

Thomas E Gorochowski

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

1,804
citations

279798

23
h-index

315739

38
g-index

60
all docs

60
docs citations

60
times ranked

1780
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Massively parallel characterization of engineered transcript isoforms using direct RNA sequencing. <i>Nature Communications</i> , 2022, 13, 434. | 12.8 | 11 |
| 2 | Improving the Robustness of Engineered Bacteria to Nutrient Stress Using Programmed Proteolysis. <i>ACS Synthetic Biology</i> , 2022, 11, 1049-1059. | 3.8 | 9 |
| 3 | An Open Platform for High-Resolution Light-Based Control of Microscopic Collectives. <i>Advanced Intelligent Systems</i> , 2022, 4, . | 6.1 | 4 |
| 4 | Harnessing the central dogma for stringent multi-level control of gene expression. <i>Nature Communications</i> , 2021, 12, 1738. | 12.8 | 26 |
| 5 | Cheetah: A Computational Toolkit for Cybergenetic Control. <i>ACS Synthetic Biology</i> , 2021, 10, 979-989. | 3.8 | 23 |
| 6 | Towards an engineering theory of evolution. <i>Nature Communications</i> , 2021, 12, 3326. | 12.8 | 33 |
| 7 | Efficient multiplexed gene regulation in <i>Saccharomyces cerevisiae</i> using dCas12a. <i>Nucleic Acids Research</i> , 2021, 49, 7775-7790. | 14.5 | 24 |
| 8 | paraSBOLv: a foundation for standard-compliant genetic design visualization tools. <i>Synthetic Biology</i> , 2021, 6, ysab022. | 2.2 | 1 |
| 9 | Characterizing Genetic Parts and Devices Using RNA Sequencing. <i>Methods in Molecular Biology</i> , 2021, 2229, 175-187. | 0.9 | 0 |
| 10 | Specifications of standards in systems and synthetic biology: status and developments in 2021. <i>Journal of Integrative Bioinformatics</i> , 2021, 18, . | 1.5 | 2 |
| 11 | The Synthetic Biology Open Language (SBOL) Version 3: Simplified Data Exchange for Bioengineering. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 1009. | 4.1 | 40 |
| 12 | Sequencing enabling design and learning in synthetic biology. <i>Current Opinion in Chemical Biology</i> , 2020, 58, 54-62. | 6.1 | 18 |
| 13 | Advances in engineering CRISPR-Cas9 as a molecular Swiss Army knife. <i>Synthetic Biology</i> , 2020, 5, ysaa021. | 2.2 | 9 |
| 14 | Self-adaptive biosystems through tunable genetic parts and circuits. <i>Current Opinion in Systems Biology</i> , 2020, 24, 78-85. | 2.6 | 17 |
| 15 | Tunable genetic devices through simultaneous control of transcription and translation. <i>Nature Communications</i> , 2020, 11, 2095. | 12.8 | 29 |
| 16 | SBOL Visual 2 Ontology. <i>ACS Synthetic Biology</i> , 2020, 9, 972-977. | 3.8 | 3 |
| 17 | Toward Engineering Biosystems With Emergent Collective Functions. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 705. | 4.1 | 22 |
| 18 | Synthetic biology open language (SBOL) version 3.0.0. <i>Journal of Integrative Bioinformatics</i> , 2020, 17, . | 1.5 | 13 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | Specifications of standards in systems and synthetic biology: status and developments in 2020. <i>Journal of Integrative Bioinformatics</i> , 2020, 17, . | 1.5 | 10 |
| 20 | <sc>P</sc> recision design of stable genetic circuits carried in highly insulated <i>E.Âcoli</i> genomic landing pads. <i>Molecular Systems Biology</i> , 2020, 16, e9584. | 7.2 | 45 |
| 21 | Communicating Structure and Function in Synthetic Biology Diagrams. <i>ACS Synthetic Biology</i> , 2019, 8, 1818-1825. | 3.8 | 30 |
| 22 | Augmented reality for the engineering of collective behaviours in microsystems. , 2019, , . | | 6 |
| 23 | CRISPR/Cas12a Multiplex Genome Editing of Saccharomyces cerevisiae and the Creation of Yeast Pixel Art. <i>Journal of Visualized Experiments</i> , 2019, , . | 0.3 | 10 |
| 24 | Absolute quantification of translational regulation and burden using combined sequencing approaches. <i>Molecular Systems Biology</i> , 2019, 15, e8719. | 7.2 | 61 |
| 25 | Pathways to cellular supremacy in biocomputing. <i>Nature Communications</i> , 2019, 10, 5250. | 12.8 | 88 |
| 26 | Living computers powered by biochemistry. <i>Biochemist</i> , 2019, 41, 14-18. | 0.5 | 13 |
| 27 | Burden-driven feedback control of gene expression. <i>Nature Methods</i> , 2018, 15, 387-393. | 19.0 | 281 |
| 28 | Organization of feed-forward loop motifs reveals architectural principles in natural and engineered networks. <i>Science Advances</i> , 2018, 4, eaap9751. | 10.3 | 40 |
| 29 | Designing efficient translation. <i>Nature Biotechnology</i> , 2018, 36, 934-935. | 17.5 | 12 |
| 30 | Automated Visualization of Genetic Designs Using DNAplotlib. <i>Methods in Molecular Biology</i> , 2018, 1772, 399-409. | 0.9 | 13 |
| 31 | Registry in a tube: multiplexed pools of retrievable parts for genetic design space exploration. <i>Nucleic Acids Research</i> , 2017, 45, gkw1226. | 14.5 | 37 |
| 32 | A standard-enabled workflow for synthetic biology. <i>Biochemical Society Transactions</i> , 2017, 45, 793-803. | 3.4 | 38 |
| 33 | How Behaviour and the Environment Influence Transmission in Mobile Groups. <i>Theoretical Biology</i> , 2017, , 17-42. | 0.1 | 4 |
| 34 | Genetic circuit characterization and debugging using <sc>RNA</sc> â€seq. <i>Molecular Systems Biology</i> , 2017, 13, 952. | 7.2 | 80 |
| 35 | DNAplotlib: Programmable Visualization of Genetic Designs and Associated Data. <i>ACS Synthetic Biology</i> , 2017, 6, 1115-1119. | 3.8 | 50 |
| 36 | Agent-based modelling in synthetic biology. <i>Essays in Biochemistry</i> , 2016, 60, 325-336. | 4.7 | 70 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 37 | A Minimal Model of Ribosome Allocation Dynamics Captures Trade-offs in Expression between Endogenous and Synthetic Genes. ACS Synthetic Biology, 2016, 5, 710-720. | 3.8 | 106 |
| 38 | Memory and Combinatorial Logic Based on DNA Inversions: Dynamics and Evolutionary Stability. ACS Synthetic Biology, 2015, 4, 1361-1372. | 3.8 | 42 |
| 39 | Beyond contact-based transmission networks: the role of spatial coincidence. Journal of the Royal Society Interface, 2015, 12, 20150705. | 3.4 | 38 |
| 40 | Trade-offs between tRNA abundance and mRNA secondary structure support smoothing of translation elongation rate. Nucleic Acids Research, 2015, 43, 3022-3032. | 14.5 | 111 |
| 41 | Computational modeling and analysis of hippocampal-prefrontal information coding during a spatial decision-making task. Frontiers in Behavioral Neuroscience, 2014, 8, 62. | 2.0 | 6 |
| 42 | Using Synthetic Biological Parts and Microbioreactors to Explore the Protein Expression Characteristics of <i>Escherichia coli</i> . ACS Synthetic Biology, 2014, 3, 129-139. | 3.8 | 36 |
| 43 | Translational sensitivity of the Escherichia coli genome to fluctuating tRNA availability. Nucleic Acids Research, 2013, 41, 8021-8033. | 14.5 | 36 |
| 44 | Using Aging to Visually Uncover Evolutionary Processes on Networks. IEEE Transactions on Visualization and Computer Graphics, 2012, 18, 1343-1352. | 4.4 | 29 |
| 45 | BSim: An Agent-Based Tool for Modeling Bacterial Populations in Systems and Synthetic Biology. PLoS ONE, 2012, 7, e42790. | 2.5 | 116 |
| 46 | Evolving dynamical networks: A formalism for describing complex systems. Complexity, 2012, 17, 18-25. | 1.6 | 34 |
| 47 | Evolving enhanced topologies for the synchronization of dynamical complex networks. Physical Review E, 2010, 81, 056212. | 2.1 | 56 |