

Sadhna Phanse

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

3,965
citations

218381

26
h-index

174990

52
g-index

58
all docs

58
docs citations

58
times ranked

6724
citing authors

#	ARTICLE	IF	CITATIONS
1	A Census of Human Soluble Protein Complexes. <i>Cell</i> , 2012, 150, 1068-1081.	13.5	781
2	Panorama of ancient metazoan macromolecular complexes. <i>Nature</i> , 2015, 525, 339-344.	13.7	478
3	Global Functional Atlas of Escherichia coli Encompassing Previously Uncharacterized Proteins. <i>PLoS Biology</i> , 2009, 7, e1000096.	2.6	331
4	A dual function of the CRISPR-Cas system in bacterial antiviral immunity and DNA repair. <i>Molecular Microbiology</i> , 2011, 79, 484-502.	1.2	241
5	eSGA: E. coli synthetic genetic array analysis. <i>Nature Methods</i> , 2008, 5, 789-795.	9.0	231
6	Interaction landscape of membrane-protein complexes in <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2012, 489, 585-589.	13.7	228
7	The binary protein-protein interaction landscape of <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2014, 32, 285-290.	9.4	218
8	Global landscape of cell envelope protein complexes in <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2018, 36, 103-112.	9.4	110
9	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. <i>Nature Methods</i> , 2015, 12, 725-731.	9.0	109
10	Quantitative Genome-Wide Genetic Interaction Screens Reveal Global Epistatic Relationships of Protein Complexes in <i>Escherichia coli</i> . <i>PLoS Genetics</i> , 2014, 10, e1004120.	1.5	96
11	Genetic Interaction Maps in <i>Escherichia coli</i> Reveal Functional Crosstalk among Cell Envelope Biogenesis Pathways. <i>PLoS Genetics</i> , 2011, 7, e1002377.	1.5	95
12	Actionable Cytopathogenic Host Responses of Human Alveolar Type 2 Cells to SARS-CoV-2. <i>Molecular Cell</i> , 2020, 80, 1104-1122.e9.	4.5	94
13	Human-Chromatin-Related Protein Interactions Identify a Demethylase Complex Required for Chromosome Segregation. <i>Cell Reports</i> , 2014, 8, 297-310.	2.9	72
14	Acyldepsipeptide Analogs Dysregulate Human Mitochondrial ClpP Protease Activity and Cause Apoptotic Cell Death. <i>Cell Chemical Biology</i> , 2018, 25, 1017-1030.e9.	2.5	72
15	EPIC: software toolkit for elution profile-based inference of protein complexes. <i>Nature Methods</i> , 2019, 16, 737-742.	9.0	67
16	BrainMap Elucidates the Macromolecular Connectivity Landscape of Mammalian Brain. <i>Cell Systems</i> , 2020, 10, 333-350.e14.	2.9	48
17	Features of the Chaperone Cellular Network Revealed through Systematic Interaction Mapping. <i>Cell Reports</i> , 2017, 20, 2735-2748.	2.9	47
18	A Map of Human Mitochondrial Protein Interactions Linked to Neurodegeneration Reveals New Mechanisms of Redox Homeostasis and NF- κ B Signaling. <i>Cell Systems</i> , 2017, 5, 564-577.e12.	2.9	44

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19	Identification of Human Neuronal Protein Complexes Reveals Biochemical Activities and Convergent Mechanisms of Action in Autism Spectrum Disorders. <i>Cell Systems</i> , 2015, 1, 361-374.	2.9	42
20	Mitochondrial Targets for Pharmacological Intervention in Human Disease. <i>Journal of Proteome Research</i> , 2015, 14, 5-21.	1.8	40
21	Novel function discovery with GeneMANIA: a new integrated resource for gene function prediction in <i>Escherichia coli</i> . <i>Bioinformatics</i> , 2015, 31, 306-310.	1.8	38
22	Rewiring of the Human Mitochondrial Interactome during Neuronal Reprogramming Reveals Regulators of the Respirasome and Neurogenesis. <i>IScience</i> , 2019, 19, 1114-1132.	1.9	38
23	Conditional Epistatic Interaction Maps Reveal Global Functional Rewiring of Genome Integrity Pathways in <i>Escherichia coli</i> . <i>Cell Reports</i> , 2016, 14, 648-661.	2.9	34
24	Systematic Genetic Screens Reveal the Dynamic Global Functional Organization of the Bacterial Translation Machinery. <i>Cell Reports</i> , 2016, 17, 904-916.	2.9	34
25	Efficient prediction of human protein-protein interactions at a global scale. <i>BMC Bioinformatics</i> , 2014, 15, 383.	1.2	32
26	Extracting high confidence protein interactions from affinity purification data: At the crossroads. <i>Journal of Proteomics</i> , 2015, 118, 63-80.	1.2	30
27	Chemical-genetic profiling reveals limited cross-resistance between antimicrobial peptides with different modes of action. <i>Nature Communications</i> , 2019, 10, 5731.	5.8	29
28	NleH Defines a New Family of Bacterial Effector Kinases. <i>Structure</i> , 2014, 22, 250-259.	1.6	28
29	Spindle Checkpoint Factors Bub1 and Bub2 Promote DNA Double-Strand Break Repair by Nonhomologous End Joining. <i>Molecular and Cellular Biology</i> , 2015, 35, 2448-2463.	1.1	21
30	ClpP protease activation results from the reorganization of the electrostatic interaction networks at the entrance pores. <i>Communications Biology</i> , 2019, 2, 410.	2.0	20
31	Scalable multiplex co-fractionation/mass spectrometry platform for accelerated protein interactome discovery. <i>Nature Communications</i> , 2022, 13, .	5.8	20
32	Yeast Mitochondrial Protein-Protein Interactions Reveal Diverse Complexes and Disease-Relevant Functional Relationships. <i>Journal of Proteome Research</i> , 2015, 14, 1220-1237.	1.8	18
33	Functional cooperativity between the trigger factor chaperone and the ClpXP proteolytic complex. <i>Nature Communications</i> , 2021, 12, 281.	5.8	16
34	Integrative network analysis of signaling in human CD34 ⁺ hematopoietic progenitor cells by global phosphoproteomic profiling using TiO ₂ enrichment combined with 2D LC-MS/MS and pathway mapping. <i>Proteomics</i> , 2013, 13, 1325-1333.	1.3	14
35	Systems analysis of the genetic interaction network of yeast molecular chaperones. <i>Molecular Omics</i> , 2018, 14, 82-94.	1.4	14
36	Assembly principles of the human R2TP chaperone complex reveal the presence of R2T and R2P complexes. <i>Structure</i> , 2022, 30, 156-171.e12.	1.6	13

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37	Insights from protein-protein interaction studies on bacterial pathogenesis. Expert Review of Proteomics, 2017, 14, 779-797.	1.3	11
38	Exploring the Impact of PARK2 Mutations on the Total and Mitochondrial Proteome of Human Skin Fibroblasts. Frontiers in Cell and Developmental Biology, 2020, 8, 423.	1.8	11
39	Mitochondria under the spotlight: On the implications of mitochondrial dysfunction and its connectivity to neuropsychiatric disorders. Computational and Structural Biotechnology Journal, 2020, 18, 2535-2546.	1.9	10
40	Ribosome-Dependent ATPase Interacts with Conserved Membrane Protein in Escherichia coli to Modulate Protein Synthesis and Oxidative Phosphorylation. PLoS ONE, 2011, 6, e18510.	1.1	10
41	ZapG (YhcB/DUF1043), a novel cell division protein in gamma-proteobacteria linking the Z-ring to septal peptidoglycan synthesis. Journal of Biological Chemistry, 2021, 296, 100700.	1.6	9
42	Human Soybean Allergies: Elucidation of the Seed Proteome and Comprehensive Protein-Protein Interaction Prediction. Journal of Proteome Research, 2021, 20, 4925-4947.	1.8	8
43	Development of a Method Combining Peptidiscs and Proteomics to Identify, Stabilize, and Purify a Detergent-Sensitive Membrane Protein Assembly. Journal of Proteome Research, 2022, 21, 1748-1758.	1.8	7
44	Misconnecting the dots: altered mitochondrial protein-protein interactions and their role in neurodegenerative disorders. Expert Review of Proteomics, 2020, 17, 119-136.	1.3	6
45	From fuzziness to precision medicine: on the rapidly evolving proteomics with implications in mitochondrial connectivity to rare human disease. iScience, 2021, 24, 102030.	1.9	6
46	Targeted protein identification, quantification and reporting for high-resolution nanoflow targeted peptide monitoring. Journal of Proteomics, 2013, 81, 159-172.	1.2	5
47	Proteome-wide dataset supporting the study of ancient metazoan macromolecular complexes. Data in Brief, 2016, 6, 715-721.	0.5	5
48	The conserved Tpk1 regulates non-homologous end joining double-strand break repair by phosphorylation of Nej1, a homolog of the human XLF. Nucleic Acids Research, 2021, 49, 8145-8160.	6.5	4
49	Novel Interactome of Saccharomyces cerevisiae Myosin Type II Identified by a Modified Integrated Membrane Yeast Two-Hybrid (iMYTH) Screen. G3: Genes, Genomes, Genetics, 2016, 6, 1469-1474.	0.8	3
50	A Gaussian process-based definition reveals new and bona fide genetic interactions compared to a multiplicative model in the Gram-negative Escherichia coli. Bioinformatics, 2020, 36, 880-889.	1.8	3
51	Auxotrophic and prototrophic conditional genetic networks reveal the rewiring of transcription factors in Escherichia coli. Nature Communications, 2022, 13, .	5.8	3
52	Macromolecular Connectivity Landscape of Mammalian Brain. SSRN Electronic Journal, 0, , .	0.4	1
53	Mechanistic Insight Regarding How NRF1 and NRF2 Protect Against Non-Alcoholic Steatohepatitis. Canadian Journal of Diabetes, 2021, 45, S8.	0.4	0