

# Sudhir Kumar

## List of Publications by Year in Descending Order

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**Version:** 2024-04-04

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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	Crp/fnr family protein binds to promoters of atxA and sodm genes that regulate the expression of exotoxins in Bacillus anthracis.. <i>Protein Expression and Purification</i> , <b>2022</b> , 193, 106059	2	
138	Development of Biosearch System For biobank management and storage of disease associated genetic information. <i>Journal of King Saud University - Science</i> , <b>2022</b> , 34, 101760	3.6	
137	MOCA for Integrated Analysis of Gene Expression and Genetic Variation in Single Cells.. <i>Frontiers in Genetics</i> , <b>2022</b> , 13, 831040	4.5	
136	Co-Digestion of Lignocellulosic Wastes with Food Waste for Sustainable Biogas Production. <i>Clean Energy Production Technologies</i> , <b>2022</b> , 77-97	0.8	1
135	Pretreatment of low-grade shredded dust e-waste to enhance silver recovery through biocyanidation by SAE1. <i>3 Biotech</i> , <b>2021</b> , 11, 454	2.8	1
134	How to Build a Super Predator: From Genotype to Phenotype. <i>American Biology Teacher</i> , <b>2021</b> , 83, 138-146		
133	Bioleaching of metals from waste printed circuit boards using bacterial isolates native to abandoned gold mine. <i>BioMetals</i> , <b>2021</b> , 34, 1043-1058	3.4	4
132	Proteins Involved in Colorectal Cancer: Identification Strategies and Possible Roles <b>2021</b> , 179-194		
131	Co-morbid conditions in COVID-19 patients in Uttarakhand state of India. <i>Journal of Global Health</i> , <b>2021</b> , 11, 03029	4.3	1
130	Common Treatment, Common Variant: Evolutionary Prediction of Functional Pharmacogenomic Variants. <i>Journal of Personalized Medicine</i> , <b>2021</b> , 11,	3.6	1
129	Adaptive Enrichment of a Thermophilic Bacterial Isolate for Enhanced Enzymatic Activity. <i>Microorganisms</i> , <b>2020</b> , 8,	4.9	3
128	Metallurgical processes unveil the unexplored "sleeping mines" e- waste: a review. <i>Environmental Science and Pollution Research</i> , <b>2020</b> , 27, 32359-32370	5.1	14
127	Wastewater ferti-irrigation: an eco-technology for sustainable agriculture. <i>Sustainable Water Resources Management</i> , <b>2020</b> , 6, 1	1.9	9
126	Molecular Memories of a Cambrian Fossil. <i>American Biology Teacher</i> , <b>2020</b> , 82, 586-595	0.3	0
125	Efficient Methods for Dating Evolutionary Divergences <b>2020</b> , 197-219		5
124	Deep Model Based Transfer and Multi-Task Learning for Biological Image Analysis. <i>IEEE Transactions on Big Data</i> , <b>2020</b> , 6, 322-333	3.2	72
123	Valorization of Lignocellulosic Residues for Cost-Effective Production of Thermo-Alkali-Stable Xylanase by Geobacillus thermodenitrificans X1 of Indian Himalayan Hot Spring. <i>Waste and Biomass Valorization</i> , <b>2020</b> , 11, 1205-1215	3.2	6

122	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> , <b>2020</b> , 155, 1181-1190	8.1	8
121	Synthesis and characterization of cross-linked enzyme aggregates (CLEAs) of thermostable xylanase from <i>Geobacillus thermodenitrificans</i> X1. <i>Process Biochemistry</i> , <b>2019</b> , 80, 72-79	4.8	24
120	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> , <b>2019</b> , 132, 1012-1023	7.9	5
119	"MINES" method for genomic DNA extraction from deep biosphere biofilms. <i>Journal of Microbiological Methods</i> , <b>2019</b> , 167, 105730	2.8	3
118	Annotation of a hypothetical protein (WP_002969292.1) from <i>Brucella abortus</i> . <i>Bioinformation</i> , <b>2019</b> , 15, 315-320	1.1	0
117	Enhancement of gold and silver recovery from discarded computer printed circuit boards by SAE1 using response surface methodology (RSM). <i>3 Biotech</i> , <b>2018</b> , 8, 100	2.8	12
116	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> , <b>2018</b> , 75, 194-201	2.4	46
115	Single pot bioconversion of prairie cordgrass into biohydrogen by thermophiles. <i>Bioresource Technology</i> , <b>2018</b> , 266, 232-241	11	28
114	Chemo-biohydrometallurgyA hybrid technology to recover metals from obsolete mobile SIM cards. <i>Environmental Nanotechnology, Monitoring and Management</i> , <b>2016</b> , 6, 130-133	3.3	15
113	Cloning, expression, purification and characterization of human mitochondrial carbonic anhydrase VA. <i>3 Biotech</i> , <b>2016</b> , 6, 16	2.8	11
112	Tree of life reveals clock-like speciation and diversification. <i>Molecular Biology and Evolution</i> , <b>2015</b> , 32, 835-45	8.3	617
111	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> , <b>2015</b> , 102, 1115-27	2.7	80
110	Phylogenetic placement of metagenomic reads using the minimum evolution principle. <i>BMC Genomics</i> , <b>2015</b> , 16 Suppl 1, S13	4.5	9
109	Evolutionary Diagnosis of non-synonymous variants involved in differential drug response. <i>BMC Medical Genomics</i> , <b>2015</b> , 8 Suppl 1, S6	3.7	8
108	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> , <b>2015</b> , 32, 1907-12	8.3	28
107	Conformational dynamics of nonsynonymous variants at protein interfaces reveals disease association. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2015</b> , 83, 428-35	4.2	22
106	Thermophilic Biohydrogen Production: Challenges at the Industrial Scale <b>2015</b> , 3-35		3
105	Structural Biology of Cysteine Biosynthetic Pathway Enzymes <b>2015</b> , 373-391		1

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> , <b>2014</b> , 21, 7913-28	5.1	105
103	Whole-genome sequencing of the snub-nosed monkey provides insights into folivory and evolutionary history. <i>Nature Genetics</i> , <b>2014</b> , 46, 1303-10	36.3	122
102	Biophysical aspects of lysozyme adduct with monocrotophos. <i>Analytical and Bioanalytical Chemistry</i> , <b>2014</b> , 406, 5477-85	4.4	4
101	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> , <b>2014</b> , 1844, 1741-8	4	8
100	MEGA-MD: molecular evolutionary genetics analysis software with mutational diagnosis of amino acid variation. <i>Bioinformatics</i> , <b>2014</b> , 30, 1305-7	7.2	26
99	No positive selection for G allele in a p53 response element in Europeans. <i>Cell</i> , <b>2014</b> , 157, 1497-9	56.2	2
98	Reoxidation of Biogenic Reduced Uranium: A Challenge Toward Bioremediation. <i>Critical Reviews in Environmental Science and Technology</i> , <b>2014</b> , 44, 391-415	11.1	21
97	Prospects for building large timetrees using molecular data with incomplete gene coverage among species. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 2542-50	8.3	42
96	Signatures of natural selection on mutations of residues with multiple posttranslational modifications. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 1641-5	8.3	9
95	myFX: a turn-key software for laboratory desktops to analyze spatial patterns of gene expression in <i>Drosophila</i> embryos. <i>Bioinformatics</i> , <b>2014</b> , 30, 1319-21	7.2	
94	Automated annotation of developmental stages of <i>Drosophila</i> embryos in images containing spatial patterns of expression. <i>Bioinformatics</i> , <b>2014</b> , 30, 266-73	7.2	11
93	MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. <i>Molecular Biology and Evolution</i> , <b>2013</b> , 30, 2725-9	8.3	30181
92	GRASP [Genomic Resource Access for Stoichioproteomics]: comparative explorations of the atomic content of 12 <i>Drosophila</i> proteomes. <i>BMC Genomics</i> , <b>2013</b> , 14, 599	4.5	2
91	A mesh generation and machine learning framework for <i>Drosophila</i> gene expression pattern image analysis. <i>BMC Bioinformatics</i> , <b>2013</b> , 14, 372	3.6	7
90	Image-level and group-level models for <i>Drosophila</i> gene expression pattern annotation. <i>BMC Bioinformatics</i> , <b>2013</b> , 14, 350	3.6	9
89	Structural dynamics flexibility informs function and evolution at a proteome scale. <i>Evolutionary Applications</i> , <b>2013</b> , 6, 423-33	4.8	69
88	Improved lignocellulose conversion to biofuels with thermophilic bacteria and thermostable enzymes. <i>Bioresource Technology</i> , <b>2013</b> , 128, 751-9	11	247
87	Genome-wide profiling of human cap-independent translation-enhancing elements. <i>Nature Methods</i> , <b>2013</b> , 10, 747-50	21.6	22

86	Evolutionary balancing is critical for correctly forecasting disease-associated amino acid variants. <i>Molecular Biology and Evolution</i> , <b>2013</b> , 30, 1252-7	8.3	17
85	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> , <b>2013</b> , 8, e56466	3.7	2
84	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> , <b>2013</b> , 4, 18	5.7	6
83	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> , <b>2013</b> , 8, e55932	3.7	6
82	Comparison of embryonic expression within multigene families using the FlyExpress discovery platform reveals more spatial than temporal divergence. <i>Developmental Dynamics</i> , <b>2012</b> , 241, 150-60	2.9	19
81	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> , <b>2012</b> , 68, 909-19		29
80	Estimating divergence times in large molecular phylogenies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 19333-8	11.5	354
79	Metals bioleaching from electronic waste by <i>Chromobacterium violaceum</i> and <i>Pseudomonads</i> sp. <i>Waste Management and Research</i> , <b>2012</b> , 30, 1151-9	4	112
78	Energy: Clean stoves already in use in rural India. <i>Nature</i> , <b>2012</b> , 491, 333	50.4	1
77	Purifying selection modulates the estimates of population differentiation and confounds genome-wide comparisons across single-nucleotide polymorphisms. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 3617-23	8.3	21
76	Evolutionary meta-analysis of association studies reveals ancient constraints affecting disease marker discovery. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 2087-94	8.3	17
75	Learning sparse representations for fruit-fly gene expression pattern image annotation and retrieval. <i>BMC Bioinformatics</i> , <b>2012</b> , 13, 107	3.6	14
74	<i>Drosophila</i> gene expression pattern annotation through multi-instance multi-label learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2012</b> , 9, 98-112	3	40
73	Human genomic disease variants: a neutral evolutionary explanation. <i>Genome Research</i> , <b>2012</b> , 22, 1383-94	9.7	32
72	Statistics and truth in phylogenomics. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 457-72	8.3	174
71	Evolutionary diagnosis method for variants in personal exomes. <i>Nature Methods</i> , <b>2012</b> , 9, 855-6	21.6	55
70	MEGA-CC: computing core of molecular evolutionary genetics analysis program for automated and iterative data analysis. <i>Bioinformatics</i> , <b>2012</b> , 28, 2685-6	7.2	214
69	Performance of computational tools in evaluating the functional impact of laboratory-induced amino acid mutations. <i>Bioinformatics</i> , <b>2012</b> , 28, 2093-6	7.2	47

68	MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. <i>Molecular Biology and Evolution</i> , <b>2011</b> , 28, 2731-9	8.3	32705
67	Stoichiogenomics: the evolutionary ecology of macromolecular elemental composition. <i>Trends in Ecology and Evolution</i> , <b>2011</b> , 26, 38-44	10.9	59
66	Phylomedicine: an evolutionary telescope to explore and diagnose the universe of disease mutations. <i>Trends in Genetics</i> , <b>2011</b> , 27, 377-86	8.5	61
65	A case study: biomedical waste management practices at city hospital in Himachal Pradesh. <i>Waste Management and Research</i> , <b>2011</b> , 29, 669-73	4	24
64	Bioconversion of herbal industry waste into vermicompost using an epigeic earthworm <i>Eudrilus eugeniae</i> . <i>Waste Management and Research</i> , <b>2011</b> , 29, 1205-12	4	10
63	Fast and slow implementations of relaxed-clock methods show similar patterns of accuracy in estimating divergence times. <i>Molecular Biology and Evolution</i> , <b>2011</b> , 28, 2439-42	8.3	27
62	TimeTree2: species divergence times on the iPhone. <i>Bioinformatics</i> , <b>2011</b> , 27, 2023-4	7.2	103
61	Rampant purifying selection conserves positions with posttranslational modifications in human proteins. <i>Molecular Biology and Evolution</i> , <b>2011</b> , 28, 1565-8	8.3	27
60	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> , <b>2011</b> , 286, 12533-41	5.4	42
59	FlyExpress: visual mining of spatiotemporal patterns for genes and publications in <i>Drosophila</i> embryogenesis. <i>Bioinformatics</i> , <b>2011</b> , 27, 3319-20	7.2	49
58	Evolution of modern birds revealed by mitogenomics: timing the radiation and origin of major orders. <i>Molecular Biology and Evolution</i> , <b>2011</b> , 28, 1927-42	8.3	183
57	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> , <b>2010</b> , 365, 3277-88	5.8	54
56	Performance of relaxed-clock methods in estimating evolutionary divergence times and their credibility intervals. <i>Molecular Biology and Evolution</i> , <b>2010</b> , 27, 1289-300	8.3	73
55	Quantitative analysis of the <i>Drosophila</i> segmentation regulatory network using pattern generating potentials. <i>PLoS Biology</i> , <b>2010</b> , 8, e1000456	9.7	58
54	Positional conservation and amino acids shape the correct diagnosis and population frequencies of benign and damaging personal amino acid mutations. <i>Genome Research</i> , <b>2009</b> , 19, 1562-9	9.7	50
53	Relationship between gene co-expression and sharing of transcription factor binding sites in <i>Drosophila melanogaster</i> . <i>Bioinformatics</i> , <b>2009</b> , 25, 2473-7	7.2	35
52	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> , <b>2009</b> , 26, 2275-84	8.3	14
51	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> , <b>2009</b> , 276, 2605-10	4.4	27

50	A bag-of-words approach for Drosophila gene expression pattern annotation. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 119	3.6	28
49	Association of orthodenticle with natural variation for early embryonic patterning in Drosophila melanogaster. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , <b>2009</b> , 312, 841-54	1.8	8
48	The origin of Metazoa: a transition from temporal to spatial cell differentiation. <i>BioEssays</i> , <b>2009</b> , 31, 758-68	4.8	79
47	Phylogenetic construction of 17 bacterial phyla by new method and carefully selected orthologs. <i>Gene</i> , <b>2009</b> , 429, 59-64	3.8	16
46	Automated annotation of Drosophila gene expression patterns using a controlled vocabulary. <i>Bioinformatics</i> , <b>2008</b> , 24, 1881-8	7.2	30
45	MEGA: a biologist-centric software for evolutionary analysis of DNA and protein sequences. <i>Briefings in Bioinformatics</i> , <b>2008</b> , 9, 299-306	13.4	2630
44	Nullomers: really a matter of natural selection?. <i>PLoS ONE</i> , <b>2007</b> , 2, e1022	3.7	31
43	Constraint and turnover in sex-biased gene expression in the genus Drosophila. <i>Nature</i> , <b>2007</b> , 450, 233-7	50.4	229
42	Evolution of genes and genomes on the Drosophila phylogeny. <i>Nature</i> , <b>2007</b> , 450, 203-18	50.4	1586
41	Lower bounds on multiple sequence alignment using exact 3-way alignment. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 140	3.6	1
40	Bioinformatics software for biologists in the genomics era. <i>Bioinformatics</i> , <b>2007</b> , 23, 1713-7	7.2	53
39	Multiple sequence alignment: in pursuit of homologous DNA positions. <i>Genome Research</i> , <b>2007</b> , 17, 127-35	3.7	99
38	MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. <i>Molecular Biology and Evolution</i> , <b>2007</b> , 24, 1596-9	8.3	24132
37	Evolutionary anatomies of positions and types of disease-associated and neutral amino acid mutations in the human genome. <i>BMC Genomics</i> , <b>2006</b> , 7, 306	4.5	57
36	Constraining fossil calibrations for molecular clocks. <i>BioEssays</i> , <b>2006</b> , 28, 770-1; author reply 772-3	4.1	8
35	Signatures of ecological resource availability in the animal and plant proteomes. <i>Molecular Biology and Evolution</i> , <b>2006</b> , 23, 1946-51	8.3	48
34	TimeTree: a public knowledge-base of divergence times among organisms. <i>Bioinformatics</i> , <b>2006</b> , 22, 2971-2	17.2	867
33	Higher intensity of purifying selection on >90% of the human genes revealed by the intrinsic replacement mutation rates. <i>Molecular Biology and Evolution</i> , <b>2006</b> , 23, 2283-7	8.3	23



32	Pushing back the expansion of introns in animal genomes. <i>Cell</i> , <b>2005</b> , 123, 1182-4	56.2	4
31	Automatic annotation techniques for gene expression images of the fruit fly embryo <b>2005</b> ,		2
30	Molecular clocks: four decades of evolution. <i>Nature Reviews Genetics</i> , <b>2005</b> , 6, 654-62	30.1	246
29	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> , <b>2005</b> , 304, 64-74	1.8	288
28	Maximum likelihood outperforms maximum parsimony even when evolutionary rates are heterotachous. <i>Molecular Biology and Evolution</i> , <b>2005</b> , 22, 2139-41	8.3	58
27	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> , <b>2005</b> , 102, 18842-7	11.5	132
26	Temporal patterns of fruit fly ( <i>Drosophila</i> ) evolution revealed by mutation clocks. <i>Molecular Biology and Evolution</i> , <b>2004</b> , 21, 36-44	8.3	452
25	Gene expression intensity shapes evolutionary rates of the proteins encoded by the vertebrate genome. <i>Genetics</i> , <b>2004</b> , 168, 373-81	4	183
24	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> , <b>2004</b> , 101, 11030-5	11.5	3177
23	Precision of molecular time estimates. <i>Trends in Genetics</i> , <b>2004</b> , 20, 242-7	8.5	199
22	Identifying spatially similar gene expression patterns in early stage fruit fly embryo images: binary feature versus invariant moment digital representations. <i>BMC Bioinformatics</i> , <b>2004</b> , 5, 202	3.6	25
21	MEGA3: Integrated software for Molecular Evolutionary Genetics Analysis and sequence alignment. <i>Briefings in Bioinformatics</i> , <b>2004</b> , 5, 150-63	13.4	9984
20	Heterogeneity of nucleotide frequencies among evolutionary lineages and phylogenetic inference. <i>Molecular Biology and Evolution</i> , <b>2003</b> , 20, 610-21	8.3	76
19	Genomic sequence of a ranavirus (family Iridoviridae) associated with salamander mortalities in North America. <i>Virology</i> , <b>2003</b> , 316, 90-103	3.6	114
18	Genomic clocks and evolutionary timescales. <i>Trends in Genetics</i> , <b>2003</b> , 19, 200-6	8.5	223
17	Quantifying the intragenic distribution of human disease mutations. <i>Annals of Human Genetics</i> , <b>2003</b> , 67, 567-79	2.2	21
16	Neutral substitutions occur at a faster rate in exons than in noncoding DNA in primate genomes. <i>Genome Research</i> , <b>2003</b> , 13, 838-44	9.7	92
15	Patterns of transitional mutation biases within and among mammalian genomes. <i>Molecular Biology and Evolution</i> , <b>2003</b> , 20, 988-93	8.3	88



14	Taxon sampling, bioinformatics, and phylogenomics. <i>Systematic Biology</i> , <b>2003</b> , 52, 119-24	8.4	99
13	Mutation rates in mammalian genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2002</b> , 99, 803-8	11.5	408
12	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> , <b>2002</b> , 45, 769-76	2.4	9
11	A genomic timescale for the origin of eukaryotes. <i>BMC Evolutionary Biology</i> , <b>2001</b> , 1, 4	3	138
10	Understanding human disease mutations through the use of interspecific genetic variation. <i>Human Molecular Genetics</i> , <b>2001</b> , 10, 2319-28	5.6	237
9	Does nonneutral evolution shape observed patterns of DNA variation in animal mitochondrial genomes?. <i>Annual Review of Genetics</i> , <b>2001</b> , 35, 539-66	14.5	114
8	MEGA2: molecular evolutionary genetics analysis software. <i>Bioinformatics</i> , <b>2001</b> , 17, 1244-5	7.2	4711
7	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> , <b>2001</b> , 98, 10751-6	11.5	240
6	Single column discrepancy and dynamic max-mini optimizations for quickly finding the most parsimonious evolutionary trees. <i>Bioinformatics</i> , <b>2000</b> , 16, 140-51	7.2	21
5	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> , <b>1998</b> , 95, 12390-7	11.5	112
4	Evolutionary relationships of eukaryotic kingdoms. <i>Journal of Molecular Evolution</i> , <b>1996</b> , 42, 183-93	3.1	135
3	Continental breakup and the ordinal diversification of birds and mammals. <i>Nature</i> , <b>1996</b> , 381, 226-9	50.4	413
2	Human origins and analysis of mitochondrial DNA sequences. <i>Science</i> , <b>1992</b> , 255, 737-9	33.3	126
1	Evaluation of e-waste status, management strategies, and legislations. <i>International Journal of Environmental Science and Technology</i> , 1	3.3	5