

List of Publications by Citations

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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.

139 papers	118,745 citations	54 h-index	144 g-index
144 ext. papers	128,571 ext. citations	8.6 avg, IF	8.67 L-index

#	Paper	IF	Citations
139	MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. <i>Molecular Biology and Evolution</i> , 2011 , 28, 2731-9	8.3	32705
138	MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. <i>Molecular Biology and Evolution</i> , 2013 , 30, 2725-9	8.3	30181
137	MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. <i>Molecular Biology and Evolution</i> , 2007 , 24, 1596-9	8.3	24132
136	MEGA3: Integrated software for Molecular Evolutionary Genetics Analysis and sequence alignment. <i>Briefings in Bioinformatics</i> , 2004 , 5, 150-63	13.4	9984
135	MEGA2: molecular evolutionary genetics analysis software. <i>Bioinformatics</i> , 2001 , 17, 1244-5	7.2	4711
134	Prospects for inferring very large phylogenies by using the neighbor-joining method. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 11030-5	11.5	3177
133	MEGA: a biologist-centric software for evolutionary analysis of DNA and protein sequences. <i>Briefings in Bioinformatics</i> , 2008 , 9, 299-306	13.4	2630
132	Evolution of genes and genomes on the Drosophila phylogeny. <i>Nature</i> , 2007 , 450, 203-18	50.4	1586
131	TimeTree: a public knowledge-base of divergence times among organisms. <i>Bioinformatics</i> , 2006 , 22, 2971-2	7.2	867
130	Tree of life reveals clock-like speciation and diversification. <i>Molecular Biology and Evolution</i> , 2015 , 32, 835-45	8.3	617
129	Temporal patterns of fruit fly (<i>Drosophila</i>) evolution revealed by mutation clocks. <i>Molecular Biology and Evolution</i> , 2004 , 21, 36-44	8.3	452
128	Continental breakup and the ordinal diversification of birds and mammals. <i>Nature</i> , 1996 , 381, 226-9	50.4	413
127	Mutation rates in mammalian genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 803-8	11.5	408
126	Estimating divergence times in large molecular phylogenies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 19333-8	11.5	354
125	Inferring species phylogenies from multiple genes: concatenated sequence tree versus consensus gene tree. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2005 , 304, 64-74	1.8	288
124	Improved lignocellulose conversion to biofuels with thermophilic bacteria and thermostable enzymes. <i>Bioresource Technology</i> , 2013 , 128, 751-9	11	247
123	Molecular clocks: four decades of evolution. <i>Nature Reviews Genetics</i> , 2005 , 6, 654-62	30.1	246

122	Incomplete taxon sampling is not a problem for phylogenetic inference. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 10751-6	11.5	240
121	Understanding human disease mutations through the use of interspecific genetic variation. <i>Human Molecular Genetics</i> , 2001 , 10, 2319-28	5.6	237
120	Constraint and turnover in sex-biased gene expression in the genus <i>Drosophila</i> . <i>Nature</i> , 2007 , 450, 233-7	50.4	229
119	Genomic clocks and evolutionary timescales. <i>Trends in Genetics</i> , 2003 , 19, 200-6	8.5	223
118	MEGA-CC: computing core of molecular evolutionary genetics analysis program for automated and iterative data analysis. <i>Bioinformatics</i> , 2012 , 28, 2685-6	7.2	214
117	Precision of molecular time estimates. <i>Trends in Genetics</i> , 2004 , 20, 242-7	8.5	199
116	Evolution of modern birds revealed by mitogenomics: timing the radiation and origin of major orders. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1927-42	8.3	183
115	Gene expression intensity shapes evolutionary rates of the proteins encoded by the vertebrate genome. <i>Genetics</i> , 2004 , 168, 373-81	4	183
114	Statistics and truth in phylogenomics. <i>Molecular Biology and Evolution</i> , 2012 , 29, 457-72	8.3	174
113	A genomic timescale for the origin of eukaryotes. <i>BMC Evolutionary Biology</i> , 2001 , 1, 4	3	138
112	Evolutionary relationships of eukaryotic kingdoms. <i>Journal of Molecular Evolution</i> , 1996 , 42, 183-93	3.1	135
111	Placing confidence limits on the molecular age of the human-chimpanzee divergence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 18842-7	11.5	132
110	Human origins and analysis of mitochondrial DNA sequences. <i>Science</i> , 1992 , 255, 737-9	33.3	126
109	Whole-genome sequencing of the snub-nosed monkey provides insights into folivory and evolutionary history. <i>Nature Genetics</i> , 2014 , 46, 1303-10	36.3	122
108	Genomic sequence of a ranavirus (family Iridoviridae) associated with salamander mortalities in North America. <i>Virology</i> , 2003 , 316, 90-103	3.6	114
107	Does nonneutral evolution shape observed patterns of DNA variation in animal mitochondrial genomes?. <i>Annual Review of Genetics</i> , 2001 , 35, 539-66	14.5	114
106	Metals bioleaching from electronic waste by <i>Chromobacterium violaceum</i> and <i>Pseudomonads</i> sp. <i>Waste Management and Research</i> , 2012 , 30, 1151-9	4	112
105	The optimization principle in phylogenetic analysis tends to give incorrect topologies when the number of nucleotides or amino acids used is small. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998 , 95, 12390-7	11.5	112

104	Informal e-waste recycling: environmental risk assessment of heavy metal contamination in Mandoli industrial area, Delhi, India. <i>Environmental Science and Pollution Research</i> , 2014 , 21, 7913-28	5.1	105
103	TimeTree2: species divergence times on the iPhone. <i>Bioinformatics</i> , 2011 , 27, 2023-4	7.2	103
102	Multiple sequence alignment: in pursuit of homologous DNA positions. <i>Genome Research</i> , 2007 , 17, 127-35	3.5	99
101	Taxon sampling, bioinformatics, and phylogenomics. <i>Systematic Biology</i> , 2003 , 52, 119-24	8.4	99
100	Neutral substitutions occur at a faster rate in exons than in noncoding DNA in primate genomes. <i>Genome Research</i> , 2003 , 13, 838-44	9.7	92
99	Patterns of transitional mutation biases within and among mammalian genomes. <i>Molecular Biology and Evolution</i> , 2003 , 20, 988-93	8.3	88
98	Exceptional reduction of the plastid genome of saguaro cactus (<i>Carnegiea gigantea</i>): Loss of the <i>ndh</i> gene suite and inverted repeat. <i>American Journal of Botany</i> , 2015 , 102, 1115-27	2.7	80
97	The origin of Metazoa: a transition from temporal to spatial cell differentiation. <i>BioEssays</i> , 2009 , 31, 758-68	4.8	79
96	Heterogeneity of nucleotide frequencies among evolutionary lineages and phylogenetic inference. <i>Molecular Biology and Evolution</i> , 2003 , 20, 610-21	8.3	76
95	Performance of relaxed-clock methods in estimating evolutionary divergence times and their credibility intervals. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1289-300	8.3	73
94	Deep Model Based Transfer and Multi-Task Learning for Biological Image Analysis. <i>IEEE Transactions on Big Data</i> , 2020 , 6, 322-333	3.2	72
93	Structural dynamics flexibility informs function and evolution at a proteome scale. <i>Evolutionary Applications</i> , 2013 , 6, 423-33	4.8	69
92	Phylomedicine: an evolutionary telescope to explore and diagnose the universe of disease mutations. <i>Trends in Genetics</i> , 2011 , 27, 377-86	8.5	61
91	Stoichiogenomics: the evolutionary ecology of macromolecular elemental composition. <i>Trends in Ecology and Evolution</i> , 2011 , 26, 38-44	10.9	59
90	Quantitative analysis of the <i>Drosophila</i> segmentation regulatory network using pattern generating potentials. <i>PLoS Biology</i> , 2010 , 8, e1000456	9.7	58
89	Maximum likelihood outperforms maximum parsimony even when evolutionary rates are heterotachous. <i>Molecular Biology and Evolution</i> , 2005 , 22, 2139-41	8.3	58
88	Evolutionary anatomies of positions and types of disease-associated and neutral amino acid mutations in the human genome. <i>BMC Genomics</i> , 2006 , 7, 306	4.5	57
87	Evolutionary diagnosis method for variants in personal exomes. <i>Nature Methods</i> , 2012 , 9, 855-6	21.6	55

86	More reliable estimates of divergence times in Pan using complete mtDNA sequences and accounting for population structure. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010 , 365, 3277-88	5.8	54
85	Bioinformatics software for biologists in the genomics era. <i>Bioinformatics</i> , 2007 , 23, 1713-7	7.2	53
84	Positional conservation and amino acids shape the correct diagnosis and population frequencies of benign and damaging personal amino acid mutations. <i>Genome Research</i> , 2009 , 19, 1562-9	9.7	50
83	FlyExpress: visual mining of spatiotemporal patterns for genes and publications in Drosophila embryogenesis. <i>Bioinformatics</i> , 2011 , 27, 3319-20	7.2	49
82	Signatures of ecological resource availability in the animal and plant proteomes. <i>Molecular Biology and Evolution</i> , 2006 , 23, 1946-51	8.3	48
81	Performance of computational tools in evaluating the functional impact of laboratory-induced amino acid mutations. <i>Bioinformatics</i> , 2012 , 28, 2093-6	7.2	47
80	Bioleaching of Gold and Silver from Waste Printed Circuit Boards by <i>Pseudomonas balearica</i> SAE1 Isolated from an e-Waste Recycling Facility. <i>Current Microbiology</i> , 2018 , 75, 194-201	2.4	46
79	Prospects for building large timetrees using molecular data with incomplete gene coverage among species. <i>Molecular Biology and Evolution</i> , 2014 , 31, 2542-50	8.3	42
78	Structural and biochemical studies of serine acetyltransferase reveal why the parasite <i>Entamoeba histolytica</i> cannot form a cysteine synthase complex. <i>Journal of Biological Chemistry</i> , 2011 , 286, 12533-41	5.4	42
77	Drosophila gene expression pattern annotation through multi-instance multi-label learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012 , 9, 98-112	3	40
76	Relationship between gene co-expression and sharing of transcription factor binding sites in <i>Drosophila melanogaster</i> . <i>Bioinformatics</i> , 2009 , 25, 2473-7	7.2	35
75	Human genomic disease variants: a neutral evolutionary explanation. <i>Genome Research</i> , 2012 , 22, 1383-94	9.7	32
74	Nullomers: really a matter of natural selection?. <i>PLoS ONE</i> , 2007 , 2, e1022	3.7	31
73	Automated annotation of Drosophila gene expression patterns using a controlled vocabulary. <i>Bioinformatics</i> , 2008 , 24, 1881-8	7.2	30
72	The narrow active-site cleft of O-acetylserine sulfhydrylase from <i>Leishmania donovani</i> allows complex formation with serine acetyltransferases with a range of C-terminal sequences. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012 , 68, 909-19		29
71	A Protocol for Diagnosing the Effect of Calibration Priors on Posterior Time Estimates: A Case Study for the Cambrian Explosion of Animal Phyla. <i>Molecular Biology and Evolution</i> , 2015 , 32, 1907-12	8.3	28
70	A bag-of-words approach for Drosophila gene expression pattern annotation. <i>BMC Bioinformatics</i> , 2009 , 10, 119	3.6	28
69	Single pot bioconversion of prairie cordgrass into biohydrogen by thermophiles. <i>Bioresource Technology</i> , 2018 , 266, 232-241	11	28

68	Signatures of nitrogen limitation in the elemental composition of the proteins involved in the metabolic apparatus. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009 , 276, 2605-10	4.4	27
67	Fast and slow implementations of relaxed-clock methods show similar patterns of accuracy in estimating divergence times. <i>Molecular Biology and Evolution</i> , 2011 , 28, 2439-42	8.3	27
66	Rampant purifying selection conserves positions with posttranslational modifications in human proteins. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1565-8	8.3	27
65	MEGA-MD: molecular evolutionary genetics analysis software with mutational diagnosis of amino acid variation. <i>Bioinformatics</i> , 2014 , 30, 1305-7	7.2	26
64	Identifying spatially similar gene expression patterns in early stage fruit fly embryo images: binary feature versus invariant moment digital representations. <i>BMC Bioinformatics</i> , 2004 , 5, 202	3.6	25
63	Synthesis and characterization of cross-linked enzyme aggregates (CLEAs) of thermostable xylanase from <i>Geobacillus thermodenitrificans</i> X1. <i>Process Biochemistry</i> , 2019 , 80, 72-79	4.8	24
62	A case study: biomedical waste management practices at city hospital in Himachal Pradesh. <i>Waste Management and Research</i> , 2011 , 29, 669-73	4	24
61	Higher intensity of purifying selection on >90% of the human genes revealed by the intrinsic replacement mutation rates. <i>Molecular Biology and Evolution</i> , 2006 , 23, 2283-7	8.3	23
60	Conformational dynamics of nonsynonymous variants at protein interfaces reveals disease association. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015 , 83, 428-35	4.2	22
59	Genome-wide profiling of human cap-independent translation-enhancing elements. <i>Nature Methods</i> , 2013 , 10, 747-50	21.6	22
58	Reoxidation of Biogenic Reduced Uranium: A Challenge Toward Bioremediation. <i>Critical Reviews in Environmental Science and Technology</i> , 2014 , 44, 391-415	11.1	21
57	Purifying selection modulates the estimates of population differentiation and confounds genome-wide comparisons across single-nucleotide polymorphisms. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3617-23	8.3	21
56	Quantifying the intragenic distribution of human disease mutations. <i>Annals of Human Genetics</i> , 2003 , 67, 567-79	2.2	21
55	Single column discrepancy and dynamic max-mini optimizations for quickly finding the most parsimonious evolutionary trees. <i>Bioinformatics</i> , 2000 , 16, 140-51	7.2	21
54	Comparison of embryonic expression within multigene families using the FlyExpress discovery platform reveals more spatial than temporal divergence. <i>Developmental Dynamics</i> , 2012 , 241, 150-60	2.9	19
53	Evolutionary meta-analysis of association studies reveals ancient constraints affecting disease marker discovery. <i>Molecular Biology and Evolution</i> , 2012 , 29, 2087-94	8.3	17
52	Evolutionary balancing is critical for correctly forecasting disease-associated amino acid variants. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1252-7	8.3	17
51	Phylogenetic construction of 17 bacterial phyla by new method and carefully selected orthologs. <i>Gene</i> , 2009 , 429, 59-64	3.8	16

50	Chemo-biohydrometallurgy: A hybrid technology to recover metals from obsolete mobile SIM cards. <i>Environmental Nanotechnology, Monitoring and Management</i> , 2016 , 6, 130-133	3.3	15
49	Metallurgical processes unveil the unexplored "sleeping mines" e- waste: a review. <i>Environmental Science and Pollution Research</i> , 2020 , 27, 32359-32370	5.1	14
48	Learning sparse representations for fruit-fly gene expression pattern image annotation and retrieval. <i>BMC Bioinformatics</i> , 2012 , 13, 107	3.6	14
47	Methods for incorporating the hypermutability of CpG dinucleotides in detecting natural selection operating at the amino acid sequence level. <i>Molecular Biology and Evolution</i> , 2009 , 26, 2275-84	8.3	14
46	Enhancement of gold and silver recovery from discarded computer printed circuit boards by SAE1 using response surface methodology (RSM). <i>3 Biotech</i> , 2018 , 8, 100	2.8	12
45	Cloning, expression, purification and characterization of human mitochondrial carbonic anhydrase VA. <i>3 Biotech</i> , 2016 , 6, 16	2.8	11
44	Automated annotation of developmental stages of Drosophila embryos in images containing spatial patterns of expression. <i>Bioinformatics</i> , 2014 , 30, 266-73	7.2	11
43	Bioconversion of herbal industry waste into vermicompost using an epigeic earthworm <i>Eudrilus eugeniae</i> . <i>Waste Management and Research</i> , 2011 , 29, 1205-12	4	10
42	Phylogenetic placement of metagenomic reads using the minimum evolution principle. <i>BMC Genomics</i> , 2015 , 16 Suppl 1, S13	4.5	9
41	Wastewater ferti-irrigation: an eco-technology for sustainable agriculture. <i>Sustainable Water Resources Management</i> , 2020 , 6, 1	1.9	9
40	Signatures of natural selection on mutations of residues with multiple posttranslational modifications. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1641-5	8.3	9
39	Image-level and group-level models for Drosophila gene expression pattern annotation. <i>BMC Bioinformatics</i> , 2013 , 14, 350	3.6	9
38	Measuring conservation of contiguous sets of autosomal markers on bovine and porcine genomes in relation to the map of the human genome. <i>Genome</i> , 2002 , 45, 769-76	2.4	9
37	Evolutionary Diagnosis of non-synonymous variants involved in differential drug response. <i>BMC Medical Genomics</i> , 2015 , 8 Suppl 1, S6	3.7	8
36	Crystal structure of serine acetyl transferase from <i>Brucella abortus</i> and its complex with coenzyme A. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014 , 1844, 1741-8	4	8
35	Association of orthodenticle with natural variation for early embryonic patterning in <i>Drosophila melanogaster</i> . <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2009 , 312, 841-54	1.8	8
34	Constraining fossil calibrations for molecular clocks. <i>BioEssays</i> , 2006 , 28, 770-1; author reply 772-3	4.1	8
33	Techno-economic analysis, kinetics, global warming potential comparison and optimization of a pilot-scale unheated semi-continuous anaerobic reactor in a hilly area: For north Indian hilly states. <i>Renewable Energy</i> , 2020 , 155, 1181-1190	8.1	8

32	A mesh generation and machine learning framework for Drosophila gene expression pattern image analysis. <i>BMC Bioinformatics</i> , 2013 , 14, 372	3.6	7
31	Presence of glucose, xylose, and glycerol fermenting bacteria in the deep biosphere of the former Homestake gold mine, South Dakota. <i>Frontiers in Microbiology</i> , 2013 , 4, 18	5.7	6
30	Single residue mutation in active site of serine acetyltransferase isoform 3 from <i>Entamoeba histolytica</i> assists in partial regaining of feedback inhibition by cysteine. <i>PLoS ONE</i> , 2013 , 8, e55932	3.7	6
29	Valorization of Lignocellulosic Residues for Cost-Effective Production of Thermo-Alkali-Stable Xylanase by <i>Geobacillus thermodenitrificans</i> X1 of Indian Himalayan Hot Spring. <i>Waste and Biomass Valorization</i> , 2020 , 11, 1205-1215	3.2	6
28	N-terminal residues are crucial for quaternary structure and active site conformation for the phosphoserine aminotransferase from enteric human parasite <i>E. histolytica</i> . <i>International Journal of Biological Macromolecules</i> , 2019 , 132, 1012-1023	7.9	5
27	Efficient Methods for Dating Evolutionary Divergences 2020 , 197-219		5
26	Evaluation of e-waste status, management strategies, and legislations. <i>International Journal of Environmental Science and Technology</i> , 1	3.3	5
25	Biophysical aspects of lysozyme adduct with monocrotophos. <i>Analytical and Bioanalytical Chemistry</i> , 2014 , 406, 5477-85	4.4	4
24	Pushing back the expansion of introns in animal genomes. <i>Cell</i> , 2005 , 123, 1182-4	56.2	4
23	Bioleaching of metals from waste printed circuit boards using bacterial isolates native to abandoned gold mine. <i>BioMetals</i> , 2021 , 34, 1043-1058	3.4	4
22	Adaptive Enrichment of a Thermophilic Bacterial Isolate for Enhanced Enzymatic Activity. <i>Microorganisms</i> , 2020 , 8,	4.9	3
21	"MINES" method for genomic DNA extraction from deep biosphere biofilms. <i>Journal of Microbiological Methods</i> , 2019 , 167, 105730	2.8	3
20	Thermophilic Biohydrogen Production: Challenges at the Industrial Scale 2015 , 3-35		3
19	No positive selection for G allele in a p53 response element in Europeans. <i>Cell</i> , 2014 , 157, 1497-9	56.2	2
18	GRASP [Genomic Resource Access for Stoichioproteomics]: comparative explorations of the atomic content of 12 <i>Drosophila</i> proteomes. <i>BMC Genomics</i> , 2013 , 14, 599	4.5	2
17	The evolutionary history of amino acid variations mediating increased resistance of <i>S. aureus</i> identifies reversion mutations in metabolic regulators. <i>PLoS ONE</i> , 2013 , 8, e56466	3.7	2
16	Automatic annotation techniques for gene expression images of the fruit fly embryo 2005 ,		2
15	Energy: Clean stoves already in use in rural India. <i>Nature</i> , 2012 , 491, 333	50.4	1

14	Lower bounds on multiple sequence alignment using exact 3-way alignment. <i>BMC Bioinformatics</i> , 2007 , 8, 140	3.6	1
13	Pretreatment of low-grade shredded dust e-waste to enhance silver recovery through biocyanidation by SAE1. <i>3 Biotech</i> , 2021 , 11, 454	2.8	1
12	Structural Biology of Cysteine Biosynthetic Pathway Enzymes 2015 , 373-391		1
11	Co-morbid conditions in COVID-19 patients in Uttarakhand state of India. <i>Journal of Global Health</i> , 2021 , 11, 03029	4.3	1
10	Common Treatment, Common Variant: Evolutionary Prediction of Functional Pharmacogenomic Variants. <i>Journal of Personalized Medicine</i> , 2021 , 11,	3.6	1
9	Co-Digestion of Lignocellulosic Wastes with Food Waste for Sustainable Biogas Production. <i>Clean Energy Production Technologies</i> , 2022 , 77-97	0.8	1
8	Molecular Memories of a Cambrian Fossil. <i>American Biology Teacher</i> , 2020 , 82, 586-595	0.3	0
7	Annotation of a hypothetical protein (WP_002969292.1) from <i>Brucella abortus</i> . <i>Bioinformation</i> , 2019 , 15, 315-320	1.1	0
6	myFX: a turn-key software for laboratory desktops to analyze spatial patterns of gene expression in <i>Drosophila</i> embryos. <i>Bioinformatics</i> , 2014 , 30, 1319-21	7.2	
5	Crp/fnr family protein binds to promoters of <i>atxA</i> and <i>sodM</i> genes that regulate the expression of exotoxins in <i>Bacillus anthracis</i> .. <i>Protein Expression and Purification</i> , 2022 , 193, 106059	2	
4	Development of Biosearch System for biobank management and storage of disease associated genetic information. <i>Journal of King Saud University - Science</i> , 2022 , 34, 101760	3.6	
3	How to Build a Super Predator: From Genotype to Phenotype. <i>American Biology Teacher</i> , 2021 , 83, 138-146		
2	Proteins Involved in Colorectal Cancer: Identification Strategies and Possible Roles 2021 , 179-194		
1	MOCA for Integrated Analysis of Gene Expression and Genetic Variation in Single Cells.. <i>Frontiers in Genetics</i> , 2022 , 13, 831040	4.5	