

Sadhna Phanse

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

49
papers

2,876
citations

22
h-index

53
g-index

58
ext. papers

3,557
ext. citations

11.9
avg, IF

3.94
L-index

#	Paper	IF	Citations
49	A census of human soluble protein complexes. <i>Cell</i> , 2012 , 150, 1068-81	56.2	612
48	Panorama of ancient metazoan macromolecular complexes. <i>Nature</i> , 2015 , 525, 339-44	50.4	325
47	Global functional atlas of Escherichia coli encompassing previously uncharacterized proteins. <i>PLoS Biology</i> , 2009 , 7, e96	9.7	280
46	A dual function of the CRISPR-Cas system in bacterial antiviral immunity and DNA repair. <i>Molecular Microbiology</i> , 2011 , 79, 484-502	4.1	199
45	eSGA: E. coli synthetic genetic array analysis. <i>Nature Methods</i> , 2008 , 5, 789-95	21.6	196
44	Interaction landscape of membrane-protein complexes in <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2012 , 489, 585-9	50.4	186
43	The binary protein-protein interaction landscape of Escherichia coli. <i>Nature Biotechnology</i> , 2014 , 32, 285-299	44.9	159
42	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. <i>Nature Methods</i> , 2015 , 12, 725-31	21.6	86
41	Genetic interaction maps in Escherichia coli reveal functional crosstalk among cell envelope biogenesis pathways. <i>PLoS Genetics</i> , 2011 , 7, e1002377	6	76
40	Quantitative genome-wide genetic interaction screens reveal global epistatic relationships of protein complexes in Escherichia coli. <i>PLoS Genetics</i> , 2014 , 10, e1004120	6	71
39	Global landscape of cell envelope protein complexes in Escherichia coli. <i>Nature Biotechnology</i> , 2018 , 36, 103-112	44.5	68
38	Human-chromatin-related protein interactions identify a demethylase complex required for chromosome segregation. <i>Cell Reports</i> , 2014 , 8, 297-310	10.6	46
37	Acyldepsipeptide Analogs Dysregulate Human Mitochondrial ClpP Protease Activity and Cause Apoptotic Cell Death. <i>Cell Chemical Biology</i> , 2018 , 25, 1017-1030.e9	8.2	42
36	Actionable Cytopathogenic Host Responses of Human Alveolar Type 2 Cells to SARS-CoV-2. <i>Molecular Cell</i> , 2020 , 80, 1104-1122.e9	17.6	38
35	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	10.6	37
34	Features of the Chaperone Cellular Network Revealed through Systematic Interaction Mapping. <i>Cell Reports</i> , 2017 , 20, 2735-2748	10.6	36
33	Mitochondrial targets for pharmacological intervention in human disease. <i>Journal of Proteome Research</i> , 2015 , 14, 5-21	5.6	35

32	EPIC: software toolkit for elution profile-based inference of protein complexes. <i>Nature Methods</i> , 2019 , 16, 737-742	21.6	34
31	Novel function discovery with GeneMANIA: a new integrated resource for gene function prediction in <i>Escherichia coli</i> . <i>Bioinformatics</i> , 2015 , 31, 306-10	7.2	31
30	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	10.6	29
29	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	10.6	23
28	Systematic Genetic Screens Reveal the Dynamic Global Functional Organization of the Bacterial Translation Machinery. <i>Cell Reports</i> , 2016 , 17, 904-916	10.6	22
27	NleH defines a new family of bacterial effector kinases. <i>Structure</i> , 2014 , 22, 250-9	5.2	20
26	Extracting high confidence protein interactions from affinity purification data: at the crossroads. <i>Journal of Proteomics</i> , 2015 , 118, 63-80	3.9	19
25	Efficient prediction of human protein-protein interactions at a global scale. <i>BMC Bioinformatics</i> , 2014 , 15, 383	3.6	19
24	Rewiring of the Human Mitochondrial Interactome during Neuronal Reprogramming Reveals Regulators of the Respirasome and Neurogenesis. <i>iScience</i> , 2019 , 19, 1114-1132	6.1	17
23	Spindle Checkpoint Factors Bub1 and Bub2 Promote DNA Double-Strand Break Repair by Nonhomologous End Joining. <i>Molecular and Cellular Biology</i> , 2015 , 35, 2448-63	4.8	17
22	Yeast mitochondrial protein-protein interactions reveal diverse complexes and disease-relevant functional relationships. <i>Journal of Proteome Research</i> , 2015 , 14, 1220-37	5.6	14
21	ClpP protease activation results from the reorganization of the electrostatic interaction networks at the entrance pores. <i>Communications Biology</i> , 2019 , 2, 410	6.7	14
20	Chemical-genetic profiling reveals limited cross-resistance between antimicrobial peptides with different modes of action. <i>Nature Communications</i> , 2019 , 10, 5731	17.4	14
19	BraInMap Elucidates the Macromolecular Connectivity Landscape of Mammalian Brain. <i>Cell Systems</i> , 2020 , 10, 333-350.e14	10.6	13
18	Systems analysis of the genetic interaction network of yeast molecular chaperones. <i>Molecular Omics</i> , 2018 , 14, 82-94	4.4	12
17	Integrative network analysis of signaling in human CD34(+) hematopoietic progenitor cells by global phosphoproteomic profiling using TiO2 enrichment combined with 2D LC-MS/MS and pathway mapping. <i>Proteomics</i> , 2013 , 13, 1325-33	4.8	12
16	Ribosome-dependent ATPase interacts with conserved membrane protein in <i>Escherichia coli</i> to modulate protein synthesis and oxidative phosphorylation. <i>PLoS ONE</i> , 2011 , 6, e18510	3.7	10
15	Insights from protein-protein interaction studies on bacterial pathogenesis. <i>Expert Review of Proteomics</i> , 2017 , 14, 779-797	4.2	8

14	Functional cooperativity between the trigger factor chaperone and the ClpXP proteolytic complex. <i>Nature Communications</i> , 2021 , 12, 281	17.4	6
13	Mitochondria under the spotlight: On the implications of mitochondrial dysfunction and its connectivity to neuropsychiatric disorders. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 2535-2546	6.8	5
12	Proteome-wide dataset supporting the study of ancient metazoan macromolecular complexes. <i>Data in Brief</i> , 2016 , 6, 715-21	1.2	5
11	Exploring the Impact of Mutations on the Total and Mitochondrial Proteome of Human Skin Fibroblasts. <i>Frontiers in Cell and Developmental Biology</i> , 2020 , 8, 423	5.7	4
10	Misconnecting the dots: altered mitochondrial protein-protein interactions and their role in neurodegenerative disorders. <i>Expert Review of Proteomics</i> , 2020 , 17, 119-136	4.2	4
9	Targeted protein identification, quantification and reporting for high-resolution nanoflow targeted peptide monitoring. <i>Journal of Proteomics</i> , 2013 , 81, 159-72	3.9	4
8	From fuzziness to precision medicine: on the rapidly evolving proteomics with implications in mitochondrial connectivity to rare human disease. <i>IScience</i> , 2021 , 24, 102030	6.1	3
7	Novel Interactome of <i>Saccharomyces cerevisiae</i> Myosin TypeIII Identified by a Modified Integrated Membrane Yeast Two-Hybrid (iMYTH) Screen. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 1469-74	3.2	3
6	ZapG (YhcB/DUF1043), a novel cell division protein in gamma-proteobacteria linking the Z-ring to septal peptidoglycan synthesis. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100700	5.4	3
5	The conserved Tpk1 regulates non-homologous end joining double-strand break repair by phosphorylation of Nej1, a homolog of the human XLF. <i>Nucleic Acids Research</i> , 2021 , 49, 8145-8160	20.1	2
4	Macromolecular Connectivity Landscape of Mammalian Brain. <i>SSRN Electronic Journal</i> ,	1	1
3	Chemical-genetic profiling reveals cross-resistance and collateral sensitivity between antimicrobial peptides		1
2	Human-Soybean Allergies: Elucidation of the Seed Proteome and Comprehensive Protein-Protein Interaction Prediction. <i>Journal of Proteome Research</i> , 2021 , 20, 4925-4947	5.6	1
1	A Gaussian process-based definition reveals new and bona fide genetic interactions compared to a multiplicative model in the Gram-negative <i>Escherichia coli</i> . <i>Bioinformatics</i> , 2020 , 36, 880-889	7.2	