Sudhir Kumar

List of Publications by Year
in descending order

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	Evaluation of e-waste status, management strategies, and legislations. International Journal of Environmental Science and Technology, 2022, 19, 6957-6966.	3.5	21
2	Energy possibilities and future strategies for municipal solid waste in Himachal Pradesh. Materials Today: Proceedings, 2022, 48, 1455-1459.	1.8	2
3	Development of â€œBiosearch Systemâ€•for biobank management and storage of disease associated genetic information. Journal of King Saud University - Science, 2022, 34, 101760.	3.5	2
4	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
5	Limitations of Phylogenomic Data Can Drive Inferred Speciation Rate Shifts. Molecular Biology and Evolution, 2022, 39, .	8.9	9
6	Waiting for the truth: is reluctance in accepting an early origin hypothesis for SARS-CoV-2 delaying our understanding of viral emergence?. BMJ Global Health, 2022, 7, e008386.	4.7	10
7	MOCA for Integrated Analysis of Gene Expression and Genetic Variation in Single Cells. Frontiers in Genetics, 2022, 13, 831040.	2.3	1
8	Co-Digestion of Lignocellulosic Wastes with Food Waste for Sustainable Biogas Production. Clean Energy Production Technologies, 2022, , 77-97.	0.5	2
9	Proteins Involved in Colorectal Cancer: Identification Strategies and Possible Roles. , 2021, , 179-194.		0
10	Co-morbid conditions in COVID-19 patients in Uttarakhand state of India. Journal of Global Health, 2021, 11, 03029.	2.7	1
11	Common Treatment, Common Variant: Evolutionary Prediction of Functional Pharmacogenomic Variants. Journal of Personalized Medicine, 2021, 11, 131.	2.5	8
12	How to Build a Super Predator. American Biology Teacher, 2021, 83, 138-146.	0.2	0
13	Bioleaching of metals from waste printed circuit boards using bacterial isolates native to abandoned gold mine. BioMetals, 2021, 34, 1043-1058.	4.1	13
14	Pretreatment of low-grade shredded dust e-waste to enhance silver recovery through biocyanidation by Pseudomonas balearica SAE1. 3 Biotech, 2021, 11, 454.	2.2	4
15	Deep Model Based Transfer and Multi-Task Learning for Biological Image Analysis. IEEE Transactions on Big Data, 2020, 6, 322-333.	6.1	101
16	Valorization of Lignocellulosic Residues for Cost-Effective Production of Thermo-Alkali-Stable Xylanase by Geobacillus thermodenitrificans X1 of Indian Himalayan Hot Spring. Waste and Biomass Valorization, 2020, 11, 1205-1215.	3.4	6
17	Adaptive Enrichment of a Thermophilic Bacterial Isolate for Enhanced Enzymatic Activity. Microorganisms, 2020, 8, 871.	3.6	11
18	Metallurgical processes unveil the unexplored â€œsleeping minesâ€• e- waste: a review. Environmental Science and Pollution Research, 2020, 27, 32359-32370.	5.3	34

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19	Wastewater ferti-irrigation: an eco-technology for sustainable agriculture. Sustainable Water Resources Management, 2020, 6, 1.	2.1	19
20	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. Renewable Energy, 2020, 155, 1181-1190.	8.9	22
21	Efficient Methods for Dating Evolutionary Divergences. , 2020, , 197-219.		14
22	The bits and bytes of biology: digitalization fuels an emerging generative platform for biological innovation. , 2020, , .		3
23	Molecular Memories of a Cambrian Fossil. American Biology Teacher, 2020, 82, 586-595.	0.2	1
24	â€œMINESâ€•method for genomic DNA extraction from deep biosphere biofilms. Journal of Microbiological Methods, 2019, 167, 105730.	1.6	4
25	Synthesis and characterization of cross-linked enzyme aggregates (CLEAs) of thermostable xylanase from Geobacillus thermodenitrificans X1. Process Biochemistry, 2019, 80, 72-79.	3.7	38
26	N-terminal residues are crucial for quaternary structure and active site conformation for the phosphoserine aminotransferase from enteric human parasite E. histolytica. International Journal of Biological Macromolecules, 2019, 132, 1012-1023.	7.5	8
27	Annotation of a hypothetical protein (WP_002969292.1) from Brucella abortus. Bioinformation, 2019, 15, 315-320.	0.5	1
28	Enhancement of gold and silver recovery from discarded computer printed circuit boards by Pseudomonas balearica SAE1 using response surface methodology (RSM). 3 Biotech, 2018, 8, 100.	2.2	18
29	Bioleaching of Gold and Silver from Waste Printed Circuit Boards by Pseudomonas balearica SAE1 Isolated from an e-Waste Recycling Facility. Current Microbiology, 2018, 75, 194-201.	2.2	79
30	Single pot bioconversion of prairie cordgrass into biohydrogen by thermophiles. Bioresource Technology, 2018, 266, 232-241.	9.6	34
31	Chemo-biohydrometallurgyâ€"A hybrid technology to recover metals from obsolete mobile SIM cards. Environmental Nanotechnology, Monitoring and Management, 2016, 6, 130-133.	2.9	20
32	Cloning, expression, purification and characterization of human mitochondrial carbonic anhydrase VA. 3 Biotech, 2016, 6, 16.	2.2	13
33	Conformational dynamics of nonsynonymous variants at protein interfaces reveals disease association. Proteins: Structure, Function and Bioinformatics, 2015, 83, 428-435.	2.6	30
34	Tree of Life Reveals Clock-Like Speciation and Diversification. Molecular Biology and Evolution, 2015, 32, 835-845.	8.9	862
35	Exceptional reduction of the plastid genome of saguaro cactus (*Carnegiea gigantea*): Loss of the *ndh* gene suite and inverted repeat. American Journal of Botany, 2015, 102, 1115-1127.	1.7	137
36	Phylogenetic placement of metagenomic reads using the minimum evolution principle. BMC Genomics, 2015, 16, S13.	2.8	16

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37	Evolutionary Diagnosis of non-synonymous variants involved in differential drug response. BMC Medical Genomics, 2015, 8, S6.	1.5	9
38	A Protocol for Diagnosing the Effect of Calibration Priors on Posterior Time Estimates: A Case Study for the Cambrian Explosion of Animal Phyla. Molecular Biology and Evolution, 2015, 32, 1907-1912.	8.9	35
39	Thermophilic Biohydrogen Production: Challenges at the Industrial Scale. , 2015, , 3-35.		5
40	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
41	Automated annotation of developmental stages of <i>Drosophila</i> embryos in images containing spatial patterns of expression. Bioinformatics, 2014, 30, 266-273.	4.1	12
42	Informal e-waste recycling: environmental risk assessment of heavy metal contamination in Mandoli industrial area, Delhi, India. Environmental Science and Pollution Research, 2014, 21, 7913-7928.	5.3	142
43	Whole-genome sequencing of the snub-nosed monkey provides insights into folivory and evolutionary history. Nature Genetics, 2014, 46, 1303-1310.	21.4	174
44	Biophysical aspects of lysozyme adduct with monocrotophos. Analytical and Bioanalytical Chemistry, 2014, 406, 5477-5485.	3.7	5
45	Crystal structure of serine acetyl transferase from Brucella abortus and its complex with coenzyme A. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 1741-1748.	2.3	13
46	MEGA-MD: molecular evolutionary genetics analysis software with mutational diagnosis of amino acid variation. Bioinformatics, 2014, 30, 1305-1307.	4.1	33
47	No Positive Selection for G Allele in a p53 Response Element in Europeans. Cell, 2014, 157, 1497-1499.	28.9	2
48	Reoxidation of Biogenic Reduced Uranium: A Challenge Toward Bioremediation. Critical Reviews in Environmental Science and Technology, 2014, 44, 391-415.	12.8	32
49	Prospects for Building Large Timetrees Using Molecular Data with Incomplete Gene Coverage among Species. Molecular Biology and Evolution, 2014, 31, 2542-2550.	8.9	57
50	Signatures of Natural Selection on Mutations of Residues with Multiple Posttranslational Modifications. Molecular Biology and Evolution, 2014, 31, 1641-1645.	8.9	10
51	MEGA6: Molecular Evolutionary Genetics Analysis Version 6.0. Molecular Biology and Evolution, 2013, 30, 2725-2729.	8.9	37,728
52	GRASP [Genomic Resource Access for Stoichioproteomics]: comparative explorations of the atomic content of 12 Drosophila proteomes. BMC Genomics, 2013, 14, 599.	2.8	2
53	A mesh generation and machine learning framework for Drosophilagene expression pattern image analysis. BMC Bioinformatics, 2013, 14, 372.	2.6	8
54	Image-level and group-level models for Drosophilagene expression pattern annotation. BMC Bioinformatics, 2013, 14, 350.	2.6	12

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55	Structural dynamics flexibility informs function and evolution at a proteome scale. Evolutionary Applications, 2013, 6, 423-433.	3.1	88
56	Improved lignocellulose conversion to biofuels with thermophilic bacteria and thermostable enzymes. Bioresource Technology, 2013, 128, 751-759.	9.6	291
57	Genome-wide profiling of human cap-independent translation-enhancing elements. Nature Methods, 2013, 10, 747-750.	19.0	29
58	Evolutionary Balancing Is Critical for Correctly Forecasting Disease-Associated Amino Acid Variants. Molecular Biology and Evolution, 2013, 30, 1252-1257.	8.9	24
59	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
60	Presence of glucose, xylose, and glycerol fermenting bacteria in the deep biosphere of the former Homestake gold mine, South Dakota. Frontiers in Microbiology, 2013, 4, 18.	3.5	9
61	Single Residue Mutation in Active Site of Serine Acetyltransferase Isoform 3 from Entamoeba histolytica Assists in Partial Regaining of Feedback Inhibition by Cysteine. PLoS ONE, 2013, 8, e55932.	2.5	10
62	Statistics and Truth in Phylogenomics. Molecular Biology and Evolution, 2012, 29, 457-472.	8.9	243
63	Evolutionary diagnosis method for variants in personal exomes. Nature Methods, 2012, 9, 855-856.	19.0	62
64	MEGA-CC: computing core of molecular evolutionary genetics analysis program for automated and iterative data analysis. Bioinformatics, 2012, 28, 2685-2686.	4.1	332
65	Performance of computational tools in evaluating the functional impact of laboratory-induced amino acid mutations. Bioinformatics, 2012, 28, 2093-2096.	4.1	51
66	The narrow active-site cleft of *O*-acetylserine sulfhydrylase from *Leishmania donovani* allows complex formation with serine acetyltransferases with a range of C-terminal sequences. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 909-919.	2.5	35
67	Estimating divergence times in large molecular phylogenies. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 19333-19338.	7.1	530
68	Metals bioleaching from electronic waste by *Chromobacterium violaceum* and *Pseudomonads* sp. Waste Management and Research, 2012, 30, 1151-1159.	3.9	142
69	Clean stoves already in use in rural India. Nature, 2012, 491, 333-333.	27.8	2
70	Purifying Selection Modulates the Estimates of Population Differentiation and Confounds Genome-Wide Comparisons across Single-Nucleotide Polymorphisms. Molecular Biology and Evolution, 2012, 29, 3617-3623.	8.9	28
71	Evolutionary Meta-Analysis of Association Studies Reveals Ancient Constraints Affecting Disease Marker Discovery. Molecular Biology and Evolution, 2012, 29, 2087-2094.	8.9	20
72	Learning Sparse Representations for Fruit-Fly Gene Expression Pattern Image Annotation and Retrieval. BMC Bioinformatics, 2012, 13, 107.	2.6	16

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73	Drosophila Gene Expression Pattern Annotation through Multi-Instance Multi-Label Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 98-112.	3.0	53
74	Human genomic disease variants: A neutral evolutionary explanation. Genome Research, 2012, 22, 1383-1394.	5.5	41
75	Comparison of embryonic expression within multigene families using the flyexpress discovery platform reveals more spatial than temporal divergence. Developmental Dynamics, 2012, 241, 150-160.	1.8	23
76	A case study: biomedical waste management practices at city hospital in Himachal Pradesh. Waste Management and Research, 2011, 29, 669-673.	3.9	31
77	Bioconversion of herbal industry waste into vermicompost using an epigeic earthworm *Eudrilus eugeniae*. Waste Management and Research, 2011, 29, 1205-1212.	3.9	13
78	MEGA5: Molecular Evolutionary Genetics Analysis Using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. Molecular Biology and Evolution, 2011, 28, 2731-2739.	8.9	36,550
79	Stoichiogenomics: the evolutionary ecology of macromolecular elemental composition. Trends in Ecology and Evolution, 2011, 26, 38-44.	8.7	77
80	Phylomedicine: an evolutionary telescope to explore and diagnose the universe of disease mutations. Trends in Genetics, 2011, 27, 377-386.	6.7	74
81	Fast and Slow Implementations of Relaxed-Clock Methods Show Similar Patterns of Accuracy in Estimating Divergence Times. Molecular Biology and Evolution, 2011, 28, 2439-2442.	8.9	30
82	TimeTree2: species divergence times on the iPhone. Bioinformatics, 2011, 27, 2023-2024.	4.1	119
83	Rampant Purifying Selection Conserves Positions with Posttranslational Modifications in Human Proteins. Molecular Biology and Evolution, 2011, 28, 1565-1568.	8.9	27
84	Structural and Biochemical Studies of Serine Acetyltransferase Reveal Why the Parasite Entamoeba histolytica Cannot Form a Cysteine Synthase Complex. Journal of Biological Chemistry, 2011, 286, 12533-12541.	3.4	50
85	FlyExpress: visual mining of spatiotemporal patterns for genes and publications in *Drosophila* embryogenesis. Bioinformatics, 2011, 27, 3319-3320.	4.1	64
86	Evolution of Modern Birds Revealed by Mitogenomics: Timing the Radiation and Origin of Major Orders. Molecular Biology and Evolution, 2011, 28, 1927-1942.	8.9	211
87	More reliable estimates of divergence times in *Pan* using complete mtDNA sequences and accounting for population structure. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 3277-3288.	4.0	65
88	Performance of Relaxed-Clock Methods in Estimating Evolutionary Divergence Times and Their Credibility Intervals. Molecular Biology and Evolution, 2010, 27, 1289-1300.	8.9	85
89	Quantitative Analysis of the Drosophila Segmentation Regulatory Network Using Pattern Generating Potentials. PLoS Biology, 2010, 8, e1000456.	5.6	69
90	Positional conservation and amino acids shape the correct diagnosis and population frequencies of benign and damaging personal amino acid mutations. Genome Research, 2009, 19, 1562-1569.	5.5	55

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91	Relationship between gene co-expression and sharing of transcription factor binding sites in *Drosophila melanogaster*. Bioinformatics, 2009, 25, 2473-2477.	4.1	45
92	Methods for Incorporating the Hypermutability of CpG Dinucleotides in Detecting Natural Selection Operating at the Amino Acid Sequence Level. Molecular Biology and Evolution, 2009, 26, 2275-2284.	8.9	18
93	Signatures of nitrogen limitation in the elemental composition of the proteins involved in the metabolic apparatus. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 2605-2610.	2.6	36
94	A bag-of-words approach for Drosophila gene expression pattern annotation. BMC Bioinformatics, 2009, 10, 119.	2.6	35
95	Association of *orthodenticle* with natural variation for early embryonic patterning in *Drosophila melanogaster*. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2009, 312B, 841-854.	1.3	11
96	The origin of Metazoa: a transition from temporal to spatial cell differentiation. BioEssays, 2009, 31, 758-768.	2.5	125
97	Phylogenetic construction of 17 bacterial phyla by new method and carefully selected orthologs. Gene, 2009, 429, 59-64.	2.2	20
98	MEGA: A biologist-centric software for evolutionary analysis of DNA and protein sequences. Briefings in Bioinformatics, 2008, 9, 299-306.	6.5	3,073
99	Automated annotation of *Drosophila* gene expression patterns using a controlled vocabulary. Bioinformatics, 2008, 24, 1881-1888.	4.1	33
100	Bioinformatics software for biologists in the genomics era. Bioinformatics, 2007, 23, 1713-1717.	4.1	63
101	Multiple sequence alignment: In pursuit of homologous DNA positions. Genome Research, 2007, 17, 127-135.	5.5	115
102	MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) Software Version 4.0. Molecular Biology and Evolution, 2007, 24, 1596-1599.	8.9	25,988
103	Nullomers: Really a Matter of Natural Selection?. PLoS ONE, 2007, 2, e1022.	2.5	43
104	Constraint and turnover in sex-biased gene expression in the genus Drosophila. Nature, 2007, 450, 233-237.	27.8	269
105	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	27.8	1,886
106	Lower bounds on multiple sequence alignment using exact 3-way alignment. BMC Bioinformatics, 2007, 8, 140.	2.6	2
107	Evolutionary anatomies of positions and types of disease-associated and neutral amino acid mutations in the human genome. BMC Genomics, 2006, 7, 306.	2.8	67
108	Constraining fossil calibrations for molecular clocks. BioEssays, 2006, 28, 770-771.	2.5	8

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109	Signatures of Ecological Resource Availability in the Animal and Plant Proteomes. Molecular Biology and Evolution, 2006, 23, 1946-1951.	8.9	65
110	TimeTree: a public knowledge-base of divergence times among organisms. Bioinformatics, 2006, 22, 2971-2972.	4.1	1,096
111	Higher Intensity of Purifying Selection on >90% of the Human Genes Revealed by the Intrinsic Replacement Mutation Rates. Molecular Biology and Evolution, 2006, 23, 2283-2287.	8.9	27
112	Automatic annotation techniques for gene expression images of the fruit fly embryo. , 2005, , .		8
113	Molecular clocks: four decades of evolution. Nature Reviews Genetics, 2005, 6, 654-662.	16.3	329
114	Inferring species phylogenies from multiple genes: Concatenated sequence tree versus consensus gene tree. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2005, 304B, 64-74.	1.3	382
115	Maximum Likelihood Outperforms Maximum Parsimony Even When Evolutionary Rates Are Heterotachous. Molecular Biology and Evolution, 2005, 22, 2139-2141.	8.9	92
116	Placing confidence limits on the molecular age of the human–chimpanzee divergence. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 18842-18847.	7.1	190
117	Pushing Back the Expansion of Introns in Animal Genomes. Cell, 2005, 123, 1182-1184.	28.9	4
118	Gene Expression Intensity Shapes Evolutionary Rates of the Proteins Encoded by the Vertebrate Genome. Genetics, 2004, 168, 373-381.	2.9	227
119	Prospects for inferring very large phylogenies by using the neighbor-joining method. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 11030-11035.	7.1	4,158
120	Precision of molecular time estimates. Trends in Genetics, 2004, 20, 242-247.	6.7	259
121	Identifying spatially similar gene expression patterns in early stage fruit fly embryo images: binary feature versus invariant moment digital representations. BMC Bioinformatics, 2004, 5, 202.	2.6	29
122	MEGA3: Integrated software for Molecular Evolutionary Genetics Analysis and sequence alignment. Briefings in Bioinformatics, 2004, 5, 150-163.	6.5	10,598
123	Genomic sequence of a ranavirus (family Iridoviridae) associated with salamander mortalities in North America. Virology, 2003, 316, 90-103.	2.4	125
124	Genomic clocks and evolutionary timescales. Trends in Genetics, 2003, 19, 200-206.	6.7	257
125	Quantifying the Intragenic Distribution of Human Disease Mutations. Annals of Human Genetics, 2003, 67, 567-579.	0.8	24
126	Neutral Substitutions Occur at a Faster Rate in Exons Than in Noncoding DNA in Primate Genomes. Genome Research, 2003, 13, 838-844.	5.5	108

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127	Patterns of Transitional Mutation Biases Within and Among Mammalian Genomes. Molecular Biology and Evolution, 2003, 20, 988-993.	8.9	110
128	Taxon Sampling, Bioinformatics, and Phylogenomics. Systematic Biology, 2003, 52, 119-124.	5.6	116
129	Heterogeneity of Nucleotide Frequencies Among Evolutionary Lineages and Phylogenetic Inference. Molecular Biology and Evolution, 2003, 20, 610-621.	8.9	88
130	Temporal Patterns of Fruit Fly (Drosophila) Evolution Revealed by Mutation Clocks. Molecular Biology and Evolution, 2003, 21, 36-44.	8.9	516
131	Mutation rates in mammalian genomes. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 803-808.	7.1	528
132	Measuring conservation of contiguous sets of autosomal markers on bovine and porcine genomes in relation to the map of the human genome. Genome, 2002, 45, 769-776.	2.0	9
133	Does Nonneutral Evolution Shape Observed Patterns of DNA Variation in Animal Mitochondrial Genomes?. Annual Review of Genetics, 2001, 35, 539-566.	7.6	124
134	MEGA2: molecular evolutionary genetics analysis software. Bioinformatics, 2001, 17, 1244-1245.	4.1	5,102
135	Incomplete taxon sampling is not a problem for phylogenetic inference. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 10751-10756.	7.1	287
136	<title>Classification and indexing of gene expression images</title>. , 2001, 4472, 471.		1
137	A genomic timescale for the origin of eukaryotes. BMC Evolutionary Biology, 2001, 1, 4.	3.2	170
138	Understanding human disease mutations through the use of interspecific genetic variation. Human Molecular Genetics, 2001, 10, 2319-2328.	2.9	289
139	Single column discrepancy and dynamic max-mini optimizations for quickly finding the most parsimonious evolutionary trees. Bioinformatics, 2000, 16, 140-151.	4.1	26
140	The optimization principle in phylogenetic analysis tends to give incorrect topologies when the number of nucleotides or amino acids used is small. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 12390-12397.	7.1	162
141	Evolutionary relationships of eukaryotic kingdoms. Journal of Molecular Evolution, 1996, 42, 183-193.	1.8	146
142	Continental breakup and the ordinal diversification of birds and mammals. Nature, 1996, 381, 226-229.	27.8	527
143	Human origins and analysis of mitochondrial DNA sequences. Science, 1992, 255, 737-739.	12.6	201