

# Jagajjit Sahu

## List of Publications by Year in descending order

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Version: 2024-02-01

37  
papers

413  
citations

1039880

9  
h-index

794469

19  
g-index

40  
all docs

40  
docs citations

40  
times ranked

739  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative genomics of cetartiodactyla: energy metabolism underpins the transition to an aquatic lifestyle. , 2021, 9, coaa136.		12
2	Role of Microbial Biofilms in Agriculture: Perspectives on Plant and Soil Health. , 2021, , 251-288.		1
3	Mining Proteome Research Reports: A Bird's Eye View. Proteomes, 2021, 9, 29.	1.7	2
4	Novel Coronavirus Disease and the Current Scenario of the Global Health Emergency. Anti-Inflammatory and Anti-Allergy Agents in Medicinal Chemistry, 2020, 19, 203-205.	1.1	0
5	Transient Sub-cellular Localization and In Vivo Protein-Protein Interaction Study of Multiple Abiotic Stress-Responsive AtELF4A-III and AtALY4 Proteins in Arabidopsis thaliana. Plant Molecular Biology Reporter, 2020, 38, 538-553.	1.0	2
6	Genomics of Extremophiles for Sustainable Agriculture and Biotechnological Applications (Part I). Current Genomics, 2020, 21, 78-79.	0.7	2
7	Genomics of Extremophiles for Sustainable Agriculture and Biotechnological Applications (Part II). Current Genomics, 2020, 21, 238-239.	0.7	1
8	Seed Biotechnology for Improvement of Staple Crops. , 2020, , 503-519.		1
9	Insights in Plant-Microbe Interaction through Genomics Approach (Part I). Current Genomics, 2020, 21, 155-156.	0.7	5
10	Insights in Plant-Microbe Interaction through Genomics Approach (Part III). Current Genomics, 2020, 21, 399-400.	0.7	2
11	Insights in Plant-Microbe Interaction through Genomics Approach (Part IV). Current Genomics, 2020, 21, 479-480.	0.7	0
12	Dissecting the Role of Promoters of Pathogen-sensitive Genes in Plant Defense. Current Genomics, 2020, 21, 491-503.	0.7	9
13	Insights in Plant-Microbe Interaction Through Genomics Approach (Part II). Current Genomics, 2020, 21, 319-320.	0.7	2
14	A Systematic Review on the Role of Mycorrhiza in Soil Genesis Using Scientometrics Analysis. , 2019, , 95-109.		1
15	A scientometric analysis on WoS reports to evaluate the research on Fusarium oxysporum since 2009. Archives of Phytopathology and Plant Protection, 2019, 52, 795-812.	0.6	4
16	Role of Natural Phenolics in Hepatoprotection: A Mechanistic Review and Analysis of Regulatory Network of Associated Genes. Frontiers in Pharmacology, 2019, 10, 509.	1.6	73
17	Revealing shared differential co-expression profiles in rice infected by virus from reoviridae and sequiviridae group. Gene, 2019, 698, 82-91.	1.0	5
18	Mining and comparative survey of EST's SSR markers among members of Euphorbiaceae family. Molecular Biology Reports, 2018, 45, 453-468.	1.0	5

#	ARTICLE	IF	CITATIONS
19	In silico mining and characterization of simple sequence repeats (SSRs) from <i>Euphorbia esula</i> expressed sequence tags (ESTs): A potential crop for biofuel. <i>Plant OMICS</i> , 2017, 10, 53-63.	0.4	1
20	Genome wide transcriptome profiling reveals differential gene expression in secondary metabolite pathway of <i>Cymbopogon winterianus</i> . <i>Scientific Reports</i> , 2016, 6, 21026.	1.6	27
21	Molecular recognition of avirulence protein ( <i>avrxa5</i> ) by eukaryotic transcription factor <i>xa5</i> of rice ( <i>Oryza sativa</i> L.): Insights from molecular dynamics simulations. <i>Journal of Molecular Graphics and Modelling</i> , 2015, 57, 49-61.	1.3	8
22	E-Microsatellite Markers for <i>Centella asiatica</i> (Gotu Kola) Genome: Validation and Cross-Transferability in Apiaceae Family for Plant Omics Research and Development. <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 52-65.	1.0	9
23	Big Next Generation Sequencing Data. <i>Transcriptomics: Open Access</i> , 2015, 03, .	0.2	0
24	Computational identification and characterization of conserved miRNAs and their target genes in garlic ( <i>Allium sativum</i> L.) expressed sequence tags. <i>Gene</i> , 2014, 537, 333-342.	1.0	43
25	Rediscovering Medicinal Plants' Potential with OMICS: Microsatellite Survey in Expressed Sequence Tags of Eleven Traditional Plants with Potent Antidiabetic Properties. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 298-309.	1.0	20
26	Structure-Based Computational Study of Two Disease Resistance Gene Homologues (Hm1 and Hm2) in Maize ( <i>Zea mays</i> L.) with Implications in Plant-Pathogen Interactions. <i>PLoS ONE</i> , 2014, 9, e97852.	1.1	28
27	Structural Insight of <i>Bos Indicus</i> ITGB6 Receptor Gene for FMDV Host Tropism. <i>Advances in Animal and Veterinary Sciences</i> , 2014, 2, 549-556.	0.1	0
28	Insights into the structure-function relationship of disease resistance protein HCTR in maize ( <i>Zea mays</i> L.) expressed sequence tags (ESTs). <i>PLoS ONE</i> , 2013, 8, e65433.	1.3	9
29	Molecular Phylogeny, Homology Modeling, and Molecular Dynamics Simulation of Race-Specific Bacterial Blight Disease Resistance Protein ( <i>xa5</i> ) of Rice: A Comparative Agriproteomics Approach. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 423-438.	1.0	9
30	In silico analyses of superoxide dismutases (SODs) of rice ( <i>Oryza sativa</i> L.). <i>Journal of Plant Biochemistry and Biotechnology</i> , 2013, 22, 150-156.	0.9	30
31	Structural analysis and molecular dynamics simulations of novel $\beta$ -endotoxin Cry1Id from <i>Bacillus thuringiensis</i> to pave the way for development of novel fusion proteins against insect pests of crops. <i>Journal of Molecular Modeling</i> , 2013, 19, 5301-5316.	0.8	12
32	In silico identification and characterization of conserved miRNAs and their target genes in sweet potato ( <i>Ipomoea batatas</i> L.) Expressed Sequence Tags (ESTs). <i>Plant Signaling and Behavior</i> , 2013, 8, e26543.	1.2	45
33	A comparative proteomic approach to analyse structure, function and evolution of rice chitinases: a step towards increasing plant fungal resistance. <i>Journal of Molecular Modeling</i> , 2012, 18, 4761-4780.	0.8	9
34	An approach to delineate primers for a group of poorly conserved sequences incorporating the common motif region. <i>Bioinformatics</i> , 2012, 8, 181-184.	0.2	1
35	Towards an efficient computational mining approach to identify EST-SSR markers. <i>Bioinformatics</i> , 2012, 8, 201-202.	0.2	6
36	ESMP: A high-throughput computational pipeline for mining SSR markers from ESTs. <i>Bioinformatics</i> , 2012, 8, 206-208.	0.2	7

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37	Mining for SSRs and FDMs from expressed sequence tags of <i>Camellia sinensis</i> . <i>Bioinformatics</i> , 2012, 8, 260-266.	0.2	19