

Debmalya Barh

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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 importance of accessory protein variants in the pathogenicity of SARS-CoV-2.. <i>Archives of Biochemistry and Biophysics</i> , 2022 , 717, 109124	4.1	2
183	Evidence of episodic positive selection in complex of species and its implementations in identification of drug and vaccine targets.. <i>PeerJ</i> , 2022 , 10, e12662	3.1	0
182	The Space-Exposed Kombucha Microbial Community Member Showed Only Minor Changes in Its Genome After Reactivation on Earth.. <i>Frontiers in Microbiology</i> , 2022 , 13, 782175	5.7	1
181	An issue of concern: unique truncated ORF8 protein variants of SARS-CoV-2.. <i>PeerJ</i> , 2022 , 10, e13136	3.1	1
180	Deep Learning applied to computational biology and agricultural sciences 2022 , 589-618		
179	Would New SARS-CoV-2 Variants Change the War against COVID-19?. <i>Epidemiologia</i> , 2022 , 3, 229-237	2.8	0
178	Associations and DiseaseDisease Interactions of COVID-19 with Congenital and Genetic Disorders: A Comprehensive Review. <i>Viruses</i> , 2022 , 14, 910	6.2	1
177	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	5.7	0
176	Emergence of unique SARS-CoV-2 ORF10 variants and their impact on protein structure and function. <i>International Journal of Biological Macromolecules</i> , 2021 , 194, 128-143	7.9	2
175	Modular network inference between miRNA-mRNA expression profiles using weighted co-expression network analysis. <i>Journal of Integrative Bioinformatics</i> , 2021 ,	3.8	2
174	Innate immunity and metal ion trafficking pathway perturbations in idiopathic Parkinson's disease and Tuberculosis: A comparative transcriptomics approach. <i>Brain Disorders</i> , 2021 , 4, 100025		
173	An immunoinformatics-based designed multi-epitope candidate vaccine (mpme-VAC/STV-1) against <i>Mycoplasma pneumoniae</i> .. <i>Computers in Biology and Medicine</i> , 2021 , 142, 105194	7	1
172	To Other Planets With Upgraded Millennial Kombucha in Rhythms of Sustainability and Health Support. <i>Frontiers in Astronomy and Space Sciences</i> , 2021 , 8,	3.8	2
171	Fused deposition modelling: Current status, methodology, applications and future prospects. <i>Additive Manufacturing</i> , 2021 , 47, 102378	6.1	18
170	Artificial Intelligence Techniques for Predicting Type 2 Diabetes. <i>Advances in Intelligent Systems and Computing</i> , 2021 , 411-430	0.4	1
169	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,	6.2	56
168	Carbon-Based Nanomaterials: Promising Antiviral Agents to Combat COVID-19 in the Microbial-Resistant Era. <i>ACS Nano</i> , 2021 , 15, 8069-8086	16.7	59

167	Pan-Resistome Insights into the Multidrug Resistance of. <i>Antibiotics</i> , 2021 , 10,	4.9	2
166	Predicting COVID-19-Comorbidity Pathway Crosstalk-Based Targets and Drugs: Towards Personalized COVID-19 Management. <i>Biomedicines</i> , 2021 , 9,	4.8	7
165	A unique view of SARS-CoV-2 through the lens of ORF8 protein. <i>Computers in Biology and Medicine</i> , 2021 , 133, 104380	7	23
164	Bacterial Cellulose Retains Robustness but Its Synthesis Declines After Exposure to a Mars-like Environment Simulated Outside the International Space Station. <i>Astrobiology</i> , 2021 , 21, 706-717	3.7	10
163	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	7.9	25
162	New putative therapeutic targets against using reverse vaccinology and subtractive genomics. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 1-16	3.6	2
161	Computational identification of putative common genomic drug and vaccine targets in <i>Mycoplasma genitalium</i> . <i>Genomics</i> , 2021 , 113, 2730-2743	4.3	1
160	COVID-19 Vaccines and Thrombosis-Roadblock or Dead-End Street?. <i>Biomolecules</i> , 2021 , 11,	5.9	13
159	The Spike of SARS-CoV-2: Uniqueness and Applications. <i>Frontiers in Immunology</i> , 2021 , 12, 663912	8.4	2
158	Reverse vaccinology and subtractive genomics approaches for identifying common therapeutics against and. <i>Journal of Venomous Animals and Toxins Including Tropical Diseases</i> , 2021 , 27, e20200027	2.2	1
157	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	4.4	13
156	Characterization of a new multidrug-resistant Brazilian isolate and 172 spp. sequenced strains: Genomic island, multilocus sequence typing and capsule locus dataset. <i>Data in Brief</i> , 2021 , 34, 106746	1.2	
155	Shotgun metagenomic analysis of kombucha mutualistic community exposed to Mars-like environment outside the International Space Station. <i>Environmental Microbiology</i> , 2021 , 23, 3727-3742	5.2	6
154	Pathophysiological features of the visual cycle, cascade and metabolic pathways in retinitis pigmentosa. <i>Rossiiskii Oftalmologicheskii Zhurnal</i> , 2021 , 14, 80-88	0.3	0
153	Comparative genomics with a multidrug-resistant <i>Klebsiella pneumoniae</i> isolate reveals the panorama of unexplored diversity in Northeast Brazil. <i>Gene</i> , 2021 , 772, 145386	3.8	1
152	Overview of key molecular and pharmacological targets for diabetes and associated diseases. <i>Life Sciences</i> , 2021 , 278, 119632	6.8	4
151	Emergence of Cardiac Glycosides as Potential Drugs: Current and Future Scope for Cancer Therapeutics. <i>Biomolecules</i> , 2021 , 11,	5.9	4
150	Autoimmunity roots of the thrombotic events after COVID-19 vaccination. <i>Autoimmunity Reviews</i> , 2021 , 20, 102941	13.6	9

149	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	1.3	2
148	Periodically aperiodic pattern of SARS-CoV-2 mutations underpins the uncertainty of its origin and evolution. <i>Environmental Research</i> , 2021 , 204, 112092	7.9	1
147	Potential Molecular Mechanisms of Rare Anti-Tumor Immune Response by SARS-CoV-2 in Isolated Cases of Lymphomas. <i>Viruses</i> , 2021 , 13,	6.2	1
146	The mechanism behind flaring/triggering of autoimmunity disorders associated with COVID-19. <i>Autoimmunity Reviews</i> , 2021 , 20, 102909	13.6	4
145	Targeting LIN28: a new hope in prostate cancer theranostics. <i>Future Oncology</i> , 2021 , 17, 3873-3880	3.6	1
144	Implications derived from S-protein variants of SARS-CoV-2 from six continents. <i>International Journal of Biological Macromolecules</i> , 2021 , 191, 934-955	7.9	1
143	Potential Chimeric Peptides to Block the SARS-CoV-2 Spike RBD 2020 ,		7
142	Fitness of Outer Membrane Vesicles From Is Altered Under the Impact of Simulated Mars-like Stressors Outside the International Space Station. <i>Frontiers in Microbiology</i> , 2020 , 11, 1268	5.7	7
141	In silico disease model: from simple networks to complex diseases 2020 , 441-460		0
140	Pan-omics focused to Crick's central dogma 2020 , 1-41		1
139	Pan-genomics of veterinary pathogens and its applications 2020 , 101-119		
138	Pan-genomics of fungi and its applications 2020 , 251-260		0
137	Computational screening for potential drug candidates against the SARS-CoV-2 main protease. <i>F1000Research</i> , 2020 , 9,	3.6	9
136	Computational screening for potential drug candidates against the SARS-CoV-2 main protease. <i>F1000Research</i> , 2020 , 9, 514	3.6	7
135	Potential chimeric peptides to block the SARS-CoV-2 spike receptor-binding domain. <i>F1000Research</i> , 2020 , 9, 576	3.6	28
134	Clinical Applications of Antimicrobial Peptides (AMPs): Where do we Stand Now?. <i>Protein and Peptide Letters</i> , 2020 , 27, 120-134	1.9	43
133	Repurposing Approved Drugs for Guiding COVID-19 Prophylaxis: A Systematic Review. <i>Frontiers in Pharmacology</i> , 2020 , 11, 590598	5.6	8
132	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	1.4	1

131	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	3.7	2
130	Cellular and Organismal Toxicity of Nanoparticles and Its Associated Health Concerns 2020 , 477-497		1
129	Analysis of the microarray gene expression for breast cancer progression after the application modified logistic regression. <i>Gene</i> , 2020 , 726, 144168	3.8	8
128	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	45
127	Current Trends in Experimental and Computational Approaches to Combat Antimicrobial Resistance. <i>Frontiers in Genetics</i> , 2020 , 11, 563975	4.5	3
126	Anticancer and Antiviral Properties of Cardiac Glycosides: A Review to Explore the Mechanism of Actions. <i>Molecules</i> , 2020 , 25,	4.8	22
125	Genomic Characterization of Multidrug-Resistant BH100 Sub-strains. <i>Frontiers in Microbiology</i> , 2020 , 11, 549254	5.7	0
124	Natural selection versus creation: a review on the origin of SARS-COV-2. <i>Infezioni in Medicina</i> , 2020 , 28, 302-311	3.6	0
123	16S rRNA Gene Amplicon Based Metagenomic Signatures of Rhizobiome Community in Rice Field During Various Growth Stages. <i>Frontiers in Microbiology</i> , 2019 , 10, 2103	5.7	10
122	Compounds Piperidine, Eugenyl Acetate, and Chlorogenic Acid Are Broad-Spectrum Anti-Compounds that Are Also Effective on MDR Strains of the Pathogen. <i>Pathogens</i> , 2019 , 8,	4.5	5
121	Protein-Protein Interactions: An Overview 2019 , 821-833		
120	Evaluation of the Common Molecular Basis in Alzheimer's and Parkinson's Diseases. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	5
119	Transcriptome profile of <i>Corynebacterium pseudotuberculosis</i> in response to iron limitation. <i>BMC Genomics</i> , 2019 , 20, 663	4.5	9
118	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,	5.9	26
117	Re-sequencing and optical mapping reveals misassemblies and real inversions on <i>Corynebacterium pseudotuberculosis</i> genomes. <i>Scientific Reports</i> , 2019 , 9, 16387	4.9	2
116	Novel frameshift mutation in gene in a Russian family with complete congenital stationary night blindness. <i>Ophthalmic Genetics</i> , 2019 , 40, 558-563	1.2	2
115	Next-Generation Sequencing and Data Analysis 2018 , 191-207		2
114	GO FEAT: a rapid web-based functional annotation tool for genomic and transcriptomic data. <i>Scientific Reports</i> , 2018 , 8, 1794	4.9	48

113	Comparative mangrove metagenome reveals global prevalence of heavy metals and antibiotic resistome across different ecosystems. <i>Scientific Reports</i> , 2018 , 8, 11187	4.9	38
112	The Druggable Pocketome of : A New Approach for Putative Druggable Targets. <i>Frontiers in Genetics</i> , 2018 , 9, 44	4.5	5
111	The Benefits of Genetic Addiction Risk Score (GARS) Testing in Substance Use Disorder (SUD) 2018 , 2018,		5
110	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> , 2018 , 18, 2731-2740	3	4
109	Linking common non-coding RNAs of human lung cancer and <i>M. tuberculosis</i> . <i>Bioinformatics</i> , 2018 , 14, 337-345	1.1	4
108	Genetic screening of Russian Usher syndrome patients toward selection for gene therapy. <i>Ophthalmic Genetics</i> , 2018 , 39, 706-713	1.2	8
107	First genome sequencing and comparative analyses of strains from Mexico. <i>Standards in Genomic Sciences</i> , 2018 , 13, 21		4
106	Putative vaccine candidates and drug targets identified by reverse vaccinology and subtractive genomics approaches to control , the causative agent of chancroid. <i>Journal of the Royal Society Interface</i> , 2018 , 15,	4.1	9
105	Bioinformatics and Systems Biology in Bioengineering 2018 , 223-243		1
104	Microbial Omics: Applications in Biotechnology 2018 , 3-20		10
103	Computational Techniques in Data Integration and Big Data Handling in Omics 2018 , 209-222		
102	Stargardt disease-associated mutation spectrum of a Russian Federation cohort. <i>European Journal of Medical Genetics</i> , 2017 , 60, 140-147	2.6	14
101	miRsig: a consensus-based network inference methodology to identify pan-cancer miRNA-miRNA interaction signatures. <i>Scientific Reports</i> , 2017 , 7, 39684	4.9	14
100	Exploration of Nitrate Reductase Metabolic Pathway in. <i>International Journal of Genomics</i> , 2017 , 2017, 9481756	2.5	7
99	An integrative in-silico approach for therapeutic target identification in the human pathogen <i>Corynebacterium diphtheriae</i> . <i>PLoS ONE</i> , 2017 , 12, e0186401	3.7	25
98	Quadruplex PCR assay for identification of <i>Corynebacterium pseudotuberculosis</i> differentiating biovar Ovis and Equi. <i>BMC Veterinary Research</i> , 2017 , 13, 290	2.7	7
97	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,	6.3	28
96	Determining causal miRNAs and their signaling cascade in diseases using an influence diffusion model. <i>Scientific Reports</i> , 2017 , 7, 8133	4.9	6

95	Searching for signatures across microbial communities: Metagenomic analysis of soil samples from mangrove and other ecosystems. <i>Scientific Reports</i> , 2017 , 7, 8859	4.9	37
94	BARHL1 Is Downregulated in Alzheimer's Disease and May Regulate Cognitive Functions through ESR1 and Multiple Pathways. <i>Genes</i> , 2017 , 8,	4.2	46
93	Two-Component Signal Transduction Systems of Pathogenic Bacteria As Targets for Antimicrobial Therapy: An Overview. <i>Frontiers in Microbiology</i> , 2017 , 8, 1878	5.7	106
92	GLOBAL OPIOID EPIDEMIC: DOOMED TO FAIL WITHOUT GENETICALLY BASED PRECISION ADDICTION MEDICINE (PAM): LESSONS LEARNED FROM AMERICA 2017 , 2, 17-22		8
91	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	3.5	15
90	SIMBA: a web tool for managing bacterial genome assembly generated by Ion PGM sequencing technology. <i>BMC Bioinformatics</i> , 2016 , 17, 456	3.6	7
89	Whole-genome optical mapping reveals a mis-assembly between two rRNA operons of <i>Corynebacterium pseudotuberculosis</i> strain 1002. <i>BMC Genomics</i> , 2016 , 17, 315	4.5	11
88	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		15
87	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	2.1	6
86	Whole-genome resequencing: Current status and future prospects in genomics-assisted crop improvement 2016 , 187-211		2
85	Novel aromatase inhibitors selection using induced fit docking and extra precision methods: Potential clinical use in ER-alpha-positive breast cancer. <i>Bioinformatics</i> , 2016 , 12, 324-331	1.1	3
84	Biotechnology for improved crop productivity and quality 2016 , 231-248		
83	KB220Z1b 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
82	Towards a Comprehensive Understanding of miRNA Regulome and miRNA Interaction Networks. <i>Journal of Pharmacogenomics & Pharmacoproteomics</i> , 2016 , 7,		1
81	<i>Corynebacterium pseudotuberculosis</i> may be under anagenesis and biovar Equi forms biovar Ovis: a phylogenetic inference from sequence and structural analysis. <i>BMC Microbiology</i> , 2016 , 16, 100	4.5	8
80	PlantOmics: The Omics of Plant Science 2015 ,		8
79	Functional Genomics: Applications in Plant Science 2015 , 65-111		4
78	Epigenetics in head and neck cancer. <i>Methods in Molecular Biology</i> , 2015 , 1238, 751-69	1.4	10

77	miRegulome: a knowledge-base of miRNA regulomics and analysis. <i>Scientific Reports</i> , 2015 , 5, 12832	4.9	10
76	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 Suppl 5, S7	4.5	8
75	DISMIRA: Prioritization of disease candidates in miRNA-disease associations based on maximum weighted matching inference model and motif-based analysis. <i>BMC Genomics</i> , 2015 , 16 Suppl 5, S12	4.5	15
74	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 Suppl 5, S9	4.5	17
73	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, 139580	3	35
72	XomAnnotate: Analysis of Heterogeneous and Complex Exome- A Step towards Translational Medicine. <i>PLoS ONE</i> , 2015 , 10, e0123569	3.7	5
71	In Silico Protein-Protein Interactions: Avoiding Data and Method Biases Over Sensitivity and Specificity. <i>Current Protein and Peptide Science</i> , 2015 , 16, 689-700	2.8	6
70	Isolation and Characterization of L-Tryptophan Ammonia Lyase from <i>Rubrivivax benzoatilyticus</i> Strain JA2. <i>Current Protein and Peptide Science</i> , 2015 , 16, 775-81	2.8	6
69	MapRepeat: an approach for effective assembly of repetitive regions in prokaryotic genomes. <i>Bioinformatics</i> , 2015 , 11, 276-9	1.1	12
68	Cytogenetic Early Markers in Gynecologic Cancers 2015 , 43-58		
67	Biomarkers for Early Detection of Familial Breast Cancer 2015 , 167-190		
66	In Silico Models 2014 , 385-404		3
65	Genetic Addiction Risk Score (GARS): molecular neurogenetic evidence for predisposition to Reward Deficiency Syndrome (RDS). <i>Molecular Neurobiology</i> , 2014 , 50, 765-96	6.2	97
64	Proteome scale comparative modeling for conserved drug and vaccine targets identification in <i>Corynebacterium pseudotuberculosis</i> . <i>BMC Genomics</i> , 2014 , 15 Suppl 7, S3	4.5	18
63	Identifying human disease genes: advances in molecular genetics and computational approaches. <i>Genetics and Molecular Research</i> , 2014 , 13, 5073-87	1.2	7
62	A Multi-Locus Approach to Treating Fibromyalgia by Boosting Dopaminergic Activity in the Meso-Limbic System of the Brain. <i>Journal of Genetic Syndromes & Gene Therapy</i> , 2014 , 5, 213		2
61	Can Genetic Testing Coupled with Enhanced Dopaminergic Activation Reduce Recidivism Rates in the Workers Compensation Legacy Cases?. <i>Journal of Alcoholism and Drug Dependence</i> , 2014 , 2,	1	3
60	An improved interolog mapping-based computational prediction of protein-protein interactions with increased network coverage. <i>Integrative Biology (United Kingdom)</i> , 2014 , 6, 1080-7	3.7	19

59	Abiotic stresses, constraints and improvement strategies in chickpea. <i>Plant Breeding</i> , 2014 , 133, 163-178.	2.4	48
58	<i>C. pseudotuberculosis</i> Phop confers virulence and may be targeted by natural compounds. <i>Integrative Biology (United Kingdom)</i> , 2014 , 6, 1088-99	3.7	11
57	Omics Approaches in Breast Cancer 2014 ,		8
56	Breast Cancer Biomarkers for Risk Assessment, Screening, Detection, Diagnosis, and Prognosis 2014 , 393-407		
55	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. <i>Journal of Addiction Research & Therapy</i> , 2014 , 5, 1-7	2.5	9
54	The conserved mitochondrial gene distribution in relatives of <i>Turritopsis nutricula</i> , an immortal jellyfish. <i>Bioinformatics</i> , 2014 , 10, 586-91	1.1	10
53	PharmacogenomicsPharmacoepigenomics of Breast Cancer Therapy: Clinical Implications 2014 , 499-518		
52	Omics of Male Breast Cancer 2014 , 265-276		
51	Breast Cancer Stem Cells and Cellomics 2014 , 245-263		
50	Omics for Personalized Medicine 2013 ,		3
49	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 Suppl 6, S5	4.5	9
48	Conserved host-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 Piper betel compounds. <i>Integrative Biology (United Kingdom)</i> , 2013 , 5, 107-109	3.7	18
47	Identification of 11 new exoproteins in <i>Corynebacterium pseudotuberculosis</i> by comparative analysis of the exoproteome. <i>Microbial Pathogenesis</i> , 2013 , 61-62, 37-42	3.8	15
46	Differential Exoproteome analysis of two <i>corynebacterium pseudotuberculosis</i> biovar ovis strains isolated from goat (1002) and sheep (C231). <i>Current Microbiology</i> , 2013 , 67, 460-5	2.4	12
45	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, 2902-12	1.2	17
44	Determining miRNA-disease associations using bipartite graph modelling 2013 ,		2
43	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, 117-24	6.3	15
42	Coupling Genetic Addiction Risk Score (GARS) with Electrotherapy: Fighting Iatrogenic Opioid Dependence. <i>Journal of Addiction Research & Therapy</i> , 2013 , 4, 1000163	2.5	13

41	PANNOTATOR: an automated tool for annotation of pan-genomes. <i>Genetics and Molecular Research</i> , 2013 , 12, 2982-9	1.2	16
40	Long term Suboxone [®] emotional reactivity as measured by automatic detection in speech. <i>PLoS ONE</i> , 2013 , 8, e69043	3.7	60
39	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	3.7	51
38	Omics Approaches in Pulses 2013 , 101-138		1
37	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	1.1	3
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 Indian scenario on renewable and sustainable energy sources with emphasis on algae. <i>Applied Microbiology and Biotechnology</i> , 2012 , 96, 1125-35	5.7	31
34	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, 40-8	6.1	70
33	Quality of prokaryote genome assembly: indispensable issues of factors affecting prokaryote genome assembly quality. <i>Gene</i> , 2012 , 505, 365-7	3.8	9
32	In Silico and Ultrahigh-Throughput Screenings (uHTS) in Drug Discovery: An Overview 2012 , 451-490		1
31	Early intervention of intravenous KB220IV--neuroadaptagen amino-acid therapy (NAAT) improves behavioral outcomes in a residential addiction treatment program: a pilot study. <i>Journal of Psychoactive Drugs</i> , 2012 , 44, 398-409	3.6	14
30	The addictive brain: all roads lead to dopamine. <i>Journal of Psychoactive Drugs</i> , 2012 , 44, 134-43	3.6	115
29	The <i>Corynebacterium pseudotuberculosis</i> in silico predicted pan-exoproteome. <i>BMC Genomics</i> , 2012 , 13 Suppl 5, S6	4.5	13
28	Cancer Biomarkers for Diagnosis, Prognosis and Therapy 2012 , 18-68		1
27	Tight controlled expression and secretion of <i>Lactobacillus brevis</i> SlpA in <i>Lactococcus lactis</i> . <i>Biotechnology Letters</i> , 2012 , 34, 1275-81	3	1
26	Optimization of enzymatic hydrolysis of prairie cordgrass for improved ethanol production. <i>Journal of Renewable and Sustainable Energy</i> , 2012 , 4, 033118	2.5	
25	Whole-genome sequence of <i>Corynebacterium pseudotuberculosis</i> strain Cp162, isolated from camel. <i>Journal of Bacteriology</i> , 2012 , 194, 5718-9	3.5	9
24	Complete genome sequence of <i>Corynebacterium pseudotuberculosis</i> biovar <i>ovis</i> strain P54B96 isolated from antelope in South Africa obtained by rapid next generation sequencing technology. <i>Standards in Genomic Sciences</i> , 2012 , 7, 189-99		6

23	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> , 2012 , 3, 139	2.5	52
22	Diagnosis and Healing In Veterans Suspected of Suffering from Post-Traumatic Stress Disorder (PTSD) Using Reward Gene Testing and Reward Circuitry Natural Dopaminergic Activation. <i>Journal of Genetic Syndromes & Gene Therapy</i> , 2012 , 3, 1000116		15
21	FunSys: Software for functional analysis of prokaryotic transcriptome and proteome. <i>Bioinformatics</i> , 2012 , 8, 529-31	1.1	1
20	Simplifier: a web tool to eliminate redundant NGS contigs. <i>Bioinformatics</i> , 2012 , 8, 996-9	1.1	11
19	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, 4425-59	4.6	87
18	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	2.9	31
17	In silico subtractive genomics for target identification in human bacterial pathogens. <i>Drug Development Research</i> , 2011 , 72, 162-177	5.1	65
16	Whole-genome sequence of <i>Corynebacterium pseudotuberculosis</i> PAT10 strain isolated from sheep in Patagonia, Argentina. <i>Journal of Bacteriology</i> , 2011 , 193, 6420-1	3.5	16
15	Complete genome sequence of <i>Corynebacterium pseudotuberculosis</i> strain CIP 52.97, isolated from a horse in Kenya. <i>Journal of Bacteriology</i> , 2011 , 193, 7025-6	3.5	16
14	miReg: a resource for microRNA regulation. <i>Journal of Integrative Bioinformatics</i> , 2010 , 7,	3.8	11
13	miReg: a resource for microRNA regulation. <i>Journal of Integrative Bioinformatics</i> , 2010 , 7,	3.8	5
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10	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	2	45
9	Molecular features, markers, drug targets, and prospective targeted therapeutics in cardiac myxoma. <i>Current Cancer Drug Targets</i> , 2009 , 9, 705-16	2.8	18
8	Biomarkers, critical disease pathways, drug targets, and alternative medicine in male breast cancer. <i>Current Drug Targets</i> , 2009 , 10, 1-8	3	8
7	Epitope Design from Transporter Targets in <i>N. gonorrhoeae</i> . <i>Journal of Proteomics and Bioinformatics</i> , 2009 , 02, 475-480	2.1	5
6	Genomic Target Database (GTD): a database of potential targets in human pathogenic bacteria. <i>Bioinformatics</i> , 2009 , 4, 50-1	1.1	9

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4	OMICS		9
3	A novel multi-omics-based identification of symptoms, comorbid conditions, and possible long-term complications in COVID-19		2
2	A potential link between tuberculosis and lung cancer through non-coding RNAs		1
1	An Issue of Concern: Unique Truncated ORF8 Protein Variants of SARS-CoV-2		1