

Debmalya Barh

List of Publications by Year in descending order

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Version: 2024-02-01

186
papers

4,114
citations

147801

31
h-index

168389

53
g-index

221
all docs

221
docs citations

221
times ranked

4521
citing authors

#	ARTICLE	IF	CITATIONS
1	Long-COVID and Post-COVID Health Complications: An Up-to-Date Review on Clinical Conditions and Their Possible Molecular Mechanisms. <i>Viruses</i> , 2021, 13, 700.	3.3	249
2	Two-Component Signal Transduction Systems of Pathogenic Bacteria As Targets for Antimicrobial Therapy: An Overview. <i>Frontiers in Microbiology</i> , 2017, 8, 1878.	3.5	176
3	Genetic Addiction Risk Score (GARS): Molecular Neurogenetic Evidence for Predisposition to Reward Deficiency Syndrome (RDS). <i>Molecular Neurobiology</i> , 2014, 50, 765-796.	4.0	157
4	The Addictive Brain: All Roads Lead to Dopamine. <i>Journal of Psychoactive Drugs</i> , 2012, 44, 134-143.	1.7	138
5	Carbon-Based Nanomaterials: Promising Antiviral Agents to Combat COVID-19 in the Microbial-Resistant Era. <i>ACS Nano</i> , 2021, 15, 8069-8086.	14.6	134
6	In silico subtractive genomics for target identification in human bacterial pathogens. <i>Drug Development Research</i> , 2011, 72, 162-177.	2.9	115
7	Generational Association Studies of Dopaminergic Genes in Reward Deficiency Syndrome (RDS) Subjects: Selecting Appropriate Phenotypes for Reward Dependence Behaviors. <i>International Journal of Environmental Research and Public Health</i> , 2011, 8, 4425-4459.	2.6	106
8	GO FEAT: a rapid web-based functional annotation tool for genomic and transcriptomic data. <i>Scientific Reports</i> , 2018, 8, 1794.	3.3	99
9	Fused deposition modelling: Current status, methodology, applications and future prospects. <i>Additive Manufacturing</i> , 2021, 47, 102378.	3.0	99
10	Exoproteome and Secretome Derived Broad Spectrum Novel Drug and Vaccine Candidates in <i>Vibrio cholerae</i> Targeted by Piper betel Derived Compounds. <i>PLoS ONE</i> , 2013, 8, e52773.	2.5	95
11	Clinical Applications of Antimicrobial Peptides (AMPs): Where do we Stand Now?. <i>Protein and Peptide Letters</i> , 2020, 27, 120-134.	0.9	85
12	Correlation of the Taq1 dopamine D2 receptor gene and percent body fat in obese and screened control subjects: A preliminary report. <i>Food and Function</i> , 2012, 3, 40-48.	4.6	82
13	Long Term Suboxone [®] Emotional Reactivity As Measured by Automatic Detection in Speech. <i>PLoS ONE</i> , 2013, 8, e69043.	2.5	73
14	Abiotic stresses, constraints and improvement strategies in chickpea. <i>Plant Breeding</i> , 2014, 133, 163-178.	1.9	73
15	Lanatoside C Induces G2/M Cell Cycle Arrest and Suppresses Cancer Cell Growth by Attenuating MAPK, Wnt, JAK-STAT, and PI3K/AKT/mTOR Signaling Pathways. <i>Biomolecules</i> , 2019, 9, 792.	4.0	73
16	Multi-omics-based identification of SARS-CoV-2 infection biology and candidate drugs against COVID-19. <i>Computers in Biology and Medicine</i> , 2020, 126, 104051.	7.0	71
17	Neurogenetics and Nutrigenomics of Neuro-Nutrient Therapy for Reward Deficiency Syndrome (RDS): Clinical Ramifications as a Function of Molecular Neurobiological Mechanisms. <i>Journal of Addiction Research & Therapy</i> , 2013, 03, 139.	0.2	65
18	Comparative mangrove metagenome reveals global prevalence of heavy metals and antibiotic resistome across different ecosystems. <i>Scientific Reports</i> , 2018, 8, 11187.	3.3	63

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19	In silico Identification of Candidate Drug and Vaccine Targets from Various Pathways in <i>Neisseria gonorrhoeae</i> . <i>In Silico Biology</i> , 2009, 9, 225-231.	0.9	60
20	BARHL1 Is Downregulated in Alzheimer's Disease and May Regulate Cognitive Functions through ESR1 and Multiple Pathways. <i>Genes</i> , 2017, 8, 245.	2.4	57
21	Searching for signatures across microbial communities: Metagenomic analysis of soil samples from mangrove and other ecosystems. <i>Scientific Reports</i> , 2017, 7, 8859.	3.3	50
22	A Novel Comparative Genomics Analysis for Common Drug and Vaccine Targets in <i>Corynebacterium pseudotuberculosis</i> and other CMN Group of Human Pathogens. <i>Chemical Biology and Drug Design</i> , 2011, 78, 73-84.	3.2	48
23	A unique view of SARS-CoV-2 through the lens of ORF8 protein. <i>Computers in Biology and Medicine</i> , 2021, 133, 104380.	7.0	48
24	Pan-Genome Analysis of Human Gastric Pathogen <i>H. pylori</i> : Comparative Genomics and Pathogenomics Approaches to Identify Regions Associated with Pathogenicity and Prediction of Potential Core Therapeutic Targets. <i>BioMed Research International</i> , 2015, 2015, 1-17.	1.9	47
25	Anticancer and Antiviral Properties of Cardiac Glycosides: A Review to Explore the Mechanism of Actions. <i>Molecules</i> , 2020, 25, 3596.	3.8	42
26	A novel strategy of epitope design in <i>Neisseria gonorrhoeae</i> . <i>Bioinformatics</i> , 2010, 5, 77-82.	0.5	42
27	Autoimmunity roots of the thrombotic events after COVID-19 vaccination. <i>Autoimmunity Reviews</i> , 2021, 20, 102941.	5.8	39
28	Potential chimeric peptides to block the SARS-CoV-2 spike receptor-binding domain. <i>F1000Research</i> , 2020, 9, 576.	1.6	38
29	An In Silico Identification of Common Putative Vaccine Candidates against <i>Treponema pallidum</i> : A Reverse Vaccinology and Subtractive Genomics Based Approach. <i>International Journal of Molecular Sciences</i> , 2017, 18, 402.	4.1	37
30	An Indian scenario on renewable and sustainable energy sources with emphasis on algae. <i>Applied Microbiology and Biotechnology</i> , 2012, 96, 1125-1135.	3.6	36
31	Notable sequence homology of the ORF10 protein introspects the architecture of SARS-CoV-2. <i>International Journal of Biological Macromolecules</i> , 2021, 181, 801-809.	7.5	36
32	An integrative in-silico approach for therapeutic target identification in the human pathogen <i>Corynebacterium diphtheriae</i> . <i>PLoS ONE</i> , 2017, 12, e0186401.	2.5	35
33	An improved interolog mapping-based computational prediction of protein-protein interactions with increased network coverage. <i>Integrative Biology (United Kingdom)</i> , 2014, 6, 1080-1087.	1.3	32
34	In silico identification of candidate drug and vaccine targets from various pathways in <i>Neisseria gonorrhoeae</i> . <i>In Silico Biology</i> , 2009, 9, 225-31.	0.9	32
35	Proteome scale comparative modeling for conserved drug and vaccine targets identification in <i>Corynebacterium pseudotuberculosis</i> . <i>BMC Genomics</i> , 2014, 15, S3.	2.8	30
36	KB220Z, a Pro-Dopamine Regulator Associated with the Protracted, Alleviation of Terrifying Lucid Dreams. Can We Infer Neuroplasticity-induced Changes in the Reward Circuit?. , 2016, 2, 3-13.		29

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37	miRsig: a consensus-based network inference methodology to identify pan-cancer miRNA-miRNA interaction signatures. <i>Scientific Reports</i> , 2017, 7, 39684.	3.3	29
38	COVID-19 Vaccines and Thrombosisâ€”Roadblock or Dead-End Street?. <i>Biomolecules</i> , 2021, 11, 1020.	4.0	28
39	Coupling Genetic Addiction Risk Score (GARS) with Electrotherapy: Fighting Iatrogenic Opioid Dependence. <i>Journal of Addiction Research & Therapy</i> , 2013, 04, 1000163.	0.2	26
40	An integrated structural proteomics approach along the druggable genome of <i>Corynebacterium pseudotuberculosis</i> species for putative druggable targets. <i>BMC Genomics</i> , 2015, 16, S9.	2.8	25
41	Analysis of the microarray gene expression for breast cancer progression after the application modified logistic regression. <i>Gene</i> , 2020, 726, 144168.	2.2	25
42	Conserved hostâ€”pathogen PPIs Globally conserved inter-species bacterial PPIs based conserved host-pathogen interactome derived novel target in <i>C. pseudotuberculosis</i> , <i>C. diphtheriae</i> , <i>M. tuberculosis</i> , <i>C. ulcerans</i> , <i>Y. pestis</i> , and <i>E. coli</i> targeted by <i>Piper betel</i> compounds. <i>Integrative Biology (United Kingdom)</i> , 2013, 5, 495-509.	1.3	24
43	In silico identification of essential proteins in <i>Corynebacterium pseudotuberculosis</i> based on protein-protein interaction networks. <i>BMC Systems Biology</i> , 2016, 10, 103.	3.0	24
44	A novel multi-omics-based highly accurate prediction of symptoms, comorbid conditions, and possible long-term complications of COVID-19. <i>Molecular Omics</i> , 2021, 17, 317-337.	2.8	24
45	A novel in silico reverse-transcriptomics-based identification and blood-based validation of a panel of sub-type specific biomarkers in lung cancer. <i>BMC Genomics</i> , 2013, 14, S5.	2.8	22
46	In silico prediction of conserved vaccine targets in <i>Streptococcus agalactiae</i> strains isolated from fish, cattle, and human samples. <i>Genetics and Molecular Research</i> , 2013, 12, 2902-2912.	0.2	22
47	PANNOTATOR: an automated tool for annotation of pan-genomes. <i>Genetics and Molecular Research</i> , 2013, 12, 2982-2989.	0.2	22
48	Emergence of Cardiac Glycosides as Potential Drugs: Current and Future Scope for Cancer Therapeutics. <i>Biomolecules</i> , 2021, 11, 1275.	4.0	22
49	Early Intervention of Intravenous KB220IV- Neuroadaptagen Amino-Acid Therapy (NAAT)â„¢ Improves Behavioral Outcomes in a Residential Addiction Treatment Program: A Pilot Study. <i>Journal of Psychoactive Drugs</i> , 2012, 44, 398-409.	1.7	21
50	Repurposing Approved Drugs for Guiding COVID-19 Prophylaxis: A Systematic Review. <i>Frontiers in Pharmacology</i> , 2020, 11, 590598.	3.5	21
51	Molecular Features, Markers, Drug Targets, and Prospective Targeted Therapeutics in Cardiac Myxoma. <i>Current Cancer Drug Targets</i> , 2009, 9, 705-716.	1.6	20
52	Hypothesizing repetitive paraphilia behavior of a medication refractive Tourette's syndrome patient having rapid clinical attenuation with KB220Z-nutrigenomic amino-acid therapy (NAAT). <i>Journal of Behavioral Addictions</i> , 2013, 2, 117-124.	3.7	20
53	The genome anatomy of <i>Corynebacterium pseudotuberculosis</i> VD57 a highly virulent strain causing Caseous lymphadenitis. <i>Standards in Genomic Sciences</i> , 2016, 11, 29.	1.5	20
54	Predicting COVID-19â€”Comorbidity Pathway Crosstalk-Based Targets and Drugs: Towards Personalized COVID-19 Management. <i>Biomedicines</i> , 2021, 9, 556.	3.2	20

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55	The importance of accessory protein variants in the pathogenicity of SARS-CoV-2. Archives of Biochemistry and Biophysics, 2022, 717, 109124.	3.0	20
56	Whole-Genome Sequence of Corynebacterium pseudotuberculosis PAT10 Strain Isolated from Sheep in Patagonia, Argentina. Journal of Bacteriology, 2011, 193, 6420-6421.	2.2	19
57	Identification of 11 new exoproteins in Corynebacterium pseudotuberculosis by a comparative analysis of the exoproteome. Microbial Pathogenesis, 2013, 61-62, 37-42.	2.9	19
58	Transcriptome profile of Corynebacterium pseudotuberculosis in response to iron limitation. BMC Genomics, 2019, 20, 663.	2.8	19
59	Diagnosis and Healing In Veterans Suspected of Suffering from Post- Traumatic Stress Disorder (PTSD) Using Reward Gene Testing and Reward Circuitry Natural Dopaminergic Activation. Journal of Genetic Syndromes & Gene Therapy, 2012, 03, 1000116.	0.2	19
60	Complete Genome Sequence of Corynebacterium pseudotuberculosis Strain CIP 52.97, Isolated from a Horse in Kenya. Journal of Bacteriology, 2011, 193, 7025-7026.	2.2	18
61	C. pseudotuberculosis Phop confers virulence and may be targeted by natural compounds. Integrative Biology (United Kingdom), 2014, 6, 1088-1099.	1.3	17
62	DISMIRA: Prioritization of disease candidates in miRNA-disease associations based on maximum weighted matching inference model and motif-based analysis. BMC Genomics, 2015, 16, S12.	2.8	17
63	Whole-genome optical mapping reveals a mis-assembly between two rRNA operons of Corynebacterium pseudotuberculosis strain 1002. BMC Genomics, 2016, 17, 315.	2.8	17
64	Microbial Omics. , 2018, , 3-20.		17
65	Shotgun metagenomic analysis of kombucha mutualistic community exposed to Mars-like environment outside the International Space Station. Environmental Microbiology, 2021, 23, 3727-3742.	3.8	17
66	The Corynebacterium pseudotuberculosis in silico predicted pan-exoproteome. BMC Genomics, 2012, 13, S6.	2.8	16
67	Stargardt disease-associated mutation spectrum of a Russian Federation cohort. European Journal of Medical Genetics, 2017, 60, 140-147.	1.3	16
68	16S rRNA Gene Amplicon Based Metagenomic Signatures of Rhizobiome Community in Rice Field During Various Growth Stages. Frontiers in Microbiology, 2019, 10, 2103.	3.5	16
69	Bacterial Cellulose Retains Robustness but Its Synthesis Declines After Exposure to a Mars-like Environment Simulated Outside the International Space Station. Astrobiology, 2021, 21, 706-717.	3.0	16
70	Differential Exoproteome Analysis of Two Corynebacterium pseudotuberculosis Biovar Ovis Strains Isolated from Goat (1002) and Sheep (C231). Current Microbiology, 2013, 67, 460-465.	2.2	15
71	Epigenetics in Head and Neck Cancer. Methods in Molecular Biology, 2015, 1238, 751-769.	0.9	15
72	Quadruplex PCR assay for identification of Corynebacterium pseudotuberculosis differentiating biovar Ovis and Equi. BMC Veterinary Research, 2017, 13, 290.	1.9	15

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73	Determining causal miRNAs and their signaling cascade in diseases using an influence diffusion model. <i>Scientific Reports</i> , 2017, 7, 8133.	3.3	14
74	Exploration of Nitrate Reductase Metabolic Pathway in <i>Corynebacterium pseudotuberculosis</i> . <i>International Journal of Genomics</i> , 2017, 2017, 1-12.	1.6	14
75	The Spike of SARS-CoV-2: Uniqueness and Applications. <i>Frontiers in Immunology</i> , 2021, 12, 663912.	4.8	14
76	Fitness of Outer Membrane Vesicles From <i>Komagataeibacter intermedius</i> Is Altered Under the Impact of Simulated Mars-like Stressors Outside the International Space Station. <i>Frontiers in Microbiology</i> , 2020, 11, 1268.	3.5	13
77	Emergence of unique SARS-CoV-2 ORF10 variants and their impact on protein structure and function. <i>International Journal of Biological Macromolecules</i> , 2022, 194, 128-143.	7.5	13
78	<i>Lactobacillus delbrueckii</i> CIDCA 133 Ameliorates Chemotherapy-Induced Mucositis by Modulating Epithelial Barrier and TLR2/4/Myd88/NF- κ B Signaling Pathway. <i>Frontiers in Microbiology</i> , 2022, 13, 858036.	3.5	13
79	miReg: a resource for microRNA regulation. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.5	12
80	miRegulome: a knowledge-base of miRNA regulomics and analysis. <i>Scientific Reports</i> , 2015, 5, 12832.	3.3	12
81	Genetic screening of Russian Usher syndrome patients toward selection for gene therapy. <i>Ophthalmic Genetics</i> , 2018, 39, 706-713.	1.2	12
82	Evaluation of the Common Molecular Basis in Alzheimer's and Parkinson's Diseases. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3730.	4.1	12
83	Current Trends in Experimental and Computational Approaches to Combat Antimicrobial Resistance. <i>Frontiers in Genetics</i> , 2020, 11, 563975.	2.3	12
84	Computational screening for potential drug candidates against the SARS-CoV-2 main protease. <i>F1000Research</i> , 2020, 9, 514.	1.6	12
85	MapRepeat: an approach for effective assembly of repetitive regions in prokaryotic genomes. <i>Bioinformatics</i> , 2015, 11, 276-279.	0.5	12
86	<i>Corynebacterium pseudotuberculosis</i> may be under anagenesis and biovar <i>Equi</i> forms biovar <i>Ovis</i> : a phylogenetic inference from sequence and structural analysis. <i>BMC Microbiology</i> , 2016, 16, 100.	3.3	11
87	Putative vaccine candidates and drug targets identified by reverse vaccinology and subtractive genomics approaches to control <i>Haemophilus ducreyi</i> , the causative agent of chancroid. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20180032.	3.4	11
88	Pan-Resistome Insights into the Multidrug Resistance of <i>Acinetobacter baumannii</i> . <i>Antibiotics</i> , 2021, 10, 596.	3.7	11
89	Simplifier: a web tool to eliminate redundant NGS contigs. <i>Bioinformatics</i> , 2012, 8, 996-999.	0.5	11
90	GLOBAL OPIOID EPIDEMIC: DOOMED TO FAIL WITHOUT GENETICALLY BASED PRECISION ADDICTION MEDICINE (PAM): LESSONS LEARNED FROM AMERICA. <i>Precision Medicine</i> , 2017, 2, 17-22.	3.5	11

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91	Whole-Genome Sequence of <i>Corynebacterium pseudotuberculosis</i> Strain Cp162, Isolated from Camel. <i>Journal of Bacteriology</i> , 2012, 194, 5718-5719.	2.2	10
92	Quantitative Electroencephalography Analysis (qEEG) of Neuro-Electro- Adaptive Therapy 12â„¢ [NEAT12] Up-Regulates Cortical Potentials in an Alcoholic during Protracted Abstinence: Putative Anti-Craving Implications. <i>Journal of Addiction Research & Therapy</i> , 2013, 05, 1-7.	0.2	10
93	Omics Approaches in Breast Cancer. , 2014, , .		10
94	Genome informatics and vaccine targets in <i>Corynebacterium urealyticum</i> using two whole genomes, comparative genomics, and reverse vaccinology. <i>BMC Genomics</i> , 2015, 16, S7.	2.8	10
95	A New Broad-Spectrum Peptide Antibiotic Produced by <i>Bacillus brevis</i> Strain MH9 Isolated from Margalla Hills of Islamabad, Pakistan. <i>International Journal of Peptide Research and Therapeutics</i> , 2016, 22, 271-279.	1.9	10
96	Potential Molecular Mechanisms of Rare Anti-Tumor Immune Response by SARS-CoV-2 in Isolated Cases of Lymphomas. <i>Viruses</i> , 2021, 13, 1927.	3.3	10
97	Implications derived from S-protein variants of SARS-CoV-2 from six continents. <i>International Journal of Biological Macromolecules</i> , 2021, 191, 934-955.	7.5	10
98	Computational screening for potential drug candidates against the SARS-CoV-2 main protease. <i>F1000Research</i> , 2020, 9, 514.	1.6	10
99	In Silico Identification of Dual Ability of <i>N. gonorrhoeae</i> ddl for Developing Drug and Vaccine Against Pathogenic <i>Neisseria</i> and Other Human Pathogens. <i>Journal of Proteomics and Bioinformatics</i> , 2010, 03, 082-090.	0.4	10
100	Genomic target database (GTD): A database of potential targets in human pathogenic bacteria. <i>Bioinformatics</i> , 2009, 4, 50-51.	0.5	10
101	The conserved mitochondrial gene distribution in relatives of <i>Turritopsis nutricula</i> , an immortal jellyfish. <i>Bioinformatics</i> , 2014, 10, 586-591.	0.5	10
102	Quality of prokaryote genome assembly: Indispensable issues of factors affecting prokaryote genome assembly quality. <i>Gene</i> , 2012, 505, 365-367.	2.2	9
103	Mini Review Identifying human disease genes: advances in molecular genetics and computational approaches. <i>Genetics and Molecular Research</i> , 2014, 13, 5073-5087.	0.2	9
104	Computational identification of putative common genomic drug and vaccine targets in <i>Mycoplasma genitalium</i> . <i>Genomics</i> , 2021, 113, 2730-2743.	2.9	9
105	Acetate Kinase (Ack) is Essential for Microbial Growth and Betel-derived Compounds Potentially Target Ack, PhoP and MDR Proteins in <i>M. tuberculosis</i> , <i>V. cholerae</i> and Pathogenic <i>E. coli</i> : An in silico and in vitro Study. <i>Current Topics in Medicinal Chemistry</i> , 2019, 18, 2731-2740.	2.1	9
106	Biomarkers, Critical Disease Pathways, Drug Targets, and Alternative Medicine in Male Breast Cancer. <i>Current Drug Targets</i> , 2009, 10, 1-8.	2.1	8
107	Complete genome sequence of <i>Corynebacterium pseudotuberculosis</i> biovar ovis strain P54B96 isolated from antelope in South Africa obtained by rapid next generation sequencing technology. <i>Standards in Genomic Sciences</i> , 2012, 7, 189-199.	1.5	8
108	In Silico Models. , 2014, , 385-404.		8

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109	SIMBA: a web tool for managing bacterial genome assembly generated by Ion PGM sequencing technology. BMC Bioinformatics, 2016, 17, 456.	2.6	8
110	First genome sequencing and comparative analyses of Corynebacterium pseudotuberculosis strains from Mexico. Standards in Genomic Sciences, 2018, 13, 21.	1.5	8
111	The Druggable Pocketome of Corynebacterium diphtheriae: A New Approach for in silico Putative Druggable Targets. Frontiers in Genetics, 2018, 9, 44.	2.3	8
112	In Silico Protein-Protein Interactions: Avoiding Data and Method Biases Over Sensitivity and Specificity. Current Protein and Peptide Science, 2015, 16, 689-700.	1.4	8
113	Novel aromatase inhibitors selection using induced fit docking and extra precision methods: Potential clinical use in ER-alpha-positive breast cancer. Bioinformatics, 2016, 12, 324-331.	0.5	8
114	Can Genetic Testing Coupled with Enhanced Dopaminergic Activation Reduce Recidivism Rates in the Workers Compensation Legacy Cases?. Journal of Alcoholism and Drug Dependence, 2014, 02, .	0.2	7
115	In silico disease model: from simple networks to complex diseases. , 2020, , 441-460.		7
116	The mechanism behind flaring/triggering of autoimmunity disorders associated with COVID-19. Autoimmunity Reviews, 2021, 20, 102909.	5.8	7
117	Isolation and Characterization of L-Tryptophan Ammonia Lyase from Rubrivivax benzoatilyticus Strain JA2. Current Protein and Peptide Science, 2015, 16, 775-781.	1.4	7
118	Epitope Design from Transporter Targets in N. gonorrhoeae. Journal of Proteomics and Bioinformatics, 2009, 02, 475-480.	0.4	7
119	To Other Planets With Upgraded Millennial Kombucha in Rhythms of Sustainability and Health Support. Frontiers in Astronomy and Space Sciences, 2021, 8, .	2.8	7
120	The Benefits of Genetic Addiction Risk Score (GARS) Testing in Substance Use Disorder (SUD). International Journal of Genomics and Data Mining, 2018, 2018, .	0.1	7
121	An issue of concern: unique truncated ORF8 protein variants of SARS-CoV-2. PeerJ, 2022, 10, e13136.	2.0	7
122	Piper betel Compounds Piperidine, Eugenyl Acetate, and Chlorogenic Acid Are Broad-Spectrum Anti-Vibrio Compounds that Are Also Effective on MDR Strains of the Pathogen. Pathogens, 2019, 8, 64.	2.8	6
123	Re-sequencing and optical mapping reveals misassemblies and real inversions on Corynebacterium pseudotuberculosis genomes. Scientific Reports, 2019, 9, 16387.	3.3	6
124	Overview of key molecular and pharmacological targets for diabetes and associated diseases. Life Sciences, 2021, 278, 119632.	4.3	6
125	Targeting LIN28: a new hope in prostate cancer theranostics. Future Oncology, 2021, 17, 3873-3880.	2.4	6
126	miReg: a resource for microRNA regulation. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	6

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127	Bacteriocins as an alternative in the treatment of infections by <i>Staphylococcus aureus</i> . <i>Anais Da Academia Brasileira De Ciencias</i> , 2020, 92, e20201216.	0.8	6
128	Taxonomic classification of strain PO100/5 shows a broader geographic distribution and genetic markers of the recently described <i>Corynebacterium silvaticum</i> . <i>PLoS ONE</i> , 2020, 15, e0244210.	2.5	6
129	Associations and Disease–Disease Interactions of COVID-19 with Congenital and Genetic Disorders: A Comprehensive Review. <i>Viruses</i> , 2022, 14, 910.	3.3	6
130	Next-Generation Sequencing and Data Analysis. , 2018, , 191-207.		5
131	Novel frameshift mutation in <i>NYX</i> gene in a Russian family with complete congenital stationary night blindness. <i>Ophthalmic Genetics</i> , 2019, 40, 558-563.	1.2	5
132	Genomic Characterization of Multidrug-Resistant <i>Escherichia coli</i> BH100 Sub-strains. <i>Frontiers in Microbiology</i> , 2020, 11, 549254.	3.5	5
133	XomAnnotate: Analysis of Heterogeneous and Complex Exome- A Step towards Translational Medicine. <i>PLoS ONE</i> , 2015, 10, e0123569.	2.5	5
134	Linking common non-coding RNAs of human lung cancer and <i>M. tuberculosis</i> . <i>Bioinformatics</i> , 2018, 14, 337-345.	0.5	5
135	Modular network inference between miRNA–mRNA expression profiles using weighted co-expression network analysis. <i>Journal of Integrative Bioinformatics</i> , 2021, 18, .	1.5	5
136	The Space-Exposed Kombucha Microbial Community Member <i>Komagataeibacter oboediens</i> Showed Only Minor Changes in Its Genome After Reactivation on Earth. <i>Frontiers in Microbiology</i> , 2022, 13, 782175.	3.5	5
137	New putative therapeutic targets against <i>Serratia marcescens</i> using reverse vaccinology and subtractive genomics. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 10106-10121.	3.5	4
138	Metagenome-Assembled Genome Sequences Obtained from a Reactivated Kombucha Microbial Community Exposed to a Mars-Like Environment outside the International Space Station. <i>Microbiology Resource Announcements</i> , 2021, 10, e0054921.	0.6	4
139	Periodically aperiodic pattern of SARS-CoV-2 mutations underpins the uncertainty of its origin and evolution. <i>Environmental Research</i> , 2022, 204, 112092.	7.5	4
140	An immunoinformatics-based designed multi-epitope candidate vaccine (mpme-VAC/STV-1) against <i>Mycoplasma pneumoniae</i> . <i>Computers in Biology and Medicine</i> , 2022, 142, 105194.	7.0	4
141	Bugs as drugs: neglected but a promising future therapeutic strategy in cancer. <i>Future Oncology</i> , 2022, 18, 1609-1626.	2.4	4
142	Natural selection versus creation: a review on the origin of SARS-COV-2. <i>Infezioni in Medicina</i> , 2020, 28, 302-311.	1.1	4
143	Tight controlled expression and secretion of <i>Lactobacillus brevis</i> SlpA in <i>Lactococcus lactis</i> . <i>Biotechnology Letters</i> , 2012, 34, 1275-1281.	2.2	3
144	Omics for Personalized Medicine. , 2013, , .		3

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145	Pan-omics focused to Crick's central dogma. , 2020, , 1-41.		3
146	Reverse vaccinology and subtractive genomics approaches for identifying common therapeutics against <i>Mycobacterium leprae</i> and <i>Mycobacterium lepromatosis</i> . <i>Journal of Venomous Animals and Toxins Including Tropical Diseases</i> , 2021, 27, e20200027.	1.4	3
147	Graphical contig analyzer for all sequencing platforms (G4ALL): a new stand-alone tool for finishing and draft generation of bacterial genomes. <i>Bioinformatics</i> , 2013, 9, 599-604.	0.5	3
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