

# 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	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
2	AlgPred: prediction of allergenic proteins and mapping of IgE epitopes. <i>Nucleic Acids Research</i> , 2006, 34, W202-W209.	14.5	612
3	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
4	Bcipep: A database of B-cell epitopes. <i>BMC Genomics</i> , 2005, 6, 79.	2.8	179
5	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
6	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
7	Prediction Methods for B-cell Epitopes. <i>Methods in Molecular Biology</i> , 2007, 409, 387-394.	0.9	106
8	Metagenomic Surveys of Gut Microbiota. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 148-158.	6.9	76
9	Prediction of Interactions between Viral and Host Proteins Using Supervised Machine Learning Methods. <i>PLoS ONE</i> , 2014, 9, e112034.	2.5	67
10	Enhanced Energy Metabolism Contributes to the Extended Life Span of Calorie-restricted <i>Caenorhabditis elegans</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 31414-31426.	3.4	60
11	LncRBase: An Enriched Resource for lncRNA Information. <i>PLoS ONE</i> , 2014, 9, e108010.	2.5	60
12	Machine-learning techniques for the prediction of protein-protein interactions. <i>Journal of Biosciences</i> , 2019, 44, 1.	1.1	53
13	piRNAQuest: searching the piRNAome for silencers. <i>BMC Genomics</i> , 2014, 15, 555.	2.8	52
14	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
15	High Throughput Screen Identifies Small Molecule Inhibitors Specific for Mycobacterium tuberculosis Phosphoserine Phosphatase. <i>Journal of Biological Chemistry</i> , 2014, 289, 25149-25165.	3.4	38
16	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
17	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
18	Allergen Databases. <i>Methods in Molecular Biology</i> , 2014, 1184, 165-181.	0.9	31

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19	HIP2: An online database of human plasma proteins from healthy individuals. BMC Medical Genomics, 2008, 1, 12.	1.5	28
20	Calcimycin mediates mycobacterial killing by inducing intracellular calcium-regulated autophagy in a P2RX7 dependent manner. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 3190-3200.	2.4	28
21	<scp>R</scp>ingâ€<scp>H</scp>ydroxylating <scp>O</scp>xygenase 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
22	Epitope Mapping of Rhi o 1 and Generation of a Hypoallergenic Variant. Journal of Biological Chemistry, 2016, 291, 18016-18029.	3.4	27
23	VGIchan: Prediction and Classification of Voltage-Gated Ion Channels. Genomics, Proteomics and Bioinformatics, 2006, 4, 253-258.	6.9	25
24	Purification, Cloning and Immuno-Biochemical Characterization of a Fungal Aspartic Protease Allergen Rhi o 1 from the Airborne Mold Rhizopus oryzae. PLoS ONE, 2015, 10, e0144547.	2.5	25
25	Allergic asthma biomarkers using systems approaches. Frontiers in Genetics, 2014, 4, 308.	2.3	23
26	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
27	Dissecting the human plasma proteome and inflammatory response biomarkers. Proteomics, 2009, 9, 470-484.	2.2	20
28	The sensor kinase MtrB of Mycobacterium tuberculosis regulates hypoxic survival and establishment of infection. Journal of Biological Chemistry, 2019, 294, 19862-19876.	3.4	19
29	Prediction of neurotoxins based on their function and source. In Silico Biology, 2007, 7, 369-87.	0.9	19
30	Regulatory role of SphK1 in TLR7/9â€dependent type I interferon response and autoimmunity. FASEB Journal, 2020, 34, 4329-4347.	0.5	16
31	DNA and Chromatin Modification Networks Distinguish Stem Cell Pluripotent Ground States. Molecular and Cellular Proteomics, 2012, 11, 1036-1047.	3.8	15
32	LMPID: A manually curated database of linear motifs mediating proteinâ€protein interactions. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	3.0	15
33	Global mapping of MtrA-binding sites links MtrA to regulation of its targets in Mycobacterium tuberculosis. Microbiology (United Kingdom), 2018, 164, 99-110.	1.8	15
34	c-Mafâ€Dependent Growth of Mycobacterium tuberculosis in a CD14hi Subpopulation of Monocyte-Derived Macrophages. Journal of Immunology, 2011, 186, 1638-1645.	0.8	14
35	LMDIPred: A web-server for prediction of linear peptide sequences binding to SH3, WW and PDZ domains. PLoS ONE, 2018, 13, e0200430.	2.5	14
36	<p>Pilot-Scale Study Of Human Plasma Proteomics Identifies ApoE And IL33 As Markers In Atopic Asthma</p>. Journal of Asthma and Allergy, 2019, Volume 12, 273-283.	3.4	14

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37	PPIMpred: a web server for high-throughput screening of small molecules targeting protein-protein interaction. <i>Royal Society Open Science</i> , 2017, 4, 160501.	2.4	13
38	Searching and Mapping of B-Cell Epitopes in Bcipep Database. <i>Methods in Molecular Biology</i> , 2007, 409, 113-124.	0.9	12
39	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
40	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
41	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
42	ROCS: a Reproducibility Index and Confidence Score for Interaction Proteomics Studies. <i>BMC Bioinformatics</i> , 2012, 13, 128.	2.6	9
43	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
44	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
45	Adaptability in protein structures: structural dynamics and implications in ligand design. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 298-321.	3.5	8
46	In silico modeling of phosphorylation dependent and independent c-Myc degradation. <i>BMC Bioinformatics</i> , 2019, 20, 230.	2.6	8
47	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
48	The Bait Compatibility Index: Computational Bait Selection for Interaction Proteomics Experiments. <i>Journal of Proteome Research</i> , 2010, 9, 4972-4981.	3.7	7
49	Machine-learning techniques for the prediction of protein-protein interactions. <i>Journal of Biosciences</i> , 2019, 44, .	1.1	7
50	Dynamic Modularity of Host Protein Interaction Networks in Salmonella Typhi Infection. <i>PLoS ONE</i> , 2014, 9, e104911.	2.5	6
51	<sc>DAAB</sc>: a manually curated database of allergy and asthma biomarkers. <i>Clinical and Experimental Allergy</i> , 2015, 45, 1259-1261.	2.9	6
52	Prediction of Intra-Species Protein-Protein Interactions in Enteropathogens Facilitating Systems Biology Study. <i>PLoS ONE</i> , 2015, 10, e0145648.	2.5	5
53	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
54	Computational approach to target USP28 for regulating Myc. <i>Computational Biology and Chemistry</i> , 2020, 85, 107208.	2.3	5

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55	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
56	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
57	In Silico Prediction of Allergenic Proteins. <i>Methods in Molecular Biology</i> , 2014, 1184, 375-388.	0.9	5
58	PSCRdb: A database of regulatory interactions and networks of pluripotent stem cell lines. <i>Journal of Biosciences</i> , 2020, 45, 1.	1.1	4
59	Prediction of allergenic proteins and mapping of IgE epitopes in allergens. <i>Protocol Exchange</i> , 0, , .	0.3	4
60	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
61	PluriPred: A Web server for predicting proteins involved in pluripotent network. <i>Journal of Biosciences</i> , 2016, 41, 743-750.	1.1	3
62	Mycobacterial heat shock protein 65 mediated metabolic shift in decidualization of human endometrial stromal cells. <i>Scientific Reports</i> , 2017, 7, 3942.	3.3	3
63	Integrative Omics for Interactomes. , 2018, , 39-49.		3
64	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
65	Predicting Virulence Factors of Immunological Interest. <i>Methods in Molecular Biology</i> , 2007, 409, 407-415.	0.9	3
66	Network-based approaches for extending the Wnt signalling pathway and identifying context-specific sub-networks. <i>International Journal of Computational Biology and Drug Design</i> , 2012, 5, 185.	0.3	2
67	DAABv2: Updated database of allergy and asthma biomarkers. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021, 76, 3829-3832.	5.7	2
68	LHSPred: A web based application for predicting lung health severity. <i>Biomedical Signal Processing and Control</i> , 2022, 77, 103745.	5.7	2
69	Systematic discovery of condition specific Wnt signaling subnetworks. , 2011, , .		1
70	Computational Proteomics. , 2016, , 11-20.		0
71	Editorial: Integrated Omics for Defining Interactomes. <i>Frontiers in Physiology</i> , 2020, 11, 81.	2.8	0
72	Systems Immunology. , 2013, , 2073-2078.		0

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73	Systems Immunology Approach in Understanding the Association of Allergy and Cancer. , 2020, , 53-72.		0