

# Sudhir Kumar

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2134333/publications.pdf>

Version: 2024-02-01

143  
papers

137,593  
citations

25034

57  
h-index

11607

135  
g-index

144  
all docs

144  
docs citations

144  
times ranked

114537  
citing authors

#	ARTICLE	IF	CITATIONS
1	MEGA6: Molecular Evolutionary Genetics Analysis Version 6.0. <i>Molecular Biology and Evolution</i> , 2013, 30, 2725-2729.	8.9	37,728
2	MEGA5: Molecular Evolutionary Genetics Analysis Using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. <i>Molecular Biology and Evolution</i> , 2011, 28, 2731-2739.	8.9	36,550
3	MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) Software Version 4.0. <i>Molecular Biology and Evolution</i> , 2007, 24, 1596-1599.	8.9	25,988
4	MEGA3: Integrated software for Molecular Evolutionary Genetics Analysis and sequence alignment. <i>Briefings in Bioinformatics</i> , 2004, 5, 150-163.	6.5	10,598
5	MEGA2: molecular evolutionary genetics analysis software. <i>Bioinformatics</i> , 2001, 17, 1244-1245.	4.1	5,102
6	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, 11030-11035.	7.1	4,158
7	MEGA: A biologist-centric software for evolutionary analysis of DNA and protein sequences. <i>Briefings in Bioinformatics</i> , 2008, 9, 299-306.	6.5	3,073
8	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886
9	TimeTree: a public knowledge-base of divergence times among organisms. <i>Bioinformatics</i> , 2006, 22, 2971-2972.	4.1	1,096
10	Tree of Life Reveals Clock-Like Speciation and Diversification. <i>Molecular Biology and Evolution</i> , 2015, 32, 835-845.	8.9	862
11	Estimating divergence times in large molecular phylogenies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19333-19338.	7.1	530
12	Mutation rates in mammalian genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 803-808.	7.1	528
13	Continental breakup and the ordinal diversification of birds and mammals. <i>Nature</i> , 1996, 381, 226-229.	27.8	527
14	Temporal Patterns of Fruit Fly ( <i>Drosophila</i> ) Evolution Revealed by Mutation Clocks. <i>Molecular Biology and Evolution</i> , 2003, 21, 36-44.	8.9	516
15	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, 304B, 64-74.	1.3	382
16	MEGA-CC: computing core of molecular evolutionary genetics analysis program for automated and iterative data analysis. <i>Bioinformatics</i> , 2012, 28, 2685-2686.	4.1	332
17	Molecular clocks: four decades of evolution. <i>Nature Reviews Genetics</i> , 2005, 6, 654-662.	16.3	329
18	Improved lignocellulose conversion to biofuels with thermophilic bacteria and thermostable enzymes. <i>Bioresource Technology</i> , 2013, 128, 751-759.	9.6	291

#	ARTICLE	IF	CITATIONS
19	Understanding human disease mutations through the use of interspecific genetic variation. <i>Human Molecular Genetics</i> , 2001, 10, 2319-2328.	2.9	289
20	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, 10751-10756.	7.1	287
21	Constraint and turnover in sex-biased gene expression in the genus <i>Drosophila</i> . <i>Nature</i> , 2007, 450, 233-237.	27.8	269
22	Precision of molecular time estimates. <i>Trends in Genetics</i> , 2004, 20, 242-247.	6.7	259
23	Genomic clocks and evolutionary timescales. <i>Trends in Genetics</i> , 2003, 19, 200-206.	6.7	257
24	Statistics and Truth in Phylogenomics. <i>Molecular Biology and Evolution</i> , 2012, 29, 457-472.	8.9	243
25	Gene Expression Intensity Shapes Evolutionary Rates of the Proteins Encoded by the Vertebrate Genome. <i>Genetics</i> , 2004, 168, 373-381.	2.9	227
26	Evolution of Modern Birds Revealed by Mitogenomics: Timing the Radiation and Origin of Major Orders. <i>Molecular Biology and Evolution</i> , 2011, 28, 1927-1942.	8.9	211
27	Human origins and analysis of mitochondrial DNA sequences. <i>Science</i> , 1992, 255, 737-739.	12.6	201
28	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, 18842-18847.	7.1	190
29	Whole-genome sequencing of the snub-nosed monkey provides insights into folivory and evolutionary history. <i>Nature Genetics</i> , 2014, 46, 1303-1310.	21.4	174
30	A genomic timescale for the origin of eukaryotes. <i>BMC Evolutionary Biology</i> , 2001, 1, 4.	3.2	170
31	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, 12390-12397.	7.1	162
32	Evolutionary relationships of eukaryotic kingdoms. <i>Journal of Molecular Evolution</i> , 1996, 42, 183-193.	1.8	146
33	Metals bioleaching from electronic waste by <i>Chromobacterium violaceum</i> and <i>Pseudomonads</i> sp. <i>Waste Management and Research</i> , 2012, 30, 1151-1159.	3.9	142
34	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, 7913-7928.	5.3	142
35	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, 1115-1127.	1.7	137
36	Genomic sequence of a ranavirus (family Iridoviridae) associated with salamander mortalities in North America. <i>Virology</i> , 2003, 316, 90-103.	2.4	125

#	ARTICLE	IF	CITATIONS
37	The origin of Metazoa: a transition from temporal to spatial cell differentiation. <i>BioEssays</i> , 2009, 31, 758-768.	2.5	125
38	Does Nonneutral Evolution Shape Observed Patterns of DNA Variation in Animal Mitochondrial Genomes?. <i>Annual Review of Genetics</i> , 2001, 35, 539-566.	7.6	124
39	TimeTree2: species divergence times on the iPhone. <i>Bioinformatics</i> , 2011, 27, 2023-2024.	4.1	119
40	Taxon Sampling, Bioinformatics, and Phylogenomics. <i>Systematic Biology</i> , 2003, 52, 119-124.	5.6	116
41	Multiple sequence alignment: In pursuit of homologous DNA positions. <i>Genome Research</i> , 2007, 17, 127-135.	5.5	115
42	Patterns of Transitional Mutation Biases Within and Among Mammalian Genomes. <i>Molecular Biology and Evolution</i> , 2003, 20, 988-993.	8.9	110
43	Neutral Substitutions Occur at a Faster Rate in Exons Than in Noncoding DNA in Primate Genomes. <i>Genome Research</i> , 2003, 13, 838-844.	5.5	108
44	Deep Model Based Transfer and Multi-Task Learning for Biological Image Analysis. <i>IEEE Transactions on Big Data</i> , 2020, 6, 322-333.	6.1	101
45	Maximum Likelihood Outperforms Maximum Parsimony Even When Evolutionary Rates Are Heterotachous. <i>Molecular Biology and Evolution</i> , 2005, 22, 2139-2141.	8.9	92
46	Heterogeneity of Nucleotide Frequencies Among Evolutionary Lineages and Phylogenetic Inference. <i>Molecular Biology and Evolution</i> , 2003, 20, 610-621.	8.9	88
47	Structural dynamics flexibility informs function and evolution at a proteome scale. <i>Evolutionary Applications</i> , 2013, 6, 423-433.	3.1	88
48	Performance of Relaxed-Clock Methods in Estimating Evolutionary Divergence Times and Their Credibility Intervals. <i>Molecular Biology and Evolution</i> , 2010, 27, 1289-1300.	8.9	85
49	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.	2.2	79
50	Stoichiogenomics: the evolutionary ecology of macromolecular elemental composition. <i>Trends in Ecology and Evolution</i> , 2011, 26, 38-44.	8.7	77
51	Phylomedicine: an evolutionary telescope to explore and diagnose the universe of disease mutations. <i>Trends in Genetics</i> , 2011, 27, 377-386.	6.7	74
52	Quantitative Analysis of the <i>Drosophila</i> Segmentation Regulatory Network Using Pattern Generating Potentials. <i>PLoS Biology</i> , 2010, 8, e1000456.	5.6	69
53	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.	2.8	67
54	Signatures of Ecological Resource Availability in the Animal and Plant Proteomes. <i>Molecular Biology and Evolution</i> , 2006, 23, 1946-1951.	8.9	65

#	ARTICLE	IF	CITATIONS
55	More reliable estimates of divergence times in <i>Pan</i> using complete mtDNA sequences and accounting for population structure. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 3277-3288.	4.0	65
56	FlyExpress: visual mining of spatiotemporal patterns for genes and publications in <i>Drosophila</i> embryogenesis. <i>Bioinformatics</i> , 2011, 27, 3319-3320.	4.1	64
57	Bioinformatics software for biologists in the genomics era. <i>Bioinformatics</i> , 2007, 23, 1713-1717.	4.1	63
58	Evolutionary diagnosis method for variants in personal exomes. <i>Nature Methods</i> , 2012, 9, 855-856.	19.0	62
59	Prospects for Building Large Timetrees Using Molecular Data with Incomplete Gene Coverage among Species. <i>Molecular Biology and Evolution</i> , 2014, 31, 2542-2550.	8.9	57
60	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, 1562-1569.	5.5	55
61	<i>Drosophila</i> Gene Expression Pattern Annotation through Multi-Instance Multi-Label Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 98-112.	3.0	53
62	Performance of computational tools in evaluating the functional impact of laboratory-induced amino acid mutations. <i>Bioinformatics</i> , 2012, 28, 2093-2096.	4.1	51
63	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, 12533-12541.	3.4	50
64	Relationship between gene co-expression and sharing of transcription factor binding sites in <i>Drosophila melanogaster</i> . <i>Bioinformatics</i> , 2009, 25, 2473-2477.	4.1	45
65	Nullomers: Really a Matter of Natural Selection?. <i>PLoS ONE</i> , 2007, 2, e1022.	2.5	43
66	Human genomic disease variants: A neutral evolutionary explanation. <i>Genome Research</i> , 2012, 22, 1383-1394.	5.5	41
67	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.	3.7	38
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, 2605-2610.	2.6	36
69	A bag-of-words approach for <i>Drosophila</i> gene expression pattern annotation. <i>BMC Bioinformatics</i> , 2009, 10, 119.	2.6	35
70	The narrow active-site cleft of <i>O</i> -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, 909-919.	2.5	35
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, 1907-1912.	8.9	35
72	Single pot bioconversion of prairie cordgrass into biohydrogen by thermophiles. <i>Bioresource Technology</i> , 2018, 266, 232-241.	9.6	34

#	ARTICLE	IF	CITATIONS
73	Metallurgical processes unveil the unexplored "sleeping mines" e-waste: a review. <i>Environmental Science and Pollution Research</i> , 2020, 27, 32359-32370.	5.3	34
74	Automated annotation of <i>Drosophila</i> gene expression patterns using a controlled vocabulary. <i>Bioinformatics</i> , 2008, 24, 1881-1888.	4.1	33
75	MEGA-MD: molecular evolutionary genetics analysis software with mutational diagnosis of amino acid variation. <i>Bioinformatics</i> , 2014, 30, 1305-1307.	4.1	33
76	Reoxidation of Biogenic Reduced Uranium: A Challenge Toward Bioremediation. <i>Critical Reviews in Environmental Science and Technology</i> , 2014, 44, 391-415.	12.8	32
77	A case study: biomedical waste management practices at city hospital in Himachal Pradesh. <i>Waste Management and Research</i> , 2011, 29, 669-673.	3.9	31
78	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, 2439-2442.	8.9	30
79	Conformational dynamics of nonsynonymous variants at protein interfaces reveals disease association. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 428-435.	2.6	30
80	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.	2.6	29
81	Genome-wide profiling of human cap-independent translation-enhancing elements. <i>Nature Methods</i> , 2013, 10, 747-750.	19.0	29
82	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, 3617-3623.	8.9	28
83	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, 2283-2287.	8.9	27
84	Rampant Purifying Selection Conserves Positions with Posttranslational Modifications in Human Proteins. <i>Molecular Biology and Evolution</i> , 2011, 28, 1565-1568.	8.9	27
85	Single column discrepancy and dynamic max-mini optimizations for quickly finding the most parsimonious evolutionary trees. <i>Bioinformatics</i> , 2000, 16, 140-151.	4.1	26
86	Quantifying the Intra-genic Distribution of Human Disease Mutations. <i>Annals of Human Genetics</i> , 2003, 67, 567-579.	0.8	24
87	Evolutionary Balancing Is Critical for Correctly Forecasting Disease-Associated Amino Acid Variants. <i>Molecular Biology and Evolution</i> , 2013, 30, 1252-1257.	8.9	24
88	Comparison of embryonic expression within multigene families using the flyexpress discovery platform reveals more spatial than temporal divergence. <i>Developmental Dynamics</i> , 2012, 241, 150-160.	1.8	23
89	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.	8.9	22
90	Evaluation of e-waste status, management strategies, and legislations. <i>International Journal of Environmental Science and Technology</i> , 2022, 19, 6957-6966.	3.5	21

#	ARTICLE	IF	CITATIONS
91	Phylogenetic construction of 17 bacterial phyla by new method and carefully selected orthologs. <i>Gene</i> , 2009, 429, 59-64.	2.2	20
92	Evolutionary Meta-Analysis of Association Studies Reveals Ancient Constraints Affecting Disease Marker Discovery. <i>Molecular Biology and Evolution</i> , 2012, 29, 2087-2094.	8.9	20
93	Chemo-biohydrometallurgy—A hybrid technology to recover metals from obsolete mobile SIM cards. <i>Environmental Nanotechnology, Monitoring and Management</i> , 2016, 6, 130-133.	2.9	20
94	Wastewater ferti-irrigation: an eco-technology for sustainable agriculture. <i>Sustainable Water Resources Management</i> , 2020, 6, 1.	2.1	19
95	Methods for Incorporating the Hypermutable CpG Dinucleotides in Detecting Natural Selection Operating at the Amino Acid Sequence Level. <i>Molecular Biology and Evolution</i> , 2009, 26, 2275-2284.	8.9	18
96	Enhancement of gold and silver recovery from discarded computer printed circuit boards by <i>Pseudomonas balearica</i> SAE1 using response surface methodology (RSM). <i>3 Biotech</i> , 2018, 8, 100.	2.2	18
97	Learning Sparse Representations for Fruit-Fly Gene Expression Pattern Image Annotation and Retrieval. <i>BMC Bioinformatics</i> , 2012, 13, 107.	2.6	16
98	Phylogenetic placement of metagenomic reads using the minimum evolution principle. <i>BMC Genomics</i> , 2015, 16, S13.	2.8	16
99	Efficient Methods for Dating Evolutionary Divergences. , 2020, , 197-219.		14
100	Bioconversion of herbal industry waste into vermicompost using an epigeic earthworm <i>Eudrilus eugeniae</i> . <i>Waste Management and Research</i> , 2011, 29, 1205-1212.	3.9	13
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> , 2014, 1844, 1741-1748.	2.3	13
102	Cloning, expression, purification and characterization of human mitochondrial carbonic anhydrase VA. <i>3 Biotech</i> , 2016, 6, 16.	2.2	13
103	Bioleaching of metals from waste printed circuit boards using bacterial isolates native to abandoned gold mine. <i>BioMetals</i> , 2021, 34, 1043-1058.	4.1	13
104	Image-level and group-level models for <i>Drosophila</i> gene expression pattern annotation. <i>BMC Bioinformatics</i> , 2013, 14, 350.	2.6	12
105	Automated annotation of developmental stages of <i>Drosophila</i> embryos in images containing spatial patterns of expression. <i>Bioinformatics</i> , 2014, 30, 266-273.	4.1	12
106	Association of <i>orthodenticle</i> 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, 312B, 841-854.	1.3	11
107	Adaptive Enrichment of a Thermophilic Bacterial Isolate for Enhanced Enzymatic Activity. <i>Microorganisms</i> , 2020, 8, 871.	3.6	11
108	Signatures of Natural Selection on Mutations of Residues with Multiple Posttranslational Modifications. <i>Molecular Biology and Evolution</i> , 2014, 31, 1641-1645.	8.9	10

#	ARTICLE	IF	CITATIONS
109	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.	2.5	10
110	Waiting for the truth: is reluctance in accepting an early origin hypothesis for SARS-CoV-2 delaying our understanding of viral emergence?. <i>BMJ Global Health</i> , 2022, 7, e008386.	4.7	10
111	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, 769-776.	2.0	9
112	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.	3.5	9
113	Evolutionary Diagnosis of non-synonymous variants involved in differential drug response. <i>BMC Medical Genomics</i> , 2015, 8, S6.	1.5	9
114	Limitations of Phylogenomic Data Can Drive Inferred Speciation Rate Shifts. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	9
115	Automatic annotation techniques for gene expression images of the fruit fly embryo. , 2005, , .		8
116	Constraining fossil calibrations for molecular clocks. <i>BioEssays</i> , 2006, 28, 770-771.	2.5	8
117	A mesh generation and machine learning framework for <i>Drosophilagene</i> expression pattern image analysis. <i>BMC Bioinformatics</i> , 2013, 14, 372.	2.6	8
118	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.	7.5	8
119	Common Treatment, Common Variant: Evolutionary Prediction of Functional Pharmacogenomic Variants. <i>Journal of Personalized Medicine</i> , 2021, 11, 131.	2.5	8
120	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.	3.4	6
121	Biophysical aspects of lysozyme adduct with monocrotophos. <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 5477-5485.	3.7	5
122	Thermophilic Biohydrogen Production: Challenges at the Industrial Scale. , 2015, , 3-35.		5
123	Pushing Back the Expansion of Introns in Animal Genomes. <i>Cell</i> , 2005, 123, 1182-1184.	28.9	4
124	â€œMINESâ€•method for genomic DNA extraction from deep biosphere biofilms. <i>Journal of Microbiological Methods</i> , 2019, 167, 105730.	1.6	4
125	Pretreatment of low-grade shredded dust e-waste to enhance silver recovery through biocyanidation by <i>Pseudomonas balearica</i> SAE1. <i>3 Biotech</i> , 2021, 11, 454.	2.2	4
126	The bits and bytes of biology: digitalization fuels an emerging generative platform for biological innovation. , 2020, , .		3



#	ARTICLE	IF	CITATIONS
127	Lower bounds on multiple sequence alignment using exact 3-way alignment. BMC Bioinformatics, 2007, 8, 140.	2.6	2
128	Clean stoves already in use in rural India. Nature, 2012, 491, 333-333.	27.8	2
129	GRASP [Genomic Resource Access for Stoichioproteomics]: comparative explorations of the atomic content of 12 Drosophila proteomes. BMC Genomics, 2013, 14, 599.	2.8	2
130	The Evolutionary History of Amino Acid Variations Mediating Increased Resistance of S. aureus Identifies Reversion Mutations in Metabolic Regulators. PLoS ONE, 2013, 8, e56466.	2.5	2
131	No Positive Selection for G Allele in a p53 Response Element in Europeans. Cell, 2014, 157, 1497-1499.	28.9	2
132	Energy possibilities and future strategies for municipal solid waste in Himachal Pradesh. Materials Today: Proceedings, 2022, 48, 1455-1459.	1.8	2
133	Development of "Biosearch System" for biobank management and storage of disease associated genetic information. Journal of King Saud University - Science, 2022, 34, 101760.	3.5	2
134	Co-Digestion of Lignocellulosic Wastes with Food Waste for Sustainable Biogas Production. Clean Energy Production Technologies, 2022, , 77-97.	0.5	2
135	<title>Classification and indexing of gene expression images</title>. , 2001, 4472, 471.		1
136	Co-morbid conditions in COVID-19 patients in Uttarakhand state of India. Journal of Global Health, 2021, 11, 03029.	2.7	1
137	Annotation of a hypothetical protein (WP_002969292.1) from Brucella abortus. Bioinformatics, 2019, 15, 315-320.	0.5	1
138	Molecular Memories of a Cambrian Fossil. American Biology Teacher, 2020, 82, 586-595.	0.2	1
139	Crp/fnr family protein binds to promoters of atxA and sodmn genes that regulate the expression of exotoxins in Bacillus anthracis. Protein Expression and Purification, 2022, 193, 106059.	1.3	1
140	MOCA for Integrated Analysis of Gene Expression and Genetic Variation in Single Cells. Frontiers in Genetics, 2022, 13, 831040.	2.3	1
141	myFX: a turn-key software for laboratory desktops to analyze spatial patterns of gene expression in Drosophila embryos. Bioinformatics, 2014, 30, 1319-1321.	4.1	0
142	Proteins Involved in Colorectal Cancer: Identification Strategies and Possible Roles. , 2021, , 179-194.		0
143	How to Build a Super Predator. American Biology Teacher, 2021, 83, 138-146.	0.2	0