

Tamir Tuller

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

155
papers

4,311
citations

33
h-index

61
g-index

170
ext. papers

5,163
ext. citations

6.2
avg, IF

6.09
L-index

#	Paper	IF	Citations
155	MPEPE, a predictive approach to improve protein expression in based on deep learning.. <i>Computational and Structural Biotechnology Journal</i> , 2022 , 20, 1142-1153	6.8	0
154	Using Computational Synthetic Biology Tools to Modulate Gene Expression Within a Microbiome. <i>Lecture Notes in Computer Science</i> , 2022 , 235-259	0.9	
153	Modeling the effect of rRNA-mRNA interactions and mRNA folding on mRNA translation in chloroplasts. <i>Computational and Structural Biotechnology Journal</i> , 2022 , 20, 2521-2538	6.8	
152	Determinants of efficient modulation of ribosomal traffic jams. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 6064-6079	6.8	
151	A Mathematical Analysis of RNA Structural Motifs in Viruses. <i>Mathematics</i> , 2021 , 9, 585	2.3	2
150	Variability in mRNA translation: a random matrix theory approach. <i>Scientific Reports</i> , 2021 , 11, 5300	4.9	5
149	Identification of conserved slow codons that are important for protein expression and function. <i>RNA Biology</i> , 2021 , 18, 2296-2307	4.8	1
148	Computational based design and tracking of synthetic variants of Porcine circovirus reveal relations between silent genomic information and viral fitness. <i>Scientific Reports</i> , 2021 , 11, 10620	4.9	0
147	Estimating the predictive power of silent mutations on cancer classification and prognosis. <i>Npj Genomic Medicine</i> , 2021 , 6, 67	6.2	1
146	Prokaryotic rRNA-mRNA interactions are involved in all translation steps and shape bacterial transcripts. <i>RNA Biology</i> , 2021 , 1-15	4.8	1
145	Codon-based indices for modeling gene expression and transcript evolution. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 2646-2663	6.8	6
144	Algorithms for ribosome traffic engineering and their potential in improving host cells' titer and growth rate. <i>Scientific Reports</i> , 2020 , 10, 21202	4.9	5
143	CSN: unsupervised approach for inferring biological networks based on the genome alone. <i>BMC Bioinformatics</i> , 2020 , 21, 190	3.6	0
142	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	18.3	14
141	Widespread non-modular overlapping codes in the coding regions. <i>Physical Biology</i> , 2020 , 17, 031002	3	12
140	Novel Driver Synonymous Mutations in the Coding Regions of GCB Lymphoma Patients Improve the Transcription Levels of BCL2. <i>Lecture Notes in Computer Science</i> , 2020 , 108-118	0.9	1
139	Exploring Potential Signals of Selection for Disordered Residues in Prokaryotic and Eukaryotic Proteins. <i>Genomics, Proteomics and Bioinformatics</i> , 2020 , 18, 549-564	6.5	2

138	Computational discovery and modeling of novel gene expression rules encoded in the mRNA. <i>Biochemical Society Transactions</i> , 2020 , 48, 1519-1528	5.1	1
137	CSO TA sequence optimization software for engineering chloroplast expression in <i>Chlamydomonas reinhardtii</i> . <i>Algal Research</i> , 2020 , 46, 101788	5	4
136	A possible universal role for mRNA secondary structure in bacterial translation revealed using a synthetic operon. <i>Nature Communications</i> , 2020 , 11, 4827	17.4	3
135	Whole cell biophysical modeling of codon-tRNA competition reveals novel insights related to translation dynamics. <i>PLoS Computational Biology</i> , 2020 , 16, e1008038	5	2
134	Quantifying the distribution of protein oligomerization degree reflects cellular information capacity. <i>Scientific Reports</i> , 2020 , 10, 17689	4.9	3
133	New computational model for miRNA-mediated repression reveals novel regulatory roles of miRNA bindings inside the coding region. <i>Bioinformatics</i> , 2020 ,	7.2	2
132	Solving the Riddle of the Evolution of Shine-Dalgarno Based Translation in Chloroplasts. <i>Molecular Biology and Evolution</i> , 2019 , 36, 2854-2860	8.3	6
131	Image-Processing Software for High-Throughput Quantification of Colony Luminescence. <i>MSphere</i> , 2019 , 4,	5	3
130	ChimeraUGEM: unsupervised gene expression modeling in any given organism. <i>Bioinformatics</i> , 2019 , 35, 3365-3371	7.2	4
129	Modelling and measuring intracellular competition for finite resources during gene expression. <i>Journal of the Royal Society Interface</i> , 2019 , 16, 20180887	4.1	17
128	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	20.1	2
127	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	3.7	2
126	Novel insights into gene expression regulation during meiosis revealed by translation elongation dynamics. <i>Npj Systems Biology and Applications</i> , 2019 , 5, 12	5	8
125	Networks of ribosome flow models for modeling and analyzing intracellular traffic. <i>Scientific Reports</i> , 2019 , 9, 1703	4.9	10
124	The Integration of Multiple Nuclear-Encoded Transgenes in the Green Alga Results in Higher Transcription Levels. <i>Frontiers in Plant Science</i> , 2019 , 10, 1784	6.2	6
123	Modeling three-dimensional genomic organization in evolution and pathogenesis. <i>Seminars in Cell and Developmental Biology</i> , 2019 , 90, 78-93	7.5	5
122	The COP9 signalosome influences the epigenetic landscape of <i>Arabidopsis thaliana</i> . <i>Bioinformatics</i> , 2019 , 35, 2718-2723	7.2	6
121	Enhancing heterologous expression in <i>Chlamydomonas reinhardtii</i> by transcript sequence optimization. <i>Plant Journal</i> , 2018 , 94, 22-31	6.9	45

120	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	7.2	9
119	Controllability Analysis and Control Synthesis for the Ribosome Flow Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018 , 15, 1351-1364	3	7
118	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	5	8
117	Generation and comparative genomics of synthetic dengue viruses. <i>BMC Bioinformatics</i> , 2018 , 19, 140	3.6	1
116	The extent of ribosome queuing in budding yeast. <i>PLoS Computational Biology</i> , 2018 , 14, e1005951	5	40
115	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	5	12
114	A code for transcription elongation speed. <i>RNA Biology</i> , 2018 , 15, 81-94	4.8	19
113	Genome-wide analysis of horizontally acquired genes in the genus <i>Mycobacterium</i> . <i>Scientific Reports</i> , 2018 , 8, 14817	4.9	14
112	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	4.5	13
111	Genome-Scale Analysis of Perturbations in Translation Elongation Based on a Computational Model. <i>Scientific Reports</i> , 2018 , 8, 16191	4.9	3
110	Modeling and Analyzing the Flow of Molecular Machines in Gene Expression. <i>RNA Technologies</i> , 2018 , 275-300	0.2	4
109	Optimal Down Regulation of mRNA Translation. <i>Scientific Reports</i> , 2017 , 7, 41243	4.9	15
108	Unsupervised detection of regulatory gene expression information in different genomic regions enables gene expression ranking. <i>BMC Bioinformatics</i> , 2017 , 18, 77	3.6	3
107	Computational analysis of nascent peptides that induce ribosome stalling and their proteomic distribution in. <i>Rna</i> , 2017 , 23, 983-994	5.8	17
106	Tracking the evolution of 3D gene organization demonstrates its connection to phenotypic divergence. <i>Nucleic Acids Research</i> , 2017 , 45, 4330-4343	20.1	6
105	A deterministic mathematical model for bidirectional excluded flow with Langmuir kinetics. <i>PLoS ONE</i> , 2017 , 12, e0182178	3.7	11
104	stAlcalc: tRNA adaptation index calculator based on species-specific weights. <i>Bioinformatics</i> , 2017 , 33, 589-591	7.2	34
103	Hidden Silent Codes in Viral Genomes 2017 , 87-110		

102	Ribosome flow model with extended objects. <i>Journal of the Royal Society Interface</i> , 2017 , 14,	4.1	10
101	Evidence of translation efficiency adaptation of the coding regions of the bacteriophage lambda. <i>DNA Research</i> , 2017 , 24, 333-342	4.5	14
100	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	4.5	12
99	Checkable Conditions for Contraction After Small Transients in Time and Amplitude. <i>Lecture Notes in Control and Information Sciences</i> , 2017 , 279-305	0.5	9
98	Generation and Comparative Genomics of Synthetic Dengue Viruses. <i>Lecture Notes in Computer Science</i> , 2017 , 31-52	0.9	
97	Evidence of a Direct Evolutionary Selection for Strong Folding and Mutational Robustness Within HIV Coding Regions. <i>Journal of Computational Biology</i> , 2016 , 23, 641-50	1.7	7
96	Complementary Post Transcriptional Regulatory Information is Detected by PUNCH-P and Ribosome Profiling. <i>Scientific Reports</i> , 2016 , 6, 21635	4.9	17
95	Estimation of ribosome profiling performance and reproducibility at various levels of resolution. <i>Biology Direct</i> , 2016 , 11, 24	7.2	49
94	Selection for reduced translation costs at the intronic 5' end in fungi. <i>DNA Research</i> , 2016 , 23, 377-94	4.5	6
93	A model for competition for ribosomes in the cell. <i>Journal of the Royal Society Interface</i> , 2016 , 13,	4.1	70
92	Contraction after small transients. <i>Automatica</i> , 2016 , 67, 178-184	5.7	25
91	On the Ribosomal Density that Maximizes Protein Translation Rate. <i>PLoS ONE</i> , 2016 , 11, e0166481	3.7	27
90	Controlling the ribosomal density profile in mRNA translation 2016 ,		1
89	Predictive biophysical modeling and understanding of the dynamics of mRNA translation and its evolution. <i>Nucleic Acids Research</i> , 2016 , 44, 9031-9049	20.1	52
88	Three-dimensional Genomic Organization of Genes Function in Eukaryotes 2016 , 233-252		2
87	Multiple roles of the coding sequence 5' end in gene expression regulation. <i>Nucleic Acids Research</i> , 2015 , 43, 13-28	20.1	125
86	Improving 3D Genome Reconstructions Using Orthologous and Functional Constraints. <i>PLoS Computational Biology</i> , 2015 , 11, e1004298	5	9
85	Rationally designed, heterologous <i>S. cerevisiae</i> transcripts expose novel expression determinants. <i>RNA Biology</i> , 2015 , 12, 972-84	4.8	35

84	Nucleotide sequence composition adjacent to intronic splice sites improves splicing efficiency via its effect on pre-mRNA local folding in fungi. <i>Rna</i> , 2015 , 21, 1704-18	5.8	19
83	Exploiting hidden information interleaved in the redundancy of the genetic code without prior knowledge. <i>Bioinformatics</i> , 2015 , 31, 1161-8	7.2	14
82	Sensitivity of mRNA Translation. <i>Scientific Reports</i> , 2015 , 5, 12795	4.9	27
81	Widespread signatures of local mRNA folding structure selection in four Dengue virus serotypes. <i>BMC Genomics</i> , 2015 , 16 Suppl 10, S4	4.5	17
80	A comparative genomics study on the effect of individual amino acids on ribosome stalling. <i>BMC Genomics</i> , 2015 , 16 Suppl 10, S5	4.5	50
79	Ribosome Flow Model on a Ring. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015 , 12, 1429-39	3	23
78	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> , 2014 , 5, 73-80	3.2	41
77	Challenges and obstacles related to solving the codon bias riddles. <i>Biochemical Society Transactions</i> , 2014 , 42, 155-9	5.1	12
76	Most associations between transcript features and gene expression are monotonic. <i>Molecular BioSystems</i> , 2014 , 10, 1426-40		3
75	The RNA polymerase flow model of gene transcription. <i>IEEE Transactions on Biomedical Circuits and Systems</i> , 2014 , 8, 54-64	5.1	16
74	Ribosomal mutations affecting the translation of genes that use non-optimal codons. <i>FEBS Journal</i> , 2014 , 281, 3701-18	5.7	5
73	Modelling the efficiency of codon-tRNA interactions based on codon usage bias. <i>DNA Research</i> , 2014 , 21, 511-26	4.5	66
72	Quantifying the effect of ribosomal density on mRNA stability. <i>PLoS ONE</i> , 2014 , 9, e102308	3.7	27
71	Maximizing Protein Translation Rate in the Ribosome Flow Model: The Homogeneous Case. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014 , 11, 1184-95	3	8
70	Accurate, model-based tuning of synthetic gene expression using introns in <i>S. cerevisiae</i> . <i>PLoS Genetics</i> , 2014 , 10, e1004407	6	22
69	The effect of tRNA levels on decoding times of mRNA codons. <i>Nucleic Acids Research</i> , 2014 , 42, 9171-81	20.1	166
68	Three-dimensional eukaryotic genomic organization is strongly correlated with codon usage expression and function. <i>Nature Communications</i> , 2014 , 5, 5876	17.4	19
67	Properties and determinants of codon decoding time distributions. <i>BMC Genomics</i> , 2014 , 15 Suppl 6, S13	4.5	18

66	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	4.1	36
65	Drosophila COP9 signalosome subunit 7 interacts with multiple genomic loci to regulate development. <i>Nucleic Acids Research</i> , 2014 , 42, 9761-70	20.1	14
64	Alternative transcription initiation and the AUG context configuration control dual-organelle targeting and functional competence of Arabidopsis Lon1 protease. <i>Molecular Plant</i> , 2014 , 7, 989-1005	14.4	25
63	Entrainment to periodic initiation and transition rates in a computational model for gene translation. <i>PLoS ONE</i> , 2014 , 9, e96039	3.7	52
62	Transcript features alone enable accurate prediction and understanding of gene expression in <i>S. cerevisiae</i> . <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 15, S1	3.6	18
61	Mapping the translation initiation landscape of an <i>S. cerevisiae</i> gene using fluorescent proteins. <i>Genomics</i> , 2013 , 102, 419-29	4.3	9
60	Explicit expression for the steady-state translation rate in the infinite-dimensional homogeneous ribosome flow model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013 , 10, 1322-8	3	26
59	New universal rules of eukaryotic translation initiation fidelity. <i>PLoS Computational Biology</i> , 2013 , 9, e1003136	7.5	
58	Ribosome flow model with positive feedback. <i>Journal of the Royal Society Interface</i> , 2013 , 10, 20130267	4.1	41
57	sbv IMPROVER Diagnostic Signature Challenge. <i>Systems Biomedicine (Austin, Tex)</i> , 2013 , 1, 208-216		2
56	The Effect of Codon Usage on the Success of Horizontal Gene Transfer		3
55	Stability analysis of the ribosome flow model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012 , 9, 1545-52	3	51
54	Conservation of the relative tRNA composition in healthy and cancerous tissues. <i>Rna</i> , 2012 , 18, 640-52	5.8	35
53	On the steady-state distribution in the homogeneous ribosome flow model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012 , 9, 1724-36	3	23
52	Coevolution of Gene Families: Models, Algorithms, and Systems Biology		2012, 65-78
51	Extensive Inter-Domain Lateral Gene Transfer in the Evolution of the Human Commensal <i>Methanospira stadtmanae</i> . <i>Frontiers in Genetics</i> , 2012 , 3, 182	4.5	11
50	The Effect of Dysregulation of tRNA Genes and Translation Efficiency Mutations in Cancer and Neurodegeneration. <i>Frontiers in Genetics</i> , 2012 , 3, 201	4.5	10
49	Determinants of translation elongation speed and ribosomal profiling biases in mouse embryonic stem cells. <i>PLoS Computational Biology</i> , 2012 , 8, e1002755	5	91

48	RFMapp: ribosome flow model application. <i>Bioinformatics</i> , 2012 , 28, 1663-4	7.2	10
47	Efficient manipulations of synonymous mutations for controlling translation rate: an analytical approach. <i>Journal of Computational Biology</i> , 2012 , 19, 200-31	1.7	22
46	Strong association between mRNA folding strength and protein abundance in <i>S. cerevisiae</i> . <i>EMBO Reports</i> , 2012 , 13, 272-7	6.5	79
45	Computational Modeling of Gene Translation and its Potential Applications in Individualized Medicine. <i>Studies in Mechanobiology, Tissue Engineering and Biomaterials</i> , 2011 , 487-503	0.5	
44	Composite effects of gene determinants on the translation speed and density of ribosomes. <i>Genome Biology</i> , 2011 , 12, R110	18.3	151
43	Sequence features of <i>E. coli</i> mRNAs affect their degradation. <i>PLoS ONE</i> , 2011 , 6, e28544	3.7	19
42	Selection for translation efficiency on synonymous polymorphisms in recent human evolution. <i>Genome Biology and Evolution</i> , 2011 , 3, 749-61	3.9	37
41	Analysis of coevolving gene families using mutually exclusive orthologous modules. <i>Genome Biology and Evolution</i> , 2011 , 3, 413-23	3.9	5
40	Efficient algorithms for reconstructing gene content by co-evolution. <i>BMC Bioinformatics</i> , 2011 , 12 Suppl 9, S12	3.6	2
39	Co-evolution is incompatible with the Markov assumption in phylogenetics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011 , 8, 1667-70	3	3
38	Codon bias, tRNA pools and horizontal gene transfer. <i>Mobile Genetic Elements</i> , 2011 , 1, 75-77		26
37	Association between translation efficiency and horizontal gene transfer within microbial communities. <i>Nucleic Acids Research</i> , 2011 , 39, 4743-55	20.1	72
36	Global map of physical interactions among differentially expressed genes in multiple sclerosis relapses and remissions. <i>Human Molecular Genetics</i> , 2011 , 20, 3606-19	5.6	16
35	Metabolic modeling of endosymbiont genome reduction on a temporal scale. <i>Molecular Systems Biology</i> , 2011 , 7, 479	12.2	30
34	Genome-scale analysis of translation elongation with a ribosome flow model. <i>PLoS Computational Biology</i> , 2011 , 7, e1002127	5	138
33	A Ribosome Flow Model for Analyzing Translation Elongation. <i>Lecture Notes in Computer Science</i> , 2011 , 358-360	0.9	1
32	Reconstructing ancestral gene content by coevolution. <i>Genome Research</i> , 2010 , 20, 122-32	9.7	44
31	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, 3645-50	11.5	388

30	Reconstructing ancestral genomic sequences by co-evolution: formal definitions, computational issues, and biological examples. <i>Journal of Computational Biology</i> , 2010 , 17, 1327-44	1.7	2
29	An evolutionarily conserved mechanism for controlling the efficiency of protein translation. <i>Cell</i> , 2010 , 141, 344-54	56.2	582
28	Translation efficiency in humans: tissue specificity, global optimization and differences between developmental stages. <i>Nucleic Acids Research</i> , 2010 , 38, 2964-74	20.1	54
27	Discovering local patterns of co-evolution: computational aspects and biological examples. <i>BMC Bioinformatics</i> , 2010 , 11, 43	3.6	6
26	Comparative classification of species and the study of pathway evolution based on the alignment of metabolic pathways. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 1, S38	3.6	20
25	Higher-order genomic organization of cellular functions in yeast. <i>Journal of Computational Biology</i> , 2009 , 16, 303-16	1.7	8
24	The NET-HMM approach: phylogenetic network inference by combining maximum likelihood and Hidden Markov Models. <i>Journal of Bioinformatics and Computational Biology</i> , 2009 , 7, 625-44	1	2
23	TP53 cancerous mutations exhibit selection for translation efficiency. <i>Cancer Research</i> , 2009 , 69, 8807-13	10.1	13
22	Properties of untranslated regions of the <i>S. cerevisiae</i> genome. <i>BMC Genomics</i> , 2009 , 10, 391	4.5	33
21	Clone clusters in autoreactive CD4 T-cell lines from probable multiple sclerosis patients form disease-characteristic signatures. <i>Immunology</i> , 2009 , 128, 287-300	7.8	15
20	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	3	20
19	Co-evolutionary networks of genes and cellular processes across fungal species. <i>Genome Biology</i> , 2009 , 10, R48	18.3	14
18	Prediction of acute multiple sclerosis relapses by transcription levels of peripheral blood cells. <i>BMC Medical Genomics</i> , 2009 , 2, 46	3.7	29
17	Co-evolutionary Models for Reconstructing Ancestral Genomic Sequences: Computational Issues and Biological Examples. <i>Lecture Notes in Computer Science</i> , 2009 , 164-180	0.9	
16	Evolutionary rate and gene expression across different brain regions. <i>Genome Biology</i> , 2008 , 9, R142	18.3	23
15	Inferring horizontal transfers in the presence of rearrangements by the minimum evolution criterion. <i>Bioinformatics</i> , 2008 , 24, 826-32	7.2	7
14	Discovering Local Patterns of Co-evolution. <i>Lecture Notes in Computer Science</i> , 2008 , 55-71	0.9	2
13	Novel Phylogenetic Network Inference by Combining Maximum Likelihood and Hidden Markov Models. <i>Lecture Notes in Computer Science</i> , 2008 , 354-368	0.9	

12	Forbidden penta-peptides. <i>Protein Science</i> , 2007 , 16, 2251-9	6.3	17
11	Determinants of protein abundance and translation efficiency in <i>S. cerevisiae</i> . <i>PLoS Computational Biology</i> , 2007 , 3, e248	5	98
10	Reconstruction of ancestral genomic sequences using likelihood. <i>Journal of Computational Biology</i> , 2007 , 14, 216-37	1.7	16
9	Biological networks: comparison, conservation, and evolution via relative description length. <i>Journal of Computational Biology</i> , 2007 , 14, 817-38	1.7	10
8	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	12.2	36
7	Inferring phylogenetic networks by the maximum parsimony criterion: a case study. <i>Molecular Biology and Evolution</i> , 2007 , 24, 324-37	8.3	63
6	Inferring Models of Rearrangements, Recombinations, and Horizontal Transfers by the Minimum Evolution Criterion. <i>Lecture Notes in Computer Science</i> , 2007 , 111-123	0.9	
5	A New Linear-Time Heuristic Algorithm for Computing the Parsimony Score of Phylogenetic Networks: Theoretical Bounds and Empirical Performance 2007 , 61-72		6
4	Maximum likelihood of phylogenetic networks. <i>Bioinformatics</i> , 2006 , 22, 2604-11	7.2	90
3	The average common substring approach to phylogenomic reconstruction. <i>Journal of Computational Biology</i> , 2006 , 13, 336-50	1.7	153
2	Time-Window Analysis of Developmental Gene Expression Data with Multiple Genetic Backgrounds. <i>Lecture Notes in Computer Science</i> , 2005 , 53-64	0.9	2
1	mRNA secondary structure stability regulates bacterial translation insulation and re-initiation		2