

# Mohit Kumar Swarnkar

## List of Publications by Year in descending order

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29  
papers

968  
citations

516710

16  
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477307

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docs citations

29  
times ranked

1427  
citing authors

#	ARTICLE	IF	CITATIONS
1	Expression of SOD and APX genes positively regulates secondary cell wall biosynthesis and promotes plant growth and yield in Arabidopsis under salt stress. <i>Plant Molecular Biology</i> , 2015, 87, 615-631.	3.9	183
2	Protein Model Discrimination Using Mutational Sensitivity Derived from Deep Sequencing. <i>Structure</i> , 2012, 20, 371-381.	3.3	83
3	Comprehensive transcriptome analysis of <i>Crocus sativus</i> for discovery and expression of genes involved in apocarotenoid biosynthesis. <i>BMC Genomics</i> , 2015, 16, 698.	2.8	81
4	Transcriptome Analysis Reveals Candidate Genes involved in Blister Blight defense in Tea ( <i>Camellia</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.3	78
5	Comprehensive transcriptomic study on horse gram ( <i>Macrotyloma uniflorum</i> ): De novo assembly, functional characterization and comparative analysis in relation to drought stress. <i>BMC Genomics</i> , 2013, 14, 647.	2.8	71
6	Molecular dissection of transcriptional reprogramming of steviol glycosides synthesis in leaf tissue during developmental phase transitions in <i>Stevia rebaudiana</i> Bert. <i>Scientific Reports</i> , 2017, 7, 11835.	3.3	51
7	A Sequence-Based Variation Map of Zebrafish. <i>Zebrafish</i> , 2013, 10, 15-20.	1.1	40
8	Complete genome sequence of <i>Arthrobacter</i> sp. ERGS1:01, a putative novel bacterium with prospective cold active industrial enzymes, isolated from East Rathong glacier in India. <i>Journal of Biotechnology</i> , 2015, 214, 139-140.	3.8	37
9	Transcriptome and Co-Expression Network Analyses Identify Key Genes Regulating Nitrogen Use Efficiency in <i>Brassica juncea</i> L.. <i>Scientific Reports</i> , 2018, 8, 7451.	3.3	37
10	Transcriptome sequencing of rhizome tissue of <i>Sinopodophyllum hexandrum</i> at two temperatures. <i>BMC Genomics</i> , 2014, 15, 871.	2.8	35
11	De Novo Transcriptome Sequencing and Analysis for <i>Venturia inaequalis</i> , the Devastating Apple Scab Pathogen. <i>PLoS ONE</i> , 2013, 8, e53937.	2.5	32
12	Complete genome sequence of <i>Arthrobacter alpinus</i> ERGS4:06, a yellow pigmented bacterium tolerant to cold and radiations isolated from Sikkim Himalaya. <i>Journal of Biotechnology</i> , 2016, 220, 86-87.	3.8	30
13	Complete Genome Sequencing of Protease-Producing Novel <i>Arthrobacter</i> sp. Strain IHBB 11108 Using PacBio Single-Molecule Real-Time Sequencing Technology. <i>Genome Announcements</i> , 2015, 3, .	0.8	23
14	Chilling Affects Phytohormone and Post-Embryonic Development Pathways during Bud Break and Fruit Set in Apple ( <i>Malus domestica</i> Borkh.). <i>Scientific Reports</i> , 2017, 7, 42593.	3.3	22
15	De novo transcriptome provides insights into the growth behaviour and resveratrol and trans-stilbenes biosynthesis in <i>Dactylorhiza hatagirea</i> - An endangered alpine terrestrial orchid of western Himalaya. <i>Scientific Reports</i> , 2019, 9, 13133.	3.3	20
16	Genome Assembly of <i>Chryseobacterium polytrichastri</i> ERM1:04, a Psychrotolerant Bacterium with Cold Active Proteases, Isolated from East Rathong Glacier in India. <i>Genome Announcements</i> , 2015, 3, .	0.8	18
17	Deciphering key regulators involved in epilepsy-induced cardiac damage through whole transcriptome and proteome analysis in a rat model. <i>Epilepsia</i> , 2021, 62, 504-516.	5.1	17
18	Complete Genome Sequence of Potential Probiotic <i>Lactobacillus</i> sp. HFC8, Isolated from Human Gut Using PacBio SMRT Sequencing. <i>Genome Announcements</i> , 2015, 3, .	0.8	14

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19	Paenibacillus ihbetae sp. nov., a cold-adapted antimicrobial producing bacterium isolated from high altitude Suraj Tal Lake in the Indian trans-Himalayas. Systematic and Applied Microbiology, 2017, 40, 430-439.	2.8	14
20	First complete genome sequence of a species in the genus Microterricola, an extremophilic cold active enzyme producing bacterial strain ERGS5:02 isolated from Sikkim Himalaya. Journal of Biotechnology, 2016, 222, 17-18.	3.8	13
21	Prickle morphogenesis in rose is coupled with secondary metabolite accumulation and governed by canonical MBW transcriptional complex. Plant Direct, 2021, 5, e00325.	1.9	13
22	Complete genome sequence of a low-temperature active and alkaline-stable endoglucanase-producing Paenibacillus sp. strain IHB B 3084 from the Indian Trans-Himalayas. Journal of Biotechnology, 2016, 230, 1-2.	3.8	11
23	Comparative transcriptome analysis of Rheum australe, an endangered medicinal herb, growing in its natural habitat and those grown in controlled growth chambers. Scientific Reports, 2021, 11, 3702.	3.3	11
24	Genome assembly of Chryseobacterium sp. strain IHBB 10212 from glacier top-surface soil in the Indian trans-Himalayas with potential for hydrolytic enzymes. Genomics Data, 2017, 13, 46-49.	1.3	9
25	Draft Genome Sequence of a Cellulase-Producing Psychrotrophic Paenibacillus Strain, IHB B 3415, Isolated from the Cold Environment of the Western Himalayas, India. Genome Announcements, 2015, 3, .	0.8	8
26	Complete Genome Sequence of the Rhizobacterium Pseudomonas trivialis Strain IHBB745 with Multiple Plant Growth-Promoting Activities and Tolerance to Desiccation and Alkalinity. Genome Announcements, 2015, 3, .	0.8	8
27	Complete Genome Sequence of Paenibacillus sp. Strain IHBB 10380 Using PacBio Single-Molecule Real-Time Sequencing Technology. Genome Announcements, 2015, 3, .	0.8	4
28	Genome Sequence of a Potential Probiotic Strain, Lactobacillus fermentum HFB3, Isolated from a Human Gut. Genome Announcements, 2015, 3, .	0.8	3
29	Draft Genome Sequence of Psychrotrophic <i>Acinetobacter</i> sp. Strain MN12 (MTCC 10786), Which Produces a Low-Temperature-Active and Alkaline-Stable Peptidase. Genome Announcements, 2014, 2, .	0.8	2