

# Sandeep Chakraborty

## List of Publications by Year in descending order

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Version: 2024-02-01

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	High-quality chromosome-scale assembly of the walnut ( <i>Juglans regia</i> L.) reference genome. <i>GigaScience</i> , 2020, 9, .	6.4	83
2	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
3	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
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	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
6	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	3
7	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
8	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
9	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
10	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
11	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
12	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. <i>F1000Research</i> , 2016, 5, 1150.	1.6	10
13	Computational analysis of perturbations in the post-fusion Dengue virus envelope protein highlights known epitopes and conserved residues in the Zika virus. <i>F1000Research</i> , 2016, 5, 1150.	1.6	12
14	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
15	YeATSAM analysis of the walnut and chickpea transcriptome reveals key genes undetected by current annotation tools. <i>F1000Research</i> , 2016, 5, 2689.	1.6	7
16	A single amino acid substitution in the $\beta$ -lactamase-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
17	YeATS - a tool suite for analyzing RNA-seq derived transcriptome identifies a highly transcribed putative extensin in heartwood/sapwood transition zone in black walnut. <i>F1000Research</i> , 2015, 4, 155.	1.6	10
18	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

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19	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
20	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
21	Promiscuity-Based Enzyme Selection for Rational Directed Evolution Experiments. Methods in Molecular Biology, 2013, 978, 205-216.	0.9	20
22	Structural phylogeny by profile extraction and multiple superimposition using electrostatic congruence as a discriminator. Intrinsically Disordered Proteins, 2013, 1, e25463.	1.9	7
23	Protein structure quality assessment based on the distance profiles of consecutive backbone C $\alpha$ atoms. F1000Research, 2013, 2, 211.	1.6	12
24	A Quantitative Measure of Electrostatic Perturbation in Holo and Apo Enzymes Induced by Structural Changes. PLoS ONE, 2013, 8, e59352.	2.5	6
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	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. PLoS ONE, 2013, 8, e70923.	2.5	21
27	The electrostatic profile of consecutive C $\alpha$ atoms applied to protein structure quality assessment. F1000Research, 2013, 2, 243.	1.6	5
28	The electrostatic profile of consecutive C $\alpha$ atoms applied to protein structure quality assessment. F1000Research, 2013, 2, 243.	1.6	4
29	Inhibition of a cold-active alkaline phosphatase by imipenem revealed by <i>in silico</i> modeling of metallo- $\beta$ -lactamase active sites. FEBS Letters, 2012, 586, 3710-3715.	2.8	28
30	A Measure of the Promiscuity of Proteins and Characteristics of Residues in the Vicinity of the Catalytic Site That Regulate Promiscuity. PLoS ONE, 2012, 7, e32011.	2.5	36
31	A Measure of the Broad Substrate Specificity of Enzymes Based on "Duplicate"™ Catalytic Residues. PLoS ONE, 2012, 7, e49313.	2.5	14
32	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
33	An Automated Flow for Directed Evolution Based on Detection of Promiscuous Scaffolds Using Spatial and Electrostatic Properties of Catalytic Residues. PLoS ONE, 2012, 7, e40408.	2.5	22
34	Active Site Detection by Spatial Conformity and Electrostatic Analysis—Unravelling a Proteolytic Function in Shrimp Alkaline Phosphatase. PLoS ONE, 2011, 6, e28470.	2.5	41
35	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
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

#	ARTICLE	IF	CITATIONS
37	Promiscuous scaffolds in proteins - non-native, non-additive and non-trivial. F1000Research, 0, 2, 260.	1.6	0
38	The electrostatic profile of consecutive C $\hat{\alpha}$ 2 atoms applied to protein structure quality assessment. F1000Research, 0, 2, 243.	1.6	1
39	Promiscuous scaffolds in proteins - non-native, non-additive and non-trivial. F1000Research, 0, 2, 260.	1.6	0
40	PREMONITION - Preprocessing motifs in protein structures for search acceleration. F1000Research, 0, 3, 217.	1.6	3
41	RNA-seq assembler artifacts can bias expression counts and differential expression analysis - application of YeATS on the chickpea transcriptome. F1000Research, 0, 5, 2394.	1.6	0
42	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