Debmalya Barh

List of Publications by Year
in descending order

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	New putative therapeutic targets against *Serratia marcescens* using reverse vaccinology and subtractive genomics. Journal of Biomolecular Structure and Dynamics, 2022, 40, 10106-10121.	3.5	4
2	Periodically aperiodic pattern of SARS-CoV-2 mutations underpins the uncertainty of its origin and evolution. Environmental Research, 2022, 204, 112092.	7.5	4
3	An immunoinformatics-based designed multi-epitope candidate vaccine (mpme-VAC/STV-1) against Mycoplasma pneumoniae. Computers in Biology and Medicine, 2022, 142, 105194.	7.0	4
4	Emergence of unique SARS-CoV-2 ORF10 variants and their impact on protein structure and function. International Journal of Biological Macromolecules, 2022, 194, 128-143.	7.5	13
5	The importance of accessory protein variants in the pathogenicity of SARS-CoV-2. Archives of Biochemistry and Biophysics, 2022, 717, 109124.	3.0	20
6	Therapeutic Challenges in COVID-19. , 2022, , 27-35.		1
7	Bugs as drugs: neglected but a promising future therapeutic strategy in cancer. Future Oncology, 2022, 18, 1609-1626.	2.4	4
8	Lessons Learned from COVID-19 and Their Implementations for Future Pandemics. , 2022, , 196-207.		0
9	Evidence of episodic positive selection in *Corynebacterium diphtheriae* complex of species and its implementations in identification of drug and vaccine targets. PeerJ, 2022, 10, e12662.	2.0	1
10	The Space-Exposed Kombucha Microbial Community Member Komagataeibacter oboediens Showed Only Minor Changes in Its Genome After Reactivation on Earth. Frontiers in Microbiology, 2022, 13, 782175.	3.5	5
11	An issue of concern: unique truncated ORF8 protein variants of SARS-CoV-2. PeerJ, 2022, 10, e13136.	2.0	7
12	Deep Learning applied to computational biology and agricultural sciences. , 2022, , 589-618.		0
13	Would New SARS-CoV-2 Variants Change the War against COVID-19?. Epidemiologia, 2022, 3, 229-237.	2.2	3
14	Associations and Disease–Disease Interactions of COVID-19 with Congenital and Genetic Disorders: A Comprehensive Review. Viruses, 2022, 14, 910.	3.3	6
15	Lactobacillus delbrueckii CIDCA 133 Ameliorates Chemotherapy-Induced Mucositis by Modulating Epithelial Barrier and TLR2/4/Myd88/NF-κB Signaling Pathway. Frontiers in Microbiology, 2022, 13, 858036.	3.5	13
16	Neuroinformatics Insights towards Multiple Neurosyphilis Complications. Venereology, 2022, 1, 135-160.	1.6	1
17	In Silico Designed Multi-Epitope Immunogen "Tpme-VAC/LGCM-2022" May Induce Both Cellular and Humoral Immunity against Treponema pallidum Infection. Vaccines, 2022, 10, 1019.	4.4	3
18	Reverse vaccinology and subtractive genomics approaches for identifying common therapeutics against Mycobacterium leprae and Mycobacterium lepromatosis. Journal of Venomous Animals and Toxins Including Tropical Diseases, 2021, 27, e20200027.	1.4	3

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19	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.	2.8	24
20	Characterization of a new multidrug-resistant Brazilian K. pneumoniae isolate and 172 Klebsiella spp. sequenced strains: Genomic island, multilocus sequence typing and capsule locus dataset. Data in Brief, 2021, 34, 106746.	1.0	0
21	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
22	Pathophysiological features of the visual cycle, cascade and metabolic pathways in retinitis pigmentosa. Rossiiskii Oftal'mologicheskii Zhurnal, 2021, 14, 80-88.	0.4	1
23	Comparative genomics with a multidrug-resistant Klebsiella pneumoniae isolate reveals the panorama of unexplored diversity in Northeast Brazil. Gene, 2021, 772, 145386.	2.2	2
24	Long-COVID and Post-COVID Health Complications: An Up-to-Date Review on Clinical Conditions and Their Possible Molecular Mechanisms. Viruses, 2021, 13, 700.	3.3	249
25	Carbon-Based Nanomaterials: Promising Antiviral Agents to Combat COVID-19 in the Microbial-Resistant Era. ACS Nano, 2021, 15, 8069-8086.	14.6	134
26	Pan-Resistome Insights into the Multidrug Resistance of Acinetobacter baumannii. Antibiotics, 2021, 10, 596.	3.7	11
27	Predicting COVID-19—Comorbidity Pathway Crosstalk-Based Targets and Drugs: Towards Personalized COVID-19 Management. Biomedicines, 2021, 9, 556.	3.2	20
28	A unique view of SARS-CoV-2 through the lens of ORF8 protein. Computers in Biology and Medicine, 2021, 133, 104380.	7.0	48
29	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
30	Notable sequence homology of the ORF10 protein introspects the architecture of SARS-CoV-2. International Journal of Biological Macromolecules, 2021, 181, 801-809.	7.5	36
31	Computational identification of putative common genomic drug and vaccine targets in Mycoplasma genitalium. Genomics, 2021, 113, 2730-2743.	2.9	9
32	COVID-19 Vaccines and Thrombosis—Roadblock or Dead-End Street?. Biomolecules, 2021, 11, 1020.	4.0	28
33	The Spike of SARS-CoV-2: Uniqueness and Applications. Frontiers in Immunology, 2021, 12, 663912.	4.8	14
34	Overview of key molecular and pharmacological targets for diabetes and associated diseases. Life Sciences, 2021, 278, 119632.	4.3	6
35	Emergence of Cardiac Glycosides as Potential Drugs: Current and Future Scope for Cancer Therapeutics. Biomolecules, 2021, 11, 1275.	4.0	22
36	Autoimmunity roots of the thrombotic events after COVID-19 vaccination. Autoimmunity Reviews, 2021, 20, 102941.	5.8	39

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37	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.	0.6	4
38	Potential Molecular Mechanisms of Rare Anti-Tumor Immune Response by SARS-CoV-2 in Isolated Cases of Lymphomas. Viruses, 2021, 13, 1927.	3.3	10
39	The mechanism behind flaring/triggering of autoimmunity disorders associated with COVID-19. Autoimmunity Reviews, 2021, 20, 102909.	5.8	7
40	Targeting LIN28: a new hope in prostate cancer theranostics. Future Oncology, 2021, 17, 3873-3880.	2.4	6
41	Implications derived from S-protein variants of SARS-CoV-2 from six continents. International Journal of Biological Macromolecules, 2021, 191, 934-955.	7.5	10
42	Artificial Intelligence Techniques for Predicting Type 2 Diabetes. Advances in Intelligent Systems and Computing, 2021, , 411-430.	0.6	1
43	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
44	Fused deposition modelling: Current status, methodology, applications and future prospects. Additive Manufacturing, 2021, 47, 102378.	3.0	99
45	Modular network inference between miRNA–mRNA expression profiles using weighted co-expression network analysis. Journal of Integrative Bioinformatics, 2021, 18, .	1.5	5
46	Innate immunity and metal ion trafficking pathway perturbations in idiopathic Parkinson's disease and Tuberculosis: A comparative transcriptomics approach. Brain Disorders, 2021, 4, 100025.	1.7	0
47	Analysis of the microarray gene expression for breast cancer progression after the application modified logistic regression. Gene, 2020, 726, 144168.	2.2	25
48	Multi-omics-based identification of SARS-CoV-2 infection biology and candidate drugs against COVID-19. Computers in Biology and Medicine, 2020, 126, 104051.	7.0	71
49	Current Trends in Experimental and Computational Approaches to Combat Antimicrobial Resistance. Frontiers in Genetics, 2020, 11, 563975.	2.3	12
50	Anticancer and Antiviral Properties of Cardiac Glycosides: A Review to Explore the Mechanism of Actions. Molecules, 2020, 25, 3596.	3.8	42
51	Fitness of Outer Membrane Vesicles From Komagataeibacter intermedius Is Altered Under the Impact of Simulated Mars-like Stressors Outside the International Space Station. Frontiers in Microbiology, 2020, 11, 1268.	3.5	13
52	In silico disease model: from simple networks to complex diseases. , 2020, , 441-460.		7
53	Pan-omics focused to Crick's central dogma. , 2020, , 1-41.		3
54	Pan-genomics of veterinary pathogens and its applications. , 2020, , 101-119.		0

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55	Pan-genomics of fungi and its applications. , 2020, , 251-260.		1
56	Genomic Characterization of Multidrug-Resistant Escherichia coli BH100 Sub-strains. Frontiers in Microbiology, 2020, 11, 549254.	3.5	5
57	Cellular and Organismal Toxicity of Nanoparticles and Its Associated Health Concerns. , 2020, , 477-497.		1
58	Computational screening for potential drug candidates against the SARS-CoV-2 main protease. F1000Research, 2020, 9, 514.	1.6	12
59	Computational screening for potential drug candidates against the SARS-CoV-2 main protease. F1000Research, 2020, 9, 514.	1.6	10
60	Potential chimeric peptides to block the SARS-CoV-2 spike receptor-binding domain. F1000Research, 2020, 9, 576.	1.6	38
61	Clinical Applications of Antimicrobial Peptides (AMPs): Where do we Stand Now?. Protein and Peptide Letters, 2020, 27, 120-134.	0.9	85
62	Repurposing Approved Drugs for Guiding COVID-19 Prophylaxis: A Systematic Review. Frontiers in Pharmacology, 2020, 11, 590598.	3.5	21
63	Bacteriocins as an alternative in the treatment of infections by Staphylococcus aureus. Anais Da Academia Brasileira De Ciencias, 2020, 92, e20201216.	0.8	6
64	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.	2.5	6
65	Natural selection versus creation: a review on the origin of SARS-COV-2. Infezioni in Medicina, 2020, 28, 302-311.	1.1	4
66	Protein-Protein Interactions: An Overview. , 2019, , 821-833.		1
67	Evaluation of the Common Molecular Basis in Alzheimer's and Parkinson's Diseases. International Journal of Molecular Sciences, 2019, 20, 3730.	4.1	12
68	Transcriptome profile of Corynebacterium pseudotuberculosis in response to iron limitation. BMC Genomics, 2019, 20, 663.	2.8	19
69	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
70	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
71	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, 792.	4.0	73
72	Re-sequencing and optical mapping reveals misassemblies and real inversions on Corynebacterium pseudotuberculosis genomes. Scientific Reports, 2019, 9, 16387.	3.3	6

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73	Novel frameshift mutation in *NYX* gene in a Russian family with complete congenital stationary night blindness. Ophthalmic Genetics, 2019, 40, 558-563.	1.2	5
74	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, 2019, 18, 2731-2740.	2.1	9
75	Next-Generation Sequencing and Data Analysis. , 2018, , 191-207.		5
76	GO FEAT: a rapid web-based functional annotation tool for genomic and transcriptomic data. Scientific Reports, 2018, 8, 1794.	3.3	99
77	Genetic screening of Russian Usher syndrome patients toward selection for gene therapy. Ophthalmic Genetics, 2018, 39, 706-713.	1.2	12
78	First genome sequencing and comparative analyses of Corynebacterium pseudotuberculosis strains from Mexico. Standards in Genomic Sciences, 2018, 13, 21.	1.5	8
79	Putative vaccine candidates and drug targets identified by reverse vaccinology and subtractive genomics approaches to control *Haemophilus ducreyi* , the causative agent of chancroid. Journal of the Royal Society Interface, 2018, 15, 20180032.	3.4	11
80	Bioinformatics and Systems Biology in Bioengineering. , 2018, , 223-243.		1
81	Microbial Omics. , 2018, , 3-20.		17
82	Computational Techniques in Data Integration and Big Data Handling in Omics. , 2018, , 209-222.		0
83	Comparative mangrove metagenome reveals global prevalence of heavy metals and antibiotic resistome across different ecosystems. Scientific Reports, 2018, 8, 11187.	3.3	63
84	The Druggable Pocketome of Corynebacterium diphtheriae: A New Approach for in silico Putative Druggable Targets. Frontiers in Genetics, 2018, 9, 44.	2.3	8
85	Linking common non-coding RNAs of human lung cancer and M. tuberculosis. Bioinformation, 2018, 14, 337-345.	0.5	5
86	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
87	Stargardt disease-associated mutation spectrum of a Russian Federation cohort. European Journal of Medical Genetics, 2017, 60, 140-147.	1.3	16
88	miRsig: a consensus-based network inference methodology to identify pan-cancer miRNA-miRNA interaction signatures. Scientific Reports, 2017, 7, 39684.	3.3	29
89	Determining causal miRNAs and their signaling cascade in diseases using an influence diffusion model. Scientific Reports, 2017, 7, 8133.	3.3	14
90	Searching for signatures across microbial communities: Metagenomic analysis of soil samples from mangrove and other ecosystems. Scientific Reports, 2017, 7, 8859.	3.3	50

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91	BARHL1 Is Downregulated in Alzheimerâ€™s Disease and May Regulate Cognitive Functions through ESR1 and Multiple Pathways. Genes, 2017, 8, 245.	2.4	57
92	Two-Component Signal Transduction Systems of Pathogenic Bacteria As Targets for Antimicrobial Therapy: An Overview. Frontiers in Microbiology, 2017, 8, 1878.	3.5	176
93	Exploration of Nitrate Reductase Metabolic Pathway in *Corynebacterium pseudotuberculosis*. International Journal of Genomics, 2017, 2017, 1-12.	1.6	14
94	An integrative in-silico approach for therapeutic target identification in the human pathogen Corynebacterium diphtheriae. PLoS ONE, 2017, 12, e0186401.	2.5	35
95	Quadruplex PCR assay for identification of Corynebacterium pseudotuberculosis differentiating biovar Ovis and Equi. BMC Veterinary Research, 2017, 13, 290.	1.9	15
96	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, 402.	4.1	37
97	GLOBAL OPIOID EPIDEMIC: DOOMED TO FAIL WITHOUT GENETICALLY BASED PRECISION ADDICTION MEDICINE (PAM): LESSONS LEARNED FROM AMERICA. Precision Medicine, 2017, 2, 17-22.	3.5	11
98	KB220Zâ„¢ 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
99	Towards a Comprehensive Understanding of miRNA Regulome and miRNA Interaction Networks. Journal of Pharmacogenomics & Pharmacoproteomics, 2016, 7, .	0.2	1
100	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.	3.3	11
101	Whole-Genome Sequence of Corynebacterium auriscanis Strain CIP 106629 Isolated from a Dog with Bilateral Otitis from the United Kingdom. Genome Announcements, 2016, 4, .	0.8	0
102	In silico identification of essential proteins in Corynebacterium pseudotuberculosis based on protein-protein interaction networks. BMC Systems Biology, 2016, 10, 103.	3.0	24
103	SIMBA: a web tool for managing bacterial genome assembly generated by Ion PGM sequencing technology. BMC Bioinformatics, 2016, 17, 456.	2.6	8
104	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
105	The genome anatomy of Corynebacterium pseudotuberculosis VD57 a highly virulent strain causing Caseous lymphadenitis. Standards in Genomic Sciences, 2016, 11, 29.	1.5	20
106	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.	1.9	10
107	Whole-genome resequencing: Current status and future prospects in genomics-assisted crop improvement. , 2016, , 187-211.		2
108	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.	0.5	8

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109	In silico characterization of 1,2-diacylglycerol cholinephosphotransferase and lysophosphaÂtidylcholine acyltransferase genes in Glycine max L. Merrill. Genetics and Molecular Research, 2016, 15, .	0.2	0
110	Biotechnology for improved crop productivity and quality. , 2016, , 231-248.		0
111	Determining influential miRNA targets in diseases using influence diffusion model. , 2015, , .		0
112	miRegulome: a knowledge-base of miRNA regulomics and analysis. Scientific Reports, 2015, 5, 12832.	3.3	12
113	Genome informatics and vaccine targets in Corynebacterium urealyticum using two whole genomes, comparative genomics, and reverse vaccinology. BMC Genomics, 2015, 16, S7.	2.8	10
114	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
115	An integrated structural proteomics approach along the druggable genome of Corynebacterium pseudotuberculosis species for putative druggable targets. BMC Genomics, 2015, 16, S9.	2.8	25
116	Are We Ready for Real-Time Applications of Clinical NGS?. Journal of Next Generation Sequencing & Applications, 2015, 02, .	0.3	0
117	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. BioMed Research International, 2015, 2015, 1-17.	1.9	47
118	Epigenetics in Head and Neck Cancer. Methods in Molecular Biology, 2015, 1238, 751-769.	0.9	15
119	XomAnnotate: Analysis of Heterogeneous and Complex Exome- A Step towards Translational Medicine. PLoS ONE, 2015, 10, e0123569.	2.5	5
120	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
121	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
122	MapRepeat: an approach for effective assembly of repetitive regions in prokaryotic genomes. Bioinformation, 2015, 11, 276-279.	0.5	12
123	Cytogenetic Early Markers in Gynecologic Cancers. , 2015, , 43-58.		0
124	Biomarkers for Early Detection of Familial Breast Cancer. , 2015, , 167-190.		0
125	Mini Review Identifying human disease genes: advances in molecular genetics and computational approaches. Genetics and Molecular Research, 2014, 13, 5073-5087.	0.2	9
126	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, 05, 213.	0.2	2

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127	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
128	An improved interolog mapping-based computational prediction of protein–protein interactions with increased network coverage. Integrative Biology (United Kingdom), 2014, 6, 1080-1087.	1.3	32
129	Abiotic stresses, constraints and improvement strategies in chickpea. Plant Breeding, 2014, 133, 163-178.	1.9	73
130	C. pseudotuberculosis Phop confers virulence and may be targeted by natural compounds. Integrative Biology (United Kingdom), 2014, 6, 1088-1099.	1.3	17
131	Omics Approaches in Breast Cancer. , 2014, , .		10
132	Breast Cancer Biomarkers for Risk Assessment, Screening, Detection, Diagnosis, and Prognosis. , 2014, , 393-407.		0
133	In Silico Models. , 2014, , 385-404.		8
134	Genetic Addiction Risk Score (GARS): Molecular Neurogenetic Evidence for Predisposition to Reward Deficiency Syndrome (RDS). Molecular Neurobiology, 2014, 50, 765-796.	4.0	157
135	Proteome scale comparative modeling for conserved drug and vaccine targets identification in Corynebacterium pseudotuberculosis. BMC Genomics, 2014, 15, S3.	2.8	30
136	The conserved mitochondrial gene distribution in relatives of Turritopsis nutricula, an immortal jellyfish. Bioinformation, 2014, 10, 586-591.	0.5	10
137	Pharmacogenomics–Pharmacoepigenomics of Breast Cancer Therapy: Clinical Implications. , 2014, , 499-518.		0
138	Omics of Male Breast Cancer. , 2014, , 265-276.		0
139	Breast Cancer Stem Cells and Cellomics. , 2014, , 245-263.		0
140	Omics for Personalized Medicine. , 2013, , .		3
141	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, S5.	2.8	22
142	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<i>Piper betel</i>compounds. Integrative Biology (United Kingdom), 2013, 5, 495-509.	1.3	24
143	Identification of 11 new exoproteins in Corynebacterium pseudotuberculosis byÂcomparative analysis of the exoproteome. Microbial Pathogenesis, 2013, 61-62, 37-42.	2.9	19
144	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

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145	In silico prediction of conserved vaccine targets in Streptococcus agalactiae strains isolated from fish, cattle, and human samples. Genetics and Molecular Research, 2013, 12, 2902-2912.	0.2	22
146	Determining miRNA-disease associations using bipartite graph modelling. , 2013, , .		2
147	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, 117-124.	3.7	20
148	Coupling Genetic Addiction Risk Score (GARS) with Electrotherapy: Fighting Iatrogenic Opioid Dependence. Journal of Addiction Research & Therapy, 2013, 04, 1000163.	0.2	26
149	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. Journal of Addiction Research & Therapy, 2013, 05, 1-7.	0.2	10
150	PANNOTATOR: an automated tool for annotation of pan-genomes. Genetics and Molecular Research, 2013, 12, 2982-2989.	0.2	22
151	Long Term Suboxoneâ„¢ Emotional Reactivity As Measured by Automatic Detection in Speech. PLoS ONE, 2013, 8, e69043.	2.5	73
152	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.	2.5	95
153	Omics Approaches in Pulses. , 2013, , 101-138.		1
154	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, 2013, 03, 139.	0.2	65
155	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.	0.5	3
156	Neurogenetics and Nutrigenomics of Reward Deficiency Syndrome (RDS): Stratification of Addiction Risk and Mesolimbic Nutrigenomic Manipulation of Hypodopaminergic Function. , 2013, , 365-398.		1
157	Optimization of enzymatic hydrolysis of prairie cordgrass for improved ethanol production. Journal of Renewable and Sustainable Energy, 2012, 4, 033118.	2.0	1
158	Whole-Genome Sequence of Corynebacterium pseudotuberculosis Strain Cp162, Isolated from Camel. Journal of Bacteriology, 2012, 194, 5718-5719.	2.2	10
159	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, 189-199.	1.5	8
160	An Indian scenario on renewable and sustainable energy sources with emphasis on algae. Applied Microbiology and Biotechnology, 2012, 96, 1125-1135.	3.6	36
161	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, 40-48.	4.6	82
162	Quality of prokaryote genome assembly: Indispensable issues of factors affecting prokaryote genome assembly quality. Gene, 2012, 505, 365-367.	2.2	9

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163	In Silico and Ultrahigh-Throughput Screenings (uHTS) in Drug Discovery: An Overview. , 2012, , 451-490.		1
164	Early Intervention of Intravenous KB220IV- Neuroadaptagen Amino-Acid Therapy (NAAT)â„¢ Improves Behavioral Outcomes in a Residential Addiction Treatment Program: A Pilot Study. Journal of Psychoactive Drugs, 2012, 44, 398-409.	1.7	21
165	The Addictive Brain: All Roads Lead to Dopamine. Journal of Psychoactive Drugs, 2012, 44, 134-143.	1.7	138
166	The Corynebacterium pseudotuberculosis in silico predicted pan-exoproteome. BMC Genomics, 2012, 13, S6.	2.8	16
167	Tight controlled expression and secretion of Lactobacillus brevis SlpA in Lactococcus lactis. Biotechnology Letters, 2012, 34, 1275-1281.	2.2	3
168	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
169	FunSys: Software for functional analysis of prokaryotic transcriptome and proteome. Bioinformation, 2012, 8, 529-531.	0.5	1
170	Simplifier: a web tool to eliminate redundant NGS contigs. Bioinformation, 2012, 8, 996-999.	0.5	11
171	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, 4425-4459.	2.6	106
172	A Novel Comparative Genomics Analysis for Common Drug and Vaccine Targets in <i>Corynebacterium pseudotuberculosis</i> and other CMN Group of Human Pathogens. Chemical Biology and Drug Design, 2011, 78, 73-84.	3.2	48
173	In silico subtractive genomics for target identification in human bacterial pathogens. Drug Development Research, 2011, 72, 162-177.	2.9	115
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