

# Sudipto Saha

## List of Publications by Year in descending order

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Version: 2024-02-01

73  
papers

3,613  
citations

279798

23  
h-index

144013

57  
g-index

73  
all docs

73  
docs citations

73  
times ranked

4549  
citing authors

#	ARTICLE	IF	CITATIONS
1	LHSPred: A web based application for predicting lung health severity. <i>Biomedical Signal Processing and Control</i> , 2022, 77, 103745.	5.7	2
2	Soybean lectin induces autophagy through P2RX7 dependent activation of NF- $\kappa$ B-ROS pathway to kill intracellular mycobacteria. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2021, 1865, 129806.	2.4	10
3	Genome-wide analysis of Indian SARS-CoV-2 genomes to identify T-cell and B-cell epitopes from conserved regions based on immunogenicity and antigenicity. <i>International Immunopharmacology</i> , 2021, 91, 107276.	3.8	5
4	Disruption of redox homeostasis with synchronized activation of apoptosis highlights the antifilarial efficacy of novel piperine derivatives: An in vitro mechanistic approach. <i>Free Radical Biology and Medicine</i> , 2021, 169, 343-360.	2.9	3
5	Cloning and immunobiochemical analyses on recombinant chymopapain allergen Cari p 2 showing pollen-fruit cross-reaction. <i>Molecular Immunology</i> , 2021, 137, 42-51.	2.2	5
6	DAAB $\alpha$ V2: Updated database of allergy and asthma biomarkers. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021, 76, 3829-3832.	5.7	2
7	RegX3 Activates whiB3 Under Acid Stress and Subverts Lysosomal Trafficking of Mycobacterium tuberculosis in a WhiB3-Dependent Manner. <i>Frontiers in Microbiology</i> , 2020, 11, 572433.	3.5	10
8	Purification and biochemical characterization of Hel a 6, a cross-reactive pectate lyase allergen from Sunflower ( <i>Helianthus annuus</i> L.) pollen. <i>Scientific Reports</i> , 2020, 10, 20177.	3.3	8
9	Survey of drug resistance associated gene mutations in Mycobacterium tuberculosis, ESKAPE and other bacterial species. <i>Scientific Reports</i> , 2020, 10, 8957.	3.3	37
10	PSCRIdb: A database of regulatory interactions and networks of pluripotent stem cell lines. <i>Journal of Biosciences</i> , 2020, 45, 1.	1.1	4
11	Editorial: Integrated Omics for Defining Interactomes. <i>Frontiers in Physiology</i> , 2020, 11, 81.	2.8	0
12	Regulatory role of SphK1 in TLR7/9 $\alpha$ dependent type I interferon response and autoimmunity. <i>FASEB Journal</i> , 2020, 34, 4329-4347.	0.5	16
13	Computational approach to target USP28 for regulating Myc. <i>Computational Biology and Chemistry</i> , 2020, 85, 107208.	2.3	5
14	Systems Immunology Approach in Understanding the Association of Allergy and Cancer. , 2020, , 53-72.		0
15	Machine-learning techniques for the prediction of protein $\alpha$ protein interactions. <i>Journal of Biosciences</i> , 2019, 44, 1.	1.1	53
16	<p>Pilot-Scale Study Of Human Plasma Proteomics Identifies ApoE And IL33 As Markers In Atopic Asthma</p>. <i>Journal of Asthma and Allergy</i> , 2019, Volume 12, 273-283.	3.4	14
17	The sensor kinase MtrB of Mycobacterium tuberculosis regulates hypoxic survival and establishment of infection. <i>Journal of Biological Chemistry</i> , 2019, 294, 19862-19876.	3.4	19
18	In silico modeling of phosphorylation dependent and independent c-Myc degradation. <i>BMC Bioinformatics</i> , 2019, 20, 230.	2.6	8

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19	Machine-learning techniques for the prediction of protein-protein interactions. <i>Journal of Biosciences</i> , 2019, 44, .	1.1	7
20	Host-Virus Protein Interaction Network Reveals the Involvement of Multiple Host Processes in the Life Cycle of Hepatitis E Virus. <i>MSystems</i> , 2018, 3, .	3.8	40
21	Integrative Omics for Interactomes. , 2018, , 39-49.		3
22	LMDIPred: A web-server for prediction of linear peptide sequences binding to SH3, WW and PDZ domains. <i>PLoS ONE</i> , 2018, 13, e0200430.	2.5	14
23	Global mapping of MtrA-binding sites links MtrA to regulation of its targets in <i>Mycobacterium tuberculosis</i> . <i>Microbiology (United Kingdom)</i> , 2018, 164, 99-110.	1.8	15
24	Modulating Interleukins and their Receptors Interactions with Small Chemicals Using In Silico Approach for Asthma. <i>Current Topics in Medicinal Chemistry</i> , 2018, 18, 1123-1134.	2.1	9
25	PPIMpred: a web server for high-throughput screening of small molecules targeting proteinâ€“protein interaction. <i>Royal Society Open Science</i> , 2017, 4, 160501.	2.4	13
26	Calcimycin mediates mycobacterial killing by inducing intracellular calcium-regulated autophagy in a P2RX7 dependent manner. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 3190-3200.	2.4	28
27	<i>Mycobacterium</i> heat shock protein 65 mediated metabolic shift in decidualization of human endometrial stromal cells. <i>Scientific Reports</i> , 2017, 7, 3942.	3.3	3
28	MYCbase: a database of functional sites and biochemical properties of Myc in both normal and cancer cells. <i>BMC Bioinformatics</i> , 2017, 18, 224.	2.6	10
29	SUMOylation pathway alteration coupled with downregulation of SUMO E2 enzyme at mucosal epithelium modulates inflammation in inflammatory bowel disease. <i>Open Biology</i> , 2017, 7, 170024.	3.6	36
30	Computational Framework for Prediction of Peptide Sequences That May Mediate Multiple Protein Interactions in Cancer-Associated Hub Proteins. <i>PLoS ONE</i> , 2016, 11, e0155911.	2.5	5
31	Computational Proteomics. , 2016, , 11-20.		0
32	Epitope Mapping of Rhi o 1 and Generation of a Hypoallergenic Variant. <i>Journal of Biological Chemistry</i> , 2016, 291, 18016-18029.	3.4	27
33	PluriPred: A Web server for predicting proteins involved in pluripotent network. <i>Journal of Biosciences</i> , 2016, 41, 743-750.	1.1	3
34	LMPID: A manually curated database of linear motifs mediating proteinâ€“protein interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	3.0	15
35	<scp>DAAB</scp>: a manually curated database of allergy and asthma biomarkers. <i>Clinical and Experimental Allergy</i> , 2015, 45, 1259-1261.	2.9	6
36	Purification, Cloning and Immuno-Biochemical Characterization of a Fungal Aspartic Protease Allergen Rhi o 1 from the Airborne Mold <i>Rhizopus oryzae</i> . <i>PLoS ONE</i> , 2015, 10, e0144547.	2.5	25

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37	Prediction of Intra-Species Protein-Protein Interactions in Enteropathogens Facilitating Systems Biology Study. PLoS ONE, 2015, 10, e0145648.	2.5	5
38	Adaptability in protein structures: structural dynamics and implications in ligand design. Journal of Biomolecular Structure and Dynamics, 2015, 33, 298-321.	3.5	8
39	Monitoring Newly Synthesized Proteins over the Adult Life Span of <i>Caenorhabditis elegans</i> . Journal of Proteome Research, 2015, 14, 1483-1494.	3.7	23
40	Metagenomic Surveys of Gut Microbiota. Genomics, Proteomics and Bioinformatics, 2015, 13, 148-158.	6.9	76
41	Dynamic Modularity of Host Protein Interaction Networks in Salmonella Typhi Infection. PLoS ONE, 2014, 9, e104911.	2.5	6
42	LncRBase: An Enriched Resource for lncRNA Information. PLoS ONE, 2014, 9, e108010.	2.5	60
43	Allergic asthma biomarkers using systems approaches. Frontiers in Genetics, 2014, 4, 308.	2.3	23
44	piRNAQuest: searching the piRNAome for silencers. BMC Genomics, 2014, 15, 555.	2.8	52
45	ringâ€hydroxylating oxygenase database: a database of bacterial aromatic ringâ€hydroxylating oxygenases in the management of bioremediation and biocatalysis of aromatic compounds. Environmental Microbiology Reports, 2014, 6, 519-523.	2.4	27
46	High Throughput Screen Identifies Small Molecule Inhibitors Specific for Mycobacterium tuberculosis Phosphoserine Phosphatase. Journal of Biological Chemistry, 2014, 289, 25149-25165.	3.4	38
47	In Silico Prediction of Allergenic Proteins. Methods in Molecular Biology, 2014, 1184, 375-388.	0.9	5
48	Allergen Databases. Methods in Molecular Biology, 2014, 1184, 165-181.	0.9	31
49	Prediction of Interactions between Viral and Host Proteins Using Supervised Machine Learning Methods. PLoS ONE, 2014, 9, e112034.	2.5	67
50	Systems Immunology. , 2013, , 2073-2078.		0
51	DNA and Chromatin Modification Networks Distinguish Stem Cell Pluripotent Ground States. Molecular and Cellular Proteomics, 2012, 11, 1036-1047.	3.8	15
52	Enhanced Energy Metabolism Contributes to the Extended Life Span of Calorie-restricted <i>Caenorhabditis elegans</i> . Journal of Biological Chemistry, 2012, 287, 31414-31426.	3.4	60
53	Network-based approaches for extending the Wnt signalling pathway and identifying context-specific sub-networks. International Journal of Computational Biology and Drug Design, 2012, 5, 185.	0.3	2
54	ROCS: a Reproducibility Index and Confidence Score for Interaction Proteomics Studies. BMC Bioinformatics, 2012, 13, 128.	2.6	9

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55	Computational Framework for Analysis of Prey-Prey Associations in Interaction Proteomics Identifies Novel Human Protein-Protein Interactions and Networks. <i>Journal of Proteome Research</i> , 2012, 11, 4476-4487.	3.7	3
56	Systematic discovery of condition specific Wnt signaling subnetworks. , 2011, , .		1
57	c-Maf-Dependent Growth of <i>Mycobacterium tuberculosis</i> in a CD14hi Subpopulation of Monocyte-Derived Macrophages. <i>Journal of Immunology</i> , 2011, 186, 1638-1645.	0.8	14
58	The Bait Compatibility Index: Computational Bait Selection for Interaction Proteomics Experiments. <i>Journal of Proteome Research</i> , 2010, 9, 4972-4981.	3.7	7
59	Dissecting the human plasma proteome and inflammatory response biomarkers. <i>Proteomics</i> , 2009, 9, 470-484.	2.2	20
60	HIP2: An online database of human plasma proteins from healthy individuals. <i>BMC Medical Genomics</i> , 2008, 1, 12.	1.5	28
61	Prediction Methods for B-cell Epitopes. <i>Methods in Molecular Biology</i> , 2007, 409, 387-394.	0.9	106
62	Support Vector Machine-based method for predicting subcellular localization of mycobacterial proteins using evolutionary information and motifs. <i>BMC Bioinformatics</i> , 2007, 8, 337.	2.6	121
63	Predicting Virulence Factors of Immunological Interest. <i>Methods in Molecular Biology</i> , 2007, 409, 407-415.	0.9	3
64	Searching and Mapping of B-Cell Epitopes in Bcipep Database. <i>Methods in Molecular Biology</i> , 2007, 409, 113-124.	0.9	12
65	Prediction of neurotoxins based on their function and source. <i>In Silico Biology</i> , 2007, 7, 369-87.	0.9	19
66	VICMpred: An SVM-based Method for the Prediction of Functional Proteins of Gram-negative Bacteria Using Amino Acid Patterns and Composition. <i>Genomics, Proteomics and Bioinformatics</i> , 2006, 4, 42-47.	6.9	111
67	VGIchan: Prediction and Classification of Voltage-Gated Ion Channels. <i>Genomics, Proteomics and Bioinformatics</i> , 2006, 4, 253-258.	6.9	25
68	Prediction of continuous B-cell epitopes in an antigen using recurrent neural network. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 40-48.	2.6	1,146
69	AlgPred: prediction of allergenic proteins and mapping of IgE epitopes. <i>Nucleic Acids Research</i> , 2006, 34, W202-W209.	14.5	612
70	Bcipep: A database of B-cell epitopes. <i>BMC Genomics</i> , 2005, 6, 79.	2.8	179
71	BcePred: Prediction of Continuous B-Cell Epitopes in Antigenic Sequences Using Physico-chemical Properties. <i>Lecture Notes in Computer Science</i> , 2004, , 197-204.	1.3	226
72	Effect of Diet on Enzyme Profile, Biochemical Changes and In sacco Degradability of Feeds in the Rumen of Buffalo. <i>Asian-Australasian Journal of Animal Sciences</i> , 2003, 16, 374-379.	2.4	9

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73	Prediction of allergenic proteins and mapping of IgE epitopes in allergens. Protocol Exchange, 0, , .	0.3	4