

# Sandeep Chakraborty

## List of Publications by Year in descending order

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42  
papers

1,016  
citations

623734

14  
h-index

477307

29  
g-index

54  
all docs

54  
docs citations

54  
times ranked

1101  
citing authors

#	ARTICLE	IF	CITATIONS
1	The walnut ( <i>Juglans regia</i> ) genome sequence reveals diversity in genes coding for the biosynthesis of non-structural polyphenols. <i>Plant Journal</i> , 2016, 87, 507-532.	5.7	233
2	High-quality chromosome-scale assembly of the walnut ( <i>Juglans regia</i> L.) reference genome. <i>GigaScience</i> , 2020, 9, .	6.4	83
3	The Type II Secreted Lipase/Esterase LesA is a Key Virulence Factor Required for <i>Xylella fastidiosa</i> Pathogenesis in Grapevines. <i>Scientific Reports</i> , 2016, 6, 18598.	3.3	80
4	Genomic Variation Among and Within Six <i>Juglans</i> Species. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2153-2165.	1.8	73
5	Sequencing a <i>Juglans regia</i> × <i>J. microcarpa</i> hybrid yields high-quality genome assemblies of parental species. <i>Horticulture Research</i> , 2019, 6, 55.	6.3	67
6	The Secreted Protease PrtA Controls Cell Growth, Biofilm Formation and Pathogenicity in <i>Xylella fastidiosa</i> . <i>Scientific Reports</i> , 2016, 6, 31098.	3.3	42
7	Active Site Detection by Spatial Conformity and Electrostatic Analysis—Unravelling a Proteolytic Function in Shrimp Alkaline Phosphatase. <i>PLoS ONE</i> , 2011, 6, e28470.	2.5	41
8	Deep RNA-Seq profile reveals biodiversity, plant-microbe interactions and a large family of NBS-LRR resistance genes in walnut ( <i>Juglans regia</i> ) tissues. <i>AMB Express</i> , 2016, 6, 12.	3.0	39
9	A Measure of the Promiscuity of Proteins and Characteristics of Residues in the Vicinity of the Catalytic Site That Regulate Promiscuity. <i>PLoS ONE</i> , 2012, 7, e32011.	2.5	36
10	Molecular Profiling of Pierce's Disease Outlines the Response Circuitry of <i>Vitis vinifera</i> to <i>Xylella fastidiosa</i> Infection. <i>Frontiers in Plant Science</i> , 2018, 9, 771.	3.6	35
11	Inhibition of a cold-active alkaline phosphatase by imipenem revealed by <i>in silico</i> modeling of metallo- $\beta$ -lactamase active sites. <i>FEBS Letters</i> , 2012, 586, 3710-3715.	2.8	28
12	An Automated Flow for Directed Evolution Based on Detection of Promiscuous Scaffolds Using Spatial and Electrostatic Properties of Catalytic Residues. <i>PLoS ONE</i> , 2012, 7, e40408.	2.5	22
13	A Computational Module Assembled from Different Protease Family Motifs Identifies PI PLC from <i>Bacillus cereus</i> as a Putative Prolyl Peptidase with a Serine Protease Scaffold. <i>PLoS ONE</i> , 2013, 8, e70923.	2.5	21
14	Promiscuity-Based Enzyme Selection for Rational Directed Evolution Experiments. <i>Methods in Molecular Biology</i> , 2013, 978, 205-216.	0.9	20
15	The plant-based chimeric antimicrobial protein SIP14a-PPC20 protects tomato against bacterial wilt disease caused by <i>Ralstonia solanacearum</i> . <i>Plant Science</i> , 2019, 280, 197-205.	3.6	16
16	A Measure of the Broad Substrate Specificity of Enzymes Based on "Duplicate" Catalytic Residues. <i>PLoS ONE</i> , 2012, 7, e49313.	2.5	14
17	Sequence/structural analysis of xylem proteome emphasizes pathogenesis-related proteins, chitinases and $\beta$ -1, 3-glucanases as key players in grapevine defense against <i>Xylella fastidiosa</i> . <i>PeerJ</i> , 2016, 4, e2007.	2.0	14
18	A single amino acid substitution in the $\beta$ -like loop of <i>E. coli</i> PBP5 disrupts its ability to maintain cell shape and intrinsic beta-lactam resistance. <i>Microbiology (United Kingdom)</i> , 2015, 161, 895-902.	1.8	13

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19	Protein structure quality assessment based on the distance profiles of consecutive backbone C $\hat{\alpha}$ atoms. F1000Research, 2013, 2, 211.	1.6	12
20	Computational analysis of perturbations in the post-fusion Dengue virus envelope protein highlights known epitopes and conserved residues in the Zika virus. F1000Research, 2016, 5, 1150.	1.6	12
21	YeATS - a tool suite for analyzing RNA-seq derived transcriptome identifies a highly transcribed putative extensin in heartwood/sapwood transition zone in black walnut. F1000Research, 2015, 4, 155.	1.6	10
22	MEPPitope: spatial, electrostatic and secondary structure perturbations in the post-fusion Dengue virus envelope protein highlights known epitopes and conserved residues in the Zika virus. F1000Research, 2016, 5, 1150.	1.6	10
23	Dipeptidyl peptidase-IV inhibitors used in type-2 diabetes inhibit a phospholipase C: a case of promiscuous scaffolds in proteins. F1000Research, 0, 2, 286.	1.6	8
24	Structural phylogeny by profile extraction and multiple superimposition using electrostatic congruence as a discriminator. Intrinsically Disordered Proteins, 2013, 1, e25463.	1.9	7
25	The dipeptidyl peptidase IV inhibitors vildagliptin and K-579 inhibit a phospholipase C: a case of promiscuous scaffolds in proteins. F1000Research, 2013, 2, 286.	1.6	7
26	DOCLASP - Docking ligands to target proteins using spatial and electrostatic congruence extracted from a known holoenzyme and applying simple geometrical transformations. F1000Research, 2014, 3, 262.	1.6	7
27	YeATSAM analysis of the walnut and chickpea transcriptome reveals key genes undetected by current annotation tools. F1000Research, 2016, 5, 2689.	1.6	7
28	A Quantitative Measure of Electrostatic Perturbation in Holo and Apo Enzymes Induced by Structural Changes. PLoS ONE, 2013, 8, e59352.	2.5	6
29	Enumerating Pathways of Proton Abstraction Based on a Spatial and Electrostatic Analysis of Residues in the Catalytic Site. PLoS ONE, 2012, 7, e39577.	2.5	5
30	The electrostatic profile of consecutive C $\hat{\alpha}$ atoms applied to protein structure quality assessment. F1000Research, 2013, 2, 243.	1.6	5
31	The electrostatic profile of consecutive C $\hat{\alpha}$ atoms applied to protein structure quality assessment. F1000Research, 2013, 2, 243.	1.6	4
32	DOCLASP - Docking ligands to target proteins using spatial and electrostatic congruence extracted from a known holoenzyme and applying simple geometrical transformations. F1000Research, 2014, 3, 262.	1.6	4
33	RNA-seq assembler artifacts can bias expression counts and differential expression analysis - case study on the chickpea transcriptome emphasizes importance of freely accessible data for reproducibility. F1000Research, 0, 5, 2394.	1.6	4
34	Inconclusive studies on possible CRISPR-Cas off-targets should moderate expectations about enzymes that have evolved to be non-specific. Journal of Biosciences, 2018, 43, 225-228.	1.1	3
35	PREMONITION - Preprocessing motifs in protein structures for search acceleration. F1000Research, 0, 3, 217.	1.6	3
36	DOCLASP - Docking ligands to target proteins using spatial and electrostatic congruence extracted from a known holoenzyme and applying simple geometrical transformations. F1000Research, 0, 3, 262.	1.6	2

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37	Inconclusive studies on possible CRISPR-Cas off-targets should moderate expectations about enzymes that have evolved to be non-specific. <i>Journal of Biosciences</i> , 2018, 43, 225-228.	1.1	2
38	Directed evolution induces tributyrin hydrolysis in a virulence factor of <i>Xylella fastidiosa</i> using a duplicated gene as a template. <i>F1000Research</i> , 2014, 3, 215.	1.6	1
39	The electrostatic profile of consecutive C $\hat{\alpha}$ atoms applied to protein structure quality assessment. <i>F1000Research</i> , 0, 2, 243.	1.6	1
40	Promiscuous scaffolds in proteins - non-native, non-additive and non-trivial. <i>F1000Research</i> , 0, 2, 260.	1.6	0
41	Promiscuous scaffolds in proteins - non-native, non-additive and non-trivial. <i>F1000Research</i> , 0, 2, 260.	1.6	0
42	RNA-seq assembler artifacts can bias expression counts and differential expression analysis - application of YeATS on the chickpea transcriptome. <i>F1000Research</i> , 0, 5, 2394.	1.6	0