Sujay Paul

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11859/publications.pdf

Version: 2024-02-01

| 57 | 1,241 | 18 | 32 |
|----------|----------------|--------------|----------------|
| papers | citations | h-index | g-index |
| 57 | 57 | 57 | 1312 |
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|----|--|-----|-----------|
| 1 | The Micro-RNA172c-APETALA2-1 Node as a Key Regulator of the Common Bean- <i>Rhizobium etli</i> Nitrogen Fixation Symbiosis. Plant Physiology, 2015, 168, 273-291. | 4.8 | 134 |
| 2 | Regulation of Copper Homeostasis and Biotic Interactions by MicroRNA 398b in Common Bean. PLoS ONE, 2014, 9, e84416. | 2.5 | 109 |
| 3 | Identification and validation of conserved microRNAs along with their differential expression in roots of Vigna unguiculata grown under salt stress. Plant Cell, Tissue and Organ Culture, 2011, 105, 233-242. | 2.3 | 75 |
| 4 | Current Status of microRNA-Based Therapeutic Approaches in Neurodegenerative Disorders. Cells, 2020, 9, 1698. | 4.1 | 71 |
| 5 | Isolation, Characterization, and Structure Analysis of a Non-TIR-NBS-LRR Encoding Candidate Gene from MYMIV-Resistant Vigna mungo. Molecular Biotechnology, 2012, 52, 217-233. | 2.4 | 66 |
| 6 | The role of microRNAs in solving COVID-19 puzzle from infection to therapeutics: A mini-review. Virus Research, 2022, 308, 198631. | 2.2 | 47 |
| 7 | High throughput sequencing reveals modulation of microRNAs in Vigna mungo upon Mungbean Yellow Mosaic India Virus inoculation highlighting stress regulation. Plant Science, 2017, 257, 96-105. | 3.6 | 46 |
| 8 | An improved method of DNA isolation suitable for PCR-based detection of begomoviruses from jute and other mucilaginous plants. Journal of Virological Methods, 2009, 159, 34-39. | 2.1 | 44 |
| 9 | MicroRNAs and Child Neuropsychiatric Disorders: A Brief Review. Neurochemical Research, 2020, 45, 232-240. | 3.3 | 36 |
| 10 | Distribution, epidemiology and molecular variability of the begomovirus complexes associated with yellow vein mosaic disease of mesta in India. Virus Research, 2009, 141, 237-246. | 2.2 | 35 |
| 11 | Human microRNAs in host–parasite interaction: a review. 3 Biotech, 2020, 10, 510. | 2.2 | 35 |
| 12 | Identification and expression profiling of <i>Vigna mungo</i> microRNAs from leaf small RNA transcriptome by deep sequencing. Journal of Integrative Plant Biology, 2014, 56, 15-23. | 8.5 | 32 |
| 13 | Transcript Dynamics at Early Stages of Molecular Interactions of MYMIV with Resistant and Susceptible Genotypes of the Leguminous Host, Vigna mungo. PLoS ONE, 2015, 10, e0124687. | 2.5 | 32 |
| 14 | Roles of microRNAs in chronic pediatric diseases and their use as potential biomarkers: A review. Archives of Biochemistry and Biophysics, 2021, 699, 108763. | 3.0 | 31 |
| 15 | Sequence variability and phylogenetic relationship of betasatellite isolates associated with yellow vein mosaic disease of mesta in India. Virus Genes, 2008, 37, 414-424. | 1.6 | 29 |
| 16 | The Emerging Role of MicroRNAs in Bone Diseases and Their Therapeutic Potential. Molecules, 2022, 27, 211. | 3.8 | 26 |
| 17 | Identification, characterization and expression analysis of passion fruit (Passiflora edulis) microRNAs. 3 Biotech, 2020, 10, 25. | 2.2 | 25 |
| 18 | Complete nucleotide sequence of a monopartite begomovirus associated with yellow vein mosaic disease of mesta from north India. Archives of Virology, 2008, 153, 1791-1796. | 2.1 | 24 |

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|----|---|------------------|--------------------------|
| 19 | Phytochemicals mediated modulation of <scp>microRNAs</scp> and long nonâ€coding <scp>RNAs</scp> in cancer prevention and therapy. Phytotherapy Research, 2022, 36, 705-729. | 5.8 | 23 |
| 20 | Identification of microRNAs and Their Expression in Leaf Tissues of Guava (Psidium guajava L.) under Salinity Stress. Agronomy, 2020, 10, 1920. | 3.0 | 20 |
| 21 | Occurrence of Begomovirus Associated with Yellow Vein Mosaic Disease of Kenaf (Hibiscus) Tj ETQq1 1 0.78431 | 4 rgBT /0\ £4 | verlock 10 Tf |
| 22 | Metagenomic analysis of microbial community of an Amazonian geothermal spring in Peru. Genomics Data, 2016, 9, 63-66. | 1.3 | 17 |
| 23 | Current insight into the functions of microRNAs in common human hair loss disorders: a mini review. Human Cell, 2021, 34, 1040-1050. | 2.7 | 16 |
| 24 | Roles of microRNAs in carbohydrate and lipid metabolism disorders and their therapeutic potential. Biochimie, 2021, 187, 83-93. | 2.6 | 16 |
| 25 | Identification of microRNAs from Medicinal Plant Murraya koenigii by High-Throughput Sequencing and Their Functional Implications in Secondary Metabolite Biosynthesis. Plants, 2022, 11, 46. | 3.5 | 16 |
| 26 | Occurrence of a DNA β-containing begomovirus associated with leaf curl disease of kenaf (Hibiscus) Tj ETQq0 0 | 0 rgBT /0ນ | verlock 10 Tf |
| 27 | First report of <i>Tomato leaf curl Joydebpur virus</i> and associated betasatellite in kenaf (<i>Hibiscus cannabinus</i>) plants showing leaf curl symptoms from southern India. Plant Pathology, 2009, 58, 403-403. | 2.4 | 13 |
| 28 | Detection of Corchorus golden mosaic virus Associated with Yellow Mosaic Disease of Jute (Corchorus capsularis). Indian Journal of Virology: an Official Organ of Indian Virological Society, 2012, 23, 70-74. | 0.7 | 13 |
| 29 | Isolation and Characterization of Cellulase Producing Bacterial Strains from an Amazonian Geothermal Spring in Peru. British Microbiology Research Journal, 2016, 15, 1-8. | 0.2 | 13 |
| 30 | Functional Implications and Clinical Potential of MicroRNAs in Irritable Bowel Syndrome: A Concise Review. Digestive Diseases and Sciences, 2023, 68, 38-53. | 2.3 | 12 |
| 31 | Insights from the genome of a high alkaline cellulase producing Aspergillus fumigatus strain obtained from Peruvian Amazon rainforest. Journal of Biotechnology, 2017, 251, 53-58. | 3.8 | 11 |
| 32 | Identification and characterization of microRNAs and their targets in high-altitude stress-adaptive plant maca (Lepidium meyenii Walp). 3 Biotech, 2017, 7, 103. | 2.2 | 11 |
| 33 | Genome-wide computational prediction and experimental validation of quinoa (<i>Chenopodium) Tj ETQq$1\ 1\ 0.7$</i> | '843]4 rg | BT ₁ Overlock |
| 34 | High-quality draft genome sequence of a biofilm forming lignocellulolytic Aspergillus niger strain ATCC 10864. Standards in Genomic Sciences, 2017, 12, 37. | 1.5 | 10 |
| 35 | First global transcriptome analysis of brown algae Macrocystis integrifolia (Phaeophyceae) under marine intertidal conditions. 3 Biotech, 2018, 8, 185. | 2.2 | 10 |
| 36 | Characterization of miRNAs from sardine (Sardina pilchardus Walbaum, 1792) and their tissue-specific expression analysis in brain and liver. 3 Biotech, 2020, 10, 318. | 2.2 | 8 |

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|----|---|------------------------|-------------|
| 37 | A Brief Review on the Regulatory Roles of MicroRNAs in Cystic Diseases and Their Use as Potential Biomarkers. Genes, 2022, 13, 191. | 2.4 | 8 |
| 38 | Engineered titania nanomaterials in advanced clinical applications. Beilstein Journal of Nanotechnology, 2022, 13, 201-218. | 2.8 | 8 |
| 39 | Developmentally regulated temporal expression and differential acid invertase activity in differentiating cotyledonary explants of mungbean [Vigna radiata (L.) Wilczek]. Plant Cell, Tissue and Organ Culture, 2011, 107, 417-425. | 2.3 | 7 |
| 40 | A de novo transcriptomic approach to study the influence of marine water depth in Macrocystis pyrifera alginate production. Aquatic Botany, 2020, 163, 103211. | 1.6 | 7 |
| 41 | Metagenomic Analysis of Microbial Communities in the Soil-mousse Surrounding of an Amazonian Geothermal Spring in Peru. British Biotechnology Journal, 2016, 15, 1-11. | 0.4 | 7 |
| 42 | Genome Wide Computational Identification of Tuna (Thunnus orientalis) MicroRNAs and Their Targets. Ocean Science Journal, 2018, 53, 727-734. | 1.3 | 6 |
| 43 | In silico Characterization of microRNAs and Their Target Transcripts from Cranberry (Vaccinium) Tj ETQq1 | l 0.784314 rgBT 0.5 | /Qverlock 1 |
| 44 | Characterization of microRNAs from neem (Azadirachta indica) and their tissue-specific expression study in leaves and stem. 3 Biotech, 2021, 11, 277. | 2,2 | 6 |
| 45 | The regulatory activities of microRNAs in non-vascular plants: a mini review. Planta, 2021, 254, 57. | 3.2 | 6 |
| 46 | Analysis of coat protein gene sequences of begomoviruses associated with different weed species in India. Phytoparasitica, 2012, 40, 95-100. | 1,2 | 5 |
| 47 | Evolutionary Pattern of Interferon Alpha Genes in Bovidae and Genetic Diversity of IFNAA in the Bovine Genome. Frontiers in Immunology, 2020, 11, 580412. | 4.8 | 5 |
| 48 | Tumor Suppressor microRNAs in Gastrointestinal Cancers: A Mini-Review. Recent Advances in Inflammation & Allergy Drug Discovery, 2022, 16, 5-15. | 0.8 | 5 |
| 49 | Molecular evidence for existence of a New World begomovirus associated with yellow mosaic disease of Corchorus capsularis in India. Australasian Plant Disease Notes, 2008, 3, 59-62. | 0.7 | 4 |
| 50 | Genome-wide Characterization of MicroRNAs from Mungbean (Vigna radiata L.). Biotechnology Journal International, 2017, 17, 1-9. | 0.2 | 3 |
| 51 | Impact of smokingâ€induced dysregulated human miRNAs in chronic disease development and their potential use in prognostic and therapeutic purposes. Journal of Biochemical and Molecular Toxicology, 0, , . | 3.0 | 3 |
| 52 | Cell Cultures and Hairy Roots as Platform for Production of High-Value Metabolites: Current Approaches, Limitations, and Future Prospects. , 2019, , 23-57. | | 2 |
| 53 | Insight into the genome data of commercially important giant kelp Macrocystis pyrifera. Data in Brief, 2022, 42, 108068. | 1.0 | 2 |
| 54 | The elusive roles of chloroplast microRNAs: an unexplored facet of the plant transcriptome. Plant Molecular Biology, 2022, 109, 667-671. | 3.9 | 2 |

SUJAY PAUL

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|----|---|-----|-----------|
| 55 | A peep into the transcriptome studies of the industrially important brown algae with special focus on Macrocystis genus. Revista Peruana De Biologia, 2020, 27, 049-053. | 0.3 | 1 |
| 56 | Extraction of Small RNA and qPCR Validation of miRNAs in Vigna mungo. Bio-protocol, 2015, 5 , . | 0.4 | 1 |
| 57 | Mungbean Yellow Mosaic India Virus (MYMIV)-infection, Small RNA Library Construction and Deep Sequencing for MicroRNA Identification in Vigna mungo. Bio-protocol, 2016, 6, . | 0.4 | 0 |