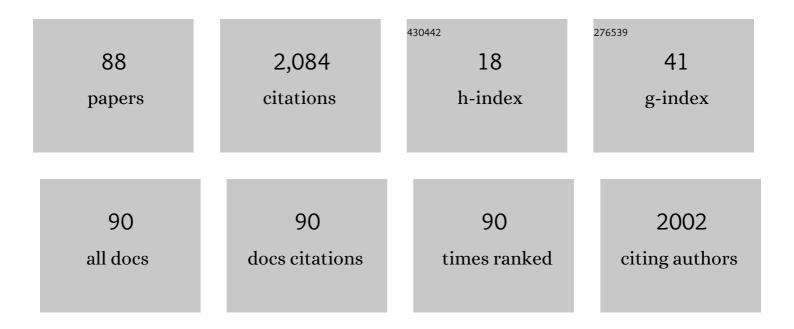
Supriyo Chakraborty, Pdf

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A review on coronary artery disease, its risk factors, and therapeutics. Journal of Cellular Physiology, 2019, 234, 16812-16823.	2.0	521
2	Interplay between miRNAs and human diseases. Journal of Cellular Physiology, 2018, 233, 2007-2018.	2.0	314
3	miRNAs and ovarian cancer: An overview. Journal of Cellular Physiology, 2018, 233, 3846-3854.	2.0	150
4	Drug resistant Tuberculosis: A review. Comparative Immunology, Microbiology and Infectious Diseases, 2021, 74, 101574.	0.7	78
5	A glance at genome editing with CRISPR–Cas9 technology. Current Genetics, 2020, 66, 447-462.	0.8	57
6	Role of miRNAs in lung cancer. Journal of Cellular Physiology, 2018, , .	2.0	51
7	Codon usage trend in mitochondrial CYB gene. Gene, 2016, 586, 105-114.	1.0	44
8	Analysis of codon usage bias of chloroplast genes in Oryza species. Planta, 2020, 252, 67.	1.6	42
9	Codon usage pattern and prediction of gene expression level in Bungarus species. Gene, 2017, 604, 48-60.	1.0	39
10	Synonymous codon usage pattern in mitochondrial <i>CYB</i> gene in pisces, aves, and mammals. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2017, 28, 187-196.	0.7	32
11	Codon usage pattern and its influencing factors in different genomes of hepadnaviruses. Archives of Virology, 2020, 165, 557-570.	0.9	29
12	Codon Usage Pattern of Genes Involved in Central Nervous System. Molecular Neurobiology, 2019, 56, 1737-1748.	1.9	28
13	Codon usage bias and its influencing factors for Y-linked genes in human. Computational Biology and Chemistry, 2017, 69, 77-86.	1.1	26
14	Analysis of codon usage patterns and influencing factors in Nipah virus. Virus Research, 2019, 263, 129-138.	1.1	26
15	The codon usage pattern of genes involved in ovarian cancer. Annals of the New York Academy of Sciences, 2019, 1440, 67-78.	1.8	23
16	Similarities and dissimilarities of codon usage in mitochondrial ATP genes among fishes, aves, and mammals. IUBMB Life, 2020, 72, 899-914.	1.5	22
17	Codon usage pattern in human SPANX genes. Bioinformation, 2015, 11, 454-459.	0.2	21
18	Composition, codon usage pattern, protein properties, and influencing factors in the genomes of members of the family Anelloviridae. Archives of Virology, 2021, 166, 461-474.	0.9	20

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19	Compositional dynamics and codon usage pattern of BRCA1 gene across nine mammalian species. Genomics, 2019, 111, 167-176.	1.3	19
20	Gaining Insights into the Codon Usage Patterns of TP53 Gene across Eight Mammalian Species. PLoS ONE, 2015, 10, e0121709.	1.1	19
21	Cytochrome P450 genes in coronary artery diseases: Codon usage analysis reveals genomic GC adaptation. Gene, 2016, 590, 35-43.	1.0	18
22	Factors influencing codon usage of mitochondrial ND1 gene in pisces, aves and mammals. Mitochondrion, 2017, 37, 17-26.	1.6	18
23	Codon bias and gene expression of mitochondrial ND2 gene in chordates. Bioinformation, 2015, 11, 407-412.	0.2	18
24	Analysis of codon usage pattern of mitochondrial protein-coding genes in different hookworms. Molecular and Biochemical Parasitology, 2018, 219, 24-32.	0.5	17
25	Understanding molecular biology of codon usage in mitochondrial complex IV genes of electron transport system: Relevance to mitochondrial diseases. Journal of Cellular Physiology, 2019, 234, 6397-6413.	2.0	17
26	Compositional properties and codon usage of TP73 gene family. Gene, 2019, 683, 159-168.	1.0	17
27	Genetic evolution and codon usage analysis of NKX-2.5 gene governing heart development in some mammals. Genomics, 2020, 112, 1319-1329.	1.3	17
28	Recombination hotspots: Models and tools for detection. DNA Repair, 2016, 40, 47-56.	1.3	16
29	A Crosstalk on Antimicrobial Peptides. International Journal of Peptide Research and Therapeutics, 2021, 27, 229-244.	0.9	16
30	Nucleotide composition determines the role of translational efficiency in human genes. Bioinformation, 2017, 13, 46-53.	0.2	16
31	Transcription factor gene GATA2 : Association of leukemia and nonsynonymous to the synonymous substitution rate across five mammals. Genomics, 2016, 107, 155-161.	1.3	15
32	Codon usage bias and phylogenetic analysis of mitochondrial ND1 gene in pisces, aves, and mammals. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 36-48.	0.7	15
33	The significance of gene mutations across eight major cancer types. Mutation Research - Reviews in Mutation Research, 2019, 781, 88-99.	2.4	15
34	Codon usage and amino acid usage influence genes expression level. Genetica, 2018, 146, 53-63.	0.5	14
35	Genomeâ€wide comparison of codon usage dynamics in mitochondrial genes across different species of amphibian genus <i>Bombina</i> . Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2019, 332, 99-112.	0.6	14
36	Role of microRNA in forming breast carcinoma. Life Sciences, 2020, 259, 118256.	2.0	13

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37	Codon usage pattern of complex III gene of respiratory chain among platyhelminths. Infection, Genetics and Evolution, 2018, 57, 128-137.	1.0	12
38	Mutation pressure and natural selection on codon usage in chloroplast genes of two species in <i>Pisum</i> L. (Fabaceae: Faboideae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2019, 30, 664-673.	0.7	12
39	Codon usage vis-a-vis start and stop codon context analysis of three dicot species. Journal of Genetics, 2018, 97, 97-107.	0.4	11
40	Prediction of Potential Epitopes for Peptide Vaccine Formulation Against Teschovirus A Using Immunoinformatics. International Journal of Peptide Research and Therapeutics, 2020, 26, 1137-1146.	0.9	11
41	Genome-wide analysis of codon usage pattern in herpesviruses and its relation to evolution. Virus Research, 2021, 292, 198248.	1.1	11
42	Insights into the Usage of Nucleobase Triplets and Codon Context Pattern in Five Influenza A Virus Subtypes. Journal of Microbiology and Biotechnology, 2016, 26, 1972-1982.	0.9	11
43	Compositional Constraint Is the Key Force in Shaping Codon Usage Bias in Hemagglutinin Gene in H1N1 Subtype of InfluenzaAVirus. International Journal of Genomics, 2014, 2014, 1-7.	0.8	10
44	A cross talk between codon usage bias in human oncogenes. Bioinformation, 2014, 10, 256-262.	0.2	10
45	Gene expression, nucleotide composition and codon usage bias of genes associated with human Y chromosome. Genetica, 2017, 145, 295-305.	0.5	9
46	Preference of A/T ending codons in mitochondrial ATP6 gene under phylum Platyhelminthes. Molecular and Biochemical Parasitology, 2018, 225, 15-26.	0.5	9
47	Japanese encephalitis virus: A multi-epitope loaded peptide vaccine formulation using reverse vaccinology approach. Infection, Genetics and Evolution, 2020, 78, 104106.	1.0	9
48	Analysis of compositional properties and codon usage bias of mitochondrial CYB gene in anura, urodela and gymnophiona. Gene, 2020, 751, 144762.	1.0	9
49	Factors affecting the codon usage bias of SRY gene across mammals. Gene, 2017, 630, 13-20.	1.0	8
50	Codon usage and expression level of human mitochondrial 13 protein coding genes across six continents. Mitochondrion, 2018, 42, 64-76.	1.6	8
51	A Study on microRNAs Targeting the Genes Overexpressed in Lung Cancer and their Codon Usage Patterns. Molecular Biotechnology, 2022, 64, 1095-1119.	1.3	8
52	Compositional properties and codon usage pattern of mitochondrial ATP gene in different classes of Arthropoda. Genetica, 2019, 147, 231-248.	0.5	7
53	Prediction of gene expression and codon usage in human parasitic helminths. Genes and Genomics, 2017, 39, 27-36.	0.5	6
54	Stress induced MAPK genes show distinct pattern of codon usage in Arabidopsis thaliana, Glycine max and Oryza sativa. Bioinformation, 2014, 10, 436-442.	0.2	6

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55	Allele frequency for Cystic fibrosis in Indians vis-a/-vis global populations. Bioinformation, 2015, 11, 348-352.	0.2	6
56	Codon Usage Bias in Two Hemipteran Insect Species: <i>Bemisia tabaci</i> and <i>Homalodisca coagulata</i> . Advances in Biology, 2014, 2014, 1-7.	1.2	5
57	Compositional bias coupled with selection and mutation pressure drives codon usage in Brassica campestris genes. Food Science and Biotechnology, 2018, 27, 725-733.	1.2	5
58	Transcript free energy positively correlates with codon usage bias in mitochondrial genes of Calypogeia species (Calypogeiaceae, Marchantiophyta). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2019, 30, 201-213.	0.7	5
59	DNA compositional dynamics and codon usage patterns of M1 and M2 matrix protein genes in influenza A virus. Infection, Genetics and Evolution, 2019, 67, 7-16.	1.0	5
60	Insights into the nucleotide composition and codon usage pattern of human tumor suppressor genes. Molecular Carcinogenesis, 2020, 59, 15-23.	1.3	5
61	Codon usage pattern and evolutionary forces of mitochondrial ND genes among orders of class Amphibia. Journal of Cellular Physiology, 2021, 236, 2850-2868.	2.0	5
62	Understanding the codon usage patterns of mitochondrial CO genes among Amphibians. Gene, 2021, 777, 145462.	1.0	5
63	Codon usage pattern and its influencing factors for mitochondrial <i>CO</i> genes among different classes of Arthropoda. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2020, 31, 313-326.	0.7	4
64	Analysis of codon usage pattern of mitochondrial ND genes in Platyhelminthes. Molecular and Biochemical Parasitology, 2020, 238, 111294.	0.5	4
65	Analysis of codon usage of Horseshoe Bat Hepatitis B virus and its host. Virology, 2021, 561, 69-79.	1.1	4
66	Synonymous codon usage and context analysis of genes associated with pancreatic cancer. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2020, 821, 111719.	0.4	3
67	Codon usage trend in genes associated with obesity. Biotechnology Letters, 2020, 42, 1865-1875.	1.1	3
68	Allele frequency analysis of GALC gene causing Krabbe disease in human and its codon usage. Gene, 2020, 747, 144673.	1.0	3
69	A Crosstalk on Codon Usage in Genes Associated with Leukemia. Biochemical Genetics, 2021, 59, 235-255.	0.8	3
70	Silencing lung cancer genes using miRNAs identified by 7mer-seed matching. Computational Biology and Chemistry, 2021, 92, 107483.	1.1	3
71	Analysis of codon usage bias in mitochondrial CO gene among platyhelminthes. Molecular and Biochemical Parasitology, 2021, 245, 111410.	0.5	3
72	Prediction of microRNAs in Pseudomonas syringae pv. tomato DC3000 and their potential target prediction in Solanum lycopersicum. Gene Reports, 2021, 25, 101360.	0.4	3

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73	Influencing elements of codon usage bias in Birnaviridae and its evolutionary analysis. Virus Research, 2022, 310, 198672.	1.1	3
74	Codon usage vis-a-vis start and stop codon context analysis of three dicot species. Journal of Genetics, 2018, 97, 97-107.	0.4	3
75	Identification of promising CD8 and CD4 T cell epitopes for peptide vaccine formulation against SARS-CoV-2. Archives of Microbiology, 2022, 204, 242.	1.0	3
76	Guanine and Cytosine at the Second Codon Position Influence Gene Expression in Cereals. Proceedings of the National Academy of Sciences India Section B - Biological Sciences, 2015, 85, 1105-1115.	0.4	2
77	Compositional features and codon usage pattern of TP63 gene. Computational Biology and Chemistry, 2019, 83, 107119.	1.1	2
78	A cross-talk on compositional dynamics and codon usage patterns of mitochondrial CYB gene in Echinodermata. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2019, 30, 351-366.	0.7	2
79	Analysis of mitochondrial proteinâ€coding genes ofAntheraea assamensis: Muga silkworm of Assam. Archives of Insect Biochemistry and Physiology, 2021, 106, e21750.	0.6	2
80	Free energy of mRNA positively correlates with GC content in chloroplast transcriptomes of edible legumes. Genomics, 2021, 113, 2826-2838.	1.3	2
81	Distinctive features gleaned from the comparative genomes analysis of clinical and non-clinical isolates of Klebsiella pneumoniae. Bioinformation, 2020, 16, 256-266.	0.2	2
82	Compositional features and pattern of codon usage for mitochondrial CO genes among reptiles. Mitochondrion, 2022, 62, 111-121.	1.6	2
83	Identification of novel microRNAs in Rous sarcoma Virus (RSV) and their target sites in tumor suppressor genes of chicken. Infection, Genetics and Evolution, 2021, 96, 105139.	1.0	2
84	Dissimilar substitution rates between two strands of DNA influence codon usage pattern in some human genes. Gene, 2018, 645, 179-187.	1.0	1
85	Chronic obstructive pulmonary disease: A crosstalk on nucleotide compositional dynamics and codon usage patterns of the genes involved in disease. Journal of Cellular Biochemistry, 2019, 120, 7649-7656.	1.2	0
86	Genome wide analysis of Mycobacterium leprae for identification of putative microRNAs and their possible targets in human. Biologia (Poland), 2021, 76, 2437-2454.	0.8	0
87	Identification of putative microRNAs in the complete genome of Mycobacterium avium and their possible interaction with human transcripts. Journal of Applied Genetics, 2021, 63, 169.	1.0	0
88	Binding sites of miRNA on the overexpressed genes of oral cancer using 7mer-seed match. Molecular and Cellular Biochemistry, 2022, 477, 1507-1526.	1.4	0