# TomÃ¡Å¡ Helikar

## List of Publications by Year
in descending order

| 59 papers | 2,087 citations | 361413<br>20 h-index | 276875<br>41 g-index |
|---|---|---|---|
| 68 all docs | 68 docs citations | 68 times ranked | 1698 citing authors |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 1 | Recent applications of quantitative systems pharmacology and machine learning models across diseases. Journal of Pharmacokinetics and Pharmacodynamics, 2022, 49, 19-37. | 1.8 | 22 |
| 2 | Two heads are better than one: current landscape of integrating QSP and machine learning. Journal of Pharmacokinetics and Pharmacodynamics, 2022, 49, 5-18. | 1.8 | 26 |
| 3 | Addressing <i>barriers in comprehensiveness, accessibility, reusability, interoperability and reproducibility of computational models in systems biology</i>. Briefings in Bioinformatics, 2022, 23, . | 6.5 | 10 |
| 4 | A practical guide to mechanistic systems modeling in biology using a logic-based approach. Briefings in Bioinformatics, 2021, 22, . | 6.5 | 19 |
| 5 | Setting the basis of best practices and standards for curation and annotation of logical models in biology—highlights of the [BC]2 2019 CoLoMoTo/SysMod Workshop. Briefings in Bioinformatics, 2021, 22, 1848-1859. | 6.5 | 25 |
| 6 | The Need for Research-Grade Systems Modeling Technologies for Life Science Education. Trends in Molecular Medicine, 2021, 27, 100-103. | 6.7 | 2 |
| 7 | Teaching Metabolism in Upper-Division Undergraduate Biochemistry Courses using Online Computational Systems and Dynamical Models Improves Student Performance. CBE Life Sciences Education, 2021, 20, ar13. | 2.3 | 14 |
| 8 | Integrative network analyses of transcriptomics data reveal potential drug targets for acute radiation syndrome. Scientific Reports, 2021, 11, 5585. | 3.3 | 4 |
| 9 | SysMod: the ISCB community for data-driven computational modelling and multi-scale analysis of biological systems. Bioinformatics, 2021, 37, 3702-3706. | 4.1 | 6 |
| 10 | A multi-approach and multi-scale platform to model CD4+ T cells responding to infections. PLoS Computational Biology, 2021, 17, e1009209. | 3.2 | 12 |
| 11 | Essential role of systemic iron mobilization and redistribution for adaptive thermogenesis through HIF2-α/hepcidin axis. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2109186118. | 7.1 | 9 |
| 12 | Integrative computational approach identifies drug targets in CD4+ T-cell-mediated immune disorders. Npj Systems Biology and Applications, 2021, 7, 4. | 3.0 | 18 |
| 13 | COVID19 Disease Map, a computational knowledge repository of virus—host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387. | 7.2 | 53 |
| 14 | The simulation experiment description markup language (SED-ML): language specification for level 1 version 4. Journal of Integrative Bioinformatics, 2021, 18, 20210021. | 1.5 | 8 |
| 15 | Using concept maps to characterise cellular respiration knowledge in undergraduate students. Journal of Biological Education, 2020, 54, 33-46. | 1.5 | 18 |
| 16 | Changes in lipid profiles of epileptic mouse model. Metabolomics, 2020, 16, 106. | 3.0 | 7 |
| 17 | Differences in Blood-Derived Francisella tularensis Type B Strains from Clinical Cases of Tularemia. Microorganisms, 2020, 8, 1515. | 3.6 | 3 |
| 18 | Simulating a Computational Biological Model, Rather Than Reading, Elicits Changes in Brain Activity during Biological Reasoning. CBE Life Sciences Education, 2020, 19, ar45. | 2.3 | 5 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 19 | Automated inference of Boolean models from molecular interaction maps using CaSQ. Bioinformatics, 2020, 36, 4473-4482. | 4.1 | 57 |
| 20 | Aberrant energy metabolism and redox balance in seizure onset zones of epileptic patients. Journal of Proteomics, 2020, 223, 103812. | 2.4 | 4 |
| 21 | ccNetViz: a WebGL-based JavaScript library for visualization of large networks. Bioinformatics, 2020, 36, 4527-4529. | 4.1 | 2 |
| 22 | Interactive learning modules with 3D printed models improve student understanding of protein structure–function relationships. Biochemistry and Molecular Biology Education, 2020, 48, 356-368. | 1.2 | 8 |
| 23 | <scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110. | 7.2 | 178 |
| 24 | Modelling activities integrating construction and simulation supported explanatory and evaluative reasoning. International Journal of Science Education, 2019, 41, 1764-1786. | 1.9 | 11 |
| 25 | Student Understanding of DNA Structure–Function Relationships Improves from Using 3D Learning Modules with Dynamic 3D Printed Models. Biochemistry and Molecular Biology Education, 2019, 47, 303-317. | 1.2 | 29 |
| 26 | Changes in students' mental models from computational modeling of gene regulatory networks. International Journal of STEM Education, 2019, 6, . | 5.0 | 10 |
| 27 | Simulation of Stimulation: Cytokine Dosage and Cell Cycle Crosstalk Driving Timing-Dependent T Cell Differentiation. Frontiers in Physiology, 2018, 9, 879. | 2.8 | 44 |
| 28 | CancerDiscover: an integrative pipeline for cancer biomarker and cancer class prediction from high-throughput sequencing data. Oncotarget, 2018, 9, 2565-2573. | 1.8 | 10 |
| 29 | A Mechanistic Computational Model Reveals That Plasticity of CD4+ T Cell Differentiation Is a Function of Cytokine Composition and Dosage. Frontiers in Physiology, 2018, 9, 878. | 2.8 | 46 |
| 30 | Identification of Biologically Essential Nodes via Determinative Power in Logical Models of Cellular Processes. Frontiers in Physiology, 2018, 9, 1185. | 2.8 | 13 |
| 31 | Visualizing the Invisible: A Guide to Designing, Printing, and Incorporating Dynamic 3D Molecular Models to Teach Structure–Function Relationships. Journal of Microbiology and Biology Education, 2018, 19, . | 1.0 | 13 |
| 32 | The CoLoMoTo Interactive Notebook: Accessible and Reproducible Computational Analyses for Qualitative Biological Networks. Frontiers in Physiology, 2018, 9, 680. | 2.8 | 67 |
| 33 | Simulated Computational Model Lesson Improves Foundational Systems Thinking Skills and Conceptual Knowledge in Biology Students. BioScience, 2018, 68, 612-621. | 4.9 | 19 |
| 34 | Computational Systems Biology Approach for the Study of Rheumatoid Arthritis: From a Molecular Map to a Dynamical Model. Genomics and Computational Biology, 2017, 4, 100050. | 0.7 | 20 |
| 35 | Identification of potential tissue-specific cancer biomarkers and development of cancer versus normal genomic classifiers. Oncotarget, 2017, 8, 85692-85715. | 1.8 | 18 |
| 36 | Systems Perturbation Analysis of a Large-Scale Signal Transduction Model Reveals Potentially Influential Candidates for Cancer Therapeutics. Frontiers in Bioengineering and Biotechnology, 2016, 4, 10. | 4.1 | 29 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 37 | Logical Modeling and Dynamical Analysis of Cellular Networks. Frontiers in Genetics, 2016, 7, 94. | 2.3 | 216 |
| 38 | Programmatic access to logical models in the Cell Collective modeling environment via a REST API. BioSystems, 2016, 139, 12-16. | 2.0 | 3 |
| 39 | SBML Level 3 package: Qualitative Models, Version 1, Release 1. Journal of Integrative Bioinformatics, 2015, 12, 691-730. | 1.5 | 15 |
| 40 | Cooperative development of logical modelling standards and tools with CoLoMoTo. Bioinformatics, 2015, 31, 1154-1159. | 4.1 | 98 |
| 41 | Integrating Interactive Computational Modeling in Biology Curricula. PLoS Computational Biology, 2015, 11, e1004131. | 3.2 | 27 |
| 42 | The Systems Biology Markup Language (SBML) Level 3 Package: Qualitative Models, Version 1, Release 1. Journal of Integrative Bioinformatics, 2015, 12, 270. | 1.5 | 21 |
| 43 | Sensitivity analysis of biological Boolean networks using information fusion based on nonadditive set functions. BMC Systems Biology, 2014, 8, 92. | 3.0 | 8 |
| 44 | Design, Assessment, and in vivo Evaluation of a Computational Model Illustrating the Role of CAV1 in CD4+ T-lymphocytes. Frontiers in Immunology, 2014, 5, 599. | 4.8 | 16 |
| 45 | Molecular phylogeny and evolutionary dynamics of influenza A nonstructural (NS) gene. Infection, Genetics and Evolution, 2014, 22, 192-200. | 2.3 | 11 |
| 46 | Dynamics of Influenza Virus and Human Host Interactions During Infection and Replication Cycle. Bulletin of Mathematical Biology, 2013, 75, 988-1011. | 1.9 | 26 |
| 47 | SBML qualitative models: a model representation format and infrastructure to foster interactions between qualitative modelling formalisms and tools. BMC Systems Biology, 2013, 7, 135. | 3.0 | 145 |
| 48 | A Cell Simulator Platform: The Cell Collective. Clinical Pharmacology and Therapeutics, 2013, 93, 393-395. | 4.7 | 38 |
| 49 | A Comprehensive, Multi-Scale Dynamical Model of ErbB Receptor Signal Transduction in Human Mammary Epithelial Cells. PLoS ONE, 2013, 8, e61757. | 2.5 | 42 |
| 50 | The Cell Collective: Toward an open and collaborative approach to systems biology. BMC Systems Biology, 2012, 6, 96. | 3.0 | 199 |
| 51 | Bio-Logic Builder: A Non-Technical Tool for Building Dynamical, Qualitative Models. PLoS ONE, 2012, 7, e46417. | 2.5 | 20 |
| 52 | Ergodic Sets as Cell Phenotype of Budding Yeast Cell Cycle. PLoS ONE, 2012, 7, e45780. | 2.5 | 32 |
| 53 | Boolean Modeling of Biochemical Networks. Open Bioinformatics Journal, 2011, 5, 16-25. | 1.0 | 28 |
| 54 | Decision Making in Cells. Systems Biology, 2010, , 295-336. | 0.1 | 0 |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 55 | ChemChains: a platform for simulation and analysis of biochemical networks aimed to laboratory scientists. BMC Systems Biology, 2009, 3, 58. | 3.0 | 79 |
| 56 | Emergent decision-making in biological signal transduction networks. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 1913-1918. | 7.1 | 183 |
| 57 | Discovering Cellular Respiration with Computational Modeling and Simulations. CourseSource, 0, 4, . | 0.0 | 8 |
| 58 | Discovering Prokaryotic Gene Regulation with Simulations of the trp Operon. CourseSource, 0, 5, . | 0.0 | 2 |
| 59 | Discovering Prokaryotic Gene Regulation by Building and Investigating a Computational Model of the lac Operon. CourseSource, 0, 6, . | 0.0 | 6 |