Debmalya Barh

List of Publications by Citations

184 papers	**2,418** citations	**26** h-index	**41** g-index
221 ext. papers	**3,349** ext. citations	**3.9** avg, IF	**5.08** L-index

#	Paper	IF	Citations
184	The addictive brain: all roads lead to dopamine. *Journal of Psychoactive Drugs*, **2012**, 44, 134-43	3.6	115
183	Two-Component Signal Transduction Systems of Pathogenic Bacteria As Targets for Antimicrobial Therapy: An Overview. *Frontiers in Microbiology*, **2017**, 8, 1878	5.7	106
182	Genetic Addiction Risk Score (GARS): molecular neurogenetic evidence for predisposition to Reward Deficiency Syndrome (RDS). *Molecular Neurobiology*, **2014**, 50, 765-96	6.2	97
181	Generational association studies of dopaminergic genes in reward deficiency syndrome (RDS) subjects: selecting appropriate phenotypes for reward dependence behaviors. *International Journal of Environmental Research and Public Health*, **2011**, 8, 4425-59	4.6	87
180	Correlation of the Taq1 dopamine D2 receptor gene and percent body fat in obese and screened control subjects: a preliminary report. *Food and Function*, **2012**, 3, 40-8	6.1	70
179	In silico subtractive genomics for target identification in human bacterial pathogens. *Drug Development Research*, **2011**, 72, 162-177	5.1	65
178	Long term Suboxone emotional reactivity as measured by automatic detection in speech. *PLoS ONE*, **2013**, 8, e69043	3.7	60
177	Carbon-Based Nanomaterials: Promising Antiviral Agents to Combat COVID-19 in the Microbial-Resistant Era. *ACS Nano*, **2021**, 15, 8069-8086	16.7	59
176	Long-COVID and Post-COVID Health Complications: An Up-to-Date Review on Clinical Conditions and Their Possible Molecular Mechanisms. *Viruses*, **2021**, 13,	6.2	56
175	Neurogenetics and Nutrigenomics of Neuro-Nutrient Therapy for Reward Deficiency Syndrome (RDS): Clinical Ramifications as a Function of Molecular Neurobiological Mechanisms. *Journal of Addiction Research & Therapy*, **2012**, 3, 139	2.5	52
174	Exoproteome and secretome derived broad spectrum novel drug and vaccine candidates in Vibrio cholerae targeted by Piper betel derived compounds. *PLoS ONE*, **2013**, 8, e52773	3.7	51
173	GO FEAT: a rapid web-based functional annotation tool for genomic and transcriptomic data. *Scientific Reports*, **2018**, 8, 1794	4.9	48
172	Abiotic stresses, constraints and improvement strategies in chickpea. *Plant Breeding*, **2014**, 133, 163-178	2.4	48
171	BARHL1 Is Downregulated in Alzheimer's Disease and May Regulate Cognitive Functions through ESR1 and Multiple Pathways. *Genes*, **2017**, 8,	4.2	46
170	In silico Identification of Candidate Drug and Vaccine Targets from Various Pathways in Neisseria gonorrhoeae. *In Silico Biology*, **2009**, 9, 225-231	2	45
169	Multi-omics-based identification of SARS-CoV-2 infection biology and candidate drugs against COVID-19. *Computers in Biology and Medicine*, **2020**, 126, 104051	7	45
168	Clinical Applications of Antimicrobial Peptides (AMPs): Where do we Stand Now?. *Protein and Peptide Letters*, **2020**, 27, 120-134	1.9	43

167	Comparative mangrove metagenome reveals global prevalence of heavy metals and antibiotic resistome across different ecosystems. *Scientific Reports*, **2018**, 8, 11187	4.9	38
166	Searching for signatures across microbial communities: Metagenomic analysis of soil samples from mangrove and other ecosystems. *Scientific Reports*, **2017**, 7, 8859	4.9	37
165	Pan-genome analysis of human gastric pathogen H. pylori: comparative genomics and pathogenomics approaches to identify regions associated with pathogenicity and prediction of potential core therapeutic targets. *BioMed Research International*, **2015**, 2015, 139580	3	35
164	A novel strategy of epitope design in Neisseria gonorrhoeae. *Bioinformation*, **2010**, 5, 77-85	1.1	34
163	An Indian scenario on renewable and sustainable energy sources with emphasis on algae. *Applied Microbiology and Biotechnology*, **2012**, 96, 1125-35	5.7	31
162	A novel comparative genomics analysis for common drug and vaccine targets in Corynebacterium pseudotuberculosis and other CMN group of human pathogens. *Chemical Biology and Drug Design*, **2011**, 78, 73-84	2.9	31
161	An In Silico Identification of Common Putative Vaccine Candidates against Treponema pallidum: A Reverse Vaccinology and Subtractive Genomics Based Approach. *International Journal of Molecular Sciences*, **2017**, 18,	6.3	28
160	Potential chimeric peptides to block the SARS-CoV-2 spike receptor-binding domain. *F1000Research*, **2020**, 9, 576	3.6	28
159	In silico identification of candidate drug and vaccine targets from various pathways in Neisseria gonorrhoeae. *In Silico Biology*, **2009**, 9, 225-31	2	28
158	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. *Biomolecules*, **2019**, 9,	5.9	26
157	An integrative in-silico approach for therapeutic target identification in the human pathogen Corynebacterium diphtheriae. *PLoS ONE*, **2017**, 12, e0186401	3.7	25
156	Notable sequence homology of the ORF10 protein introspects the architecture of SARS-CoV-2. *International Journal of Biological Macromolecules*, **2021**, 181, 801-809	7.9	25
155	A unique view of SARS-CoV-2 through the lens of ORF8 protein. *Computers in Biology and Medicine*, **2021**, 133, 104380	7	23
154	Anticancer and Antiviral Properties of Cardiac Glycosides: A Review to Explore the Mechanism of Actions. *Molecules*, **2020**, 25,	4.8	22
153	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		21
152	An improved interolog mapping-based computational prediction of protein-protein interactions with increased network coverage. *Integrative Biology (United Kingdom)*, **2014**, 6, 1080-7	3.7	19
151	Proteome scale comparative modeling for conserved drug and vaccine targets identification in Corynebacterium pseudotuberculosis. *BMC Genomics*, **2014**, 15 Suppl 7, S3	4.5	18
150	Conserved host-pathogen PPIs. Globally conserved inter-species bacterial PPIs based conserved host-pathogen interactome derived novel target in C. pseudotuberculosis, C. diphtheriae, M. tuberculosis, C. ulcerans, Y. pestis, and E. coli targeted by Piper betel compounds. *Integrative Biology (United Kingdom)*, **2013**, 5, 495-509	3.7	18

149	Molecular features, markers, drug targets, and prospective targeted therapeutics in cardiac myxoma. *Current Cancer Drug Targets*, **2009**, 9, 705-16	2.8	18
148	Fused deposition modelling: Current status, methodology, applications and future prospects. *Additive Manufacturing*, **2021**, 47, 102378	6.1	18
147	An integrated structural proteomics approach along the druggable genome of Corynebacterium pseudotuberculosis species for putative druggable targets. *BMC Genomics*, **2015**, 16 Suppl 5, S9	4.5	17
146	In silico prediction of conserved vaccine targets in Streptococcus agalactiae strains isolated from fish, cattle, and human samples. *Genetics and Molecular Research*, **2013**, 12, 2902-12	1.2	17
145	PANNOTATOR: an automated tool for annotation of pan-genomes. *Genetics and Molecular Research*, **2013**, 12, 2982-9	1.2	16
144	Whole-genome sequence of Corynebacterium pseudotuberculosis PAT10 strain isolated from sheep in Patagonia, Argentina. *Journal of Bacteriology*, **2011**, 193, 6420-1	3.5	16
143	Complete genome sequence of Corynebacterium pseudotuberculosis strain CIP 52.97, isolated from a horse in Kenya. *Journal of Bacteriology*, **2011**, 193, 7025-6	3.5	16
142	In silico identification of essential proteins in Corynebacterium pseudotuberculosis based on protein-protein interaction networks. *BMC Systems Biology*, **2016**, 10, 103	3.5	15
141	The genome anatomy of Corynebacterium pseudotuberculosis VD57 a highly virulent strain causing Caseous lymphadenitis. *Standards in Genomic Sciences*, **2016**, 11, 29		15
140	DISMIRA: Prioritization of disease candidates in miRNA-disease associations based on maximum weighted matching inference model and motif-based analysis. *BMC Genomics*, **2015**, 16 Suppl 5, S12	4.5	15
139	Identification of 11 new exoproteins in Corynebacterium pseudotuberculosis by comparative analysis of the exoproteome. *Microbial Pathogenesis*, **2013**, 61-62, 37-42	3.8	15
138	Hypothesizing repetitive paraphilia behavior of a medication refractive Tourette's syndrome patient having rapid clinical attenuation with KB220Z-nutrigenomic amino-acid therapy (NAAT). *Journal of Behavioral Addictions*, **2013**, 2, 117-24	6.3	15
137	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**, 3, 1000116		15
136	Stargardt disease-associated mutation spectrum of a Russian Federation cohort. *European Journal of Medical Genetics*, **2017**, 60, 140-147	2.6	14
135	miRsig: a consensus-based network inference methodology to identify pan-cancer miRNA-miRNA interaction signatures. *Scientific Reports*, **2017**, 7, 39684	4.9	14
134	Early intervention of intravenous KB220IV--neuroadaptagen amino-acid therapy (NAAT) improves behavioral outcomes in a residential addiction treatment program: a pilot study. *Journal of Psychoactive Drugs*, **2012**, 44, 398-409	3.6	14
133	The Corynebacterium pseudotuberculosis in silico predicted pan-exoproteome. *BMC Genomics*, **2012**, 13 Suppl 5, S6	4.5	13
132	Coupling Genetic Addiction Risk Score (GARS) with Electrotherapy: Fighting Iatrogenic Opioid Dependence. *Journal of Addiction Research & Therapy*, **2013**, 4, 1000163	2.5	13

131	COVID-19 Vaccines and Thrombosis-Roadblock or Dead-End Street?. *Biomolecules*, **2021**, 11,	5.9	13
130	A novel multi-omics-based highly accurate prediction of symptoms, comorbid conditions, and possible long-term complications of COVID-19. *Molecular Omics*, **2021**, 17, 317-337	4.4	13
129	Differential Exoproteome analysis of two corynebacterium pseudotuberculosis biovar ovis strains isolated from goat (1002) and sheep (C231). *Current Microbiology*, **2013**, 67, 460-5	2.4	12
128	MapRepeat: an approach for effective assembly of repetitive regions in prokaryotic genomes. *Bioinformation*, **2015**, 11, 276-9	1.1	12
127	Whole-genome optical mapping reveals a mis-assembly between two rRNA operons of Corynebacterium pseudotuberculosis strain 1002. *BMC Genomics*, **2016**, 17, 315	4.5	11
126	C. pseudotuberculosis Phop confers virulence and may be targeted by natural compounds. *Integrative Biology (United Kingdom)*, **2014**, 6, 1088-99	3.7	11
125	miReg: a resource for microRNA regulation. *Journal of Integrative Bioinformatics*, **2010**, 7,	3.8	11
124	Simplifier: a web tool to eliminate redundant NGS contigs. *Bioinformation*, **2012**, 8, 996-9	1.1	11
123	16S rRNA Gene Amplicon Based Metagenomic Signatures of Rhizobiome Community in Rice Field During Various Growth Stages. *Frontiers in Microbiology*, **2019**, 10, 2103	5.7	10
122	Epigenetics in head and neck cancer. *Methods in Molecular Biology*, **2015**, 1238, 751-69	1.4	10
121	miRegulome: a knowledge-base of miRNA regulomics and analysis. *Scientific Reports*, **2015**, 5, 12832	4.9	10
120	The conserved mitochondrial gene distribution in relatives of Turritopsis nutricula, an immortal jellyfish. *Bioinformation*, **2014**, 10, 586-91	1.1	10
119	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	3.7	10
118	Microbial Omics: Applications in Biotechnology **2018**, 3-20		10
117	Transcriptome profile of Corynebacterium pseudotuberculosis in response to iron limitation. *BMC Genomics*, **2019**, 20, 663	4.5	9
116	A novel in silico reverse-transcriptomics-based identification and blood-based validation of a panel of sub-type specific biomarkers in lung cancer. *BMC Genomics*, **2013**, 14 Suppl 6, S5	4.5	9
115	Quality of prokaryote genome assembly: indispensable issues of factors affecting prokaryote genome assembly quality. *Gene*, **2012**, 505, 365-7	3.8	9
114	Quantitative Electroencephalography Analysis (qEEG) of Neuro-Electro-Adaptive Therapy 12 [NEAT12] Up-Regulates Cortical Potentials in an Alcoholic during Protracted Abstinence: Putative Anti-Craving Implications. *Journal of Addiction Research & Therapy*, **2014**, 5, 1-7	2.5	9

113	Whole-genome sequence of Corynebacterium pseudotuberculosis strain Cp162, isolated from camel. *Journal of Bacteriology*, **2012**, 194, 5718-9	3.5	9
112	OMICS		9
111	Computational screening for potential drug candidates against the SARS-CoV-2 main protease. *F1000Research*, **2020**, 9,	3.6	9
110	Genomic Target Database (GTD): a database of potential targets in human pathogenic bacteria. *Bioinformation*, **2009**, 4, 50-1	1.1	9
109	Putative vaccine candidates and drug targets identified by reverse vaccinology and subtractive genomics approaches to control , the causative agent of chancroid. *Journal of the Royal Society Interface*, **2018**, 15,	4.1	9
108	Autoimmunity roots of the thrombotic events after COVID-19 vaccination. *Autoimmunity Reviews*, **2021**, 20, 102941	13.6	9
107	PlantOmics: The Omics of Plant Science **2015**,		8
106	Genome informatics and vaccine targets in Corynebacterium urealyticum using two whole genomes, comparative genomics, and reverse vaccinology. *BMC Genomics*, **2015**, 16 Suppl 5, S7	4.5	8
105	Omics Approaches in Breast Cancer **2014**,		8
104	Biomarkers, critical disease pathways, drug targets, and alternative medicine in male breast cancer. *Current Drug Targets*, **2009**, 10, 1-8	3	8
103	GLOBAL OPIOID EPIDEMIC: DOOMED TO FAIL WITHOUT GENETICALLY BASED PRECISION ADDICTION MEDICINE (PAM): LESSONS LEARNED FROM AMERICA **2017**, 2, 17-22		8
102	Repurposing Approved Drugs for Guiding COVID-19 Prophylaxis: A Systematic Review. *Frontiers in Pharmacology*, **2020**, 11, 590598	5.6	8
101	In Silico Identification of Dual Ability of N. gonorrhoeae ddl for Developing Drug and Vaccine Against Pathogenic Neisseria and Other Human Pathogens. *Journal of Proteomics and Bioinformatics*, **2010**, 03, 082-090	2.1	8
100	Analysis of the microarray gene expression for breast cancer progression after the application modified logistic regression. *Gene*, **2020**, 726, 144168	3.8	8
99	Corynebacterium pseudotuberculosis may be under anagenesis and biovar Equi forms biovar Ovis: a phylogenic inference from sequence and structural analysis. *BMC Microbiology*, **2016**, 16, 100	4.5	8
98	Genetic screening of Russian Usher syndrome patients toward selection for gene therapy. *Ophthalmic Genetics*, **2018**, 39, 706-713	1.2	8
97	Potential Chimeric Peptides to Block the SARS-CoV-2 Spike RBD **2020**,		7
96	Fitness of Outer Membrane Vesicles From Is Altered Under the Impact of Simulated Mars-like Stressors Outside the International Space Station. *Frontiers in Microbiology*, **2020**, 11, 1268	5.7	7

95	Exploration of Nitrate Reductase Metabolic Pathway in. *International Journal of Genomics*, **2017**, 2017, 9481756	2.5	7
94	Quadruplex PCR assay for identification of Corynebacterium pseudotuberculosis differentiating biovar Ovis and Equi. *BMC Veterinary Research*, **2017**, 13, 290	2.7	7
93	SIMBA: a web tool for managing bacterial genome assembly generated by Ion PGM sequencing technology. *BMC Bioinformatics*, **2016**, 17, 456	3.6	7
92	Identifying human disease genes: advances in molecular genetics and computational approaches. *Genetics and Molecular Research*, **2014**, 13, 5073-87	1.2	7
91	Computational screening for potential drug candidates against the SARS-CoV-2 main protease. *F1000Research*, **2020**, 9, 514	3.6	7
90	Predicting COVID-19-Comorbidity Pathway Crosstalk-Based Targets and Drugs: Towards Personalized COVID-19 Management. *Biomedicines*, **2021**, 9,	4.8	7
89	A New Broad-Spectrum Peptide Antibiotic Produced by Bacillus brevis Strain MH9 Isolated from Margalla Hills of Islamabad, Pakistan. *International Journal of Peptide Research and Therapeutics*, **2016**, 22, 271-279	2.1	6
88	Determining causal miRNAs and their signaling cascade in diseases using an influence diffusion model. *Scientific Reports*, **2017**, 7, 8133	4.9	6
87	Complete genome sequence of Corynebacterium pseudotuberculosis biovar ovis strain P54B96 isolated from antelope in South Africa obtained by rapid next generation sequencing technology. *Standards in Genomic Sciences*, **2012**, 7, 189-99		6
86	In Silico Protein-Protein Interactions: Avoiding Data and Method Biases Over Sensitivity and Specificity. *Current Protein and Peptide Science*, **2015**, 16, 689-700	2.8	6
85	Isolation and Characterization of L-Tryptophan Ammonia Lyase from Rubrivivax benzoatilyticus Strain JA2. *Current Protein and Peptide Science*, **2015**, 16, 775-81	2.8	6
84	Shotgun metagenomic analysis of kombucha mutualistic community exposed to Mars-like environment outside the International Space Station. *Environmental Microbiology*, **2021**, 23, 3727-3742	5.2	6
83	Compounds Piperidine, Eugenyl Acetate, and Chlorogenic Acid Are Broad-Spectrum Anti-Compounds that Are Also Effective on MDR Strains of the Pathogen. *Pathogens*, **2019**, 8,	4.5	5
82	The Druggable Pocketome of : A New Approach for Putative Druggable Targets. *Frontiers in Genetics*, **2018**, 9, 44	4.5	5
81	Evaluation of the Common Molecular Basis in Alzheimer's and Parkinson's Diseases. *International Journal of Molecular Sciences*, **2019**, 20,	6.3	5
80	XomAnnotate: Analysis of Heterogeneous and Complex Exome- A Step towards Translational Medicine. *PLoS ONE*, **2015**, 10, e0123569	3.7	5
79	The Benefits of Genetic Addiction Risk Score (GARS) Testing in Substance Use Disorder (SUD) **2018**, 2018,		5
78	miReg: a resource for microRNA regulation. *Journal of Integrative Bioinformatics*, **2010**, 7,	3.8	5

77	Epitope Design from Transporter Targets in N. gonorrhoeae. *Journal of Proteomics and Bioinformatics*, **2009**, 02, 475-480	2.1	5
76	Functional Genomics: Applications in Plant Science **2015**, 65-111		4
75	Acetate Kinase (AcK) is Essential for Microbial Growth and Betel-derived Compounds Potentially Target AcK, PhoP and MDR Proteins in M. tuberculosis, V. cholerae and Pathogenic E. coli: An in silico and in vitro Study. *Current Topics in Medicinal Chemistry*, **2018**, 18, 2731-2740	3	4
74	Linking common non-coding RNAs of human lung cancer and M. tuberculosis. *Bioinformation*, **2018**, 14, 337-345	1.1	4
73	First genome sequencing and comparative analyses of strains from Mexico. *Standards in Genomic Sciences*, **2018**, 13, 21		4
72	Overview of key molecular and pharmacological targets for diabetes and associated diseases. *Life Sciences*, **2021**, 278, 119632	6.8	4
71	Emergence of Cardiac Glycosides as Potential Drugs: Current and Future Scope for Cancer Therapeutics. *Biomolecules*, **2021**, 11,	5.9	4
70	The mechanism behind flaring/triggering of autoimmunity disorders associated with COVID-19. *Autoimmunity Reviews*, **2021**, 20, 102909	13.6	4
69	In Silico Models **2014**, 385-404		3
68	Omics for Personalized Medicine **2013**,		3
67	Can Genetic Testing Coupled with Enhanced Dopaminergic Activation Reduce Recidivism Rates in the Workers Compensation Legacy Cases?. *Journal of Alcoholism and Drug Dependence*, **2014**, 2,	1	3
66	Graphical contig analyzer for all sequencing platforms (G4ALL): a new stand-alone tool for finishing and draft generation of bacterial genomes. *Bioinformation*, **2013**, 9, 599-604	1.1	3
65	Novel aromatase inhibitors selection using induced fit docking and extra precision methods: Potential clinical use in ER-alpha-positive breast cancer. *Bioinformation*, **2016**, 12, 324-331	1.1	3
64	Current Trends in Experimental and Computational Approaches to Combat Antimicrobial Resistance. *Frontiers in Genetics*, **2020**, 11, 563975	4.5	3
63	Next-Generation Sequencing and Data Analysis **2018**, 191-207		2
62	A Multi-Locus Approach to Treating Fibromyalgia by Boosting Dopaminergic Activity in the Meso-Limbic System of the Brain. *Journal of Genetic Syndromes & Gene Therapy*, **2014**, 5, 213		2
61	Determining miRNA-disease associations using bipartite graph modelling **2013**,		2
60	Emergence of unique SARS-CoV-2 ORF10 variants and their impact on protein structure and function. *International Journal of Biological Macromolecules*, **2021**, 194, 128-143	7.9	2

59	The importance of accessory protein variants in the pathogenicity of SARS-CoV-2.. *Archives of Biochemistry and Biophysics*, **2022**, 717, 109124	4.1	2
58	Whole-genome resequencing: Current status and future prospects in genomics-assisted crop improvement **2016**, 187-211		2
57	Modular network inference between miRNA-mRNA expression profiles using weighted co-expression network analysis. *Journal of Integrative Bioinformatics*, **2021**,	3.8	2
56	To Other Planets With Upgraded Millennial Kombucha in Rhythms of Sustainability and Health Support. *Frontiers in Astronomy and Space Sciences*, **2021**, 8,	3.8	2
55	Taxonomic classification of strain PO100/5 shows a broader geographic distribution and genetic markers of the recently described Corynebacterium silvaticum. *PLoS ONE*, **2020**, 15, e0244210	3.7	2
54	A novel multi-omics-based identification of symptoms, comorbid conditions, and possible long-term complications in COVID-19		2
53	Pan-Resistome Insights into the Multidrug Resistance of. *Antibiotics*, **2021**, 10,	4.9	2
52	New putative therapeutic targets against using reverse vaccinology and subtractive genomics. *Journal of Biomolecular Structure and Dynamics*, **2021**, 1-16	3.6	2
51	The Spike of SARS-CoV-2: Uniqueness and Applications. *Frontiers in Immunology*, **2021**, 12, 663912	8.4	2
50	Re-sequencing and optical mapping reveals misassemblies and real inversions on Corynebacterium pseudotuberculosis genomes. *Scientific Reports*, **2019**, 9, 16387	4.9	2
49	Novel frameshift mutation in gene in a Russian family with complete congenital stationary night blindness. *Ophthalmic Genetics*, **2019**, 40, 558-563	1.2	2
48	Metagenome-Assembled Genome Sequences Obtained from a Reactivated Kombucha Microbial Community Exposed to a Mars-Like Environment outside the International Space Station. *Microbiology Resource Announcements*, **2021**, 10, e0054921	1.3	2
47	Pan-omics focused to Crick's central dogma **2020**, 1-41		1
46	In Silico and Ultrahigh-Throughput Screenings (uHTS) in Drug Discovery: An Overview **2012**, 451-490		1
45	Cancer Biomarkers for Diagnosis, Prognosis and Therapy **2012**, 18-68		1
44	Tight controlled expression and secretion of Lactobacillus brevis SlpA in Lactococcus lactis. *Biotechnology Letters*, **2012**, 34, 1275-81	3	1
43	Omics Approaches in Pulses **2013**, 101-138		1
42	An immunoinformatics-based designed multi-epitope candidate vaccine (mpme-VAC/STV-1) against Mycoplasma pneumoniae.. *Computers in Biology and Medicine*, **2021**, 142, 105194	7	1

41 FunSys: Software for functional analysis of prokaryotic transcriptome and proteome. *Bioinformation*, **2012**, 8, 529-31 — 1.1 — 1

40 Bacteriocins as an alternative in the treatment of infections by Staphylococcus aureus. *Anais Da Academia Brasileira De Ciencias*, **2020**, 92, e20201216 — 1.4 — 1

39 Artificial Intelligence Techniques for Predicting Type 2 Diabetes. *Advances in Intelligent Systems and Computing*, **2021**, 411-430 — 0.4 — 1

38 Cellular and Organismal Toxicity of Nanoparticles and Its Associated Health Concerns **2020**, 477-497 — 1

37 A potential link between tuberculosis and lung cancer through non-coding RNAs — 1

36 Neurogenetics and Nutrigenomics of Reward Deficiency Syndrome (RDS): Stratification of Addiction Risk and Mesolimbic Nutrigenomic Manipulation of Hypodopaminergic Function **2013**, 365-398 — 1

35 An Issue of Concern: Unique Truncated ORF8 Protein Variants of SARS-CoV-2 — 1

34 Computational identification of putative common genomic drug and vaccine targets in Mycoplasma genitalium. *Genomics*, **2021**, 113, 2730-2743 — 4.3 — 1

33 Towards a Comprehensive Understanding of miRNA Regulome and miRNA Interaction Networks. *Journal of Pharmacogenomics & Pharmacoproteomics*, **2016**, 7, — 1

32 Reverse vaccinology and subtractive genomics approaches for identifying common therapeutics against and. *Journal of Venomous Animals and Toxins Including Tropical Diseases*, **2021**, 27, e20200027 — 2.2 — 1

31 Comparative genomics with a multidrug-resistant Klebsiella pneumoniae isolate reveals the panorama of unexplored diversity in Northeast Brazil. *Gene*, **2021**, 772, 145386 — 3.8 — 1

30 Bioinformatics and Systems Biology in Bioengineering **2018**, 223-243 — 1

29 Periodically aperiodic pattern of SARS-CoV-2 mutations underpins the uncertainty of its origin and evolution. *Environmental Research*, **2021**, 204, 112092 — 7.9 — 1

28 Potential Molecular Mechanisms of Rare Anti-Tumor Immune Response by SARS-CoV-2 in Isolated Cases of Lymphomas. *Viruses*, **2021**, 13, — 6.2 — 1

27 Targeting LIN28: a new hope in prostate cancer theranostics. *Future Oncology*, **2021**, 17, 3873-3880 — 3.6 — 1

26 Implications derived from S-protein variants of SARS-CoV-2 from six continents. *International Journal of Biological Macromolecules*, **2021**, 191, 934-955 — 7.9 — 1

25 The Space-Exposed Kombucha Microbial Community Member Showed Only Minor Changes in Its Genome After Reactivation on Earth.. *Frontiers in Microbiology*, **2022**, 13, 782175 — 5.7 — 1

24 An issue of concern: unique truncated ORF8 protein variants of SARS-CoV-2.. *PeerJ*, **2022**, 10, e13136 — 3.1 — 1

23	Associations and Disease Disease Interactions of COVID-19 with Congenital and Genetic Disorders: A Comprehensive Review. *Viruses*, **2022**, 14, 910	6.2	1
22	In silico disease model: from simple networks to complex diseases **2020**, 441-460		0
21	Pan-genomics of fungi and its applications **2020**, 251-260		0
20	Genomic Characterization of Multidrug-Resistant BH100 Sub-strains. *Frontiers in Microbiology*, **2020** , 11, 549254	5.7	0
19	Pathophysiological features of the visual cycle, cascade and metabolic pathways in retinitis pigmentosa. *Rossiiskii Oftalmologicheskii Zhurnal*, **2021**, 14, 80-88	0.3	0
18	Natural selection versus creation: a review on the origin of SARS-COV-2. *Infezioni in Medicina*, **2020**, 28, 302-311	3.6	0
17	Evidence of episodic positive selection in complex of species and its implementations in identification of drug and vaccine targets.. *PeerJ*, **2022**, 10, e12662	3.1	0
16	Would New SARS-CoV-2 Variants Change the War against COVID-19?. *Epidemiologia*, **2022**, 3, 229-237	2.8	0
15	CIDCA 133 Ameliorates Chemotherapy-Induced Mucositis by Modulating Epithelial Barrier and TLR2/4/Myd88/NF-B Signaling Pathway.. *Frontiers in Microbiology*, **2022**, 13, 858036	5.7	0
14	Pan-genomics of veterinary pathogens and its applications **2020**, 101-119		
13	Protein-Protein Interactions: An Overview **2019**, 821-833		
12	Breast Cancer Biomarkers for Risk Assessment, Screening, Detection, Diagnosis, and Prognosis **2014**, 393-407		
11	Optimization of enzymatic hydrolysis of prairie cordgrass for improved ethanol production. *Journal of Renewable and Sustainable Energy*, **2012**, 4, 033118	2.5	
10	Innate immunity and metal ion trafficking pathway perturbations in idiopathic Parkinson's disease and Tuberculosis: A comparative transcriptomics approach. *Brain Disorders*, **2021**, 4, 100025		
9	Cytogenetic Early Markers in Gynecologic Cancers **2015**, 43-58		
8	Biomarkers for Early Detection of Familial Breast Cancer **2015**, 167-190		
7	Biotechnology for improved crop productivity and quality **2016**, 231-248		
6	Pharmacogenomics Pharmacoepigenomics of Breast Cancer Therapy: Clinical Implications **2014**, 499-518		

5   Omics of Male Breast Cancer **2014**, 265-276

4   Breast Cancer Stem Cells and Cellomics **2014**, 245-263

3   Characterization of a new multidrug-resistant Brazilian isolate and 172 spp. sequenced strains: Genomic island, multilocus sequence typing and capsule locus dataset. *Data in Brief*, **2021**, 34, 106746   [1,2]

2   Computational Techniques in Data Integration and Big Data Handling in Omics **2018**, 209-222

1   Deep Learning applied to computational biology and agricultural sciences **2022**, 589-618