

Ayan Roy

List of Publications by Year in descending order

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35
papers

534
citations

759233

12
h-index

713466

21
g-index

36
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36
docs citations

36
times ranked

619
citing authors

#	ARTICLE	IF	CITATIONS
1	Natural compounds from <i>Clerodendrum</i> spp. as possible therapeutic candidates against SARS-CoV-2: An <i>in silico</i> investigation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 4774-4785.	3.5	57
2	Biosurfactants and anti-inflammatory activity: A potential new approach towards COVID-19. <i>Current Opinion in Environmental Science and Health</i> , 2020, 17, 72-81.	4.1	48
3	Environmental survival of SARS-CoV-2 – A solid waste perspective. <i>Environmental Research</i> , 2021, 197, 111015.	7.5	46
4	Cyanobacterial metabolites as promising drug leads against the M ^{pro} and PL ^{pro} of SARS-CoV-2: an <i>in silico</i> analysis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 6218-6230.	3.5	35
5	Anisotine and amarogentin as promising inhibitory candidates against SARS-CoV-2 proteins: a computational investigation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 4532-4542.	3.5	35
6	Evolutionary complexities of swine flu H1N1 gene sequences of 2009. <i>Biochemical and Biophysical Research Communications</i> , 2009, 390, 349-351.	2.1	28
7	Comparative investigation of the various determinants that influence the codon and amino acid usage patterns in the genus <i>Bifidobacterium</i> . <i>World Journal of Microbiology and Biotechnology</i> , 2015, 31, 959-981.	3.6	26
8	Base Composition and Host Adaptation of the SARS-CoV-2: Insight From the Codon Usage Perspective. <i>Frontiers in Microbiology</i> , 2021, 12, 548275.	3.5	26
9	Strategies to trace back the origin of COVID-19. <i>Journal of Infection</i> , 2020, 80, e39-e40.	3.3	24
10	Evolutionary Patterning of Hemagglutinin Gene Sequence of 2009 H1N1 Pandemic. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012, 29, 733-742.	3.5	17
11	Hen raising helps chicks establish gut microbiota in their early life and improve microbiota stability after H9N2 challenge. <i>Microbiome</i> , 2022, 10, 14.	11.1	17
12	HIV Progression Depends on Codon and Amino Acid Usage Profile of Envelope Protein and Associated Host-Genetic Influence. <i>Frontiers in Microbiology</i> , 2017, 8, 1083.	3.5	16
13	Isolation and <i>in silico</i> prediction of potential drug-like compounds from <i>Anethum sowa</i> L. root extracts targeted towards cancer therapy. <i>Computational Biology and Chemistry</i> , 2019, 78, 242-259.	2.3	14
14	Adaptation of gut microbiome and host metabolic systems to lignocellulosic degradation in bamboo rats. <i>ISME Journal</i> , 2022, 16, 1980-1992.	9.8	14
15	The antioxidant rich active principles of <i>Clerodendrum</i> sp. controls haloalkane xenobiotic induced hepatic damage in murine model. <i>Saudi Journal of Biological Sciences</i> , 2019, 26, 1539-1547.	3.8	12
16	Host Adaptation and Evolutionary Analysis of Zaire ebolavirus: Insights From Codon Usage Based Investigations. <i>Frontiers in Microbiology</i> , 2020, 11, 570131.	3.5	12
17	Emergence of SARS-like coronavirus in China: An update. <i>Journal of Infection</i> , 2020, 80, e28-e29.	3.3	12
18	Structural Insight into the Binding of Cyanovirin-N with the Spike Glycoprotein, M ^{pro} and PL ^{pro} of SARS-CoV-2: Protein-Protein Interactions, Dynamics Simulations and Free Energy Calculations. <i>Molecules</i> , 2021, 26, 5114.	3.8	11

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19	A Database for Mycobacterium Secretome Analysis: MycoSec™ to Accelerate Global Health Research. OMICS A Journal of Integrative Biology, 2013, 17, 502-509.	2.0	9
20	Comprehensive profiling of codon usage signatures and codon context variations in the genus Ustilago. World Journal of Microbiology and Biotechnology, 2019, 35, 118.	3.6	9
21	Computational profiling of natural compounds as promising inhibitors against the spike proteins of SARS-CoV-2 wildtype and the variants of concern, viral cell entry process, and cytokine storm in COVID-19. Journal of Cellular Biochemistry, 2022, 123, 964-986.	2.6	8
22	Synthesis of potent neuroprotective butenolides based on plant smoke derived 3,4,5-Trimethylfuran-2(5H)-one and 3-methyl-2H-furo[2,3-c]pyrone-2-one. Phytochemistry, 2019, 163, 187-194.	2.9	7
23	Insights into the riddles of codon usage patterns and codon context signatures in fungal genus <i>Puccinia</i> , a persistent threat to global agriculture. Journal of Cellular Biochemistry, 2019, 120, 19555-19566.	2.6	6
24	Host Adaptive Evolution of Avian-Origin H3N2 Canine Influenza Virus. Frontiers in Microbiology, 2021, 12, 655228.	3.5	6
25	Similarity of currently circulating H1N1 virus with the 2009 pandemic clone: Viability of an imminent pandemic. Infection, Genetics and Evolution, 2015, 32, 107-112.	2.3	5
26	Comparative genomics of Mycobacterium reveals evolutionary trends of M. avium complex. Genomics, 2019, 111, 426-435.	2.9	5
27	Codon usage signatures in the genus <i>Cryptococcus</i> : A complex interplay of gene expression, translational selection and compositional bias. Genomics, 2021, 113, 821-830.	2.9	5
28	HIV long-term non-progressors share similar features with simian immunodeficiency virus infection of chimpanzees. Journal of Biomolecular Structure and Dynamics, 2021, 39, 2447-2454.	3.5	4
29	Comprehensive profiling of functional attributes, virulence potential and evolutionary dynamics in mycobacterial secretomes. World Journal of Microbiology and Biotechnology, 2018, 34, 5.	3.6	4
30	Molecular characterization influencing metal resistance in the <i>Cupriavidus</i> / <i>Ralstonia</i> genomes. Journal of Biomolecular Structure and Dynamics, 2015, 33, 2330-2346.	3.5	3
31	Comparative evolutionary genomics of <i>Corynebacterium</i> with special reference to codon and amino acid usage diversities. Genetica, 2018, 146, 13-27.	1.1	3
32	A natural derivative from ethnomedicinal mushroom potentiates apoptosis, autophagy and attenuates cell migration, via fine tuning the Akt signaling in human lung adenocarcinoma cells (A549). Environmental Toxicology, 2022, 37, 52-68.	4.0	3
33	Structural insights into the amino acid usage variations in the profilin gene family. Amino Acids, 2022, 54, 411-419.	2.7	3
34	Evolutionary perspectives and adaptation dynamics of human seasonal influenza viruses from 2009 to 2019: An insight from codon usage. Infection, Genetics and Evolution, 2021, 96, 105067.	2.3	2
35	Rhizospheric soil metabarcoding analysis of <i>Alnus nepalensis</i> from Darjeeling hills reveals the abundance of nitrogen-fixing symbiotic microbes. Journal of Forest Research, 0, , 1-7.	1.4	2