

# Dhurvas Chandrasekaran Dinesh

## List of Publications by Year in descending order

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13  
papers

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1040056

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1125743

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docs citations

13  
times ranked

1597  
citing authors

#	ARTICLE	IF	CITATIONS
1	Iron-Dependent Callose Deposition Adjusts Root Meristem Maintenance to Phosphate Availability. <i>Developmental Cell</i> , 2015, 33, 216-230.	7.0	271
2	Structural basis of RNA recognition by the SARS-CoV-2 nucleocapsid phosphoprotein. <i>PLoS Pathogens</i> , 2020, 16, e1009100.	4.7	206
3	Arabidopsis Calmodulin-binding Protein IQ67-Domain 1 Localizes to Microtubules and Interacts with Kinesin Light Chain-related Protein-1. <i>Journal of Biological Chemistry</i> , 2013, 288, 1871-1882.	3.4	116
4	Structure-based virtual screening and molecular dynamics simulation of SARS-CoV-2 Guanine-N7 methyltransferase (nsp14) for identifying antiviral inhibitors against COVID-19. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 4582-4593.	3.5	73
5	Solution structure of the PsIAA4 oligomerization domain reveals interaction modes for transcription factors in early auxin response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6230-6235.	7.1	52
6	Structural Biology of Nuclear Auxin Action. <i>Trends in Plant Science</i> , 2016, 21, 302-316.	8.8	45
7	Microsecond MD Simulation and Multiple-Conformation Virtual Screening to Identify Potential Anti-COVID-19 Inhibitors Against SARS-CoV-2 Main Protease. <i>Frontiers in Chemistry</i> , 2020, 8, 595273.	3.6	32
8	Antiviral Drug Targets of Single-Stranded RNA Viruses Causing Chronic Human Diseases. <i>Current Drug Targets</i> , 2020, 21, 105-124.	2.1	18
9	High-Throughput Screening and Quantum Mechanics for Identifying Potent Inhibitors Against Mac1 Domain of SARS-CoV-2 Nsp3. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1262-1270.	3.0	17
10	An <i>in silico</i> molecular dynamics simulation study on the inhibitors of SARS-CoV-2 proteases (3CL <sup>pro</sup> and PL <sup>pro</sup> ) to combat COVID-19. <i>Molecular Simulation</i> , 2021, 47, 1168-1184.	2.0	10
11	Structural insights of macromolecules involved in bacteria-induced apoptosis in the pathogenesis of human diseases. <i>Advances in Protein Chemistry and Structural Biology</i> , 2021, 126, 1-38.	2.3	5
12	Structural Understanding of SARS-CoV-2 Drug Targets, Active Site Contour Map Analysis and COVID-19 Therapeutics. <i>Current Molecular Pharmacology</i> , 2021, 14, .	1.5	4
13	Molecular Insights into Agonist/Antagonist Effects on Macromolecules Involved in Human Disease Mechanisms. <i>Current Molecular Pharmacology</i> , 2022, 15, 263-264.	1.5	2