

Tamir Tuller

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9189524/publications.pdf>

Version: 2024-02-01

160
papers

5,673
citations

109137

35
h-index

102304

66
g-index

170
all docs

170
docs citations

170
times ranked

4939
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | An Evolutionarily Conserved Mechanism for Controlling the Efficiency of Protein Translation. <i>Cell</i> , 2010, 141, 344-354. | 13.5 | 759 |
| 2 | Translation efficiency is determined by both codon bias and folding energy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 3645-3650. | 3.3 | 489 |
| 3 | The effect of tRNA levels on decoding times of mRNA codons. <i>Nucleic Acids Research</i> , 2014, 42, 9171-9181. | 6.5 | 222 |
| 4 | Composite effects of gene determinants on the translation speed and density of ribosomes. <i>Genome Biology</i> , 2011, 12, R110. | 13.9 | 185 |
| 5 | The Average Common Substring Approach to Phylogenomic Reconstruction. <i>Journal of Computational Biology</i> , 2006, 13, 336-350. | 0.8 | 184 |
| 6 | Genome-Scale Analysis of Translation Elongation with a Ribosome Flow Model. <i>PLoS Computational Biology</i> , 2011, 7, e1002127. | 1.5 | 175 |
| 7 | Multiple roles of the coding sequence 5' end in gene expression regulation. <i>Nucleic Acids Research</i> , 2015, 43, 13-28. | 6.5 | 165 |
| 8 | Determinants of Protein Abundance and Translation Efficiency in <i>S. cerevisiae</i> . <i>PLoS Computational Biology</i> , 2007, 3, e248. | 1.5 | 116 |
| 9 | Maximum likelihood of phylogenetic networks. <i>Bioinformatics</i> , 2006, 22, 2604-2611. | 1.8 | 112 |
| 10 | Determinants of Translation Elongation Speed and Ribosomal Profiling Biases in Mouse Embryonic Stem Cells. <i>PLoS Computational Biology</i> , 2012, 8, e1002755. | 1.5 | 106 |
| 11 | Association between translation efficiency and horizontal gene transfer within microbial communities. <i>Nucleic Acids Research</i> , 2011, 39, 4743-4755. | 6.5 | 99 |
| 12 | Modelling the Efficiency of Codon-tRNA Interactions Based on Codon Usage Bias. <i>DNA Research</i> , 2014, 21, 511-526. | 1.5 | 94 |
| 13 | A model for competition for ribosomes in the cell. <i>Journal of the Royal Society Interface</i> , 2016, 13, 20151062. | 1.5 | 94 |
| 14 | Strong association between mRNA folding strength and protein abundance in <i>S. cerevisiae</i> . <i>EMBO Reports</i> , 2012, 13, 272-277. | 2.0 | 89 |
| 15 | New Universal Rules of Eukaryotic Translation Initiation Fidelity. <i>PLoS Computational Biology</i> , 2013, 9, e1003136. | 1.5 | 89 |
| 16 | Inferring Phylogenetic Networks by the Maximum Parsimony Criterion: A Case Study. <i>Molecular Biology and Evolution</i> , 2006, 24, 324-337. | 3.5 | 74 |
| 17 | Predictive biophysical modeling and understanding of the dynamics of mRNA translation and its evolution. <i>Nucleic Acids Research</i> , 2016, 44, gkw764. | 6.5 | 70 |
| 18 | Translation efficiency in humans: tissue specificity, global optimization and differences between developmental stages. <i>Nucleic Acids Research</i> , 2010, 38, 2964-2974. | 6.5 | 69 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | Stability Analysis of the Ribosome Flow Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1545-1552. | 1.9 | 68 |
| 20 | stAlcalc: tRNA adaptation index calculator based on species-specific weights. <i>Bioinformatics</i> , 2017, 33, 589-591. | 1.8 | 68 |
| 21 | Estimation of ribosome profiling performance and reproducibility at various levels of resolution. <i>Biology Direct</i> , 2016, 11, 24. | 1.9 | 67 |
| 22 | Entrainment to Periodic Initiation and Transition Rates in a Computational Model for Gene Translation. <i>PLoS ONE</i> , 2014, 9, e96039. | 1.1 | 65 |
| 23 | Enhancing heterologous expression in <i>Chlamydomonas reinhardtii</i> by transcript sequence optimization. <i>Plant Journal</i> , 2018, 94, 22-31. | 2.8 | 62 |
| 24 | A comparative genomics study on the effect of individual amino acids on ribosome stalling. <i>BMC Genomics</i> , 2015, 16, S5. | 1.2 | 58 |
| 25 | The extent of ribosome queuing in budding yeast. <i>PLoS Computational Biology</i> , 2018, 14, e1005951. | 1.5 | 55 |
| 26 | Mean of the Typical Decoding Rates: A New Translation Efficiency Index Based on the Analysis of Ribosome Profiling Data. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 73-80. | 0.8 | 54 |
| 27 | Reconstructing ancestral gene content by coevolution. <i>Genome Research</i> , 2010, 20, 122-132. | 2.4 | 49 |
| 28 | Codon bias, tRNA pools, and horizontal gene transfer. <i>Mobile Genetic Elements</i> , 2011, 1, 75-77. | 1.8 | 49 |
| 29 | Ribosome flow model with positive feedback. <i>Journal of the Royal Society Interface</i> , 2013, 10, 20130267. | 1.5 | 47 |
| 30 | Maximizing protein translation rate in the non-homogeneous ribosome flow model: a convex optimization approach. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20140713. | 1.5 | 45 |
| 31 | Properties of untranslated regions of the <i>S. cerevisiae</i> genome. <i>BMC Genomics</i> , 2009, 10, 391. | 1.2 | 44 |
| 32 | Conservation of the relative tRNA composition in healthy and cancerous tissues. <i>Rna</i> , 2012, 18, 640-652. | 1.6 | 42 |
| 33 | Genomic analysis of COP9 signalosome function in <i>Drosophila melanogaster</i> reveals a role in temporal regulation of gene expression. <i>Molecular Systems Biology</i> , 2007, 3, 108. | 3.2 | 41 |
| 34 | Selection for Translation Efficiency on Synonymous Polymorphisms in Recent Human Evolution. <i>Genome Biology and Evolution</i> , 2011, 3, 749-761. | 1.1 | 41 |
| 35 | Rationally designed, heterologous <i>S. cerevisiae</i> transcripts expose novel expression determinants. <i>RNA Biology</i> , 2015, 12, 972-984. | 1.5 | 39 |
| 36 | On the Ribosomal Density that Maximizes Protein Translation Rate. <i>PLoS ONE</i> , 2016, 11, e0166481. | 1.1 | 35 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 37 | Prediction of acute multiple sclerosis relapses by transcription levels of peripheral blood cells. BMC Medical Genomics, 2009, 2, 46. | 0.7 | 34 |
| 38 | Metabolic modeling of endosymbiont genome reduction on a temporal scale. Molecular Systems Biology, 2011, 7, 479. | 3.2 | 34 |
| 39 | Quantifying the Effect of Ribosomal Density on mRNA Stability. PLoS ONE, 2014, 9, e102308. | 1.1 | 34 |
| 40 | Ribosome Flow Model on a Ring. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 1429-1439. | 1.9 | 34 |
| 41 | Codon-based indices for modeling gene expression and transcript evolution. Computational and Structural Biotechnology Journal, 2021, 19, 2646-2663. | 1.9 | 33 |
| 42 | Accurate, Model-Based Tuning of Synthetic Gene Expression Using Introns in <i>S. cerevisiae</i> . PLoS Genetics, 2014, 10, e1004407. | 1.5 | 31 |
| 43 | Alternative Transcription Initiation and the AUG Context Configuration Control Dual-Organellar Targeting and Functional Competence of Arabidopsis Lon1 Protease. Molecular Plant, 2014, 7, 989-1005. | 3.9 | 31 |
| 44 | Sensitivity of mRNA Translation. Scientific Reports, 2015, 5, 12795. | 1.6 | 31 |
| 45 | Contraction after small transients. Automatica, 2016, 67, 178-184. | 3.0 | 31 |
| 46 | Evolutionary Rate and Gene Expression Across Different Brain Regions. Genome Biology, 2008, 9, R142. | 13.9 | 30 |
| 47 | Comparative classification of species and the study of pathway evolution based on the alignment of metabolic pathways. BMC Bioinformatics, 2010, 11, S38. | 1.2 | 29 |
| 48 | Computational analysis of nascent peptides that induce ribosome stalling and their proteomic distribution in <i>Saccharomyces cerevisiae</i> . Rna, 2017, 23, 983-994. | 1.6 | 29 |
| 49 | Explicit Expression for the Steady-State Translation Rate in the Infinite-Dimensional Homogeneous Ribosome Flow Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1322-1328. | 1.9 | 28 |
| 50 | Nucleotide sequence composition adjacent to intronic splice sites improves splicing efficiency via its effect on pre-mRNA local folding in fungi. Rna, 2015, 21, 1704-1718. | 1.6 | 28 |
| 51 | Modelling and measuring intracellular competition for finite resources during gene expression. Journal of the Royal Society Interface, 2019, 16, 20180887. | 1.5 | 28 |
| 52 | Forbidden pentapeptides. Protein Science, 2007, 16, 2251-2259. | 3.1 | 26 |
| 53 | On the Steady-State Distribution in the Homogeneous Ribosome Flow Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1724-1736. | 1.9 | 26 |
| 54 | Complementary Post Transcriptional Regulatory Information is Detected by PUNCH-P and Ribosome Profiling. Scientific Reports, 2016, 6, 21635. | 1.6 | 25 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 55 | Parsimony Score of Phylogenetic Networks: Hardness Results and a Linear-Time Heuristic. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 495-505. | 1.9 | 24 |
| 56 | Efficient Manipulations of Synonymous Mutations for Controlling Translation Rate: An Analytical Approach. <i>Journal of Computational Biology</i> , 2012, 19, 200-231. | 0.8 | 24 |
| 57 | Three-dimensional eukaryotic genomic organization is strongly correlated with codon usage expression and function. <i>Nature Communications</i> , 2014, 5, 5876. | 5.8 | 24 |
| 58 | Widespread signatures of local mRNA folding structure selection in four Dengue virus serotypes. <i>BMC Genomics</i> , 2015, 16, S4. | 1.2 | 24 |
| 59 | A code for transcription elongation speed. <i>RNA Biology</i> , 2018, 15, 81-94. | 1.5 | 24 |
| 60 | High-resolution modeling of the selection on local mRNA folding strength in coding sequences across the tree of life. <i>Genome Biology</i> , 2020, 21, 63. | 3.8 | 24 |
| 61 | Transcript features alone enable accurate prediction and understanding of gene expression in <i>S. cerevisiae</i> . <i>BMC Bioinformatics</i> , 2013, 14, S1. | 1.2 | 23 |
| 62 | Sequence Features of <i>E. coli</i> mRNAs Affect Their Degradation. <i>PLoS ONE</i> , 2011, 6, e28544. | 1.1 | 22 |
| 63 | Genome scale analysis of <i>Escherichia coli</i> with a comprehensive prokaryotic sequence-based biophysical model of translation initiation and elongation. <i>DNA Research</i> , 2018, 25, 195-205. | 1.5 | 22 |
| 64 | Widespread non-modular overlapping codes in the coding regions*. <i>Physical Biology</i> , 2020, 17, 031002. | 0.8 | 22 |
| 65 | Genome-wide analysis of horizontally acquired genes in the genus <i>Mycobacterium</i> . <i>Scientific Reports</i> , 2018, 8, 14817. | 1.6 | 21 |
| 66 | Global map of physical interactions among differentially expressed genes in multiple sclerosis relapses and remissions. <i>Human Molecular Genetics</i> , 2011, 20, 3606-3619. | 1.4 | 20 |
| 67 | Properties and determinants of codon decoding time distributions. <i>BMC Genomics</i> , 2014, 15, S13. | 1.2 | 20 |
| 68 | Optimal Down Regulation of mRNA Translation. <i>Scientific Reports</i> , 2017, 7, 41243. | 1.6 | 19 |
| 69 | Significant differences in terms of codon usage bias between bacteriophage early and late genes: a comparative genomics analysis. <i>BMC Genomics</i> , 2017, 18, 866. | 1.2 | 19 |
| 70 | Overcoming the expression barrier of the ferredoxin-hydrogenase chimera in <i>Chlamydomonas reinhardtii</i> supports a linear increment in photosynthetic hydrogen output. <i>Algal Research</i> , 2018, 33, 310-315. | 2.4 | 19 |
| 71 | <i>Drosophila</i> COP9 signalosome subunit 7 interacts with multiple genomic loci to regulate development. <i>Nucleic Acids Research</i> , 2014, 42, 9761-9770. | 6.5 | 18 |
| 72 | The RNA Polymerase Flow Model of Gene Transcription. <i>IEEE Transactions on Biomedical Circuits and Systems</i> , 2014, 8, 54-64. | 2.7 | 18 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 73 | Exploiting hidden information interleaved in the redundancy of the genetic code without prior knowledge. <i>Bioinformatics</i> , 2015, 31, 1161-1168. | 1.8 | 18 |
| 74 | Reconstruction of Ancestral Genomic Sequences Using Likelihood. <i>Journal of Computational Biology</i> , 2007, 14, 216-237. | 0.8 | 17 |
| 75 | Clone clusters in autoreactive CD4 T cell lines from probable multiple sclerosis patients form disease characteristic signatures. <i>Immunology</i> , 2009, 128, 287-300. | 2.0 | 17 |
| 76 | Evidence of translation efficiency adaptation of the coding regions of the bacteriophage lambda. <i>DNA Research</i> , 2017, 24, 333-342. | 1.5 | 17 |
| 77 | <i>TP53</i> Cancerous Mutations Exhibit Selection for Translation Efficiency. <i>Cancer Research</i> , 2009, 69, 8807-8813. | 0.4 | 16 |
| 78 | Ribosome flow model with extended objects. <i>Journal of the Royal Society Interface</i> , 2017, 14, 20170128. | 1.5 | 16 |
| 79 | Novel insights into gene expression regulation during meiosis revealed by translation elongation dynamics. <i>Npj Systems Biology and Applications</i> , 2019, 5, 12. | 1.4 | 16 |
| 80 | Networks of ribosome flow models for modeling and analyzing intracellular traffic. <i>Scientific Reports</i> , 2019, 9, 1703. | 1.6 | 16 |
| 81 | Co-evolutionary networks of genes and cellular processes across fungal species. <i>Genome Biology</i> , 2009, 10, R48. | 13.9 | 15 |
| 82 | RFMapp: ribosome flow model application. <i>Bioinformatics</i> , 2012, 28, 1663-1664. | 1.8 | 15 |
| 83 | Algorithms for ribosome traffic engineering and their potential in improving host cells' titer and growth rate. <i>Scientific Reports</i> , 2020, 10, 21202. | 1.6 | 15 |
| 84 | Extensive inter-domain lateral gene transfer in the evolution of the human commensal <i>Methanospaera stadtmannae</i> . <i>Frontiers in Genetics</i> , 2012, 3, 182. | 1.1 | 14 |
| 85 | Challenges and obstacles related to solving the codon bias riddles. <i>Biochemical Society Transactions</i> , 2014, 42, 155-159. | 1.6 | 13 |
| 86 | A deterministic mathematical model for bidirectional excluded flow with Langmuir kinetics. <i>PLoS ONE</i> , 2017, 12, e0182178. | 1.1 | 13 |
| 87 | Quantifying the distribution of protein oligomerization degree reflects cellular information capacity. <i>Scientific Reports</i> , 2020, 10, 17689. | 1.6 | 13 |
| 88 | The Integration of Multiple Nuclear-Encoded Transgenes in the Green Alga <i>Chlamydomonas reinhardtii</i> Results in Higher Transcription Levels. <i>Frontiers in Plant Science</i> , 2020, 10, 1784. | 1.7 | 13 |
| 89 | Biological Networks: Comparison, Conservation, and Evolution via Relative Description Length. <i>Journal of Computational Biology</i> , 2007, 14, 817-838. | 0.8 | 12 |
| 90 | Maximizing Protein Translation Rate in the Ribosome Flow Model: The Homogeneous Case. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 1184-1195. | 1.9 | 12 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 91 | Computational analysis of the oscillatory behavior at the translation level induced by mRNA levels oscillations due to finite intracellular resources. <i>PLoS Computational Biology</i> , 2018, 14, e1006055. | 1.5 | 12 |
| 92 | Higher-Order Genomic Organization of Cellular Functions in Yeast. <i>Journal of Computational Biology</i> , 2009, 16, 303-316. | 0.8 | 11 |
| 93 | Universal evolutionary selection for high dimensional silent patterns of information hidden in the redundancy of viral genetic code. <i>Bioinformatics</i> , 2018, 34, 3241-3248. | 1.8 | 11 |
| 94 | Controllability Analysis and Control Synthesis for the Ribosome Flow Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1351-1364. | 1.9 | 11 |
| 95 | A possible universal role for mRNA secondary structure in bacterial translation revealed using a synthetic operon. <i>Nature Communications</i> , 2020, 11, 4827. | 5.8 | 11 |
| 96 | Variability in mRNA translation: a random matrix theory approach. <i>Scientific Reports</i> , 2021, 11, 5300. | 1.6 | 11 |
| 97 | Inferring horizontal transfers in the presence of rearrangements by the minimum evolution criterion. <i>Bioinformatics</i> , 2008, 24, 826-832. | 1.8 | 10 |
| 98 | The Effect of Dysregulation of tRNA Genes and Translation Efficiency Mutations in Cancer and Neurodegeneration. <i>Frontiers in Genetics</i> , 2012, 3, 201. | 1.1 | 10 |
| 99 | Improving 3D Genome Reconstructions Using Orthologous and Functional Constraints. <i>PLoS Computational Biology</i> , 2015, 11, e1004298. | 1.5 | 10 |
| 100 | Evidence of a Direct Evolutionary Selection for Strong Folding and Mutational Robustness Within HIV Coding Regions. <i>Journal of Computational Biology</i> , 2016, 23, 641-650. | 0.8 | 10 |
| 101 | Modeling three-dimensional genomic organization in evolution and pathogenesis. <i>Seminars in Cell and Developmental Biology</i> , 2019, 90, 78-93. | 2.3 | 10 |
| 102 | Solving the Riddle of the Evolution of Shine-Dalgarno Based Translation in Chloroplasts. <i>Molecular Biology and Evolution</i> , 2019, 36, 2854-2860. | 3.5 | 10 |
| 103 | Whole cell biophysical modeling of codon-tRNA competition reveals novel insights related to translation dynamics. <i>PLoS Computational Biology</i> , 2020, 16, e1008038. | 1.5 | 10 |
| 104 | Estimating the predictive power of silent mutations on cancer classification and prognosis. <i>Npj Genomic Medicine</i> , 2021, 6, 67. | 1.7 | 10 |
| 105 | Checkable Conditions for Contraction After Small Transients in Time and Amplitude. <i>Lecture Notes in Control and Information Sciences</i> , 2017, , 279-305. | 0.6 | 10 |
| 106 | Mapping the translation initiation landscape of an <i>S. cerevisiae</i> gene using fluorescent proteins. <i>Genomics</i> , 2013, 102, 419-429. | 1.3 | 9 |
| 107 | Selection for reduced translation costs at the intronic 5' end in fungi. <i>DNA Research</i> , 2016, 23, 377-394. | 1.5 | 9 |
| 108 | Prediction and large-scale analysis of primary operons in plastids reveals unique genetic features in the evolution of chloroplasts. <i>Nucleic Acids Research</i> , 2019, 47, 3344-3352. | 6.5 | 9 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 109 | The COP9 signalosome influences the epigenetic landscape of <i>Arabidopsis thaliana</i> . <i>Bioinformatics</i> , 2019, 35, 2718-2723. | 1.8 | 9 |
| 110 | Discovering local patterns of co - evolution: computational aspects and biological examples. <i>BMC Bioinformatics</i> , 2010, 11, 43. | 1.2 | 8 |
| 111 | ChimeraUGEM: unsupervised gene expression modeling in any given organism. <i>Bioinformatics</i> , 2019, 35, 3365-3371. | 1.8 | 8 |
| 112 | MPEPE, a predictive approach to improve protein expression in <i>E. coli</i> based on deep learning. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1142-1153. | 1.9 | 8 |
| 113 | Ribosomal mutations affecting the translation of genes that use non-optimal codons. <i>FEBS Journal</i> , 2014, 281, 3701-3718. | 2.2 | 7 |
| 114 | Tracking the evolution of 3D gene organization demonstrates its connection to phenotypic divergence. <i>Nucleic Acids Research</i> , 2017, 45, 4330-4343. | 6.5 | 7 |
| 115 | Identification of conserved slow codons that are important for protein expression and function. <i>RNA Biology</i> , 2021, 18, 2296-2307. | 1.5 | 7 |
| 116 | A New Linear-Time Heuristic Algorithm for Computing the Parsimony Score of Phylogenetic Networks: Theoretical Bounds and Empirical Performance. , 2007, , 61-72. | | 7 |
| 117 | Evolutionary Stability Optimizer (ESO): A Novel Approach to Identify and Avoid Mutational Hotspots in DNA Sequences While Maintaining High Expression Levels. <i>ACS Synthetic Biology</i> , 2022, 11, 1142-1151. | 1.9 | 7 |
| 118 | Image-Processing Software for High-Throughput Quantification of Colony Luminescence. <i>MSphere</i> , 2019, 4, . | 1.3 | 6 |
| 119 | CSO – A sequence optimization software for engineering chloroplast expression in <i>Chlamydomonas reinhardtii</i> . <i>Algal Research</i> , 2020, 46, 101788. | 2.4 | 6 |
| 120 | Analysis of Coevolving Gene Families Using Mutually Exclusive Orthologous Modules. <i>Genome Biology and Evolution</i> , 2011, 3, 413-423. | 1.1 | 5 |
| 121 | Modeling and Analyzing the Flow of Molecular Machines in Gene Expression. <i>RNA Technologies</i> , 2018, , 275-300. | 0.2 | 5 |
| 122 | Prediction of the Wingate anaerobic mechanical power outputs from a maximal incremental cardiopulmonary exercise stress test using machine-learning approach. <i>PLoS ONE</i> , 2019, 14, e0212199. | 1.1 | 5 |
| 123 | Prokaryotic rRNA-mRNA interactions are involved in all translation steps and shape bacterial transcripts. <i>RNA Biology</i> , 2021, 18, 684-698. | 1.5 | 5 |
| 124 | Co-evolution Is Incompatible with the Markov Assumption in Phylogenetics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 1667-1670. | 1.9 | 4 |
| 125 | Efficient algorithms for reconstructing gene content by co-evolution. <i>BMC Bioinformatics</i> , 2011, 12, S12. | 1.2 | 4 |
| 126 | Most associations between transcript features and gene expression are monotonic. <i>Molecular BioSystems</i> , 2014, 10, 1426-1440. | 2.9 | 4 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 127 | Three-dimensional Genomic Organization of Genesâ€™ Function in Eukaryotes. , 2016, , 233-252. | | 4 |
| 128 | Genome-Scale Analysis of Perturbations in Translation Elongation Based on a Computational Model. Scientific Reports, 2018, 8, 16191. | 1.6 | 4 |
| 129 | Evolutionary selection against short nucleotide sequences in viruses and their related hosts. DNA Research, 2020, 27, . | 1.5 | 4 |
| 130 | New computational model for miRNA-mediated repression reveals novel regulatory roles of miRNA bindings inside the coding region. Bioinformatics, 2021, 36, 5398-5404. | 1.8 | 4 |
| 131 | A Mathematical Analysis of RNA Structural Motifs in Viruses. Mathematics, 2021, 9, 585. | 1.1 | 4 |
| 132 | THE NET-HMM APPROACH: PHYLOGENETIC NETWORK INFERENCE BY COMBINING MAXIMUM LIKELIHOOD AND HIDDEN MARKOV MODELS. Journal of Bioinformatics and Computational Biology, 2009, 07, 625-644. | 0.3 | 3 |
| 133 | Unsupervised detection of regulatory gene expression information in different genomic regions enables gene expression ranking. BMC Bioinformatics, 2017, 18, 77. | 1.2 | 3 |
| 134 | The Effect of Codon Usage on the Success of Horizontal Gene Transfer. , 2013, , 147-158. | | 3 |
| 135 | Exploring Potential Signals of Selection for Disordered Residues in Prokaryotic and Eukaryotic Proteins. Genomics, Proteomics and Bioinformatics, 2020, 18, 549-564. | 3.0 | 3 |
| 136 | Reconstructing Ancestral Genomic Sequences by Co-Evolution: Formal Definitions, Computational Issues, and Biological Examples. Journal of Computational Biology, 2010, 17, 1327-1344. | 0.8 | 2 |
| 137 | sbv IMPROVER Diagnostic Signature Challenge. Systems Biomedicine (Austin, Tex), 2013, 1, 208-216. | 0.7 | 2 |
| 138 | A Mathematical Analysis of HDV Genotypes: From Molecules to Cells. Mathematics, 2021, 9, 2063. | 1.1 | 2 |
| 139 | Discovering Local Patterns of Co-evolution. Lecture Notes in Computer Science, 2008, , 55-71. | 1.0 | 2 |
| 140 | Modeling the ribosomal small subunit dynamic in Saccharomyces cerevisiae based on TCP-seq data. Nucleic Acids Research, 2022, , . | 6.5 | 2 |
| 141 | Controlling the ribosomal density profile in mRNA translation. , 2016, , . | | 1 |
| 142 | Generation and comparative genomics of synthetic dengue viruses. BMC Bioinformatics, 2018, 19, 140. | 1.2 | 1 |
| 143 | CSN: unsupervised approach for inferring biological networks based on the genome alone. BMC Bioinformatics, 2020, 21, 190. | 1.2 | 1 |
| 144 | Computational based design and tracking of synthetic variants of Porcine circovirus reveal relations between silent genomic information and viral fitness. Scientific Reports, 2021, 11, 10620. | 1.6 | 1 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 145 | A Ribosome Flow Model for Analyzing Translation Elongation. Lecture Notes in Computer Science, 2011, , 358-360. | 1.0 | 1 |
| 146 | Computational discovery and modeling of novel gene expression rules encoded in the mRNA. Biochemical Society Transactions, 2020, 48, 1519-1528. | 1.6 | 1 |
| 147 | Co-evolutionary Models for Reconstructing Ancestral Genomic Sequences: Computational Issues and Biological Examples. Lecture Notes in Computer Science, 2009, , 164-180. | 1.0 | 1 |
| 148 | Novel Driver Synonymous Mutations in the Coding Regions of GCB Lymphoma Patients Improve the Transcription Levels of BCL2. Lecture Notes in Computer Science, 2020, , 108-118. | 1.0 | 1 |
| 149 | Accelerating Whole-Cell Simulations of mRNA Translation Using a Dedicated Hardware. ACS Synthetic Biology, 2021, , . | 1.9 | 1 |
| 150 | Modeling the effect of rRNA-mRNA interactions and mRNA folding on mRNA translation in chloroplasts. Computational and Structural Biotechnology Journal, 2022, 20, 2521-2538. | 1.9 | 1 |
| 151 | Editing Bayesian Networks: A New Approach for Combining Prior Knowledge and Gene Expression Measurements for Researching Diseases. , 2008, , . | | 0 |
| 152 | Computational Modeling of Gene Translation and its Potential Applications in Individualized Medicine. Studies in Mechanobiology, Tissue Engineering and Biomaterials, 2011, , 487-503. | 0.7 | 0 |
| 153 | Flow models for efficient simulation and engineering of transcription and translation elongation. , 2012, , . | | 0 |
| 154 | Coevolution of Gene Families: Models, Algorithms, and Systems Biology. , 2012, , 65-78. | | 0 |
| 155 | Hidden Silent Codes in Viral Genomes. , 2017, , 87-110. | | 0 |
| 156 | Inferring Models of Rearrangements, Recombinations, and Horizontal Transfers by the Minimum Evolution Criterion. Lecture Notes in Computer Science, 2007, , 111-123. | 1.0 | 0 |
| 157 | Novel Phylogenetic Network Inference by Combining Maximum Likelihood and Hidden Markov Models. Lecture Notes in Computer Science, 2008, , 354-368. | 1.0 | 0 |
| 158 | Generation and Comparative Genomics of Synthetic Dengue Viruses. Lecture Notes in Computer Science, 2017, , 31-52. | 1.0 | 0 |
| 159 | Temporal mRNA Translation Efficiency Is Encoded In Viral Coding Regions. , 2017, , . | | 0 |
| 160 | Determinants of efficient modulation of ribosomal traffic jams. Computational and Structural Biotechnology Journal, 2021, 19, 6064-6079. | 1.9 | 0 |