

# Tal Pupko

## List of Publications by Year in descending order

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127  
papers

17,523  
citations

34105  
52  
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16183  
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137  
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137  
docs citations

137  
times ranked

22950  
citing authors

#	ARTICLE	IF	CITATIONS
1	ConSurf 2016: an improved methodology to estimate and visualize evolutionary conservation in macromolecules. <i>Nucleic Acids Research</i> , 2016, 44, W344-W350.	14.5	2,395
2	ConSurf 2010: calculating evolutionary conservation in sequence and structure of proteins and nucleic acids. <i>Nucleic Acids Research</i> , 2010, 38, W529-W533.	14.5	1,592
3	ConSurf 2005: the projection of evolutionary conservation scores of residues on protein structures. <i>Nucleic Acids Research</i> , 2005, 33, W299-W302.	14.5	1,255
4	ConSurf: Identification of Functional Regions in Proteins by Surface-Mapping of Phylogenetic Information. <i>Bioinformatics</i> , 2003, 19, 163-164.	4.1	1,082
5	GUIDANCE2: accurate detection of unreliable alignment regions accounting for the uncertainty of multiple parameters. <i>Nucleic Acids Research</i> , 2015, 43, W7-W14.	14.5	707
6	GUIDANCE: a web server for assessing alignment confidence scores. <i>Nucleic Acids Research</i> , 2010, 38, W23-W28.	14.5	560
7	Rate4Site: an algorithmic tool for the identification of functional regions in proteins by surface mapping of evolutionary determinants within their homologues. <i>Bioinformatics</i> , 2002, 18, S71-S77.	4.1	536
8	ConSurf: Using Evolutionary Data to Raise Testable Hypotheses about Protein Function. <i>Israel Journal of Chemistry</i> , 2013, 53, 199-206.	2.3	459
9	ConSeq: the identification of functionally and structurally important residues in protein sequences. <i>Bioinformatics</i> , 2004, 20, 1322-1324.	4.1	458
10	Comparison of Site-Specific Rate-Inference Methods for Protein Sequences: Empirical Bayesian Methods Are Superior. <i>Molecular Biology and Evolution</i> , 2004, 21, 1781-1791.	8.9	405
11	A Fast Algorithm for Joint Reconstruction of Ancestral Amino Acid Sequences. <i>Molecular Biology and Evolution</i> , 2000, 17, 890-896.	8.9	329
12	An Alignment Confidence Score Capturing Robustness to Guide Tree Uncertainty. <i>Molecular Biology and Evolution</i> , 2010, 27, 1759-1767.	8.9	313
13	FastML: a web server for probabilistic reconstruction of ancestral sequences. <i>Nucleic Acids Research</i> , 2012, 40, W580-W584.	14.5	295
14	Selecton 2007: advanced models for detecting positive and purifying selection using a Bayesian inference approach. <i>Nucleic Acids Research</i> , 2007, 35, W506-W511.	14.5	290
15	Comparative Analysis Identifies Exonic Splicing Regulatory Sequencesâ€”The Complex Definition of Enhancers and Silencers. <i>Molecular Cell</i> , 2006, 22, 769-781.	9.7	275
16	Model selection may not be a mandatory step for phylogeny reconstruction. <i>Nature Communications</i> , 2019, 10, 934.	12.8	266
17	Differential GC Content between Exons and Introns Establishes Distinct Strategies of Splice-Site Recognition. <i>Cell Reports</i> , 2012, 1, 543-556.	6.4	249
18	Rodent phylogeny revised: analysis of six nuclear genes from all major rodent clades. <i>BMC Evolutionary Biology</i> , 2009, 9, 71.	3.2	242

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19	Genome-Scale Identification of <i>Legionella pneumophila</i> Effectors Using a Machine Learning Approach. PLoS Pathogens, 2009, 5, e1000508.	4.7	236
20	Genomic analysis of 38 <i>Legionella</i> species identifies large and diverse effector repertoires. Nature Genetics, 2016, 48, 167-175.	21.4	235
21	Computational characterization of B-cell epitopes. Molecular Immunology, 2008, 45, 3477-3489.	2.2	194
22	The interface of protein structure, protein biophysics, and molecular evolution. Protein Science, 2012, 21, 769-785.	7.6	188
23	The Complexity Hypothesis Revisited: Connectivity Rather Than Function Constitutes a Barrier to Horizontal Gene Transfer. Molecular Biology and Evolution, 2011, 28, 1481-1489.	8.9	187
24	Epitopia: a web-server for predicting B-cell epitopes. BMC Bioinformatics, 2009, 10, 287.	2.6	177
25	Combined Analysis of Variation in Core, Accessory and Regulatory Genome Regions Provides a Super-Resolution View into the Evolution of Bacterial Populations. PLoS Genetics, 2016, 12, e1006280.	3.5	177
26	Computational modeling and experimental validation of the <i>Legionella</i> and <i>Coxiella</i> virulence-related type-IVB secretion signal. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E707-15.	7.1	166
27	Large-scale comparative analysis of splicing signals and their corresponding splicing factors in eukaryotes. Genome Research, 2008, 18, 88-103.	5.5	161
28	Combining Multiple Data Sets in a Likelihood Analysis: Which Models are the Best?. Molecular Biology and Evolution, 2002, 19, 2294-2307.	8.9	136
29	A Model-Based Approach for Detecting Coevolving Positions in a Molecule. Molecular Biology and Evolution, 2005, 22, 1919-1928.	8.9	131
30	Selecton: a server for detecting evolutionary forces at a single amino-acid site. Bioinformatics, 2005, 21, 2101-2103.	4.1	129
31	A Gamma mixture model better accounts for among site rate heterogeneity. Bioinformatics, 2005, 21, ii151-ii158.	4.1	129
32	Pepitope: epitope mapping from affinity-selected peptides. Bioinformatics, 2007, 23, 3244-3246.	4.1	129
33	Improving the Performance of Positive Selection Inference by Filtering Unreliable Alignment Regions. Molecular Biology and Evolution, 2012, 29, 1-5.	8.9	124
34	A Combined Empirical and Mechanistic Codon Model. Molecular Biology and Evolution, 2006, 24, 388-397.	8.9	123
35	GLOOME: gain loss mapping engine. Bioinformatics, 2010, 26, 2914-2915.	4.1	122
36	The ConSurf-HSSP database: The mapping of evolutionary conservation among homologs onto PDB structures. Proteins: Structure, Function and Bioinformatics, 2004, 58, 610-617.	2.6	115

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37	A machine-learning approach for predicting B-cell epitopes. <i>Molecular Immunology</i> , 2009, 46, 840-847.	2.2	108
38	A branch-and-bound algorithm for the inference of ancestral amino-acid sequences when the replacement rate varies among sites: Application to the evolution of five gene families. <i>Bioinformatics</i> , 2002, 18, 1116-1123.	4.1	102
39	Epitope mapping using combinatorial phage-display libraries: a graph-based algorithm. <i>Nucleic Acids Research</i> , 2007, 35, 69-78.	14.5	102
40	A Structural EM Algorithm for Phylogenetic Inference. <i>Journal of Computational Biology</i> , 2002, 9, 331-353.	1.6	95
41	Changes in exon–intron structure during vertebrate evolution affect the splicing pattern of exons. <i>Genome Research</i> , 2012, 22, 35-50.	5.5	88
42	M1CROB1AL1Z3Râ€”a user-friendly web server for the analysis of large-scale microbial genomics data. <i>Nucleic Acids Research</i> , 2019, 47, W88-W92.	14.5	86
43	Stepwise prediction of conformational discontinuous B-cell epitopes using the Mapitope algorithm. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 294-304.	2.6	82
44	Inference and Characterization of Horizontally Transferred Gene Families Using Stochastic Mapping. <i>Molecular Biology and Evolution</i> , 2010, 27, 703-713.	8.9	81
45	SMARCA2 and other genome-wide supported schizophrenia-associated genes: regulation by REST/NRSF, network organization and primate-specific evolution. <i>Human Molecular Genetics</i> , 2010, 19, 2841-2857.	2.9	78
46	A covarion-based method for detecting molecular adaptation: application to the evolution of primate mitochondrial genomes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2002, 269, 1313-1316.	2.6	67
47	Identification of novel <i>Xanthomonas euvesicatoria</i> type III effector proteins by a machine-learning approach. <i>Molecular Plant Pathology</i> , 2016, 17, 398-411.	4.2	66
48	The “Alternative” Choice of Constitutive Exons throughout Evolution. <i>PLoS Genetics</i> , 2007, 3, e203.	3.5	63
49	DNA motifs determining the efficiency of adaptation into the <i>Escherichia coli</i> CRISPR array. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14396-14401.	7.1	62
50	Towards realistic codon models: among site variability and dependency of synonymous and non-synonymous rates. <i>Bioinformatics</i> , 2007, 23, i319-i327.	4.1	60
51	Transfer of noncoding DNA drives regulatory rewiring in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 16112-16117.	7.1	59
52	The Conserved Carboxy Terminus of the Capsid Domain of Human Immunodeficiency Virus Type 1 Gag Protein Is Important for Virion Assembly and Release. <i>Journal of Virology</i> , 2004, 78, 9675-9688.	3.4	57
53	Evolution of Microsatellites in the Yeast <i>Saccharomyces cerevisiae</i> : Role of Length and Number of Repeated Units. <i>Journal of Molecular Evolution</i> , 1999, 48, 313-316.	1.8	56
54	Identification of Novel <i>Coxiella burnetii</i> Icm/Dot Effectors and Genetic Analysis of Their Involvement in Modulating a Mitogen-Activated Protein Kinase Pathway. <i>Infection and Immunity</i> , 2014, 82, 3740-3752.	2.2	55

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55	The Permian Bacterium that Isn't. <i>Molecular Biology and Evolution</i> , 2001, 18, 1143-1146.	8.9	54
56	Incomplete Directed Perfect Phylogeny. <i>SIAM Journal on Computing</i> , 2004, 33, 590-607.	1.0	54
57	Evolutionary Models Accounting for Layers of Selection in Protein-Coding Genes and their Impact on the Inference of Positive Selection. <i>Molecular Biology and Evolution</i> , 2011, 28, 3297-3308.	8.9	54
58	In silico identification of functional regions in proteins. <i>Bioinformatics</i> , 2005, 21, i328-i337.	4.1	51
59	State-of the art methodologies dictate new standards for phylogenetic analysis. <i>BMC Evolutionary Biology</i> , 2013, 13, 161.	3.2	51
60	Type III secretion system effectors form robust and flexible intracellular virulence networks. <i>Science</i> , 2021, 371, .	12.6	50
61	Deep Panning: Steps towards Probing the IgOme. <i>PLoS ONE</i> , 2012, 7, e41469.	2.5	46
62	Inference of Gain and Loss Events from Phyletic Patterns Using Stochastic Mapping and Maximum Parsimony—A Simulation Study. <i>Genome Biology and Evolution</i> , 2011, 3, 1265-1275.	2.5	45
63	A likelihood framework to analyse phyletic patterns. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 3903-3911.	4.0	44
64	Show me your secret(ed) weapons: a multifaceted approach reveals a wide arsenal of type III secreted effectors in the cucurbit pathogenic bacterium <i>Acidovorax citrulli</i> and novel effectors in the <i>Acidovorax</i> genus. <i>Molecular Plant Pathology</i> , 2020, 21, 17-37.	4.2	42
65	Evolution of the Metazoan Protein Phosphatase 2C Superfamily. <i>Journal of Molecular Evolution</i> , 2007, 64, 61-70.	1.8	38
66	Phosphatidylserine Increases IKBKAP Levels in Familial Dysautonomia Cells. <i>PLoS ONE</i> , 2010, 5, e15884.	2.5	38
67	Novel Type III Effectors in <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2015, 6, e00161.	4.1	37
68	An Evolutionary Analysis of Lateral Gene Transfer in Thymidylate Synthase Enzymes. <i>Systematic Biology</i> , 2010, 59, 212-225.	5.6	36
69	Uncovering the co-evolutionary network among prokaryotic genes. <i>Bioinformatics</i> , 2012, 28, i389-i394.	4.1	36
70	Assessing the prediction fidelity of ancestral reconstruction by a library approach. <i>Protein Engineering, Design and Selection</i> , 2015, 28, 507-518.	2.1	35
71	Site-Specific Evolutionary Rate Inference: Taking Phylogenetic Uncertainty into Account. <i>Journal of Molecular Evolution</i> , 2005, 60, 345-353.	1.8	34
72	An Integrated Model of Phenotypic Trait Changes and Site-Specific Sequence Evolution. <i>Systematic Biology</i> , 2017, 66, 917-933.	5.6	34

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73	HENA, heterogeneous network-based data set for Alzheimer's disease. Scientific Data, 2019, 6, 151.	5.3	34
74	<scp>COVID</scp> - 19 pandemic-related lockdown: response time is more important than its strictness. EMBO Molecular Medicine, 2020, 12, e13171.	6.9	31
75	Evolutionary Modeling of Rate Shifts Reveals Specificity Determinants in HIV-1 Subtypes. PLoS Computational Biology, 2008, 4, e1000214.	3.2	30
76	CoPAP: Coevolution of Presence-Absence Patterns. Nucleic Acids Research, 2013, 41, W232-W237.	14.5	30
77	Phage display peptide libraries: deviations from randomness and correctives. Nucleic Acids Research, 2018, 46, e52-e52.	14.5	30
78	ModelTeller: Model Selection for Optimal Phylogenetic Reconstruction Using Machine Learning. Molecular Biology and Evolution, 2020, 37, 3338-3352.	8.9	30
79	Native homing endonucleases can target conserved genes in humans and in animal models. Nucleic Acids Research, 2011, 39, 6646-6659.	14.5	27
80	Indel Reliability in Indel-Based Phylogenetic Inference. Genome Biology and Evolution, 2014, 6, 3199-3209.	2.5	26
81	A Machine Learning Approach To Identify Hydrogenosomal Proteins in Trichomonas vaginalis. Eukaryotic Cell, 2012, 11, 217-228.	3.4	24
82	Synonymous site conservation in the HIV-1 genome. BMC Evolutionary Biology, 2013, 13, 164.	3.2	24
83	Multiple Sequence Alignment Averaging Improves Phylogeny Reconstruction. Systematic Biology, 2019, 68, 117-130.	5.6	24
84	Revealing bacterial targets of growth inhibitors encoded by bacteriophage T7. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18715-18720.	7.1	23
85	Alignment Errors Strongly Impact Likelihood-Based Tests for Comparing Topologies. Molecular Biology and Evolution, 2014, 31, 3057-3067.	8.9	23
86	Revealing the inventory of type III effectors in <i>Pantoea agglomerans</i> gall-forming pathovars using draft genome sequences and a machine learning approach. Molecular Plant Pathology, 2018, 19, 381-392.	4.2	23
87	Interleukin-6 and Interferon- $\gamma$ Signaling via JAK-STAT Differentially Regulate Oncolytic versus Cytoprotective Antiviral States. Frontiers in Immunology, 2018, 9, 94.	4.8	22
88	An Evolutionary Space-Time Model with Varying Among-Site Dependencies. Molecular Biology and Evolution, 2006, 23, 392-400.	8.9	20
89	Harnessing machine learning to guide phylogenetic-tree search algorithms. Nature Communications, 2021, 12, 1983.	12.8	20
90	Insights from the Genome Sequence of Acidovorax citrulli M6, a Group I Strain of the Causal Agent of Bacterial Fruit Blotch of Cucurbits. Frontiers in Microbiology, 2016, 7, 430.	3.5	19

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91	The Prevalence and Evolutionary Conservation of Inverted Repeats in Proteobacteria. <i>Genome Biology and Evolution</i> , 2018, 10, 918-927.	2.5	19
92	A Probabilistic Model for Indel Evolution: Differentiating Insertions from Deletions. <i>Molecular Biology and Evolution</i> , 2021, 38, 5769-5781.	8.9	19
93	Effectidor: an automated machine-learning-based web server for the prediction of type-III secretion system effectors. <i>Bioinformatics</i> , 2022, 38, 2341-2343.	4.1	19
94	Sequence analysis of malacoherpesvirus proteins: Pan-herpesvirus capsid module and replication enzymes with an ancient connection to "Megavirales". <i>Virology</i> , 2018, 513, 114-128.	2.4	18
95	Harnessing Machine Learning To Unravel Protein Degradation in <i>Escherichia coli</i> . <i>MSystems</i> , 2021, 6, .	3.8	18
96	Detecting excess radical replacements in phylogenetic trees. <i>Gene</i> , 2003, 319, 127-135.	2.2	17
97	Regulation of alternative splicing at the single-cell level. <i>Molecular Systems Biology</i> , 2015, 11, 845.	7.2	17
98	The Cytoskeleton of Parabasalian Parasites Comprises Proteins that Share Properties Common to Intermediate Filament Proteins. <i>Protist</i> , 2016, 167, 526-543.	1.5	17
99	ASAP - A Webserver for Immunoglobulin-Sequencing Analysis Pipeline. <i>Frontiers in Immunology</i> , 2018, 9, 1686.	4.8	17
100	Ancestral sequence reconstruction: accounting for structural information by averaging over replacement matrices. <i>Bioinformatics</i> , 2019, 35, 2562-2568.	4.1	14
101	Independent Evolution of Strychnine Recognition by Bitter Taste Receptor Subtypes. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 9.	3.5	12
102	PASA: Proteomic analysis of serum antibodies web server. <i>PLoS Computational Biology</i> , 2021, 17, e1008607.	3.2	12
103	A structural EM algorithm for phylogenetic inference. , 2001, , .		11
104	Emergence of an HIV-1 cluster harbouring the major protease L90M mutation among treatment-naïve patients in T <sup>+</sup> A <sup>+</sup> I <sup>+</sup> srael. <i>HIV Medicine</i> , 2012, 13, 202-206.	2.2	10
105	Evolution of the U.S. Biological Select Agent <i>Rathayibacter toxicus</i> . <i>MBio</i> , 2018, 9, .	4.1	10
106	Paths of lateral gene transfer of lysyl-aminoacyl-tRNA synthetases with a unique evolutionary transition stage of prokaryotes coding for class I and II varieties by the same organisms. <i>BMC Evolutionary Biology</i> , 2006, 6, 22.	3.2	8
107	Phylogeny reconstruction: increasing the accuracy of pairwise distance estimation using Bayesian inference of evolutionary rates. <i>Bioinformatics</i> , 2007, 23, e136-e141.	4.1	8
108	TraitRateProp: a web server for the detection of trait-dependent evolutionary rate shifts in sequence sites. <i>Nucleic Acids Research</i> , 2017, 45, W260-W264.	14.5	8

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109	A phage mechanism for selective nicking of dUMP-containing DNA. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	8
110	Inferring Rates and Length-Distributions of Indels Using Approximate Bayesian Computation. Genome Biology and Evolution, 2017, 9, 1280-1294.	2.5	7
111	A Simulation-Based Approach to Statistical Alignment. Systematic Biology, 2019, 68, 252-266.	5.6	7
112	Motifier: An IgOme Profiler Based on Peptide Motifs Using Machine Learning. Journal of Molecular Biology, 2021, 433, 167071.	4.2	7
113	The Operonic Location of Auto-transcriptional Repressors Is Highly Conserved in Bacteria. Molecular Biology and Evolution, 2011, 28, 3309-3318.	8.9	6
114	Inferring Indel Parameters using a Simulation-based Approach. Genome Biology and Evolution, 2015, 7, 3226-3238.	2.5	6
115	Probabilistic models and their impact on the accuracy of reconstructed ancestral protein sequences. , 2007, , 43-57.		6
116	Detection and analysis of conservation at synonymous sites. , 2012, , 218-228.		6
117	SpartaABC: a web server to simulate sequences with indel parameters inferred using an approximate Bayesian computation algorithm. Nucleic Acids Research, 2017, 45, W453-W457.	14.5	5
118	Phylogenetic Distribution and Evolution of Type VI Secretion System in the Genus Xanthomonas. Frontiers in Microbiology, 2022, 13, 840308.	3.5	5
119	Fast computation of maximum likelihood trees by numerical approximation of amino acid replacement probabilities. Computational Statistics and Data Analysis, 2002, 40, 285-291.	1.2	4
120	Machine-learning of complex evolutionary signals improves classification of SNVs. NAR Genomics and Bioinformatics, 2022, 4, lqac025.	3.2	4
121	EvoRator: Prediction of Residue-level Evolutionary Rates from Protein Structures Using Machine Learning. Journal of Molecular Biology, 2022, 434, 167538.	4.2	4
122	Transduplication resulted in the incorporation of two protein-coding sequences into the Turmoil-1 transposable element of C. elegans. Biology Direct, 2008, 3, 41.	4.6	3
123	Domain-Scan: Combinatorial Sero-Diagnosis of Infectious Diseases Using Machine Learning. Frontiers in Immunology, 2020, 11, 619896.	4.8	3
124	A Chemical-Distance-Based Test for Positive Darwinian Selection. Lecture Notes in Computer Science, 2001, , 142-155.	1.3	2
125	The Complexity Hypothesis and Other Connectivity Barriers to Lateral Gene Transfer. , 2013, , 137-145.		2
126	Evolution after gene duplication. Trends in Evolutionary Biology, 2011, 3, 1.	0.4	1



#	ARTICLE	IF	CITATIONS
127	A LASSO-based approach to sample sites for phylogenetic tree search. Bioinformatics, 2022, 38, i118-i124.	4.1	1