious attacks. Copyright (c) 2015 John Wiley & Sons, Ltd.

Author(s) affiliation: [Iftikhar, Saman; Anwar, Zahid] Natl Univ Sci & Technol, Sch Elect Engn & Comp Sci, Islamabad, Pakistan.

[Kamran, M.] Comsat Inst Informat Technol, Wah Cantt, Pakistan.

Reprint Address: Iftikhar, S (reprint author), Natl Univ Sci & Technol, Sch Elect Engn & Comp Sci, Islamabad, Pakistan.

E-mail Author(s) affiliation: iftikhar.saman@gmail.com

Times Cited: 0

Number of references: 78

Tags: Applications - Cryptography/Information security, Synthetic biology

[Trichocyanines: a Red-Hair-Inspired Modular Platform for Dye-Based One-Time-Pad Molecular Cryptography \(Italy\) 2015](#)

Author(s): Leone, L (Leone, Loredana); Pezzella, A (Pezzella, Alessandro); Crescenzi, O (Crescenzi, Orlando); Napolitano, A (Napolitano, Alessandra); Barone, V (Barone, Vincenzo); d'Ischia, M (d'Ischia, Marco)

Source: CHEMISTRYOPEN Volume: 4 Issue: 3 Pages: 370-377 DOI: 10.1002/open.201402164 Published: JUN 2015

ABSTRACT: Current molecular cryptography (MoCryp) systems are almost exclusively based on DNA chemistry and reports of cryptography technologies based on other less complex chemical systems are lacking. We describe herein, as proof of concept, the prototype of the first asymmetric MoCryp system, based on an 8-compound set of a novel bioinspired class of cyanine-type dyes called trichocyanines. These novel acidichromic cyanine-type dyes inspired by red hair pigments were synthesized and characterized with the aid of density functional theory (DFT) calculations. Trichocyanines consist of a modular scaffold easily accessible via an expedient condensation of 3-phenyl- or 3-methyl-2H-1,4-benzothiazines with N-dimethyl- or o-methoxyhydroxy-substituted benzaldehyde or cinnamaldehyde derivatives. The eight representative members synthesized herein can be classified as belonging to two three-state systems tunable through four different control points. This versatile dye platform can generate an expandable palette of colors and appears to be specifically suited to implement an unprecedented single-use asymmetric molecular cryptography system. With this system, we intend to pioneer the translation of digital public-key cryptography into a chemical-coding one-time-pad-like system.

Author(s) affiliation: [Leone, Loredana; Pezzella, Alessandro; Crescenzi, Orlando; Napolitano, Alessandra; d'Ischia, Marco] Univ

Naples Federico II, Dept Chem Sci, I-80126 Naples, Italy.

[Barone, Vincenzo] Scuola Normale Super Pisa, I-56126 Pisa, Italy.

Reprint Address: Leone, L (reprint author), Univ Naples Federico II, Dept Chem Sci, Via Cintia 4, I-80126 Naples, Italy.

E-mail Author(s) affiliation: alesnapo@unina.it

Times Cited: 0

Number of references: 45

Tags: Applications - Cryptography/Information security, Synthetic biology

'Yeast Mail' : A Novel Saccharomyces Application (NSA) to Encrypt Messages (Germany) 2014

Author(s): Rosemeyer, H (Rosemeyer, Helmut); Paululat, A (Paululat, Achim); Heinisch, JJ (Heinisch, Juergen J.)

Source: CHEMISTRY & BIODIVERSITY Volume: 11 Issue: 9 Pages: 1364-1373 DOI: 10.1002/cbdv.201400160 Published: SEP 2014

ABSTRACT: Here, we describe an experimental system to stably integrate encrypted messages within the yeast genome using a polymerase chain reaction (PCR)-based, one-step homologous recombination system. Thus, DNA sequences encoding alphabetical and/or numerical information will be inherited by yeast propagation and can be sent in the form of dried yeast. Moreover, due to the availability of triple shuttle vectors, *Saccharomyces cerevisiae* can also be used as an intermediate construction device for transfer of information to either *Drosophila* or mammalian cells as steganographic containers. Besides its classical use in alcoholic fermentation and its modern use for heterologous gene expression, we here show that baker's yeast can thus be employed in a novel *Saccharomyces* application (NSA) as a simple steganographic container to hide and convey messages.

Author(s) affiliation: [Rosemeyer, Helmut] Univ Osnabruck, Inst Chem New Mat, D-49069 Osnabruck, Germany.

[Paululat, Achim] Univ Osnabruck, Dept Zool, D-49069 Osnabruck, Germany.

[Heinisch, Juergen J.] Univ Osnabruck, Dept Genet, D-49069 Osnabruck, Germany.

Reprint Address: Rosemeyer, H (reprint author), Univ Osnabruck, Inst Chem New Mat, Barbarastr 7, D-49069 Osnabruck, Germany.

E-mail Author(s) affiliation: Helmut.Rosemeyer@uos.de; Paululat@biologie.uni-osnabrueck.de; Heinisch@biologie.uni-osnabrueck.de

Times Cited: 0

Number of references: 20

Tags: Applications - Cryptography/Information security, Synthetic biology

Applications - Energy

2,3 Butanediol production in an obligate photoautotrophic cyanobacterium in dark conditions via diverse sugar consumption (USA) 2016

Author(s): McEwen, JT (McEwen, Jordan T.); Kanno, M (Kanno, Masahiro); Atsumi, S (Atsumi, Shota)

Source: METABOLIC ENGINEERING Volume: 36 Pages: 28-36 DOI: 10.1016/j.ymben.2016.03.004 Published: JUL 2016

ABSTRACT: Cyanobacteria are under investigation as a means to utilize light energy to directly recycle CO₂ into chemical compounds currently derived from petroleum. Any large-scale photosynthetic production scheme must rely on natural sunlight for energy, thereby limiting production time to only lighted hours during the day. Here, an obligate photoautotrophic cyanobacterium was engineered for enhanced production of 2,3-butanediol (23BD) in continuous light, 12 h:12 h light-dark diurnal, and continuous dark conditions via supplementation with glucose or xylose. This study achieved 23BD production under diurnal conditions comparable to production under continuous light conditions. The maximum 23BD titer was 3.0 g L⁻¹ in 10 d. Also achieving chemical production under dark conditions, this work enhances the feasibility of using Cyanobacteria as industrial chemical-producing microbes. (C) 2016 International Metabolic Engineering Society. Published by Elsevier Inc. All rights reserved.

Author(s) affiliation: [McEwen, Jordan T.; Kanno, Masahiro; Atsumi, Shota] Univ Calif Davis, Dept Chem, One Shields Ave, Davis, CA 95616 USA.

[Kanno, Masahiro] Asahi Kasei Corp, 2-1 Samejima, Fuji, Shizuoka 4168501, Japan.

Reprint Address: Atsumi, S (reprint author), Univ Calif Davis, Dept Chem, One Shields Ave, Davis, CA 95616 USA.

E-mail Author(s) affiliation: satsumi@ucdavis.edu

Times cited: 1

Number of references: 44

Tags: Applications - Energy, Synthetic biology

Advances in bioprocessing for efficient bio manufacture (China) 2015

Author(s): Zhang, GL (Zhang, Genlin); Qj, F (Qj, Feng); Jia, HY (Jia, Haiyang); Zou, CL (Zou, Changling); Li, C (Li, Chun)

Source: RSC ADVANCES Volume: 5 Issue: 65 Pages: 52444-52451 DOI: 10.1039/c5ra07699d Published: 2015

ABSTRACT: Bioprocesses use cost-effective renewable resources as feedstock to produce various products with less energy consumption under mild conditions. The technical progress in the modification of biocatalysts including enzymes and cells has significantly improved their efficiencies. In this article, the strategies involving molecular, cellular and community levels

for improving various bioprocesses are reviewed with specific examples presented. To modify of enzyme molecule to better fit biomanufacture, semi-rational design of enzyme molecules and intensification of substrate channelling have been proved as effective methods. Progress in metabolic engineering and synthetic biology has promoted engineering the intelligent microbial cell factories. Through modularization of non-native synthesis pathways, microbial cell factories can be optimized at whole cellular levels, and consequently achieved the efficient production of pharmaceuticals, biofuels and chemical compounds as well as natural products. The use of synergistic interactions in microbial communities would provide an opportunity to engineer more complex and robust functions. In addition, several special technologies including bioprocessing under microgravity conditions and nanobiotechnology provide novel ways for developing new applied areas and opportunity to improve bioprocess efficiency.

Author(s) affiliation: [Zhang, Genlin; Qi, Feng; Jia, Haiyang; Li, Chun] Beijing Inst Technol, Sch Life Sci, Beijing 100081, Peoples R China.

Reprint Address: Li, C (reprint author), Beijing Inst Technol, Sch Life Sci, Beijing 100081, Peoples R China.

E-mail Author(s) affiliation: lichun@bit.edu.cn

Times cited: 2

Number of references: 59

Tags: Applications - Energy, Synthetic biology

Better together: engineering and application of microbial symbioses (USA) 2015

Author(s): Hays, SG (Hays, Stephanie G.); Patrick, WG (Patrick, William G.); Ziesack, M (Ziesack, Marika); Oxman, N (Oxman, Neri); Silver, PA (Silver, Pamela A.)

Source: CURRENT OPINION IN BIOTECHNOLOGY Volume: 36 Pages: 40-49 DOI: 10.1016/j.copbio.2015.08.008 Published: DEC 2015

ABSTRACT: Symbioses provide a way to surpass the limitations of individual microbes. Natural communities exemplify this in symbioses like lichens and biofilms that are robust to perturbations, an essential feature in fluctuating environments. Metabolic capabilities also expand in consortia enabling the division of labor across organisms as seen in photosynthetic and methanogenic communities. In engineered consortia, the external environment provides levers of control for microbes repurposed from nature or engineered to interact through synthetic biology. Consortia have successfully been applied to real-world problems including remediation and energy, however there are still fundamental questions to be answered. It is clear that continued study is necessary for the understanding and engineering of microbial systems that are more than the sum of their parts.

Author(s) affiliation: [Hays, Stephanie G.; Ziesack, Marika; Silver, Pamela A.] Harvard Univ, Sch Med, Dept Syst Biol, Boston, MA 02115 USA.

[Patrick, William G.; Oxman, Neri] MIT, Media Lab, Sch Architecture & Planning, Cambridge, MA 02139 USA.

Reprint Address: Silver, PA (reprint author), Harvard Univ, Sch Med, Dept Syst Biol, 200 Longwood Ave, WAB 563, Boston, MA 02115 USA.

E-mail Author(s) affiliation: stephaniehays@fas.harvard.edu; pamela_silver@hms.harvard.edu

Times cited: 6

Number of references: 90

Tags: Applications - Energy, Synthetic biology

Biotechnological and bioinformatics approaches for augmentation of biohydrogen production: A review (India) 2016

Author(s): Kumar, GR (Kumar, Gopal Ramesh); Chowdhary, N (Chowdhary, Nupoor)

Source: RENEWABLE & SUSTAINABLE ENERGY REVIEWS Volume: 56 Pages: 1194-1206 DOI: 10.1016/j.rser.2015.12.022 Published: APR 2016

ABSTRACT: Biohydrogen production (BHP) from biomass is a characteristic feature of prokaryotes and is considered to be a vital source of renewable energy. It is considered as the cleanest fuel with no emanation of greenhouse gases on ignition. The major biological processes for hydrogen (H₂) production are: biophotolysis of water by algae and cyanobacteria, dark fermentation and photo-fermentation. For the past fifty years, lot of work has been carried out for understanding and improving BHP and still it has to overcome some of the serious limitations so that it becomes viable proposition. The bottlenecks include thermodynamic inefficiency, difficulty in using lignocellulosics as feed material, raw material cost and lower hydrogen yield. To overcome these major problems, the conventional approach is not enough and one has to vigorously think modern bioinformatics approaches to conquer them. The accessibility of huge sequenced genomes, functional genomics studies, the development of in silico models at the genome scale, metabolic pathway reconstruction, and synthetic biology approach predicts engineering strategies to enhance H₂ production in an organism. This review investigates the recent status and advancements that have been made in the area of biotechnology and bioinformatics, to understand and enhance the H₂ generation to overcome current limitations and make biohydrogen, a reality in near future. (C) 2015 Elsevier Ltd. All rights reserved.

Author(s) affiliation: [Kumar, Gopal Ramesh; Chowdhary, Nupoor] Anna Univ, Bioinformat Lab, AU KBC Res Ctr, MIT Campus, Chennai 600044, Tamil Nadu, India.

Reprint Address: Kumar, GR (reprint author), Anna Univ, Bioinformat Lab, AU KBC Res Ctr, MIT Campus, Chennai 600044, Tamil Nadu, India.

E-mail Author(s) affiliation: grameshpub@au-kbc.org

Times cited: 1

Number of references: 151

Tags: Applications - Energy, Synthetic biology

Cellular and molecular engineering of yeast *Saccharomyces cerevisiae* for advanced biobutanol production (Japan) 2016

Author(s): Kuroda, K (Kuroda, Kouichi); Ueda, M (Ueda, Mitsuyoshi)

Source: FEMS MICROBIOLOGY LETTERS Volume: 363 Issue: 3 Article Number: fnv247 DOI: [10.1093/femsle/fnv247](https://doi.org/10.1093/femsle/fnv247)

Published: FEB 2016

ABSTRACT: Butanol is an attractive alternative energy fuel owing to several advantages over ethanol. Among the microbial hosts for biobutanol production, yeast *Saccharomyces cerevisiae* has a great potential as a microbial host due to its powerful genetic tools, a history of successful industrial use, and its inherent tolerance to higher alcohols. Butanol production by *S. cerevisiae* was first attempted by transferring the 1-butanol-producing metabolic pathway from native microorganisms or using the endogenous Ehrlich pathway for isobutanol synthesis. Utilizing alternative enzymes with higher activity, eliminating competitive pathways, and maintaining cofactor balance achieved significant improvements in butanol production. Meeting future challenges, such as enhancing butanol tolerance and implementing a comprehensive strategy by high-throughput screening, would further elevate the biobutanol-producing ability of *S. cerevisiae* toward an ideal microbial cell factory exhibiting high productivity of biobutanol.

Author(s) affiliation: [Kuroda, Kouichi; Ueda, Mitsuyoshi] Kyoto Univ, Grad Sch Agr, Div Appl Life Sci, Sakyo Ku, Kyoto 6068502, Japan.

Reprint Address: Ueda, M (reprint author), Kyoto Univ, Grad Sch Agr, Sakyo Ku, Kyoto 6068502, Japan.

E-mail Author(s) affiliation: miueda@kais.kyoto-u.ac.jp

Times cited: 1

Number of references: 25

Tags: Applications - Energy, Synthetic biology

Computational Approaches for Microalgal Biofuel Optimization: A Review (United Arab Emirates) 2014

Author(s): Koussa, J (Koussa, Joseph); Chaiboonchoe, A (Chaiboonchoe, Amphun); Salehi-Ashtiani, K (Salehi-Ashtiani, Kourosh)

Source: BIOMED RESEARCH INTERNATIONAL Article Number: 649453 DOI: [10.1155/2014/649453](https://doi.org/10.1155/2014/649453) Published: 2014

ABSTRACT: The advent of next generation sequencing and other high throughput methods has led to a major increase in availability of biological data. Integration of such disparate data can help define the emergent metabolic system properties, which is of crucial importance in addressing biofuel production optimization. Herein, we review major computational tools and approaches developed and used in order to potentially identify target genes, pathways, and reactions of particular interest to biofuel production in algae. As the use of these tools and approaches has not been fully implemented in algal biofuel research, the aim of this review is to highlight the potential utility of these resources toward their future implementation in algal research.

Author(s) affiliation: [Salehi-Ashtiani, Kourosh] New York Univ Abu Dhabi, Div Sci & Math, Abu Dhabi, U Arab Emirates.

New York Univ Abu Dhabi, Ctr Genom & Syst Biol, Abu Dhabi, U Arab Emirates.

Reprint Address: Salehi-Ashtiani, K (reprint author), New York Univ Abu Dhabi, Div Sci & Math, POB 129188, Abu Dhabi, U Arab Emirates.

E-mail Author(s) affiliation: ksa3@nyu.edu

Times cited: 0

Number of references: 87

Tags: Applications - Energy, Synthetic biology

Cyanobacterial chassis engineering for enhancing production of biofuels and chemicals (China) 2016

Author(s): Gao, XY (Gao, Xinyan); Sun, T (Sun, Tao); Pei, GS (Pei, Guangsheng); Chen, L (Chen, Lei); Zhang, WW (Zhang, Weiwen)

Source: APPLIED MICROBIOLOGY AND BIOTECHNOLOGY Volume: 100 Issue: 8 Pages: 3401-3413 DOI: [10.1007/s00253-016-7374-2](https://doi.org/10.1007/s00253-016-7374-2) Published: APR 2016

ABSTRACT: To reduce dependence on fossil fuels and curb greenhouse effect, cyanobacteria have emerged as an important chassis candidate for producing biofuels and chemicals due to their capability to directly utilize sunlight and CO₂ as the sole energy and carbon sources, respectively. Recent progresses in developing and applying various synthetic biology tools have led to the successful constructions of novel pathways of several dozen green fuels and chemicals utilizing cyanobacterial chassis.

Meanwhile, it is increasingly recognized that in order to enhance productivity of the synthetic cyanobacterial systems, optimizing and engineering more robust and high-efficient cyanobacterial chassis should not be omitted. In recent years, numerous research studies have been conducted to enhance production of green fuels and chemicals through cyanobacterial chassis modifications involving photosynthesis, CO₂ uptake and fixation, products exporting, tolerance, and cellular regulation. In this article, we critically reviewed recent progresses and universal strategies in cyanobacterial chassis engineering to make it more robust and effective for bio-chemicals production.

Author(s) affiliation: [Gao, Xinyan; Sun, Tao; Pei, Guangsheng; Chen, Lei; Zhang, Weiwen] Tianjin Univ, Lab Synthet Microbiol, Sch Chem Engr & Technol, Tianjin 300072, Peoples R China.

Reprint Address: Chen, L (reprint author), Tianjin Univ, Lab Synthet Microbiol, Sch Chem Engr & Technol, Tianjin 300072, Peoples R China.

Chen, L (reprint author), Tianjin Univ, Minist Educ, Key Lab Syst Bioengn, Tianjin 300072, Peoples R China.

Chen, L (reprint author), Collaborat Innovat Ctr Chem Sci & Engr, SynBio Res Platform, Tianjin 300072, Peoples R China.

E-mail Author(s) affiliation: lchen@tju.edu.cn

Times cited: 0

Number of references: 139

Tags: Applications - Energy, Synthetic biology

Decoupling production from growth by magnesium sulfate limitation boosts de novo limonene production (Germany) 2016

Author(s): Willrodt, C (Willrodt, Christian); Hoschek, A (Hoschek, Anna); Buhler, B (Buehler, Bruno); Schmid, A (Schmid, Andreas); Julsing, MK (Julsing, Mattijs K.)

Source: BIOTECHNOLOGY AND BIOENGINEERING Volume: 113 Issue: 6 Pages: 1305-1314 DOI: 10.1002/bit.25883

Published: JUN 2016

ABSTRACT: Non-growing but metabolically active *E. coli* cells were evaluated in this study as alternative biocatalyst configurations to reduce energy and carbon loss towards biomass formation. The use of non-growing cells in an optimized fermentation medium resulted in more than fivefold increased specific limonene yields on cell dry weight and glucose, as compared to the traditional growing-cell-approach. Initially, the stability of the resting-cell activity was limited. This instability was overcome via the optimization of the minimal fermentation medium enabling high and stable limonene production rates for up to 8h and a high specific yield of 50mg limonene per gram cell dry weight. Omitting MgSO₄ from the fermentation medium was very promising to prohibit growth and allow high productivities. Applying a MgSO₄-limitation also improved limonene formation by growing cells during non-exponential growth involving a reduced biomass yield on glucose and a fourfold increase in specific limonene yields on biomass as compared to non-limited cultures. The control of microbial growth via the medium composition was identified as a key but yet underrated strategy for efficient isoprenoid production. *Biotechnol. Bioeng.* 2016;113: 1305-1314. (c) 2015 Wiley Periodicals, Inc.

Author(s) affiliation: [Willrodt, Christian; Schmid, Andreas] Helmholtz Ctr Environm Res UFZ, Dept Solar Mat, Leipzig, Germany.

Reprint Address: Schmid, A (reprint author), Helmholtz Ctr Environm Res UFZ, Dept Solar Mat, Leipzig, Germany.

E-mail Author(s) affiliation: andreas.schmid@ufz.de

Times cited: 1

Number of references: 55

Tags: Applications - Energy, Synthetic biology

Engineering biofuel tolerance in non-native producing microorganisms (China) 2014

Author(s): Jin, H (Jin, Hu); Chen, L (Chen, Lei); Wang, JX (Wang, Jiangxin); Zhang, WW (Zhang, Weiwen)

Source: BIOTECHNOLOGY ADVANCES Volume: 32 Issue: 2 Pages: 541-548 DOI: 10.1016/j.biotechadv.2014.02.001

Published: MAR-APR 2014

ABSTRACT: Compared to native producers, these non-native systems carry the advantages of fast growth, simple nutrient requirements, readiness for genetic modifications, and even the capability to assimilate CO₂ and solar energy, making them competitive alternative systems to further decrease the biofuel production cost. However, the tolerance of these non-native microorganisms to toxic biofuels is naturally low, which has restricted the potentials of their application for high-efficiency biofuel production. To address the issues, researches have been recently conducted to explore the biofuel tolerance mechanisms and to construct robust high-tolerance strains for non-native biofuel-producing microorganisms. In this review, we critically summarize the recent progress in this area, focusing on three popular non-native biofuel-producing systems, i.e. *Escherichia coli*, *Lactobacillus* and photosynthetic cyanobacteria. (C) 2014 Elsevier Inc. All rights reserved.

Author(s) affiliation: [Zhang, Weiwen] Tianjin Univ, Sch Chem Engr & Technol, Lab Synthet Microbiol, Tianjin 300072, Peoples R China.

Minist Educ, Key Lab Syst Bioengn, Tianjin 300072, Peoples R China.

Collaborat Innovat Ctr Chem Sci & Engr, Tianjin, Peoples R China.

Reprint Address: Zhang, WW (reprint author), Tianjin Univ, Sch Chem Engn & Technol, Lab Synthet Microbiol, Tianjin 300072, Peoples R China.

E-mail Author(s) affiliation: wwzhang8@tju.edu.cn

Times cited: 19

Number of references: 128

Tags: Applications - Energy, Synthetic biology

From cyanochemicals to cyanofactories: a review and perspective (China) 2016

Author(s): Zhou, J (Zhou, Jie); Zhu, TC (Zhu, Taicheng); Cai, Z (Cai, Zhen); Li, Y (Li, Yin)

Source: MICROBIAL CELL FACTORIES Volume: 15 Article Number: 2 DOI: 10.1186/s12934-015-0405-3 Published: JAN 8 2016

ABSTRACT: Engineering cyanobacteria for production of chemicals from solar energy, CO₂ and water is a potential approach to address global energy and environment issues such as greenhouse effect. To date, more than 20 chemicals have been synthesized by engineered cyanobacteria using CO₂ as raw materials, and these studies have been well reviewed. However, unlike heterotrophic microorganisms, the low CO₂ fixation rate makes it a long way to go from cyanochemicals to cyanofactories. Here we review recent progresses on improvement of carbon fixation and redistribution of intercellular carbon flux, and discuss the challenges for developing cyanofactories in the future.

Author(s) affiliation: [Zhou, Jie; Zhu, Taicheng; Cai, Zhen; Li, Yin] Chinese Acad Sci, Inst Microbiol, CAS Key Lab Microbial Physiol & Metab Engn, Beijing 100101, Peoples R China.

Reprint Address: Li, Y (reprint author), Chinese Acad Sci, Inst Microbiol, CAS Key Lab Microbial Physiol & Metab Engn, 1 West Beichen Rd, Beijing 100101, Peoples R China.

E-mail Author(s) affiliation: yli@im.ac.cn

Times cited: 0

Number of references: 77

Tags: Applications - Energy, Synthetic biology

Frontiers in microbial 1-butanol and isobutanol production (USA) 2016

Author(s): Chen, CT (Chen, Chang-Ting); Liao, JC (Liao, James C.)

Source: FEMS MICROBIOLOGY LETTERS Volume: 363 Issue: 5 Article Number: fnw020 DOI: 10.1093/femsle/fnw020 Published: MAR 2016

ABSTRACT: The heavy dependence on petroleum-derived fuel has raised concerns about energy sustainability and climate change, which have prompted researchers to explore fuel production from renewable sources. 1-Butanol and isobutanol are promising biofuels that have favorable properties and can also serve as solvents or chemical feedstocks. Microbial production of these alcohols provides great opportunities to access a wide spectrum of renewable resources. In recent years, research has improved the native 1-butanol production and has engineered isobutanol production in various organisms to explore metabolic diversity and a broad range of substrates. This review focuses on progress in metabolic engineering for the production of these two compounds using various resources.

Author(s) affiliation: [Chen, Chang-Ting; Liao, James C.] Univ Calif Los Angeles, Dept Chem & Biomol Engn, 420 Westwood Plaza, Los Angeles, CA 90095 USA.

Reprint Address: Liao, JC (reprint author), Univ Calif Los Angeles, Dept Chem & Biomol Engn, 420 Westwood Plaza, Los Angeles, CA 90095 USA.

E-mail Author(s) affiliation: liaoj@ucla.edu

Times cited: 1

Number of references: 86

Tags: Applications - Energy, Synthetic biology

Genetic resources for advanced biofuel production described with the Gene Ontology (USA) 2014

Author(s): Torto-Alalibo, T (Torto-Alalibo, Trudy); Purwantini, E (Purwantini, Endang); Lomax, J (Lomax, Jane); Setubal, JC (Setubal, Joao C.); Mukhopadhyay, B (Mukhopadhyay, Biswarup); Tyler, BM (Tyler, Brett M.)

Source: FRONTIERS IN MICROBIOLOGY Volume: 5 Article Number: 528 DOI: 10.3389/fmicb.2014.00528 Published: OCT 10 2014

ABSTRACT: The Microbial ENergy processes Gene Ontology (<http://www.mengo.biochem.vt.edu>) project is extending the GO to include new terms to describe microbial processes of interest to bioenergy production. Our effort has added over 600 bioenergy related terms to the Gene Ontology. These terms will aid in the comprehensive annotation of gene products from diverse energy-related microbial genomes. An area of microbial energy research that has received a lot of attention is microbial production of advanced biofuels. These include alcohols such as butanol, isopropanol, isobutanol, and fuels derived from fatty acids, isoprenoids, and polyhydroxyalkanoates. These fuels are superior to first generation biofuels (ethanol and biodiesel esterified from vegetable oil or animal fat), can be generated from non-food feedstock sources, can be used as supplements or substitutes for gasoline,

diesel and jet fuels, and can be stored and distributed using existing infrastructure. Here we review the roles of genes associated with synthesis of advanced biofuels, and at the same time introduce the use of the GO to describe the functions of these genes in a standardized way.

Author(s) affiliation: [Torto-Alalibo, Trudy; Purwantini, Endang; Mukhopadhyay, Biswarup] Virginia Polytech Inst & State Univ, Dept Biochem, Blacksburg, VA 24061 USA.

Reprint Address: Tyler, BM (reprint author), Oregon State Univ, Ctr Genome Res & Biocomp, 4750 Campus Way ALS3021, Corvallis, OR 97331 USA.

E-mail Author(s) affiliation: brett.tyler@oregonstate.edu

Times cited: 4

Number of references: 155

Tags: Applications - Energy, Synthetic biology

Microalgal bioengineering for sustainable energy development: Recent transgenesis and metabolic engineering strategies (India) 2016

Author(s): Banerjee, C (Banerjee, Chiranjib); Singh, PK (Singh, Puneet Kumar); Shukla, P (Shukla, Pratyosh)

Source: BIOTECHNOLOGY JOURNAL Volume: 11 Issue: 3 Special Issue: SI DOI: 10.1002/biot.201500284 Published: MAR 2016

ABSTRACT: Exploring the efficiency of algae to produce remarkable products can be directly benefitted by studying its mechanism at systems level. Recent advents in biotechnology like flux balance analysis (FBA), genomics and in silico proteomics minimize the wet lab exertion. It is understood that FBA predicts the metabolic products, metabolic pathways and alternative pathway to maximize the desired product, and these are key components for microalgae bio-engineering. This review encompasses recent transgenesis techniques and metabolic engineering strategies applied to different microalgae for improving different traits. Further it also throws light on RNAi and riboswitch engineering based methods which may be advantageous for high throughput microalgal research. A valid and optimally designed microalga can be developed where every engineering strategies meet each other successfully and will definitely fulfill the market needs. It is also to be noted that Omics (viz. genetic and metabolic manipulation with bioinformatics) should be integrated to develop a strain which could prove to be a futuristic solution for sustainable development for energy.

Author(s) affiliation: [Banerjee, Chiranjib] Indian Sch Mines, Dept Environm Sci & Engn, Dhanbad 826004, Bihar, India.

[Singh, Puneet Kumar; Shukla, Pratyosh] Maharshi Dayanand Univ, Dept Microbiol, Enzyme Technol & Prot Bioinformat Lab, Rohtak 124001, Haryana, India.

Reprint Address: Shukla, P (reprint author), Maharshi Dayanand Univ, Dept Microbiol, Enzyme Technol & Prot Bioinformat Lab, Rohtak 124001, Haryana, India.

E-mail Author(s) affiliation: pratyosh.shukla@gmail.com

Times cited: 2

Number of references: 81

Tags: Applications - Energy, Synthetic biology

Modular and selective biosynthesis of gasoline-range alkanes (USA) 2016

Author(s): Sheppard, MJ (Sheppard, Micah J.); Kunjapur, AM (Kunjapur, Aditya M.); Prather, KLJ (Prather, Kristala L. J.)

Source: METABOLIC ENGINEERING Volume: 33 Pages: 28-40 DOI: 10.1016/j.ymben.2015.10.010 Published: JAN 2016

ABSTRACT: Our modular pathway framework achieves carbon-chain extension by two different mechanisms. A fatty acid synthesis route is used to generate longer chains heptane and nonane, while a more energy efficient alternative, reverse-beta-oxidation, is used for synthesis of propane, butane, and pentane. We demonstrate that both upstream (thiolase) and intermediate (thioesterase) reactions can act as control points for chain-length specificity. Specific free fatty acids are subsequently converted to alkanes using a broad-specificity carboxylic acid reductase and a cyanobacterial aldehyde decarbonylase (AD). The selectivity obtained by different module pairings provides a foundation for tuning alkane product distribution for desired fuel properties. Alternate ADs that have greater activity on shorter substrates improve observed alkane titer. However, even in an engineered host strain that significantly reduces endogenous conversion of aldehyde intermediates to alcohol byproducts, AD activity is observed to be limiting for all chain lengths. Given these insights, we discuss guiding principles for pathway selection and potential opportunities for pathway improvement. (C) 2015 International Metabolic Engineering Society. Published by Elsevier Inc. All rights reserved.

Author(s) affiliation: [Sheppard, Micah J.; Kunjapur, Aditya M.; Prather, Kristala L. J.] MIT, Dept Chem Engn, Cambridge, MA 02139 USA.

[Kunjapur, Aditya M.; Prather, Kristala L. J.] MIT, Synthet Biol Engn Res Ctr SynBERC, Cambridge, MA 02139 USA.

Reprint Address: Prather, KLJ (reprint author), MIT, Dept Chem Engn, Cambridge, MA 02139 USA.

Times cited: 0

Number of references: 71

Tags: Applications - Energy, Synthetic biology

Rationally Engineered Synthetic Coculture for Improved Biomass and Product Formation (Finland) 2014

Author(s): Santala, S (Santala, Suvi); Karp, M (Karp, Matti); Santala, V (Santala, Ville)

Source: PLOS ONE Volume: 9 Issue: 12 Article Number: e113786 DOI: 10.1371/journal.pone.0113786 Published: DEC 3 2014

ABSTRACT: In this study, a rationally engineered coculture with a carbon channeling system was constructed using two well-characterized model strains *Escherichia coli* K12 and *Acinetobacter baylyi* ADP1. The directed carbon flow resulted in efficient acetate removal, and the coculture showed symbiotic nature in terms of substrate utilization and growth. Recombinant protein production was used as a proof-of-principle example to demonstrate the coculture utility and the effects on product formation. As a result, the biomass and recombinant protein titers of *E. coli* were enhanced in both minimal and rich medium simple batch cocultures. Finally, harnessing both the strains to the production resulted in enhanced recombinant protein titers. The study demonstrates the potential of rationally engineered cocultures for synthetic biology applications.

Author(s) affiliation: [Santala, Suvi; Karp, Matti; Santala, Ville] Tampere Univ Technol, Dept Chem & Bioengn, FIN-33101 Tampere, Finland.

Reprint Address: Santala, S (reprint author), Tampere Univ Technol, Dept Chem & Bioengn, FIN-33101 Tampere, Finland.

E-mail Author(s) affiliation: suvi.santala@tut.fi

Times cited: 2

Number of references: 36

Tags: Applications - Energy, Synthetic biology

Recent advances and challenges of the use of cyanobacteria towards the production of biofuels (France) 2016

Author(s): Singh, V (Singh, Vijai); Chaudhary, DK (Chaudhary, Dharmendra Kumar); Mani, I (Mani, Indra); Dhar, PK (Dhar, Pawan Kumar)

Source: RENEWABLE & SUSTAINABLE ENERGY REVIEWS Volume: 60 Pages: 1-10 DOI: 10.1016/j.rser.2016.01.099 Published: JUL 2016

ABSTRACT: Higher oil prices and the necessity for long-term energy security have increased the public and scientific attention on the production of biofuels. Bioenergy is much cleaner, safer, and more economical source of energy than fossil-based fuels. Of several organisms, cyanobacteria are attractive source of biofuels because of their genetic tractability, photosynthetic capability and lack of dependency on fertile land. Synthetic biology and metabolic engineering approaches have been successfully used towards the production of biofuels including ethanol, butanol, biodiesel and hydrogen. This review highlights the recent advances of pathway engineering and uses of synthetic biology tools in cyanobacteria for the production of economical and ecologically biofuels. (C) 2016 Elsevier Ltd. All rights reserved.

Author(s) affiliation: [Singh, Vijai] Univ Evry Val Essonne, Inst Syst & Synthet Biol, Synth Bio Grp, Genopole Campus 1, Batiment Genavenir 6, F-91030 Evry, France.

[Chaudhary, Dharmendra Kumar] Babasahab Bhimrao Ambedkar Cent Univ, Dept Nucl Med, Rai Bareilly Rd, Lucknow 226025, Uttar Pradesh, India.

[Mani, Indra] Tulane Univ, Hlth Sci Ctr, Dept Physiol, 1430 Tulane Ave, New Orleans, LA 70112 USA.

Reprint Address: Singh, V (reprint author), Univ Evry Val Essonne, Inst Syst & Synthet Biol, Synth Bio Grp, Genopole Campus 1, Batiment Genavenir 6, F-91030 Evry, France.

E-mail Author(s) affiliation: vijaisingh15@gmail.com

Times cited: 0

Number of references: 104

Tags: Applications - Energy, Synthetic biology

Recent Progress on Systems and Synthetic Biology Approaches to Engineer Fungi As Microbial Cell Factories (Brazil) 2016

Author(s): Amores, GR (Amores, Gerardo Ruiz); Guazzaroni, ME (Guazzaroni, Maria-Eugenia); Arruda, LM (Arruda, Leticia Magalhaes); Silva-Rocha, R (Silva-Rocha, Rafael)

Source: CURRENT GENOMICS Volume: 17 Issue: 2 Pages: 85-98 DOI: 10.2174/1389202917666151116212255 Published: 2016

ABSTRACT: In this review, we discuss some aspects related to significant progress in the understating and engineering of fungi for biotechnological applications, with special focus on the construction of synthetic promoters and circuits in organisms relevant for industry. Different engineering approaches are shown, and their potential and limitations for the construction of complex synthetic circuits in these organisms are examined. Finally, we discuss the impact of engineered promoter architecture in the single-cell behavior of the system, an often-neglected relationship with a tremendous impact in the final performance of the process of interest. We expect to provide here some new directions to drive future research directed to the construction of high-performance, engineered fungal strains working as microbial cell factories.

continued

Author(s) affiliation: [Amores, Gerardo Ruiz; Arruda, Leticia Magalhaes; Silva-Rocha, Rafael] Univ Sao Paulo, FMRP, Ave Bandeirantes 3-900, BR-14049900 Ribeirao Preto, SP, Brazil.

[Guazzaroni, Maria-Eugenia] Univ Sao Paulo, FFCLRP, BR-14049900 Ribeirao Preto, SP, Brazil.

Reprint Address: Silva-Rocha, R (reprint author), Univ Sao Paulo, FMRP, Ave Bandeirantes 3-900, BR-14049900 Ribeirao Preto, SP, Brazil.

E-mail Author(s) affiliation: silvarochar@gmail.com

Times cited: 0

Number of references: 164

Tags: Applications - Energy, Synthetic biology

Synthetic biology for microbial production of lipid-based biofuels (USA) 2015

Author(s): d'Espaux, L (d'Espaux, Leo); Mendez-Perez, D (Mendez-Perez, Daniel); Li, R (Li, Rachel); Keasling, JD (Keasling, Jay D.)

Source: CURRENT OPINION IN CHEMICAL BIOLOGY Volume: 29 Pages: 58-65 DOI: 10.1016/j.cbpa.2015.09.009 Published: DEC 2015

ABSTRACT: The risks of maintaining current CO₂ emission trends have led to interest in producing biofuels using engineered microbes. Microbial biofuels reduce emissions because CO₂ produced by fuel combustion is offset by CO₂ captured by growing biomass, which is later used as feedstock for biofuel fermentation. Hydrocarbons found in petroleum fuels share striking similarity with biological lipids. Here we review synthetic metabolic pathways based on fatty acid and isoprenoid metabolism to produce alkanes and other molecules suitable as biofuels. We further discuss engineering strategies to optimize engineered biosynthetic routes, as well as the potential of synthetic biology for sustainable manufacturing.

Author(s) affiliation: [d'Espaux, Leo; Mendez-Perez, Daniel; Li, Rachel; Keasling, Jay D.] Lawrence Berkeley Natl Lab, Joint BioEnergy Inst, Emeryville, CA 94608 USA.

[Li, Rachel; Keasling, Jay D.] Univ Calif Berkeley, Dept Plant & Microbial Biol, Berkeley, CA 94270 USA.

[Keasling, Jay D.] Univ Calif Berkeley, Dept Chem & Biomol Engr, Inst QB3, Berkeley, CA 94270 USA.

Reprint Address: Keasling, JD (reprint author), Lawrence Berkeley Natl Lab, Joint BioEnergy Inst, Emeryville, CA 94608 USA.

E-mail Author(s) affiliation: jdkeasling@lbl.gov

Times cited: 1

Number of references: 71

Tags: Applications - Energy, Synthetic biology

Synthetic methylotrophy: engineering the production of biofuels and chemicals based on the biology of aerobic methanol utilization (USA) 2015

Author(s): Whitaker, WB (Whitaker, William B.); Sandoval, NR (Sandoval, Nicholas R.); Bennett, RK (Bennett, Robert K.); Fast, AG (Fast, Alan G.); Papoutsakis, ET (Papoutsakis, Eleftherios T.)

Source: CURRENT OPINION IN BIOTECHNOLOGY Volume: 33 Pages: 165-175 DOI: 10.1016/j.copbio.2015.01.007 Published: JUN 2015

ABSTRACT: Synthetic methylotrophy is the development of non-native methylotrophs that can utilize methane and methanol as sole carbon and energy sources or as co-substrates with carbohydrates to produce metabolites as biofuels and chemicals. The availability of methane (from natural gas) and its oxidation product, methanol, has been increasing, while prices have been decreasing, thus rendering them as attractive fermentation substrates. As they are more reduced than most carbohydrates, methane and methanol, as co-substrates, can enhance the yields of biologically produced metabolites. Here we discuss synthetic biology and metabolic engineering strategies based on the native biology of aerobic methylotrophs for developing synthetic strains grown on methanol, with *Escherichia coli* as the prototype.

Author(s) affiliation: [Whitaker, William B.; Sandoval, Nicholas R.; Bennett, Robert K.; Fast, Alan G.; Papoutsakis, Eleftherios T.] Univ Delaware, Dept Chem & Biomol Engr, Newark, DE 19711 USA.

[Whitaker, William B.; Sandoval, Nicholas R.; Bennett, Robert K.; Fast, Alan G.; Papoutsakis, Eleftherios T.] Univ Delaware, Delaware Biotechnol Inst, Newark, DE 19711 USA.

[Papoutsakis, Eleftherios T.] Univ Delaware, Dept Biol Sci, Newark, DE 19711 USA.

Reprint Address: Papoutsakis, ET (reprint author), Univ Delaware, Dept Chem & Biomol Engr, 15 Innovat Way, Newark, DE 19711 USA.

E-mail Author(s) affiliation: papoutsakis@dbl.udel

Times cited: 7

Number of references: 50

Tags: Applications - Energy, Synthetic biology

Transforming exoelectrogens for biotechnology using synthetic biology (USA) 2016

Author(s): TerAvest, MA (TerAvest, Michaela A.); Ajo-Franklin, CM (Ajo-Franklin, Caroline M.)

Source: BIOTECHNOLOGY AND BIOENGINEERING Volume: 113 Issue: 4 Pages: 687-697 DOI: 10.1002/bit.25723 Published: APR 2016

ABSTRACT: Here we first briefly summarize recent discoveries in understanding extracellular electron transfer pathways, then review in-depth the creation of customized and novel exoelectrogens for biotechnological applications. We analyze engineering efforts to increase current production in native exoelectrogens, which reveals that modulating certain processes within extracellular electron transfer are more effective than others. We also review efforts to create new exoelectrogens and highlight common challenges in this work. Lastly, we summarize work utilizing engineered exoelectrogens for biotechnological applications and the key obstacles to their future development. Fueled by the development of genetic tools, these approaches will continue to expand and genetically modified organisms will continue to improve the outlook for microbial electrochemical technologies. (c) 2015 Wiley Periodicals, Inc.

Author(s) affiliation: [TerAvest, Michaela A.] Univ Calif Berkeley, Calif Inst Quantitat Biosci, Berkeley, CA 94720 USA.

Reprint Address: Ajo-Franklin, CM (reprint author), Univ Calif Berkeley, Lawrence Berkeley Natl Lab, Phys Biosci Div, Berkeley, CA 94720 USA.

Ajo-Franklin, CM (reprint author), Univ Calif Berkeley, Lawrence Berkeley Natl Lab, Div Mat Sci, Berkeley, CA 94720 USA.

Ajo-Franklin, CM (reprint author), Univ Calif Berkeley, Lawrence Berkeley Natl Lab, Synthet Biol Inst, Berkeley, CA 94720 USA.

E-mail Author(s) affiliation: cajo-franklin@lbl.gov

Times cited: 2

Number of references: 83

Tags: Applications - Energy, Synthetic biology

Yeast synthetic biology toolbox and applications for biofuel production (USA) 2015

Author(s): Tsai, CS (Tsai, Ching-Sung); Kwak, S (Kwak, Suryang); Turner, TL (Turner, Timothy L.); Jin, YS (Jin, Yong-Su)

Source: FEMS YEAST RESEARCH Volume: 15 Issue: 1 DOI: 10.1111/1567-1364.12206 Published: FEB 2015

ABSTRACT: Here we review the current status of synthetic biological tools and their applications for biofuel production, focusing on the model strain *Saccharomyces cerevisiae*. We describe assembly techniques that have been developed for constructing genes, pathways, and genomes in yeast. Moreover, we discuss synthetic parts for allowing precise control of gene expression at both transcriptional and translational levels. Applications of these synthetic biological approaches have led to identification of effective gene targets that are responsible for desirable traits, such as cellulosic sugar utilization, advanced biofuel production, and enhanced tolerance against toxic products for biofuel production from renewable biomass. Although an array of synthetic biology tools and devices are available, we observed some gaps existing in tool development to achieve industrial utilization. Looking forward, future tool development should focus on industrial cultivation conditions utilizing industrial strains.

Author(s) affiliation: [Tsai, Ching-Sung; Kwak, Suryang; Turner, Timothy L.; Jin, Yong-Su] Univ Illinois, Inst Genom Biol, Urbana, IL 61801 USA.

Reprint Address: Jin, YS (reprint author), Univ Illinois, Inst Genom Biol, Urbana, IL 61801 USA.

E-mail Author(s) affiliation: ysjin@illinois.edu

Times cited: 1

Number of references: 137

Tags: Applications - Energy, Synthetic biology

Applications - Information Storage

Codes for DNA Sequence Profiles (Singapore) 2016

Author(s): Kiah, HM (Kiah, Han Mao); Puleo, GJ (Puleo, Gregory J.); Milenkovic, O (Milenkovic, Olgica)

Source: IEEE TRANSACTIONS ON INFORMATION THEORY Volume: 62 Issue: 6 Pages: 3125-3146 DOI: 10.1109/TIT.2016.2555321 Published: JUN 2016

ABSTRACT: We consider the problem of storing and retrieving information from synthetic DNA media. We introduce the DNA storage channel and model the read process through the use of profile vectors. We provide an asymptotic analysis of the number of profile vectors and propose new asymmetric coding techniques to combat the effects of synthesis and sequencing noise. Furthermore, we construct two families of codes for this new channel model.

Author(s) affiliation: [Kiah, Han Mao] Nanyang Technol Univ, Sch Phys & Math Sci, Singapore 637371, Singapore.

[Puleo, Gregory J.; Milenkovic, Olgica] Univ Illinois, Coordinated Sci Lab, Urbana, IL 61801 USA.

Reprint Address: Kiah, HM (reprint author), Nanyang Technol Univ, Sch Phys & Math Sci, Singapore 637371, Singapore.

E-mail Author(s) affiliation: hmkih@ntu.edu.sg; puleo@illinois.edu; milenkov@illinois.edu

Times Cited: 0

Number of references: 48

Tags: Applications - Information storage, Synthetic biology

continued

Coding Macromolecules: Inputting Information in Polymers Using Monomer-Based Alphabets (France) 2015

Author(s): Lutz, JF (Lutz, Jean-Francois)

Source: MACROMOLECULES Volume: 48 Issue: 14 Pages: 4759-4767 DOI: 10.1021/acs.macromol.5b00890 Published: JUL 28 2015

ABSTRACT: The monomer units of a polymer can be used to encode a Message. The aim of the present Perspective is to Show that significant progress has been done in that direction during the past two years. For instance, convenient strategies have been reported for the preparation of monodisperse sequence-defined macromolecules. In addition, encouraging advances have been made for the sequencing of non-natural polymers. These recent results are discussed and critically analyzed herein. Altogether, monomer-based information storage should be regarded as a new property of synthetic matter.

Author(s) affiliation: CNRS, Precis Macromol Chem, Inst Charles Sadron, UPR22, F-67034 Strasbourg 2, France.

Reprint Address: Lutz, JF (reprint author), CNRS, Precis Macromol Chem, Inst Charles Sadron, UPR22, 23 Rue Loess, F-67034 Strasbourg 2, France.

E-mail Author(s) affiliation: jflutz@unistra.fr

Times Cited: 17

Number of references: 117

Tags: Applications - Information storage, Synthetic biology

Configuration Synthesis for Programmable Analog Devices with Arco (USA) 2016

Author(s): Achour, S (Achour, Sara); Sarpeshkar, R (Sarpeshkar, Rahul); Rinard, MC (Rinard, Martin C.)

Source: ACM SIGPLAN NOTICES Volume: 51 Issue: 6 Pages: 177-193 DOI: 10.1145/2908080.2908116 Published: JUN 2016

ABSTRACT: Programmable analog devices have emerged as a powerful computing substrate for performing complex neuromorphic and cytomorphic computations. We present Arco, a new solver that, given a dynamical system specification in the form of a set of differential equations, generates physically realizable configurations for programmable analog devices that are algebraically equivalent to the specified system. On a set of benchmarks from the biological domain, Arco generates configurations with 35 to 534 connections and 28 to 326 components in 1 to 54 minutes.

Author(s) affiliation: [Achour, Sara; Rinard, Martin C.] MIT CSAIL, Cambridge, MA USA.

[Sarpeshkar, Rahul] Dartmouth Coll, MIT RLE, Hanover, NH 03755 USA.

Reprint Address: Achour, S (reprint author), MIT CSAIL, Cambridge, MA USA.

E-mail Author(s) affiliation: sachour@csail.mit.edu; rahul.sarpeshkar@dartmouth.edu; rinard@csail.mit.edu

Times Cited: 0

Number of references: 40

Tags: Applications - Information storage, Synthetic biology

A Cytomorphic Chip for Quantitative Modeling of Fundamental Bio-Molecular Circuits (USA) 2015

Author(s): Woo, SS (Woo, Sung Sik); Kim, J (Kim, Jaewook); Sarpeshkar, R (Sarpeshkar, Rahul)

Source: IEEE TRANSACTIONS ON BIOMEDICAL CIRCUITS AND SYSTEMS Volume: 9 Issue: 4 Pages: 527-542 DOI: 10.1109/TBCAS.2015.2446431 Published: AUG 2015

ABSTRACT: We describe a 0.35 μm BiCMOS silicon chip that quantitatively models fundamental molecular circuits via efficient log-domain cytomorphic transistor equivalents. These circuits include those for biochemical binding with automatic representation of non-modular and loading behavior, e.g., in cascade and fan-out topologies; for representing variable Hill-coefficient operation and cooperative binding; for representing inducer, transcription-factor, and DNA binding; for probabilistic gene transcription with analogic representations of log-linear and saturating operation; for gain, degradation, and dynamics of mRNA and protein variables in transcription and translation; and, for faithfully representing biological noise via tunable stochastic transistor circuits. The use of on-chip DACs and ADCs enables multiple chips to interact via incoming and outgoing molecular digital data packets and thus create scalable biochemical reaction networks. The use of off-chip digital processors and on-chip digital memory enables programmable connectivity and parameter storage. We show that published static and dynamic MATLAB models of synthetic biological circuits including repressilators, feed-forward loops, and feedback oscillators are in excellent quantitative agreement with those from transistor circuits on the chip. Computationally intensive stochastic Gillespie simulations of molecular production are also rapidly reproduced by the chip and can be reliably tuned over the range of signal-to-noise ratios observed in biological cells.

Author(s) affiliation: [Woo, Sung Sik; Kim, Jaewook; Sarpeshkar, Rahul] MIT, Elect Res Lab, Cambridge, MA 02139 USA.

Reprint Address: Woo, SS (reprint author), MIT, Analog Circuits & Biol Syst Grp, Cambridge, MA 02139 USA.

E-mail Author(s) affiliation: rahul.sarpeshkar@dartmouth.edu

Times Cited: 2

Number of references: 53

Tags: Applications - Information storage, Synthetic biology

[A DNA-Based Archival Storage System \(USA\) 2016](#)

Author(s): Bornhol, J (Bornhol, James); Lopez, R (Lopez, Randolph); Carmean, DM (Carmean, Douglas M.); Ceze, L (Ceze, Luis); Seelig, G (Seelig, Georg); Strauss, K (Strauss, Karin)

Source: ACM SIGPLAN NOTICES Volume: 51 Issue: 4 Pages: 637-649 DOI: 10.1145/2872362.2872397 Published: APR 2016

ABSTRACT: Demand for data storage is growing exponentially, but the capacity of existing storage media is not keeping up. Using DNA to archive data is an attractive possibility because it is extremely dense, with a raw limit of 1 exabyte/mm³ (10⁹ GB/mm³), and long-lasting, with observed half-life of over 500 years.

This paper presents an architecture for a DNA-based archival storage system. It is structured as a key-value store, and leverages common biochemical techniques to provide random access. We also propose a new encoding scheme that offers controllable redundancy, trading off reliability for density. We demonstrate feasibility, random access, and robustness of the proposed encoding with wet lab experiments involving 151 kB of synthesized DNA and a 42 kB random-access subset, and simulation experiments of larger sets calibrated to the wet lab experiments. Finally, we highlight trends in biotechnology that indicate the impending practicality of DNA storage for much larger datasets.

Author(s) affiliation: [Bornhol, James; Lopez, Randolph; Ceze, Luis; Seelig, Georg] Univ Washington, Seattle, WA 98195 USA.

[Carmean, Douglas M.; Strauss, Karin] Microsoft Res, Redmond, WA USA.

Reprint Address: Bornhol, J (reprint author), Univ Washington, Seattle, WA 98195 USA.

Times Cited: 0

Number of references: 29

Tags: Applications - Information storage, Synthetic biology

[DNA nanotechnology: new adventures for an old warhorse \(USA\) 2015](#)

Author(s): Zakeri, B (Zakeri, Bijan); Lu, TK (Lu, Timothy K.)

Source: CURRENT OPINION IN CHEMICAL BIOLOGY Volume: 28 Pages: 9-14 DOI: 10.1016/j.cbpa.2015.05.020 Published: OCT 2015

ABSTRACT: As the blueprint of life, the natural exploits of DNA are admirable. However, DNA should not only be viewed within a biological context. It is an elegantly simple yet functionally complex chemical polymer with properties that make it an ideal platform for engineering new nanotechnologies. Rapidly advancing synthesis and sequencing technologies are enabling novel unnatural applications for DNA beyond the realm of genetics. Here we explore the chemical biology of DNA nanotechnology for emerging applications in communication and digital data storage. Early studies of DNA as an alternative to magnetic and optical storage mediums have not only been promising, but have demonstrated the potential of DNA to revolutionize the way we interact with digital data in the future.

Author(s) affiliation: [Zakeri, Bijan; Lu, Timothy K.] MIT, Elect Res Lab, Dept Biol Engr, Dept Elect Engr & Comp Sci, Cambridge, MA 02139 USA.

[Zakeri, Bijan; Lu, Timothy K.] MIT, Synthet Biol Ctr, Cambridge, MA 02139 USA.

Reprint Address: Zakeri, B (reprint author), MIT, Elect Res Lab, Dept Biol Engr, Dept Elect Engr & Comp Sci, 77 Massachusetts Ave, Cambridge, MA 02139 USA.

E-mail Author(s) affiliation: bijan.zakeri@oxfordalumni.org; timlu@mit.edu

Times Cited: 1

Number of references: 49

Tags: Applications - Information storage, Synthetic biology

[Empirical Laws and Foreseeing the Future of Technological Progress \(Portugal\) 2016](#)

Author(s): Lopes, AM (Lopes, Antonio M.); Machado, JAT (Tenreiro Machado, Jose A.); Galhano, AM (Galhano, Alexandra M.)

Source: ENTROPY Volume: 18 Issue: 6 Article Number: 217 DOI: 10.3390/e18060217 Published: JUN 2016

ABSTRACT: The Moore's law (ML) is one of many empirical expressions that is used to characterize natural and artificial phenomena. The ML addresses technological progress and is expected to predict future trends. Yet, the "art" of predicting is often confused with the accurate fitting of trendlines to past events. Presently, data-series of multiple sources are available for scientific and computational processing. The data can be described by means of mathematical expressions that, in some cases, follow simple expressions and empirical laws. However, the extrapolation toward the future is considered with skepticism by the scientific community, particularly in the case of phenomena involving complex behavior. This paper addresses these issues in the light of entropy and pseudo-state space. The statistical and dynamical techniques lead to a more assertive perspective on the adoption of a given candidate law.

Author(s) affiliation: [Lopes, Antonio M.] Univ Porto, Fac Engr, UISPA LAETA INEGI, Rua Dr Roberto Frias, P-4200465 Oporto, Portugal.

[Tenreiro Machado, Jose A.; Galhano, Alexandra M.] Polytech Porto, Inst Engr, Dept Elect Engr, Rua Dr Antonio Bernardino de

Almeida 431, P-4249015 Oporto, Portugal.

Reprint Address: Lopes, AM (reprint author), Univ Porto, Fac Engr, UISPA LAETA INEGI, Rua Dr Roberto Frias, P-4200465 Oporto, Portugal.

E-mail Author(s) affiliation: aml@fe.up.pt; jtenreiromachado@gmail.com; amf@isep.ipp.pt

Times Cited: 0

Number of references: 56

Tags: Applications - Information storage, Synthetic biology

Feasibility study of molecular memory device based on DNA using methylation to store information (Australia) 2016

Author(s): Jiang, LM (Jiang, Liming); Qiu, WZ (Qiu, Wanzhi); Al-Dirini, F (Al-Dirini, Feras); Hossain, FM (Hossain, Faruque M.); Evans, R (Evans, Robin); Skafidas, E (Skafidas, Efstratios)

Source: JOURNAL OF APPLIED PHYSICS Volume: 120 Issue: 2 Article Number: 025501 DOI: 10.1063/1.4954219

Published: JUL 14 2016

ABSTRACT: DNA, because of its robustness and dense information storage capability, has been proposed as a potential candidate for next-generation storage media. However, encoding information into the DNA sequence requires molecular synthesis technology, which to date is costly and prone to synthesis errors. Reading the DNA strand information is also complex. Ideally, DNA storage will provide methods for modifying stored information. Here, we conduct a feasibility study investigating the use of the DNA 5-methylcytosine (5mC) methylation state as a molecular memory to store information. We propose a new 1-bit memory device and study, based on the density functional theory and non-equilibrium Green's function method, the feasibility of electrically reading the information. Our results show that changes to methylation states lead to changes in the peak of negative differential resistance which can be used to interrogate memory state. Our work demonstrates a new memory concept based on methylation state which can be beneficial in the design of next generation DNA based molecular electronic memory devices. Published by AIP Publishing.

Author(s) affiliation: [Jiang, Liming; Qiu, Wanzhi; Al-Dirini, Feras; Evans, Robin; Skafidas, Efstratios] Univ Melbourne, Dept Elect & Elect Engr, Parkville, Vic 3010, Australia.

[Jiang, Liming; Qiu, Wanzhi; Al-Dirini, Feras; Hossain, Faruque M.; Skafidas, Efstratios] Univ Melbourne, CfNE, Carlton, Vic 3053, Australia.

[Jiang, Liming; Al-Dirini, Feras] Univ Melbourne, Natl ICT Australia, Parkville, Vic 3010, Australia.

Reprint Address: Skafidas, E (reprint author), Univ Melbourne, Dept Elect & Elect Engr, Parkville, Vic 3010, Australia.

Skafidas, E (reprint author), Univ Melbourne, CfNE, Carlton, Vic 3053, Australia.

E-mail Author(s) affiliation: sskaf@unimelb.edu.au

Times Cited: 0

Number of references: 33

Tags: Applications - Information storage, Synthetic biology

Information-containing macromolecules (England) 2014

Author(s): Colquhoun, H (Colquhoun, Howard); Lutz, JF (Lutz, Jean-Francois)

Source: NATURE CHEMISTRY Volume: 6 Issue: 6 Pages: 455-456 DOI: 10.1038/nchem.1958 Published: JUN 2014

Author(s) affiliation: [Colquhoun, Howard] Univ Reading, Dept Chem, Reading RG6 6AD, Berks, England.

[Lutz, Jean-Francois] Inst Charles Sadron, F-67034 Strasbourg, France.

Reprint Address: Colquhoun, H (reprint author), Univ Reading, Dept Chem, Reading RG6 6AD, Berks, England.

E-mail Author(s) affiliation: h.m.colquhoun@rdg.ac.uk; jflutz@unistra.fr

Times Cited: 26

Number of references: 22

Tags: Applications - Information storage, Synthetic biology

Molecular computing: paths to chemical Turing machines (the Netherlands) 2015

Author(s): Varghese, S (Varghese, Shaji); Elemans, JAAW (Elemans, Johannes A. A. W.); Rowan, AE (Rowan, Alan E.); Nolte, RJM (Nolte, Roeland J. M.)

Source: CHEMICAL SCIENCE Volume: 6 Issue: 11 Pages: 6050-6058 DOI: 10.1038/nchem.1958 Published: 2015

ABSTRACT: To comply with the rapidly increasing demand of information storage and processing, new strategies for computing are needed. The idea of molecular computing, where basic computations occur through molecular, supramolecular, or biomolecular approaches, rather than electronically, has long captivated researchers. The prospects of using molecules and (bio)macromolecules for computing is not without precedent. Nature is replete with examples where the handling and storing of data occurs with high efficiencies, low energy costs, and high-density information encoding. The design and assembly of computers that function according to the universal approaches of computing, such as those in a Turing machine, might be realized in a chemical way in the future; this is both fascinating and extremely challenging. In this perspective, we highlight molecular and (bio) macromolecular systems that have been designed and synthesized so far with the objective of using them for computing purposes. We also present

a blueprint of a molecular Turing machine, which is based on a catalytic device that glides along a polymer tape and, while moving, prints binary information on this tape in the form of oxygen atoms.

Author(s) affiliation: [Varghese, Shaji; Elemans, Johannes A. A. W.; Rowan, Alan E.; Nolte, Roeland J. M.] Radboud Univ Nijmegen, Inst Mol & Mat, NL-6525 AJ Nijmegen, Netherlands.

Reprint Address: Varghese, S (reprint author), Radboud Univ Nijmegen, Inst Mol & Mat, Heyendaalseweg 135, NL-6525 AJ Nijmegen, Netherlands.

E-mail Author(s) affiliation: s.varghese@science.ru.nl; r.nolte@science.ru.nl

Times Cited: 2

Number of references: 104

Tags: Applications - Information storage, Synthetic biology

Molecular logic gates based on DNA tweezers responsive to multiplex restriction endonucleases (China) 2016

Author(s): Li, XY (Li, Xiao-Yu); Huang, J (Huang, Juan); Jiang, HX (Jiang, Hong-Xin); Du, YC (Du, Yi-Chen); Han, GM (Han, Gui-Mei); Kong, DM (Kong, De-Ming)

Source: RSC ADVANCES Volume: 6 Issue: 44 Pages: 38315-38320 DOI: 10.1039/c6ra05132d Published: 2016

ABSTRACT: DNA logic gates have received significant attention as biocompatible building blocks of molecular circuits. Herein, we described the construction of DNA self-assembled molecular tweezers containing four different restriction endonuclease recognition sites and application of the tweezers in the construction of DNA logic gates. An open tweezer is formed by three DNA oligonucleotides, one of which is labelled with a fluorophore and a quencher at the two ends. Addition of the fourth oligonucleotide might close the tweezers, thus turning off the fluorescence signal. The quenched fluorescence of the closed tweezers can be turned on again by any one of the four restriction endonucleases, thus conferring the tweezers with the ability for multiplex detection of the four endonucleases. Based on the fluorescence responses to DNA oligonucleotide and restriction endonucleases, a set of DNA logic gates, including one-input NOT and YES logic gates, two-input IMPLICATION logic gates, two, three and four-input OR logic gates, were constructed.

Author(s) affiliation: [Li, Xiao-Yu; Huang, Juan; Jiang, Hong-Xin; Du, Yi-Chen; Han, Gui-Mei; Kong, De-Ming] Nankai Univ, Coll Chem, State Key Lab Med Chem Biol, Tianjin 300071, Peoples R China.

[Kong, De-Ming] Collaborat Innovat Ctr Chem Sci & Engrn Tianjin, Tianjin 300071, Peoples R China.

[Kong, De-Ming] Nankai Univ, Res Ctr Analyt Sci, Tianjin Key Lab Biosensing & Mol Recognit, Tianjin 300071, Peoples R China.

Reprint Address: Kong, DM (reprint author), Nankai Univ, Coll Chem, State Key Lab Med Chem Biol, Tianjin 300071, Peoples R China.

Kong, DM (reprint author), Collaborat Innovat Ctr Chem Sci & Engrn Tianjin, Tianjin 300071, Peoples R China.

Kong, DM (reprint author), Nankai Univ, Res Ctr Analyt Sci, Tianjin Key Lab Biosensing & Mol Recognit, Tianjin 300071, Peoples R China.

E-mail Author(s) affiliation: kongdem@nankai.edu.cn

Times Cited: 0

Number of references: 53

Tags: Applications - Information storage, Synthetic biology

Molecules with a sense of logic: a progress report (Sweden) 2015

Author(s): Andreasson, J (Andreasson, Joakim); Pischel, U (Pischel, Uwe)

Source: CHEMICAL SOCIETY REVIEWS Volume: 44 Issue: 5 Pages: 1053-1069 DOI: 10.1039/c4cs00342j Published: MAR 7 2015

ABSTRACT: In this tutorial review, the most recent developments in the field of molecular logic and information processing are discussed. Special emphasis is given to the report of progress in the concatenation of molecular logic devices and switches, the design of memory systems working according to the principles of sequential logic, the mimicking of transistors, and the research on photochromic platforms with an unprecedented degree of functional integration. Furthermore, a series of achievements that add up to the conceptual diversity of molecular logic is introduced, such as the realization of highly complex and logically reversible Toffoli and Fredkin gates by the action of DNAzymes or the use of a multifluorophoric platform as a viable approach towards keypad lock functions.

Author(s) affiliation: [Andreasson, Joakim] Chalmers, Phys Chem, Dept Chem & Biol Engrn, SE-41296 Gothenburg, Sweden.

[Pischel, Uwe] Univ Huelva, CIQSO Ctr Res Sustainable Chem, E-21071 Huelva, Spain.

[Pischel, Uwe] Univ Huelva, Dept Chem Engrn Phys Chem & Organ Chem, E-21071 Huelva, Spain.

Reprint Address: Andreasson, J (reprint author), Chalmers, Phys Chem, Dept Chem & Biol Engrn, SE-41296 Gothenburg, Sweden.

E-mail Author(s) affiliation: a-son@chalmers.se; uwe.pischel@diq.uhu.es

Times Cited: 39

Number of references: 50

Tags: Applications - Information storage, Synthetic biology

Multiple types of logic gates based on a single G-quadruplex DNA strand (China) 2014

Author(s): Guo, YH (Guo, Yahui); Zhou, L (Zhou, Lu); Xu, LJ (Xu, Lijun); Zhou, XD (Zhou, Xiaodong); Hu, JM (Hu, Jiming); Pei, RJ (Pei, Renjun)

Source: SCIENTIFIC REPORTS Volume: 4 Article Number: 7315 DOI: 10.1038/srep07315 Published: DEC 4 2014

ABSTRACT: In this work, we demonstrate the use of a single DNA strand and G-quadruplex-specific dye NMM as a label-free switch for the construction of series of basic logic gates (YES, NOT, OR, INHIBIT, NOR, AND). The simple GT-rich sequence could be used to interact with several molecules (K⁺, thrombin, Hg²⁺, and Pb²⁺) to form different structures that can be distinguished by the label-free dye NMM. Our study showed that a single G-quadruplex DNA strand can function as multiple types of one-input and two-input logic gates with different combinations of input molecules.

Author(s) affiliation: [Guo, Yahui; Zhou, Lu; Xu, Lijun; Pei, Renjun] Chinese Acad Sci, Collaborat Innovat Ctr Suzhou Nano Sci & Technol, Suzhou Inst Nanotech & Nanobion, Div Nanobiomed, Key Lab Nanobio Interface, Suzhou 215123, Peoples R China.

[Guo, Yahui; Zhou, Xiaodong; Hu, Jiming] Wuhan Univ, Coll Chem & Mol Sci, Key Lab Analyt Chem Biol & Med, Minist Educ, Wuhan 430072, Peoples R China.

Reprint Address: Hu, JM (reprint author), Wuhan Univ, Coll Chem & Mol Sci, Key Lab Analyt Chem Biol & Med, Minist Educ, Wuhan 430072, Peoples R China.

E-mail Author(s) affiliation: jmhu@whu.edu.cn; rjpei2011@sinano.ac.cn

Times Cited: 9

Number of references: 44

Tags: Applications - Information storage, Synthetic biology

Multiplexed Sequence Encoding: A Framework for DNA Communication (USA) 2016

Author(s): Zakeri, B (Zakeri, Bijan); Carr, PA (Carr, Peter A.); Lu, TK (Lu, Timothy K.)

Source: PLOS ONE Volume: 11 Issue: 4 Article Number: e0152774 DOI: 10.1371/journal.pone.0152774 Published: APR 6 2016

ABSTRACT: Synthetic DNA has great propensity for efficiently and stably storing non-biological information. With DNA writing and reading technologies rapidly advancing, new applications for synthetic DNA are emerging in data storage and communication. Traditionally, DNA communication has focused on the encoding and transfer of complete sets of information. Here, we explore the use of DNA for the communication of short messages that are fragmented across multiple distinct DNA molecules. We identified three pivotal points in a communication-data encoding, data transfer & data extraction-and developed novel tools to enable communication via molecules of DNA. To address data encoding, we designed DNA-based individualized keyboards (iKeys) to convert plaintext into DNA, while reducing the occurrence of DNA homopolymers to improve synthesis and sequencing processes. To address data transfer, we implemented a secret-sharing system-Multiplexed Sequence Encoding (MuSE)-that conceals messages between multiple distinct DNA molecules, requiring a combination key to reveal messages. To address data extraction, we achieved the first instance of chromatogram patterning through multiplexed sequencing, thereby enabling a new method for data extraction. We envision these approaches will enable more widespread communication of information via DNA.

Author(s) affiliation: [Zakeri, Bijan; Lu, Timothy K.] MIT, Dept Elect Engn & Comp Sci, Dept Biol Engn, Elect Res Lab, 77 Massachusetts Ave, Cambridge, MA 02139 USA.

[Zakeri, Bijan; Carr, Peter A.; Lu, Timothy K.] MIT, Synthet Biol Ctr, 500 Technol Sq, Cambridge, MA 02139 USA.

[Carr, Peter A.] MIT, Lincoln Lab, 244 Wood St, Lexington, MA 02420 USA.

Reprint Address: Zakeri, B (reprint author), MIT, Dept Elect Engn & Comp Sci, Dept Biol Engn, Elect Res Lab, 77 Massachusetts Ave, Cambridge, MA 02139 USA.

Zakeri, B; Carr, PA (reprint author), MIT, Synthet Biol Ctr, 500 Technol Sq, Cambridge, MA 02139 USA.

Carr, PA (reprint author), MIT, Lincoln Lab, 244 Wood St, Lexington, MA 02420 USA.

E-mail Author(s) affiliation: bijan.zakeri@oxfordalumni.org; carr@ll.mit.edu

Times Cited: 0

Number of references: 24

Tags: Applications - Information storage, Synthetic biology

Nucleic Acid Based Logical Systems (USA) 2014

Author(s): Han, D (Han, Da); Kang, HZ (Kang, Huaizhi); Zhang, T (Zhang, Tao); Wu, CC (Wu, Cuichen); Zhou, CS (Zhou, Cuisong); You, MX (You, Mingxu); Chen, Z (Chen, Zhuo); Zhang, XB (Zhang, Xiaobing); Tan, WH (Tan, Weihong)

Source: CHEMISTRY-A EUROPEAN JOURNAL Volume: 20 Issue: 20 Pages: 5866-5873 DOI: 10.1002/chem.201304891 Published: MAY 12 2014

ABSTRACT: Researchers increasingly visualize a significant role for artificial biochemical logical systems in biological engineering, much like digital logic circuits in electrical engineering. Those logical systems could be utilized as a type of servomechanism to control nanodevices in vitro, monitor chemical reactions in situ, or regulate gene expression in vivo. Nucleic acids (NA), as carriers of genetic information with well-regulated and predictable structures, are promising materials for the design and engineering of

biochemical circuits. A number of logical devices based on nucleic acids (NA) have been designed to handle various processes for technological or biotechnological purposes. This article focuses on the most recent and important developments in NA-based logical devices and their evolution from in vitro, through cellular, even towards in vivo biological applications.

Author(s) affiliation: [Han, Da; Zhang, Tao; Wu, Cuichen; Zhou, Cuisong; You, Mingxu; Tan, Weihong] Univ Florida, Dept Chem, Ctr Res Bionano Interface, Gainesville, FL 32611 USA.

[Kang, Huaizhi] Xiamen Univ, Dept Chem, Coll Chem & Chem Engr, Xiamen 361005, Fujian, Peoples R China.

Reprint Address: Zhang, XB (reprint author), Hunan Univ, Collaborat Innovat Ctr Chem & Mol Med, Coll Biol, State Key Lab Chemo Biosensing & Chemometr, Mol Sci & Biomed Lab, Coll Chem & Chem Engr, Changsha 410082, Hunan, Peoples R China.

E-mail Author(s) affiliation: tan@chem.ufl.edu

Times Cited: 11

Number of references: 48

Tags: Applications - Information storage, Synthetic biology

Nucleic acid memory (USA) 2016

Author(s): Zhirnov, V (Zhirnov, Victor); Zadegan, RM (Zadegan, Reza M.); Sandhu, GS (Sandhu, Gurtej S.); Church, GM (Church, George M.); Hughes, WL (Hughes, William L.)

Source: NATURE MATERIALS Volume: 15 Issue: 4 Pages: 366-370 Published: APR 2016

ABSTRACT: Nucleic acid memory has a retention time far exceeding electronic memory. As an alternative storage media, DNA surpasses the information density and energy of operation offered by flash memory.

Author(s) affiliation: [Zhirnov, Victor] Semicond Res Corp, 1101 Slater Rd, Durham, NC 27703 USA.

[Zadegan, Reza M.; Hughes, William L.] Boise State Univ, Dept Mat Sci & Engr, 1910 Univ Dr, Boise, ID 83725 USA.

[Sandhu, Gurtej S.] Micron Technol Inc, POB 6,8000 South Fed Way, Boise, ID 83707 USA.

[Church, George M.] Harvard Univ, Dept Genet, 77 Ave Louis Pasteur, Boston, MA 02115 USA.

Reprint Address: Hughes, WL (reprint author), Boise State Univ, Dept Mat Sci & Engr, 1910 Univ Dr, Boise, ID 83725 USA.

Church, GM (reprint author), Harvard Univ, Dept Genet, 77 Ave Louis Pasteur, Boston, MA 02115 USA.

E-mail Author(s) affiliation: gmc@harvard.edu; willhughes@boisestate.edu

Times Cited: 2

Number of references: 50

Tags: Applications - Information storage, Synthetic biology

Particles with an identity: Tracking and tracing in commodity products (Switzerland) 2016

Author(s): Paunescu, D (Paunescu, Daniela); Stark, WJ (Stark, Wendelin J.); Grass, RN (Grass, Robert N.)

Source: POWDER TECHNOLOGY Volume: 291 Pages: 344-350 DOI: 10.1016/j.powtec.2015.12.035 Published: APR 2016

ABSTRACT: Identity is value. Knowledge of the origin, processing and supply chain of a product determines its market price. As particles can be used to carry very unique information (size/shape/optical/electronic/chemical), and at the same time be of extremely small dimensions and invisible, powders are an ideal choice to be used as a taggant as an information carrying entity that is added to another product to identify it. Recent advantages in synthesizing and analyzing unique features of particles address the growing need of identifying products in the product life cycle. This is illustrated by particulate tracers, which are of non-toxic composition and can be uniquely analyzed at part per billion (ppb) concentration ranges in fully automated procedures. It is envisioned that these technological advances in powder technology will help to build a global materials identification system, guaranteeing product value and increasing manufacturer responsibility and liability. (C) 2016 Elsevier B.V. All rights reserved.

Author(s) affiliation: [Paunescu, Daniela; Stark, Wendelin J.; Grass, Robert N.] ETH, Inst Chem & Bioengn, Vladimir Prelog Weg 1, CH-8093 Zurich, Switzerland.

Reprint Address: Grass, RN (reprint author), ETH, Inst Chem & Bioengn, Vladimir Prelog Weg 1, CH-8093 Zurich, Switzerland.

E-mail Author(s) affiliation: robert.grass@chem.ethz.ch

Times Cited: 1

Number of references: 59

Tags: Applications - Information storage, Synthetic biology

Programmable DNA-Mediated Multitasking Processor (Singapore) 2015

Author(s): Shu, JJ (Shu, Jian-Jun); Wang, QW (Wang, Qi-Wen); Yong, KY (Yong, Kian-Yan); Shao, FW (Shao, Fangwei); Lee, KJ (Lee, Kee Jin)

Source: JOURNAL OF PHYSICAL CHEMISTRY B Volume: 119 Issue: 17 Pages: 5639-5644 DOI: 10.1021/acs.jpccb.5b02165 Published: APR 30 2015

ABSTRACT: Because of DNA appealing features as perfect material, including minuscule size, defined structural repeat and rigidity, programmable DNA-mediated processing is a promising computing paradigm, which employs DNAs as information storing and processing substrates to tackle the computational problems. The massive parallelism of DNA hybridization exhibits transcendent potential to improve multitasking capabilities and yield a tremendous speed-up over the conventional electronic processors

with stepwise signal cascade. As an example of multitasking capability, we present an in vitro programmable DNA-mediated optimal route planning processor as a functional unit embedded in contemporary navigation systems. The novel programmable DNA-mediated processor has several advantages over the existing silicon-mediated methods, such as conducting massive data storage and simultaneous processing via much fewer materials than conventional silicon devices.

Author(s) affiliation: [Shu, Jian-Jun; Wang, Qi-Wen; Yong, Kian-Yan; Lee, Kee Jin] Nanyang Technol Univ, Sch Mech & Aerosp Engr, Singapore 639798, Singapore.

[Shao, Fangwei] Nanyang Technol Univ, Sch Phys & Math Sci, Singapore 637371, Singapore.

Reprint Address: Shu, JJ (reprint author), Nanyang Technol Univ, Sch Mech & Aerosp Engr, 50 Nanyang Ave, Singapore 639798, Singapore.

E-mail Addresses: mjjshu@ntu.edu.sg

Times Cited: 0

Number of references: 15

Tags: Applications - Information storage, Synthetic biology

Reading Polymers: Sequencing of Natural and Synthetic Macromolecules (France) 2014

Author(s): Mutlu, H (Mutlu, Hatice); Lutz, JF (Lutz, Jean-Francois)

Source: ANGEWANDTE CHEMIE-INTERNATIONAL EDITION Volume: 53 Issue: 48 Pages: 13010-13019 DOI: 10.1002/anie.201406766 Published: NOV 24 2014

ABSTRACT: The sequencing of biopolymers such as proteins and DNA is among the most significant scientific achievements of the 20th century. Indeed, modern chemical methods for sequence analysis allow reading and understanding the codes of life. Thus, sequencing methods currently play a major role in applications as diverse as genomics, gene therapy, biotechnology, and data storage. However, in terms of fundamental science, sequencing is not really a question of molecular biology but rather a more general topic in macromolecular chemistry. Broadly speaking, it can be defined as the analysis of comonomer sequences in copolymers. However, relatively different approaches have been used in the past to study monomer sequences in biological and manmade polymers. Yet, these “cultural” differences are slowly fading away with the recent development of synthetic sequence-controlled polymers. In this context, the aim of this Minireview is to present an overview of the tools that are currently available for sequence analysis in macromolecular science.

Author(s) affiliation: [Mutlu, Hatice; Lutz, Jean-Francois] CNRS, UPR22, Inst Charles Sadron, F-67034 Strasbourg 2, France.

Reprint Address: Lutz, JF (reprint author), CNRS, UPR22, Inst Charles Sadron, 23 Rue Loess, BP 84047, F-67034 Strasbourg 2, France.

E-mail Author(s) affiliation: jflutz@unistra.fr

Times Cited: 23

Number of references: 158

Tags: Applications - Information storage, Synthetic biology

A Rewritable, Random-Access DNA-Based Storage System (USA) 2015

Author(s): Yazdi, SMHT (Yazdi, S. M. Hossein Tabatabaei); Yuan, YB (Yuan, Yongbo); Ma, J (Ma, Jian); Zhao, HM (Zhao, Huimin); Milenkovic, O (Milenkovic, Olgica)

Source: SCIENTIFIC REPORTS Volume: 5 Article Number: 14138 DOI: 10.1038/srep14138 Published: SEP 18 2015

ABSTRACT: We describe the first DNA-based storage architecture that enables random access to data blocks and rewriting of information stored at arbitrary locations within the blocks. The newly developed architecture overcomes drawbacks of existing read-only methods that require decoding the whole file in order to read one data fragment. Our system is based on new constrained coding techniques and accompanying DNA editing methods that ensure data reliability, specificity and sensitivity of access, and at the same time provide exceptionally high data storage capacity. As a proof of concept, we encoded parts of the Wikipedia pages of six universities in the USA, and selected and edited parts of the text written in DNA corresponding to three of these schools. The results suggest that DNA is a versatile media suitable for both ultrahigh density archival and rewritable storage applications.

Author(s) affiliation: [Yazdi, S. M. Hossein Tabatabaei; Milenkovic, Olgica] Univ Illinois, Dept Elect & Comp Engr, Urbana, IL 61801 USA.

[Yuan, Yongbo; Zhao, Huimin] Univ Illinois, Dept Chem & Biomol Engr, Urbana, IL 61801 USA.

[Ma, Jian] Univ Illinois, Dept Bioengn, Urbana, IL 61801 USA.

[Ma, Jian] Univ Illinois, Inst Genom Biol, Urbana, IL 61801 USA.

Reprint Address: Milenkovic, O (reprint author), Univ Illinois, Dept Elect & Comp Engr, 1406 W Green St, Urbana, IL 61801 USA.

E-mail Author(s) affiliation: milenkov@illinois.edu

Times Cited: 2

Number of references: 22

Tags: Applications - Information storage, Synthetic biology

Robust Chemical Preservation of Digital Information on DNA in Silica with Error-Correcting Codes (Switzerland) 2015

Author(s): Grass, RN (Grass, Robert N.); Heckel, R (Heckel, Reinhard); Puddu, M (Puddu, Michela); Paunescu, D (Paunescu, Daniela); Stark, WJ (Stark, Wendelin J.)

Source: ANGEWANDTE CHEMIE-INTERNATIONAL EDITION Volume: 54 Issue: 8 Pages: 2552-2555 DOI: 10.1002/anie.201411378 Published: FEB 16 2015

ABSTRACT: Information, such as text printed on paper or images projected onto microfilm, can survive for over 500years. However, the storage of digital information for time frames exceeding 50years is challenging. Here we show that digital information can be stored on DNA and recovered without errors for considerably longer time frames. To allow for the perfect recovery of the information, we encapsulate the DNA in an inorganic matrix, and employ error-correcting codes to correct storage-related errors. Specifically, we translated 83kB of information to 4991 DNA segments, each 158nucleotides long, which were encapsulated in silica. Accelerated aging experiments were performed to measure DNA decay kinetics, which show that data can be archived on DNA for millennia under a wide range of conditions. The original information could be recovered error free, even after treating the DNA in silica at 70 degrees C for one week. This is thermally equivalent to storing information on DNA in central Europe for 2000years.

Author(s) affiliation: [Grass, Robert N.; Puddu, Michela; Paunescu, Daniela; Stark, Wendelin J.] ETH, Inst Chem & Bioengn, CH-8093 Zurich, Switzerland.

[Heckel, Reinhard] ETH, Dept Informat Technol & Elect Engn, CH-8092 Zurich, Switzerland.

Reprint Address: Grass, RN (reprint author), ETH, Inst Chem & Bioengn, Vladimir Prelog Weg 1, CH-8093 Zurich, Switzerland.

E-mail Author(s) affiliation: robert.grass@chem.ethz.ch

Times Cited: 18

Number of references: 28

Tags: Applications - Information storage, Synthetic biology

Synthetic DNA The next generation of big data storage (Ireland) 2013

Author(s): Driscoll, AO (Driscoll, Aisling O'); Sleator, RD (Sleator, Roy D.)

Source: BIOENGINEERED Volume: 4 Issue: 3 Pages: 123-125 DOI: 10.4161/bioe.24296 Published: MAY-JUN 2013

ABSTRACT: With world wide data predicted to exceed 40 trillion gigabytes by 2020, big data storage is a very real and escalating problem. Herein, we discuss the utility of synthetic DNA as a robust and eco-friendly archival data storage solution of the future.

Author(s) affiliation: [Driscoll, Aisling O'] Cork Inst Technol, Dept Comp, Cork, Ireland.

[Sleator, Roy D.] Cork Inst Technol, Dept Biol Sci, Cork, Ireland.

Reprint Address: Sleator, RD (reprint author), Cork Inst Technol, Dept Biol Sci, Cork, Ireland.

E-mail Author(s) affiliation: roy.sleator@cit.ie

Times Cited: 0

Number of references: 21

Tags: Applications - Information storage, Synthetic biology

Applications - Materials

Adding Functions to Biomaterial Surfaces through Protein Incorporation (Ireland) 2016

Author(s): Wronska, MA (Wronska, Malgorzata A.); O'Connor, IB (O'Connor, Iain B.); Tilbury, MA (Tilbury, Maura A.); Srivastava, A (Srivastava, Akshay); Wall, JG (Wall, J. Gerard)

Source: ADVANCED MATERIALS Volume: 28 Issue: 27 Special Issue: SI Pages: 5485-5508 DOI: 10.1002/adma.201504310 Published: JUL 20 2016

ABSTRACT: The concept of biomaterials has evolved from one of inert mechanical supports with a long-term, biologically inactive role in the body into complex matrices that exhibit selective cell binding, promote proliferation and matrix production, and may ultimately become replaced by newly generated tissues in vivo. Functionalization of material surfaces with biomolecules is critical to their ability to evade immunorecognition, interact productively with surrounding tissues and extracellular matrix, and avoid bacterial colonization. Antibody molecules and their derived fragments are commonly immobilized on materials to mediate coating with specific cell types in fields such as stent endothelialization and drug delivery. The incorporation of growth factors into biomaterials has found application in promoting and accelerating bone formation in osteogenerative and related applications. Peptides and extracellular matrix proteins can impart biomolecule- and cell-specificities to materials while antimicrobial peptides have found roles in preventing biofilm formation on devices and implants. In this progress report, we detail developments in the use of diverse proteins and peptides to modify the surfaces of hard biomaterials in vivo and in vitro. Chemical approaches to immobilizing active biomolecules are presented, as well as platform technologies for isolation or generation of natural or synthetic molecules suitable for biomaterial functionalization.

Author(s) affiliation: [Wronska, Malgorzata A.; O'Connor, Iain B.; Tilbury, Maura A.; Srivastava, Akshay; Wall, J. Gerard] Natl Univ

Ireland, Microbiol, Galway, Ireland.

[Wronska, Malgorzata A.; O'Connor, Iain B.; Tilbury, Maura A.; Srivastava, Akshay; Wall, J. Gerard] Natl Univ Ireland, Ctr Res Med Devices CURAM, Galway, Ireland.

Reprint Address: Wall, JG (reprint author), Natl Univ Ireland, Microbiol, Galway, Ireland.

Wall, JG (reprint author), Natl Univ Ireland, Ctr Res Med Devices CURAM, Galway, Ireland.

E-mail Author(s) affiliation: gerard.wall@nuigalway.ie

Times Cited: 0

Number of references: 409

Tags: Applications - Materials, Syntetic biology

Advanced Biotechnology: Metabolically Engineered Cells for the Bio-Based Production of Chemicals and Fuels, Materials, and Health-Care Products (Germany) 2015

Author(s): Becker, J (Becker, Judith); Wittmann, C (Wittmann, Christoph)

Source: ANGEWANDTE CHEMIE-INTERNATIONAL EDITION Volume: 54 Issue: 11 Special Issue: SI Pages: 3328-3350 DOI: 10.1002/anie.201409033 Published: MAR 9 2015

ABSTRACT: Corynebacterium glutamicum, Escherichia coli, and Saccharomyces cerevisiae in particular, have become established as important industrial workhorses in biotechnology. Recent years have seen tremendous progress in their advance into tailor-made producers, driven by the upcoming demand for sustainable processes and renewable raw materials. Here, the diversity and complexity of nature is simultaneously a challenge and a benefit. Harnessing biodiversity in the right manner through synergistic progress in systems metabolic engineering and chemical synthesis promises a future innovative bio-economy.

Author(s) affiliation: [Becker, Judith; Wittmann, Christoph] Univ Saarland, Inst Syst Biotechnol, D-66123 Saarbrücken, Germany.

Reprint Address: Wittmann, C (reprint author), Univ Saarland, Inst Syst Biotechnol, Campus A1-5, D-66123 Saarbrücken, Germany.

E-mail Author(s) affiliation: christoph.wittmann@uni-saarland.de

Times Cited: 17

Number of references: 418

Tags: Applications - Materials, Syntetic biology

Bioengineering microbial communities: Their potential to help, hinder and disgust (Australia) 2016

Author(s): Sivasubramaniam, D (Sivasubramaniam, Diane); Franks, AE (Franks, Ashley E.)

Source: BIOENGINEERED Volume: 7 Issue: 3 Pages: 137-144 DOI: 10.1080/21655979.2016.1187346 Published: 2016

ABSTRACT: The bioengineering of individual microbial organisms or microbial communities has great potential in agriculture, bioremediation and industry. Understanding community level drivers can improve community level functions to enhance desired outcomes in complex environments, whereas individual microbes can be reduced to a programmable biological unit for specific output goals. While understanding the bioengineering potential of both approaches leads to a wide range of potential uses, public acceptance of such technology may be the greatest hindrance to its application. Public perceptions and expectations of "naturalness," as well as notions of disgust and dread, may delay the development of such technologies to their full benefit. We discuss these bioengineering approaches and draw on the psychological literature to suggest strategies that scientists can use to allay public concerns over the implementation of this technology.

Author(s) affiliation: [Sivasubramaniam, Diane] Swinburne Univ, Dept Psychol Sci, Melbourne, Vic, Australia.

[Franks, Ashley E.] La Trobe Univ, Dept Physiol Anat & Microbiol, Melbourne, Vic, Australia.

Reprint Address: Franks, AE (reprint author), La Trobe Univ, Dept Physiol Anat & Microbiol, Melbourne, Vic, Australia.

E-mail Author(s) affiliation: A.Franks@latrobe.edu.au

Times Cited: 0

Number of references: 50

Tags: Applications - Materials, Syntetic biology

Bioengineering Virus-Like Particles as Vaccines (Australia) 2014

Author(s): Lua, LHL (Lua, Linda H. L.); Connors, NK (Connors, Natalie K.); Sainsbury, F (Sainsbury, Frank); Chuan, YP (Chuan, Yap P.); Wibowo, N (Wibowo, Nani); Middelberg, APJ (Middelberg, Anton P. J.)

Source: BIOTECHNOLOGY AND BIOENGINEERING Volume: 111 Issue: 3 Pages: 425-440 DOI: 10.1002/bit.25159 Published: MAR 2014

ABSTRACT: Virus-like particle (VLP) technology seeks to harness the optimally tuned immunostimulatory properties of natural viruses while omitting the infectious trait. In this review, we highlight historical and emerging VLP vaccine approaches. We overview approaches that seek to specifically engineer a desirable immune response through modular VLP design, and those that seek to improve bioprocess efficiency through inhibition of intracellular assembly to allow optimal use of existing purification technologies prior to cell-free VLP assembly. Greater understanding of VLP assembly and increased interdisciplinary activity will see enormous progress in VLP technology over the coming decade, driven by clear translational opportunity. Biotechnol. Bioeng.

2014;111: 425-440. (c) 2013 Wiley Periodicals, Inc.

Author(s) affiliation: [Lui, Linda H. L.] Univ Queensland, Prot Express Facil, St Lucia, Qld 4072, Australia.

[Connors, Natalie K.; Sainsbury, Frank; Chuan, Yap P.; Wibowo, Nani; Middelberg, Anton P. J.] Univ Queensland, Ctr Biomol Engr, Australian Inst Bioengn & Nanotechnol, St Lucia, Qld 4072, Australia.

Reprint Address: Lui, LHL (reprint author), Univ Queensland, Prot Express Facil, St Lucia, Qld 4072, Australia.

E-mail Author(s) affiliation: l.lui@uq.edu.au

Source Item Page Count: 16

Times Cited: 53

Number of references: 188

Tags: Applications - Materials, Syntetic biology

Bridging the gap between systems biology and synthetic biology (USA) 2013

Author(s): Liu, D (Liu, Di); Hoynes-O'Connor, A (Hoynes-O'Connor, Allison); Zhang, FZ (Zhang, Fuzhong)

Source: FRONTIERS IN MICROBIOLOGY Volume: 4 Article Number: 211 DOI: 10.3389/fmicb.2013.00211 Published: JUL 25 2013

ABSTRACT: Systems biology is an inter-disciplinary science that studies the complex interactions and the collective behavior of a cell or an organism. Synthetic biology, as a technological subject, combines biological science and engineering, allowing the design and manipulation of a system for certain applications. Both systems and synthetic biology have played important roles in the recent development of microbial platforms for energy, materials, and environmental applications. More importantly, systems biology provides the knowledge necessary for the development of synthetic biology tools, which in turn facilitates the manipulation and understanding of complex biological systems. Thus, the combination of systems and synthetic biology has huge potential for studying and engineering microbes, especially to perform advanced tasks, such as producing biofuels. Although there have been very few studies in integrating systems and synthetic biology, existing examples have demonstrated great power in extending microbiological capabilities. This review focuses on recent efforts in microbiological genomics, transcriptomics, proteomics, and metabolomics, aiming to fill the gap between systems and synthetic biology.

Author(s) affiliation: [Liu, Di; Hoynes-O'Connor, Allison; Zhang, Fuzhong] Washington Univ, Dept Energy Environm & Chem Engr, St Louis, MO 63130 USA.

Reprint Address: Zhang, FZ (reprint author), Washington Univ, Dept Energy Environm & Chem Engr, 1 Brookings Dr, St Louis, MO 63130 USA.

E-mail Author(s) affiliation: fzhang@seas.wustl.edu

Times Cited: 1

Number of references: 71

Tags: Applications - Materials, Syntetic biology

Chemically Modifying Viruses for Diverse Applications (USA) 2016

Author(s): Mohan, K (Mohan, Kritika); Weiss, GA (Weiss, Gregory A.)

Source: ACS CHEMICAL BIOLOGY Volume: 11 Issue: 5 Pages: 1167-1179 DOI: 10.1021/acscchembio.6b00060 Published: MAY 2016

ABSTRACT: Long fascinating to biologists, viruses offer nanometer-scale benchtops for building molecular-scale devices and materials. Viruses tolerate a wide range of chemical modifications including reaction conditions, pH values, and temperatures. Recent examples of nongenetic manipulation of viral surfaces have extended viruses into applications ranging from biomedical imaging, drug delivery, tissue regeneration, and biosensors to materials for catalysis and energy generation. Chemical reactions on the phage surface include both covalent and noncovalent modifications, including some applied in conjunction with genetic modifications. Here, we survey viruses chemically augmented with capabilities limited only by imagination.

Author(s) affiliation: [Mohan, Kritika; Weiss, Gregory A.] Univ Calif Irvine, Dept Chem, Irvine, CA 92697 USA.

[Weiss, Gregory A.] Univ Calif Irvine, Dept Mol Biol & Biochem, Irvine, CA 92697 USA.

Reprint Address: Weiss, GA (reprint author), Univ Calif Irvine, Dept Chem, Irvine, CA 92697 USA.

Weiss, GA (reprint author), Univ Calif Irvine, Dept Mol Biol & Biochem, Irvine, CA 92697 USA.

E-mail Author(s) affiliation: gweiss@uci.edu

Times Cited: 0

Number of references: 119

Tags: Applications - Materials, Syntetic biology

Creating biological nanomaterials using synthetic biology (USA) 2014

Author(s): Rice, MK (Rice, MaryJoe K.); Ruder, WC (Ruder, Warren C.)

Source: SCIENCE AND TECHNOLOGY OF ADVANCED MATERIALS Volume: 15 Issue: 1 Article Number: 014401 DOI: 10.1088/1468-6996/15/1/014401 Published: FEB 2014

ABSTRACT: Synthetic biology is a new discipline that combines science and engineering approaches to precisely control biological networks. These signaling networks are especially important in fields such as biomedicine and biochemical engineering.

continued

Additionally, biological networks can also be critical to the production of naturally occurring biological nanomaterials, and as a result, synthetic biology holds tremendous potential in creating new materials. This review introduces the field of synthetic biology, discusses how biological systems naturally produce materials, and then presents examples and strategies for incorporating synthetic biology approaches in the development of new materials. In particular, strategies for using synthetic biology to produce both organic and inorganic nanomaterials are discussed. Ultimately, synthetic biology holds the potential to dramatically impact biological materials science with significant potential applications in medical systems.

Author(s) affiliation: [Rice, MaryJoe K.; Ruder, Warren C.] Virginia Tech, Dept Biol Syst Engr, Blacksburg, VA 24061 USA.

Reprint Address: Rice, MK (reprint author), Virginia Tech, Dept Biol Syst Engr, Blacksburg, VA 24061 USA.

E-mail Author(s) affiliation: wruder@vt.edu

Source Item Page Count: 11

Times Cited: 4

Number of references: 91

Tags: Applications - Materials, Syntetic biology

Designing Synthetic Biology (USA) 2014

Author(s): Agapakis, CM (Agapakis, Christina M.)

Source: ACS SYNTHETIC BIOLOGY Volume: 3 Issue: 3 Pages: 121-128 DOI: 10.1021/sb4001068 Published: MAR 2014

ABSTRACT: Synthetic biology is frequently defined as the application of engineering design principles to biology. Such principles are intended to streamline the practice of biological engineering, to shorten the time required to design, build, and test synthetic gene networks. This review is inspired by the session titled "Design and Synthetic Biology: Connecting People and Technology" at Synthetic Biology 6.0 and covers a range of literature on design practice in synthetic biology and beyond. Critical engagement with how design is used to shape the discipline opens up new possibilities for how we might design the future of synthetic biology.

Author(s) affiliation: [Agapakis, Christina M.] Univ Calif Los Angeles, Dept Mol Cell & Dev Biol, Los Angeles, CA 90095 USA.

Reprint Address: Agapakis, CM (reprint author), Univ Calif Los Angeles, Dept Mol Cell & Dev Biol, Los Angeles, CA 90095 USA.

E-mail Author(s) affiliation: christina@agapakis.com

Times Cited: 8

Number of references: 94

Tags: Applications - Materials, Syntetic biology

DNA Nanostructures on Membranes as Tools for Synthetic Biology (Poland) 2016

Author(s): Czogalla, A (Czogalla, Aleksander); Franquelim, HG (Franquelim, Henri G.); Schwille, P (Schwille, Petra)

Source: BIOPHYSICAL JOURNAL Volume: 110 Issue: 8 Pages: 1698-1707 DOI: 10.1016/j.bpj.2016.03.015 Published: APR 26 2016

ABSTRACT: Over the last decade, functionally designed DNA nanostructures applied to lipid membranes prompted important achievements in the fields of biophysics and synthetic biology. As described throughout this review, hybrid DNA-lipid nanostructures can mediate events such as vesicle docking and fusion, or selective partitioning of molecules into phase-separated membranes. Moreover, the major benefit of DNA structural constructs, such as DNA tiles and DNA origami, is the reproducibility and simplicity of their design. DNA nanotechnology can produce functional structures with subnanometer precision and allow for a tight control over their biochemical functionality, e.g., interaction partners. DNA-based membrane nanopores and origami structures able to assemble into two-dimensional networks on top of lipid bilayers are recent examples of the manifold of complex devices that can be achieved. In this review, we will shortly present some of the potentially most relevant avenues and accomplishments of membrane-anchored DNA nanostructures for investigating, engineering, and mimicking lipid membrane-related biophysical processes.

Author(s) affiliation: [Czogalla, Aleksander] Univ Wroclaw, Fac Biotechnol, Dept Cytobiochem, PL-50138 Wroclaw, Poland.

[Franquelim, Henri G.; Schwille, Petra] Max Planck Inst Biochem, Dept Cellular & Mol Biophys, Klopferspitz 18A, D-82152

Martinsried, Germany. *Reprint Address:* Czogalla, A (reprint author), Univ Wroclaw, Fac Biotechnol, Dept Cytobiochem, PL-50138

Wroclaw, Poland. Schwille, P (reprint author), Max Planck Inst Biochem, Dept Cellular & Mol Biophys, Klopferspitz 18A, D-82152

Martinsried, Germany. *E-mail Author(s) affiliation:* aleksander.czogalla@uwr.edu.pl; schwille@biochem.mpg.de

Times Cited: 0

Number of references: 73

Tags: Applications - Materials, Syntetic biology

Engineering control of bacterial cellulose production using a genetic toolkit and a new cellulose-producing strain (England) 2016

Author(s): Florea, M (Florea, Michael); Hagemann, H (Hagemann, Henrik); Santosa, G (Santosa, Gabriella); Abbott, J (Abbott, James); Micklem, CN (Micklem, Chris N.); Spencer-Milnes, X (Spencer-Milnes, Xenia); Garcia, LD (Garcia, Laura de Arroyo); Paschou, D (Paschou, Despoina); Lazenbatt, C (Lazenbatt, Christopher); Kong, DZ (Kong, Deze); Chughtai, H (Chughtai, Haroon); Jensen, K (Jensen, Kirsten); Freemont, PS (Freemont, Paul S.); Kitney, R (Kitney, Richard); Reeve, B (Reeve, Benjamin); Ellis, T (Ellis, Tom)

continued

Source: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA Volume: 113 Issue: 24 Pages: E3431-E3440 DOI: 10.1073/pnas.1522985113 Published: JUN 14 2016

ABSTRACT: Bacterial cellulose is a strong and ultrapure form of cellulose produced naturally by several species of the Acetobacteraceae. Its high strength, purity, and biocompatibility make it of great interest to materials science; however, precise control of its biosynthesis has remained a challenge for biotechnology. Here we isolate a strain of *Komagataeibacter rhaeticus* (K. rhaeticus iGEM) that can produce cellulose at high yields, grow in low-nitrogen conditions, and is highly resistant to toxic chemicals. We achieved external control over its bacterial cellulose production through development of a modular genetic toolkit that enables rational reprogramming of the cell. To further its use as an organism for biotechnology, we sequenced its genome and demonstrate genetic circuits that enable functionalization and patterning of heterologous gene expression within the cellulose matrix. This work lays the foundations for using genetic engineering to produce cellulose-based materials, with numerous applications in basic science, materials engineering, and biotechnology.

Author(s) affiliation: [Florea, Michael; Hagemann, Henrik; Santosa, Gabriella; Micklem, Chris N.; Spencer-Milnes, Xenia; Garcia, Laura de Arroyo; Paschou, Despoina; Lazenbatt, Christopher; Kong, Deze; Chughtai, Haroon; Jensen, Kirsten; Freemont, Paul S.; Kitney, Richard; Reeve, Benjamin; Ellis, Tom] Univ London Imperial Coll Sci Technol & Med, Ctr Synthet Biol & Innovat, London SW7 2AZ, England.

Reprint Address: Ellis, T (reprint author), Univ London Imperial Coll Sci Technol & Med, Ctr Synthet Biol & Innovat, London SW7 2AZ, England.

Ellis, T (reprint author), Univ London Imperial Coll Sci Technol & Med, Dept Bioengn, London SW7 2AZ, England.

E-mail Author(s) affiliation: t.ellis@imperial.ac.uk

Times Cited: 0

Number of references: 56

Tags: Applications - Materials, Syntetic biology

Engineering microbial cell factories: Metabolic engineering of *Corynebacterium glutamicum* with a focus on non-natural products (Germany) 2015

Author(s): Heider, SAE (Heider, Sabine A. E.); Wendisch, VF (Wendisch, Volker F.)

Source: BIOTECHNOLOGY JOURNAL Volume: 10 Issue: 8 Special Issue: SI Pages: 1170-1184 DOI: 10.1002/biot.201400590 Published: AUG 2015

ABSTRACT: *Corynebacterium glutamicum* is the workhorse of biotechnological amino acid production. For more than 50 years amino acid producing strains of this actinomycete have been improved by classical breeding, metabolic engineering and systems and synthetic biology approaches. This review focusses mainly on recent developments on *C. glutamicum* strain development for non-natural products. Recently, metabolite sensors have accelerated classical strain breeding. Synthetic pathways for access to alternative carbon sources, such as pentoses, and to new products, such as alpha,omega-amino acids, alpha,omega-diamines, alpha-keto acids, isobutanol, carotenoids and terpenes, have been embedded in the central metabolism of *C. glutamicum*. Furthermore, *C. glutamicum* is a chassis for new and improved production processes that has been improved in two ways: by rendering it biotin prototrophic and by curing it from its prophage DNA followed by further genome reduction. The first combinations of this chassis approach with production will be highlighted. Although their transfer to industrial scale processes will have to be evaluated, these recent achievements indicate how synthetic biology helps realizing proof-of-principles. Moreover, current and future synthetic biology technology developments hold the promise to explore the full potential of *C. glutamicum* as production host for value-added chemicals.

Author(s) affiliation: [Wendisch, Volker F.] Univ Bielefeld, Fac Biol, Chair Genet Prokaryotes, D-33615 Bielefeld, Germany.

[Wendisch, Volker F.] Univ Bielefeld, CeBiTec, D-33615 Bielefeld, Germany.

Reprint Address: Wendisch, VF (reprint author), Univ Bielefeld, Fac Biol, Chair Genet Prokaryotes, Univ Str 25, D-33615 Bielefeld, Germany.

E-mail Author(s) affiliation: volker.wendisch@uni-bielefeld.de

Times Cited: 9

Number of references: 187

Tags: Applications - Materials, Syntetic biology

Exploring the potential of metallic nanoparticles within synthetic biology (Scotland) 2014

Author(s): Edmundson, MC (Edmundson, Matthew C.); Capeness, M (Capeness, Michael); Horsfall, L (Horsfall, Louise)

Source: NEW BIOTECHNOLOGY Volume: 31 Issue: 6 Pages: 572-578 DOI: 10.1016/j.nbt.2014.03.004 Published: DEC 25 2014

ABSTRACT: The fields of metallic nanoparticle study and synthetic biology have a great deal to offer one another. Metallic nanoparticles as a class of material have many useful properties. Examples given here include the potential use of quantum dots (QDs) and gold nanoparticles as sensing mechanisms in synthetic biology, and the use of synthetic biology to create nanoparticle-sensing devices based on current methods of detecting metals and metalloids such as arsenate. There are a number of organisms

which are able to produce a range of metallic nanoparticles naturally, such as species of the fungus *Phoma* which produces anti-microbial silver nanoparticles. The biological synthesis of nanoparticles may have many advantages over their more traditional industrial synthesis. If the proteins involved in biological nanoparticle synthesis can be put into a suitable bacterial chassis then they might be manipulated and the pathways engineered in order to produce more valuable nanoparticles.

Author(s) affiliation: [Edmundson, Matthew C.; Capeness, Michael; Horsfall, Louise] Univ Edinburgh, Sch Biol Sci, Edinburgh EH9 3JR, Midlothian, Scotland.

Reprint Address: Edmundson, MC (reprint author), Univ Edinburgh, Sch Biol Sci, Edinburgh EH9 3JR, Midlothian, Scotland.

E-mail Author(s) affiliation: medmunds@staffmail.ed.ac.uk; louise.horsfall@ed.ac.uk

Times Cited: 7

Number of references: 40

Tags: Applications - Materials, Syntetic biology

Integrated Micro/Nanoengineered Functional Biomaterials for Cell Mechanics and Mechanobiology: A Materials Perspective (USA) 2014

Author(s): Shao, Y (Shao, Yue); Fu, JP (Fu, Jianping)

Source: **ADVANCED MATERIALS** Volume: 26 Issue: 10 Pages: 1494-1533 DOI: 10.1002/adma.201304431 Published: MAR 2014

ABSTRACT: Working at the interface between materials science and engineering, biology, and medicine, we are now at the beginning of a great exploration using micro/nanoengineered functional biomaterials for both fundamental biology study and clinical and biomedical applications such as regenerative medicine and drug screening. In this review, an overview of state of the art micro/nanoengineered functional biomaterials that can control precisely individual aspects of cell-microenvironment interactions is presented and they are highlighted them as well-controlled platforms for mechanistic studies of mechano-sensitive and -responsive cellular behaviors and integrative biology research. The recent exciting trend where micro/nanoengineered biomaterials are integrated into miniaturized biological and biomimetic systems for dynamic multiparametric microenvironmental control of emergent and integrated cellular behaviors is also discussed. The impact of integrated micro/nanoengineered functional biomaterials for future in vitro studies of regenerative medicine, cell biology, as well as human development and disease models are discussed.

Author(s) affiliation: [Shao, Yue; Fu, Jianping] Univ Michigan, Dept Mech Engn, Integrated Biosyst & Biomech Lab, Ann Arbor, MI 48109 USA.

Reprint Address: Fu, JP (reprint author), Univ Michigan, Dept Mech Engn, Integrated Biosyst & Biomech Lab, Ann Arbor, MI 48109 USA.

Source Item Page Count: 40

Times Cited: 23

Number of references: 349

Tags: Applications - Materials, Syntetic biology

Modern approaches to the creation of industrial microorganism strains (Russia) 2015

Author(s): Debabov, VG (Debabov, V. G.)

Source: **RUSSIAN JOURNAL OF GENETICS** Volume: 51 Issue: 4 Pages: 365-376 DOI: 10.1134/S1022795415040043 Published: APR 2015

ABSTRACT: Microorganism producer strains are the basis of industrial biotechnology. Their properties determine the economical parameters of the production. Methods of rational design (metabolic engineering) and combinatorial methods of mutagenesis and selection (laboratory evolution, adaptive evolution, protein and genomic shuffling) are used for the construction of microorganism strains. Combination of these methods is frequently used. Modern strains usually do not contain plasmids and markers of drug resistance. All changes are introduced into the chromosome by the methods of homologous and site-specific recombination. The sum of such approaches is called recombineering. Gene expression is carried out at the optimal level under the control of promoters of a certain power (frequently regulated). Knowledge of a complete genomic sequence is almost a mandatory condition for the use of methods of metabolic engineering. Bioinformatics significantly assists in the selection of enzymes and the search for necessary genes and metabolic reactions. Measurement of metabolic fluxes largely assists in the construction of strains. The current level of science makes it possible to construct metabolic pathways de novo in strains for the production of chemicals and biofuel. Carbon dioxide has potential as a raw material for microbiological industry; therefore, the study of CO₂ fixation by acetogens and electrogens is a promising direction of studies.

Author(s) affiliation: State Res Inst Genet & Select Ind Microorganisms, Moscow 117545, Russia.

Reprint Address: Debabov, VG (reprint author), State Res Inst Genet & Select Ind Microorganisms, Moscow 117545, Russia.

E-mail Author(s) affiliation: genetika@genetika.ru

Times Cited: 1

Number of references: 107

Tags: Applications - Materials, Syntetic biology

Novel theranostic agents for next-generation personalized medicine: small molecules, nanoparticles, and engineered mammalian cells (Switzerland) 2015

Author(s): Kojima, R (Kojima, Ryosuke); Aubel, D (Aubel, Dominique); Fussenegger, M (Fussenegger, Martin)

Source: CURRENT OPINION IN CHEMICAL BIOLOGY Volume: 28 Pages: 29-38 DOI: 10.1016/j.cbpa.2015.05.021 Published: OCT 2015

ABSTRACT: Modern medicine is currently undergoing a paradigm shift from conventional disease treatments based on the diagnosis of a generalized disease state to a more personalized, customized treatment model based on molecular-level diagnosis. This uses novel biosensors that can precisely extract disease-related information from complex biological systems. Moreover, with the recent progress in chemical biology, materials science, and synthetic biology, it has become possible to simultaneously conduct diagnosis and targeted therapy (theranostics/theragnosis) by directly connecting the readout of a biosensor to a therapeutic output. These advances pave the way for more advanced and better personalized treatment for intractable diseases with fewer side effects. In this review, we describe recent advances in the development of cutting-edge theranostic agents that contain both diagnostic and therapeutic functions in a single integrated system. By comparing the advantages and disadvantages of each modality, we discuss the future challenges and prospects of developing ideal theranostic agents for the next generation of personalized medicine.

Author(s) affiliation: [Kojima, Ryosuke; Fussenegger, Martin] ETH, Dept Biosyst Sci & Engr, CH-4058 Basel, Switzerland.

[Aubel, Dominique] Univ Lyon 1, IUTA, Dept Genie Biol, F-69622 Villeurbanne, France.

[Fussenegger, Martin] Univ Basel, Fac Life Sci, CH-4058 Basel, Switzerland.

Reprint Address: Fussenegger, M (reprint author), ETH, Dept Biosyst Sci & Engr, Mattenstr 26, CH-4058 Basel, Switzerland.

E-mail Author(s) affiliation: martin.fussenegger@bsse.ethz.ch

Times Cited: 5

Number of references: 66

Tags: Applications - Materials, Syntetic biology

Opportunities in plant synthetic biology (England) 2014

Author(s): Cook, C (Cook, Charis); Martin, L (Martin, Lisa); Bastow, R (Bastow, Ruth)

Source: JOURNAL OF EXPERIMENTAL BOTANY Volume: 65 Issue: 8 Pages: 1921-1926 DOI: 10.1093/jxb/eru013 Published: MAY 2014

ABSTRACT: A report of the 2013 GARNet workshop An Introduction to Opportunities in Plant Synthetic Biology, highlighting exciting synthetic biology initiatives presented at the meeting, including research, methods, and online resources. Synthetic biology is an emerging field uniting scientists from all disciplines with the aim of designing or re-designing biological processes. Initially, synthetic biology breakthroughs came from microbiology, chemistry, physics, computer science, materials science, mathematics, and engineering disciplines. A transition to multicellular systems is the next logical step for synthetic biologists and plants will provide an ideal platform for this new phase of research. This meeting report highlights some of the exciting plant synthetic biology projects, and tools and resources, presented and discussed at the 2013 GARNet workshop on plant synthetic biology.

Author(s) affiliation: [Cook, Charis; Martin, Lisa; Bastow, Ruth] Univ Warwick, Sch Life Sci, Coventry CV4 7AL, W Midlands, England.

Reprint Address: Cook, C (reprint author), Univ Warwick, Sch Life Sci, Gibbet Hill Campus, Coventry CV4 7AL, W Midlands, England.

E-mail Author(s) affiliation: Charis@garnetcommunity.org.uk

Times Cited: 2

Number of references: 47

Tags: Applications - Materials, Syntetic biology

A survey of enabling technologies in synthetic biology

Author(s): Kahl, LJ (Kahl, Linda J.); Endy, D (Endy, Drew)

Source: JOURNAL OF BIOLOGICAL ENGINEERING Volume: 7 Issue: 1 Article Number: 13 DOI: 10.1186/1754-1611-7-13 Published: 2013

ABSTRACT: The set of enabling technologies compiled from this survey provide insight into the many and varied technologies that support innovation in synthetic biology. Many of these technologies are widely accessible for use, either by virtue of being in the public domain or through legal tools such as non-exclusive licensing. Access to some patent protected technologies is less clear and use of these technologies may be subject to restrictions imposed by material transfer agreements or other contract terms. We expect the technologies considered enabling for synthetic biology to change as the field advances. By monitoring the enabling technologies of synthetic biology and addressing the policies and practices that impact their development and use, our hope is that the field will be better able to realize its full potential.

Author(s) affiliation: [Kahl, Linda J.; Endy, Drew] Stanford Univ, Dept Bioengn, Stanford, CA 94305 USA.

Reprint Address: Kahl, LJ (reprint author), Stanford Univ, Dept Bioengn, Y2E2 Room 269C, 473 Via Ortega, Stanford, CA 94305 USA.

continued

E-mail Author(s) affiliation: linda.sciscript@gmail.com

Times Cited: 21

Number of references: 90

Tags: Applications - Materials, Synthetic biology

Synthetic biology to access and expand nature's chemical diversity (USA) 2016

Author(s): Smanski, MJ (Sanski, Michael J.); Zhou, H (Zhou, Hui); Claesen, J (Claesen, Jan); Shen, B (Shen, Ben); Fischbach, MA (Fischbach, Michael A.); Voigt, CA (Voigt, Christopher A.)

Source: NATURE REVIEWS MICROBIOLOGY Volume: 14 Issue: 3 Pages: 135-149 DOI: 10.1038/nrmicro.2015.24 Published: MAR 2016

ABSTRACT: Bacterial genomes encode the biosynthetic potential to produce hundreds of thousands of complex molecules with diverse applications, from medicine to agriculture and materials. Accessing these natural products promises to reinvigorate drug discovery pipelines and provide novel routes to synthesize complex chemicals. The pathways leading to the production of these molecules often comprise dozens of genes spanning large areas of the genome and are controlled by complex regulatory networks with some of the most interesting molecules being produced by non-model organisms. In this Review, we discuss how advances in synthetic biology-including novel DNA construction technologies, the use of genetic parts for the precise control of expression and for synthetic regulatory circuits-and multiplexed genome engineering can be used to optimize the design and synthesis of pathways that produce natural products.

Author(s) affiliation: [Sanski, Michael J.] Univ Minnesota Twin Cities, Dept Biochem Mol Biol & Biophys, St Paul, MN 55108 USA.

[Claesen, Jan; Fischbach, Michael A.] Univ Calif San Francisco, Dept Bioengn & Therapeut Sci, San Francisco, CA 94158 USA.

[Shen, Ben] Scripps Res Inst, Dept Chem & Mol Therapeut, Jupiter, FL 33458 USA.

Reprint Address: Voigt, CA (reprint author), MIT, Dept Biol Engr, Synthet Biol Ctr, 77 Massachusetts Ave, Cambridge, MA 02139 USA.

E-mail Author(s) affiliation: cavoigt@gmail.com

Times Cited: 5

Number of references: 157

Tags: Applications - Materials, Synthetic biology

Synthetic biology for mammalian cell technology and materials sciences (Germany) 2013

Author(s): Gubeli, RJ (Gubeli, Raphael J.); Burger, K (Burger, Katharina); Weber, W (Weber, Wilfried)

Source: BIOTECHNOLOGY ADVANCES Volume: 31 Issue: 1 Special Issue: SI Pages: 68-78 DOI: 10.1016/j.biotechadv.2012.01.007 Published: JAN-FEB 2013

ABSTRACT: The synthetic reconstruction of natural gene networks and the de novo design of artificial genetic circuits provide new insights into the cell's regulatory mechanisms and will open new opportunities for drug discovery and intelligent therapeutic schemes. We will present how modular synthetic biology tools like repressors, promoters and enzymes can be assembled into complex systems in order to discover small molecules to shut off antibiotic resistance in tubercle bacteria and to design self-sufficient therapeutic networks. The transfer of these synthetic biological modules to the materials science field enables the construction of novel drug-inducible biohybrid materials for biomedical applications. (c) 2012 Elsevier Inc. All rights reserved.

Author(s) affiliation: [Gubeli, Raphael J.; Burger, Katharina; Weber, Wilfried] Univ Freiburg, Fac Biol, D-79104 Freiburg, Germany.

[Weber, Wilfried] Univ Freiburg, FIT Freiburg Ctr Interact Mat & Bioinspired Techn, D-79104 Freiburg, Germany.

Reprint Address: Weber, W (reprint author), Schanzlestr 1, D-79104 Freiburg, Germany.

E-mail Author(s) affiliation: wilfried.weber@biologie.uni-freiburg.de

Times Cited: 3

Number of references: 32

Tags: Applications - Materials, Synthetic biology

Viruses, Artificial Viruses and Virus-Based Structures for Biomedical Applications (the Netherlands) 2016

Author(s): van Rijn, P (van Rijn, Patrick); Schirhagl, R (Schirhagl, Romana)

Source: ADVANCED HEALTHCARE MATERIALS Volume: 5 Issue: 12 Pages: 1386-1400 DOI: 10.1002/adhm.201501000 Published: JUN 22 2016

ABSTRACT: Nanobiomaterials such as virus particles and artificial virus particles offer tremendous opportunities to develop new biomedical applications such as drug- or gene-delivery, imaging and sensing but also improve understanding of biological mechanisms. Recent advances within the field of virus-based systems give insights in how to mimic viral structures and virus assembly processes as well as understanding biodistribution, cell/tissue targeting, controlled and triggered disassembly or release and circulation times. All these factors are of high importance for virus-based functional systems. This review illustrates advances in mimicking and enhancing or controlling these aspects to a high degree toward delivery and imaging applications.

Author(s) affiliation: [van Rijn, Patrick; Schirhagl, Romana] Univ Groningen, Univ Med Ctr Groningen, Biomed Engr FB40, WJ Kolff Inst Biomed Engr & Mat Sci FB41, Antonius Deusinglaan 1, NL-9713 AW Groningen, Netherlands.

[van Rijn, Patrick] Univ Groningen, Zernike Inst Adv Mat, Nijenborgh 4, NL-9747 AG Groningen, Netherlands.

continued

Reprint Address: van Rijn, P; Schirhagl, R (reprint author), Univ Groningen, Univ Med Ctr Groningen, Biomed Engn FB40, WJ Kolff Inst Biomed Engn & Mat Sci FB41, Antonius Deusinglaan 1, NL-9713 AW Groningen, Netherlands.

van Rijn, P (reprint author), Univ Groningen, Zernike Inst Adv Mat, Nijenborgh 4, NL-9747 AG Groningen, Netherlands.

E-mail Author(s) affiliation: p.van.rijn@umcg.nl; romana.schirhagl@gmail.com

Times Cited: 0

Number of references: 161

Tags: Applications - Materials, Syntetic biology

Applications - Sensors/Sensing

Application of genetically engineered microbial whole-cell biosensors for combined chemosensing (China) 2016

Author(s): He, W (He, Wei); Yuan, S (Yuan, Sheng); Zhong, WH (Zhong, Wen-Hui); Siddikee, MA (Siddikee, Md. Ashaduzzaman); Dai, CC (Dai, Chuan-Chao)

Source: APPLIED MICROBIOLOGY AND BIOTECHNOLOGY Volume: 100 Issue: 3 Pages: 1109-1119 DOI: 10.1007/s00253-015-7160-6 Published: FEB 2016

ABSTRACT: The progress of genetically engineered microbial whole-cell biosensors for chemosensing and monitoring has been developed in the last 20 years. Those biosensors respond to target chemicals and produce output signals, which offer a simple and alternative way of assessment approaches. As actual pollution caused by human activities usually contains a combination of different chemical substances, how to employ those biosensors to accurately detect real contaminant samples and evaluate biological effects of the combined chemicals has become a realistic object of environmental researches. In this review, we outlined different types of the recent method of genetically engineered microbial whole-cell biosensors for combined chemical evaluation, epitomized their detection performance, threshold, specificity, and application progress that have been achieved up to now. We also discussed the applicability and limitations of this biosensor technology and analyzed the optimum conditions for their environmental assessment in a combined way.

Author(s) affiliation: [He, Wei; Yuan, Sheng; Dai, Chuan-Chao] Nanjing Normal Univ, Coll Life Sci, Nanjing 210023, Jiangsu, Peoples R China.

[Zhong, Wen-Hui] Nanjing Normal Univ, Coll Geog Sci, Nanjing 210023, Jiangsu, Peoples R China.

Reprint Address: Dai, CC (reprint author), Nanjing Normal Univ, Coll Life Sci, Nanjing 210023, Jiangsu, Peoples R China.

E-mail Author(s) affiliation: daichuancho@njnu.edu.cn

Times cited: 1

Number of references: 73

Tags: Applicatons - sensors, Synthetic biology

Approaches towards molecular amplification for sensing (England) 2016

Author(s): Goggins, S (Goggins, Sean); Frost, CG (Frost, Christopher G.)

Source: ANALYST Volume: 141 Issue: 11 Pages: 3157-3218 DOI: 10.1039/c6an00348f Published: 2016

ABSTRACT: This review has been created with the focus on how each conceptually unique molecular amplification methodology achieves amplification, not just its sensitivity, while highlighting any key processes. Excluded are any references that were not found to contain an obvious molecular amplifier or amplification component, or that did not use an appropriate signal readout that could be incorporated into a sensing application. Additionally, methodologies where amplification is achieved through advances in instrumentation are also excluded. Depending upon the type of approach employed, amplification strategies are divided into four categories: target, label, signal or receptor amplification. More recent, more complex protocols combine a number of approaches and are therefore categorised by which amplification component described within was considered as the biggest advancement. The advantages and disadvantages of each methodology are discussed along with any limits of detection, if stated in the original article. Any subsequent use of the methodology within sensing or any other application is also mentioned to draw attention to its practicality. The importance of amplification within sensing is wholly emphasised while perspectives on the future direction of the field are also shared.

Author(s) affiliation: [Goggins, Sean; Frost, Christopher G.] Univ Bath, Sch Chem, 1 South,Claverton Down, Bath BA2 7AY, Avon, England.

Reprint Address: Goggins, S (reprint author), Univ Bath, Sch Chem, 1 South,Claverton Down, Bath BA2 7AY, Avon, England.

E-mail Author(s) affiliation: s.goggins@bath.ac.uk

Times cited: 0

Number of references: 345

Tags: Applicatons - sensors, Synthetic biology

Development of a highly specific and sensitive cadmium and lead microbial biosensor using synthetic CadC-T7 genetic circuitry (South Korea) 2016

Author(s): Kim, HJ (Kim, Hyun Ju); Lim, JW (Lim, Ji Won); Jeong, H (Jeong, Haeyoung); Lee, SJ (Lee, Sang-Jae); Lee, DW (Lee, Dong-Woo); Kim, T (Kim, Taesung); Lee, SJ (Lee, Sang Jun)

Source: *BIOSENSORS & BIOELECTRONICS* Volume: 79 Pages: 701-708 DOI: 10.1016/j.bios.2015.12.101 Published: MAY 15 2016

ABSTRACT: Multiple copies of a cadC homolog encoding a heavy metal-responsive transcription factor were found in the genome of a bacterium isolated from ocean sediment, and the heavy metal responses of the encoded proteins were characterized using a fluorescence reporter assay. Each CadC regulator exhibited distinct specificity in response to heavy metal ions, indicating their potential use as modular heavy metal biosensors. Next, we constructed CadC-controlled T7 RNA transcription systems for intracellular signal amplification, i.e., higher sensitivity. Flow cytometry revealed that cadmium and lead ions could be recognized specifically by CadC-T7 biosensors, which could be combined with a microfluidic platform to generate heavy metal biosensor devices with increased sensitivity. Our results demonstrate the successful development of synthetic CadC-T7 genetic circuitry for use in improved heavy metal biosensor microfluidic devices. (C) 2015 Elsevier B.V. All rights reserved.

Author(s) affiliation: [Kim, Hyun Ju; Lee, Sang Jun] KRIBB, Infect & Immun Res Ctr, 125 Gwahak Ro, Daejeon 34141, South Korea.

[Jeong, Haeyoung] KRIBB, Superbacteria Res Ctr, Daejeon, South Korea.

[Lee, Sang-Jae] Silla Univ, Dept Biofood Mat, Busan, South Korea.

Kim, T (reprint author), UNIST, Dept Mech Engn, 50 UNIST Gil, Ulsan 44919, South Korea.

E-mail Author(s) affiliation: tskim@unist.ac.kr; leesj@kribb.re.kr

Times cited: 0

Number of references: 33

Tags: *Applicatons - sensors, Synthetic biology*

DNA nanotechnology-enabled biosensors (China) 2016

Author(s): Chao, J (Chao, Jie); Zhu, D (Zhu, Dan); Zhang, YN (Zhang, Yinan); Wang, LH (Wang, Lianhui); Fan, CH (Fan, Chunhai)

Source: *BIOSENSORS & BIOELECTRONICS* Volume: 76 Special Issue: SI Pages: 68-79 DOI: 10.1016/j.bios.2015.07.007 Published: FEB 15 2016

ABSTRACT: Biosensors employ biological molecules to recognize the target and utilize output elements which can translate the biorecognition event into electrical, optical or mass-sensitive signals to determine the quantities of the target. DNA-based biosensors, as a sub-field to biosensor, utilize DNA strands with short oligonucleotides as probes for target recognition. Although DNA-based biosensors have offered a promising alternative for fast, simple and cheap detection of target molecules, there still exist key challenges including poor stability and reproducibility that hinder their competition with the current gold standard for DNA assays. By exploiting the self-recognition properties of DNA molecules, researchers have dedicated to make versatile DNA nanostructures in a highly rigid, controllable and fiunctionalized manner, which offers unprecedented opportunities for developing DNA-based biosensors. In this review, we will briefly introduce the recent advances on design and fabrication of static and dynamic DNA nanostructures, and summarize their applications for fabrication and functionalization of DNA-based biosensors. (C) 2015 Elsevier B.V. All rights reserved.

Author(s) affiliation: [Chao, Jie; Wang, Lianhui] Nanjing Univ Posts & Telecommun, Key Lab Organ Elect & Informat Displays, Nanjing 210023, Jiangsu, Peoples R China.

Reprint Address: Fan, CH (reprint author), Chinese Acad Sci, Div Phys Biol, Shanghai 201800, Peoples R China.

Times cited: 2

Number of references: 103

Tags: *Applicatons - sensors, Synthetic biology*

Environmental Sensing of Heavy Metals Through Whole Cell Microbial Biosensors: A Synthetic Biology Approach (Australia) 2015

Author(s): Bereza-Malcolm, LT (Bereza-Malcolm, Lara Tess); Mann, G (Mann, Guelay); Franks, AE (Franks, Ashley Edwin)

Source: *ACS SYNTHETIC BIOLOGY* Volume: 4 Issue: 5 Pages: 535-546 DOI: 10.1021/sb500286r Published: MAY 2015

ABSTRACT: Whole cell microbial biosensors are offering an alternative means for rapid, on-site heavy metal detection. Based in microorganisms, biosensing constructs are designed and constructed to produce both qualitative and quantitative outputs in response to heavy metal ions. Previous microbial biosensors designs are focused on single-input constructs; however, development of multiplexed systems is resulting in more flexible designs. The movement of microbial biosensors from laboratory based designs toward on-site, functioning heavy metal detectors has been hindered by the toxic nature of heavy metals, along with the lack of specificity of heavy metals promoter elements. Applying a synthetic biology approach with alternative, microbial chassis may increase the robustness of microbial biosensors and mitigate these issues. Before full applications are achieved, further

consideration has to be made regarding the risk and regulations of whole cell microbial biosensor use in the environment To this end, a standard framework for future whole cell microbial biosensor design and use is proposed.

Author(s) affiliation: [Bereza-Malcolm, Lara Tess; Franks, Ashley Edwin] La Trobe Univ, Dept Microbiol, Bundoora, Vic 3086, Australia.

[Mann, Guelay] Def Sci & Technol Org, Port Melbourne, Vic 3207, Australia.

Reprint Address: Franks, AE (reprint author), La Trobe Univ, Dept Microbiol, Bundoora, Vic 3086, Australia.

Source Item Page Count: 12

Times cited: 7

Number of references: 109

[Enzyme-driven i-motif DNA folding for logic operations and fluorescent biosensing \(China\) 2015](#)

Author(s): Wang, M (Wang, Ming); Zhang, GX (Zhang, Guanxin); Zhang, DQ (Zhang, Deqing)

Source: CHEMICAL COMMUNICATIONS Volume: 51 Issue: 18 Pages: 3812-3815 DOI: 10.1039/c4cc09905b Published: 2015

ABSTRACT: DNA nanodevices capable of “NOR” and “NAND” logic operations were developed using enzymatic reactions to generate an acidic pH gradient and drive the conformation change of cytosine-rich DNA. Due to the high selectivity and sensitivity of the enzymatic reactions in driving DNA logic gates, novel fluorescent biosensors were further designed for enzyme activity assay and glucose sensing.

Author(s) affiliation: [Wang, Ming; Zhang, Guanxin; Zhang, Deqing] Chinese Acad Sci, Beijing Natl Lab Mol Sci, Inst Chem, Organ Solids Lab, Beijing 100190, Peoples R China.

Reprint Address: Zhang, DQ (reprint author), Chinese Acad Sci, Beijing Natl Lab Mol Sci, Inst Chem, Organ Solids Lab, Beijing 100190, Peoples R China.

E-mail Author(s) affiliation: dqzhang@iccas.ac.cn

Times cited: 3

Number of references: 31

[Fluigi: Microfluidic Device Synthesis for Synthetic Biology \(USA\) 2014](#)

Author(s): Huang, HY (Huang, Haiyao); Densmore, D (Densmore, Douglas)

Source: ACM JOURNAL ON EMERGING TECHNOLOGIES IN COMPUTING SYSTEMS Volume: 11 Issue: 3 Special Issue: SI Article Number: 26 DOI: 10.1145/2660773 Published: DEC 2014

ABSTRACT: One goal of synthetic biology is to design and build genetic circuits in living cells for a range of applications. Our incomplete knowledge of the effects of metabolic load and biological “crosstalk” on the host cell make it difficult to construct multilevel genetic logic circuits in a single cell, limiting the scalability of engineered biological systems. Microfluidic technologies provide reliable and scalable construction of synthetic biological systems by allowing compartmentalization of cells encoding simple genetic circuits and the spatiotemporal control of communication among these cells. This control is achieved via valves on the microfluidics chip which restrict fluid flow when activated. We describe a Computer Aided Design (CAD) framework called “Fluigi” for optimizing the layout of genetic circuits on a microfluidic chip, generating the control sequence of the associated signaling fluid valves, and simulating the behavior of the configured biological circuits. We demonstrate the capabilities of Fluigi on a set of Boolean algebraic benchmark circuits found in both synthetic biology and electrical engineering and a set of assay-based benchmark circuits. The integration of microfluidics and synthetic biology has the capability to increase the scale of engineered biological systems for applications in DNA assembly, biosensors, and screening assays for novel orthogonal genetic parts.

Author(s) affiliation: [Huang, Haiyao; Densmore, Douglas] Boston Univ, Boston, MA 02215 USA.

Reprint Address: Huang, HY (reprint author), Boston Univ, 8 St Marys St, Boston, MA 02215 USA.

E-mail Author(s) affiliation: huangh@bu.edu; dougd@bu.edu

Times cited: 0

Number of references: 58

Tags: Applicatons - sensors, Synthetic biology

[Global transcriptomic responses of Escherichia coli K-12 to volatile organic compounds \(Singapore\) 2016](#)

Author(s): Yung, PY (Yung, Pui Yi); Lo Grasso, L (Lo Grasso, Letizia); Mohidin, AF (Mohidin, Abeed Fatima); Acerbi, E (Acerbi, Enzo); Hinks, J (Hinks, Jamie); Seviour, T (Seviour, Thomas); Marsili, E (Marsili, Enrico); Lauro, FM (Lauro, Federico M.)

Source: SCIENTIFIC REPORTS Volume: 6 Article Number: 19899 DOI: 10.1038/srep19899 Published: JAN 28 2016

ABSTRACT: Volatile organic compounds (VOCs) are commonly used as solvents in various industrial settings. Many of them present a challenge to receiving environments, due to their toxicity and low bioavailability for degradation. Microorganisms are capable of sensing and responding to their surroundings and this makes them ideal detectors for toxic compounds. This study investigates the global transcriptomic responses of Escherichia coli K-12 to selected VOCs at sub-toxic levels. Cells grown in the presence of VOCs were harvested during exponential growth, followed by whole transcriptome shotgun sequencing (RNAseq). The analysis of the

data revealed both shared and unique genetic responses compared to cells without exposure to VOCs. Results suggest that various functional gene categories, for example, those relating to Fe/S cluster biogenesis, oxidative stress responses and transport proteins, are responsive to selected VOCs in *E. coli*. The differential expression (DE) of genes was validated using GFP-promoter fusion assays. A variety of genes were differentially expressed even at non-inhibitory concentrations and when the cells are at their balanced-growth. Some of these genes belong to generic stress response and others could be specific to VOCs. Such candidate genes and their regulatory elements could be used as the basis for designing biosensors for selected VOCs.

Author(s) affiliation: [Yung, Pui Yi; Lo Grasso, Letizia; Mohidin, Abeed Fatima; Acerbi, Enzo; Hinks, Jamie; Seviour, Thomas; Marsili, Enrico; Lauro, Federico M.] SCELSE, 60 Nanyang Dr, SBS-01N-27, Singapore 637551, Singapore.

[Marsili, Enrico] Nanyang Technol Univ, Sch Chem & Biomed Engn, 62 Nanyang Dr, Singapore 637459, Singapore.

Lauro, FM (reprint author), Nanyang Technol Univ, Asian Sch Environm, 50 Nanyang Ave, N2-01C-45, Singapore 639798, Singapore.

E-mail Author(s) affiliation: FLauro@ntu.edu.sg

Times cited: 0

Number of references: 89

Tags: Applicatons - sensors, Synthetic biology

Initiator-catalyzed self-assembly of duplex-looped DNA hairpin motif based on strand displacement reaction for logic operations and amplified biosensing (China) 2016

Author(s): Bi, S (Bi, Sai); Yue, SZ (Yue, Shuzhen); Wu, Q (Wu, Qiang); Ye, JY (Ye, Jiayan)

Source: BIOSENSORS & BIOELECTRONICS Volume: 83 Pages: 281-286 DOI: 10.1016/j.bios.2016.04.059 Published: SEP 15 2016

ABSTRACT: Here we program an initiator-catalyzed self-assembly of duplex-looped DNA hairpin motif based on strand displacement reaction. Due to the recycling of initiator and performance in a cascade manner, this system is versatily extended to logic operations, including the construction of concatenated logic circuits with a feedback function and a biocomputing keypad-lock security system. Compared with previously reported molecular security systems, the prominent feature of our keypad lock is that it can be spontaneously reset and recycled with no need of any external stimulus and human intervention. Moreover, through integrating with an isothermal amplification technique of rolling circle amplification (RCA), this programming catalytic DNA self-assembly strategy readily achieves sensitive and selective biosensing of initiator. Importantly, a magnetic graphene oxide (MGO) is introduced to remarkably reduced background, which plays an important role in enhancing the signal-to-noise ratio and improving the detection sensitivity. Therefore, the proposed sophisticated DNA strand displacement-based methodology with engineering dynamic functions may find broad applications in the construction of programming DNA nanostructures, amplification biosensing platform, and large-scale DNA circuits. (C) 2016 Elsevier B.V. All rights reserved.

Author(s) affiliation: [Bi, Sai; Yue, Shuzhen] Qingdao Univ, Collaborat Innovat Ctr Marine Biomass Fiber Mat &, Shandong Sino Japanese Ctr Collaborat Res Carbon, Lab Fiber Mat & Modern Text, Growing Base State Ke, Qingdao 266071, Peoples R China.

[Wu, Qiang] Chinese Acad Fishery Sci, Shandong Prov Key Lab Fishery Resources & Ecoenvi, Key Lab Sustainable Dev Marine Fisheries, Minist Agr, Yellow Sea Fisheries Res Inst, Qingdao 266071, Peoples R China.

[Ye, Jiayan] Qingdao Univ Sci & Technol, Coll Chem & Mol Engn, Minist Educ, Key Lab Sensor Anal Tumor Marker, Qingdao 266042, Peoples R China.

Reprint Address: Bi, S (reprint author), Qingdao Univ, Collaborat Innovat Ctr Marine Biomass Fiber Mat &, Shandong Sino Japanese Ctr Collaborat Res Carbon, Lab Fiber Mat & Modern Text, Growing Base State Ke, Qingdao 266071, Peoples R China.

E-mail Author(s) affiliation: bisai11@126.com

Times cited: 0

Number of references: 45

Tags: Applicatons - sensors, Synthetic biology

Synthetic biology and biomimetic chemistry as converging technologies fostering a new generation of smart biosensors (Italy) 2015

Author(s): Scognamiglio, V (Scognamiglio, Viviana); Antonacci, A (Antonacci, Amina); Lambrea, MD (Lambrea, Maya D.); Litescu, SC (Litescu, Simona C.); Rea, G (Rea, Giuseppina)

Source: BIOSENSORS & BIOELECTRONICS Volume: 74 Pages: 1076-1086 DOI: 10.1016/j.bios.2015.07.078 Published: DEC 15 2015

ABSTRACT: The present review considered the role of synthetic biology in sustaining biosensor technology, reporting examples from the literature and reflecting on the features that make it a useful tool for designing and constructing engineered biological systems for sensing application. Besides, a section dedicated to bioinspired synthetic molecules as powerful tools to enhance biosensor potential is reported, and treated as an extension of the concept of biomimetic chemistry, where organic synthesis is used to generate artificial molecules that mimic natural molecules. Thus, the design of synthetic molecules, such as aptamers, biomimetics, molecular imprinting polymers, peptide nucleic acids, and ribozymes were encompassed as "products" of biomimetic chemistry. (C) 2015 Elsevier B.V. All rights reserved.

Author(s) affiliation: [Scognamiglio, Viviana; Antonacci, Amina; Lambreva, Maya D.; Rea, Giuseppina] Natl Res Council Italy CNR, IC, I-00015 Rome, Italy.

[Litescu, Simona C.] Natl Inst Biol Sci, Ctr Bioanal, Bucharest 060031 6, Romania.

Reprint Address: Scognamiglio, V (reprint author), CNR, Inst Crystallog, Dept Agrofood, I-00015 Rome, Italy.

E-mail Author(s) affiliation: viviana.scognamiglio@milib.ic.cnr.it

Times cited: 2

Number of references: 88

Tags: Applicatons - sensors, Synthetic biology

Synthetic Biology and Microdevices: A Powerful Combination (Belgium) 2013

Author(s): Venken, L (Venken, Lyn); Marchal, K (Marchal, Kathleen); Vanderleyden, J (Vanderleyden, Jos)

Source: ACM JOURNAL ON EMERGING TECHNOLOGIES IN COMPUTING SYSTEMS Volume: 9 Issue: 4 Special Issue: SI Article Number: 30 DOI: 10.1145/2504775 Published: NOV 2013

ABSTRACT: Recent developments demonstrate that the combination of microbiology with micro-and nanoelectronics is a successful approach to develop new miniaturized sensing devices and other technologies. In the last decade, there has been a shift from the optimization of the abiotic components, for example, the chip, to the improvement of the processing capabilities of cells through genetic engineering. The synthetic biology approach will not only give rise to systems with new functionalities, but will also improve the robustness and speed of their response towards applied signals. To this end, the development of new genetic circuits has to be guided by computational design methods that enable to tune and optimize the circuit response. As the successful design of genetic circuits is highly dependent on the quality and reliability of its composing elements, intense characterization of standard biological parts will be crucial for an efficient rational design process in the development of new genetic circuits. Microengineered devices can thereby offer a new analytical approach for the study of complex biological parts and systems. By summarizing the recent techniques in creating new synthetic circuits and in integrating biology with microdevices, this review aims at emphasizing the power of combining synthetic biology with microfluidics and microelectronics.

Author(s) affiliation: [Venken, Lyn; Marchal, Kathleen] Katholieke Univ Leuven, CMPG, B-3001 Heverlee, Belgium.

[Marchal, Kathleen; Vanderleyden, Jos] UGent, Dept Plant Biotechnol & Bioinformat, B-9052 Ghent, Belgium.

Reprint Address: Venken, L (reprint author), Katholieke Univ Leuven, CMPG, Kasteelpk Arenberg 20, Bus 2460, B-3001 Heverlee, Belgium.

E-mail Author(s) affiliation: lyn.venken@biw.kuleuven.be

Times cited: 0

Number of references: 112

Tags: Applicatons - sensors, Synthetic biology

A tutorial review for employing enzymes for the construction of G-quadruplex-based sensing platforms (China) 2016

Author(s): Ma, DL (Ma, Dik-Lung); Wang, WH (Wang, Wanhe); Mao, ZF (Mao, Zhifeng); Yang, C (Yang, Chao); Chen, XP (Chen, Xiu-Ping); Lu, JJ (Lu, Jin-Jian); Han, QB (Han, Quan-Bin); Leung, CH (Leung, Chung-Hang)

Source: ANALYTICA CHIMICA ACTA Volume: 913 Pages: 41-54 DOI: 10.1016/j.aca.2016.01.043 Published: MAR 24 2016

ABSTRACT: With rapid advances in the field of DNA chemistry, nucleic acids and DNA-modifying enzymes have recently emerged as versatile components for the construction of oligonucleotide-based sensors. Meanwhile, the G-quadruplex motif has been widely employed for the development of DNA-based assays due to its diverse structural variety. In this tutorial, we introduce the principles of G-quadruplex-based sensing and the use of DNA-modifying enzymes for sensor platform development. We also highlight recent studies of the application of DNA-modifying enzymes for the development of G-quadruplex-based luminescent detection platforms with a view towards how those enzymes play an important role in sensitivity enhancement. (C) 2016 Elsevier B.V. All rights reserved.

Author(s) affiliation: [Ma, Dik-Lung; Wang, Wanhe; Mao, Zhifeng] Hong Kong Baptist Univ, Dept Chem, Kowloon Tong, Hong Kong, Peoples R China.

[Yang, Chao; Chen, Xiu-Ping; Lu, Jin-Jian; Leung, Chung-Hang] Univ Macau, Inst Chinese Med Sci, State Key Lab Qual Res Chinese Med, Macau, Peoples R China.

[Han, Quan-Bin] Hong Kong Baptist Univ, Sch Chinese Med, Kowloon, Hong Kong, Peoples R China.

Reprint Address: Ma, DL (reprint author), Hong Kong Baptist Univ, Dept Chem, Kowloon Tong, Hong Kong, Peoples R China.

Times cited: 0

Number of references: 159

Tags: Applicatons - sensors, Synthetic biology

Ultraspecific electrochemical DNA biosensor by coupling spontaneous cascade DNA branch migration and dual-signaling sensing strategy (China) 2016

Author(s): Wang, T (Wang, Ting); Zhou, LL (Zhou, Lili); Bai, SL (Bai, Shulian); Zhang, Z (Zhang, Zhang); Li, JL (Li, Junlong); Jing, XY (Jing, Xiaoying); Xie, GM (Xie, Guoming)

Source: *BIOSENSORS & BIOELECTRONICS* Volume: 78 Pages: 464-470 DOI: 10.1016/j.bios.2015.11.071 Published: APR 15 2016

ABSTRACT: Using spontaneous cascade DNA branch migration and dual-signaling sensing strategy, we developed a novel universal electrochemical biosensor for the highly specific and sensitive detection of nucleic acids. A target strand (Ts) competitively hybridized with a ferrocene (Fc)-labeled signal probe (Fc-S1), which was blocked by a protector strand (Ps), after strand displacement to form the Ts/Fc-S1 duplex. A methylene blue (MB)-modified signal probe (MB-S2) was immobilized on the Au electrode surface by hybridizing with a thiolated capture probe (Cp). Then, the obtained reactants (Ts/Fc-S1 and MB-S2/Cp) suffered spontaneous DNA branch migration and produced two hybridization products (Fc-S1/Cp and MB-S2/Ts). These reactions led to the dissociation of MB molecules and the collection of Fc molecules. The detection mechanism of this DNA biosensor involved distance variation between the redox tags and the Au electrode, which was associated with target-induced cascade DNA branch migration. Moreover, we rationally designed the cascade DNA branch migration to occur spontaneously with Delta G degrees approximate to 0, at which slight thermodynamic changes caused by base mismatch exerted a disproportionately large effect on the hybridization yield. This "signal-on/off" sensing system exhibited a remarkable analytical performance and an ultrahigh discrimination capability even against a single-base mismatch. The maximum discrimination factor (DF) of base mutations or alterations can reach 17.9. Therefore, our electrochemical biosensor might hold a great potential for further applications in biomedical research and early clinical diagnosis. (C) 2015 Elsevier B.V. All rights reserved.

Author(s) affiliation: [Wang, Ting; Zhou, Lili; Bai, Shulian; Zhang, Zhang; Li, Junlong; Xie, Guoming] Chongqing Med Univ, Dept Lab Med, Key Lab Lab Med Diagnost, Minist Educ, 1 Yi Xue Yuan Rd, Chongqing 400016, Peoples R China.

[Jing, Xiaoying] Nanjing Med Univ, Dept Lab Med, Affiliated Wuxi Peoples Hosp, Wuxi 214023, Peoples R China.

Reprint Address: Xie, GM (reprint author), Chongqing Med Univ, Dept Lab Med, Key Lab Lab Med Diagnost, Minist Educ, 1 Yi Xue Yuan Rd, Chongqing 400016, Peoples R China.

E-mail Author(s) affiliation: guomingxie@cqmu.edu.cn

Times cited: 0

Number of references: 31

Tags: Applicatons - sensors, Synthetic biology

Understanding and exploiting feedback in synthetic biology (USA) 2013

Author(s): Afroz, T (Afroz, Taliman); Beisel, CL (Beisel, Chase L.)

Source: *CHEMICAL ENGINEERING SCIENCE* Volume: 103 Pages: 79-90 DOI: 10.1016/j.ces.2013.02.017 Published: NOV 15 2013

ABSTRACT: Synthetic biology employs traditional engineering concepts in the construction of cells and organisms. One of the most fundamental concepts is feedback, where the activity of a system is influenced by its output. Feedback can imbue the system with a range of desirable properties such as reducing the rise time or exhibiting an ultrasensitive response. Feedback is also commonly found in nature, further supporting the incorporation of feedback into synthetic biological systems. In this review, we discuss the common attributes of negative and positive feedback loops in gene regulatory networks, whether alone or in combination, and describe recent applications of feedback in metabolic engineering, population control, and the development of advanced biosensors. The examples principally come from synthetic systems in the bacterium *Escherichia coli* and in the budding yeast *Saccharomyces cerevisiae*, the two major workhorses of synthetic biology. Through this review, we argue that biological feedback represents a powerful yet underutilized tool that can advance the construction of biological systems. (C) 2013 Elsevier Ltd. All rights reserved.

Author(s) affiliation: [Afroz, Taliman; Beisel, Chase L.] N Carolina State Univ, Dept Biomol & Chem Engr, Raleigh, NC 27695 USA.

Reprint Address: Beisel, CL (reprint author), N Carolina State Univ, Dept Biomol & Chem Engr, Raleigh, NC 27695 USA.

E-mail Author(s) affiliation: cbeisel@ncsu.edu

Times cited: 5

Number of references: 98

Tags: Applicatons - sensors, Synthetic biology ■

ABOUT THIS PUBLICATION

The S&T IN-DEPTH BULLETIN is a compilation of selected recent technical articles on emerging fields in science and technology which may have long or short term implication for national security. Articles are selected from peer-reviewed journals and focus on providing a more detailed insight to the R&E community. Each quarter we will feature a topic and provide abstracts from the most timely and relevant review articles. Providing a comprehensive bibliography is beyond the scope of this publication but full articles may be requested via the Pentagon library or via your local Command's library. Personnel assigned to the Pentagon may request articles from John Mills at john.mills@whs.mil.

We welcome your feedback to improve the publication and make it more relevant to your work. To subscribe (or unsubscribe), visit <https://tin-ly.sainc.com/ASDRE>. To provide feedback or ask questions, contact us at asdre-st-bulletin-reply@sainc.com.

This publication is authored and distributed by:

Ryan Zelnio, Ph.D., Associate Director - Tech Watch / Horizon Scans,
Office of Net Technical Assessments, OSD AT&L/OASD(R&E)

Ms. Hema Viswanath, TW/HS, ONTA Corporate Librarian

The appearance of external hyperlinks in this publication does not constitute endorsement by the United States Department of Defense (DoD) of the linked web sites, nor the information, products or services contained therein. In addition, the content featured does not necessarily reflect DoD's views or priorities.