

# S Stephen Yi

## List of Publications by Year in descending order

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Version: 2024-02-01

48  
papers

4,897  
citations

218677

26  
h-index

233421

45  
g-index

52  
all docs

52  
docs citations

52  
times ranked

8609  
citing authors

#	ARTICLE	IF	CITATIONS
1	Timing of Resumption of Anticoagulation After Polypectomy and Frequency of Post-procedural Complications: A Post-hoc Analysis. <i>Digestive Diseases and Sciences</i> , 2022, 67, 3210-3219.	2.3	2
2	Metabolomics-based phenotypic screens for evaluation of drug synergy via direct-infusion mass spectrometry. <i>IScience</i> , 2022, 25, 104221.	4.1	8
3	Transcranial Near Infrared Light Stimulations Improve Cognition in Patients with Dementia. , 2021, 12, 954.		46
4	mi-IsoNet: systems-scale microRNA landscape reveals rampant isoform-mediated gain of target interaction diversity and signaling specificity. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	9
5	Gender Differences of Dementia in Response to Intensive Self-Administered Transcranial and Intraocular Near-Infrared Stimulation. <i>Cureus</i> , 2021, 13, e16188.	0.5	7
6	e-MutPath: computational modeling reveals the functional landscape of genetic mutations rewiring interactome networks. <i>Nucleic Acids Research</i> , 2021, 49, e2-e2.	14.5	10
7	Pathway perturbations in signaling networks: Linking genotype to phenotype. <i>Seminars in Cell and Developmental Biology</i> , 2020, 99, 3-11.	5.0	13
8	Integrated Genomic Characterization of the Human Immunome in Cancer. <i>Cancer Research</i> , 2020, 80, 4854-4867.	0.9	11
9	Gain-of-Function Mutations: An Emerging Advantage for Cancer Biology. <i>Trends in Biochemical Sciences</i> , 2019, 44, 659-674.	7.5	38
10	MERIT: Systematic Analysis and Characterization of Mutational Effect on RNA Interactome Topology. <i>Hepatology</i> , 2019, 70, 532-546.	7.3	28
11	Multi-omics analysis reveals neoantigen-independent immune cell infiltration in copy-number driven cancers. <i>Nature Communications</i> , 2018, 9, 1317.	12.8	94
12	LncMAP: Pan-cancer atlas of long noncoding RNA-mediated transcriptional network perturbations. <i>Nucleic Acids Research</i> , 2018, 46, 1113-1123.	14.5	115
13	Systematic Functional Annotation of Somatic Mutations in Cancer. <i>Cancer Cell</i> , 2018, 33, 450-462.e10.	16.8	213
14	Polycomb Repressive Complex 2 is essential for development and maintenance of a functional TEC compartment. <i>Scientific Reports</i> , 2018, 8, 14335.	3.3	5
15	Gene Regulatory Network Perturbation by Genetic and Epigenetic Variation. <i>Trends in Biochemical Sciences</i> , 2018, 43, 576-592.	7.5	20
16	In Situ Peroxidase Labeling and Mass-Spectrometry Connects Alpha-Synuclein Directly to Endocytic Trafficking and mRNA Metabolism in Neurons. <i>Cell Systems</i> , 2017, 4, 242-250.e4.	6.2	91
17	HSP90 Shapes the Consequences of Human Genetic Variation. <i>Cell</i> , 2017, 168, 856-866.e12.	28.9	117
18	Regulome networks and mutational landscape in liver cancer: An informative path to precision medicine. <i>Hepatology</i> , 2017, 66, 280-282.	7.3	2

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19	Functional variomics and network perturbation: connecting genotype to phenotype in cancer. <i>Nature Reviews Genetics</i> , 2017, 18, 395-410.	16.3	84
20	Base-resolution stratification of cancer mutations using functional variomics. <i>Nature Protocols</i> , 2017, 12, 2323-2341.	12.0	11
21	Revealing the Determinants of Widespread Alternative Splicing Perturbation in Cancer. <i>Cell Reports</i> , 2017, 21, 798-812.	6.4	51
22	Signal Transduction and Regulation: Insights into Evolution. <i>BioMed Research International</i> , 2016, 2016, 1-2.	1.9	0
23	Multi-OMICs and Genome Editing Perspectives on Liver Cancer Signaling Networks. <i>BioMed Research International</i> , 2016, 2016, 1-14.	1.9	7
24	Pooled matrix protein interaction screens using Barcode Fusion Genetics. <i>Molecular Systems Biology</i> , 2016, 12, 863.	7.2	102
25	An extended set of yeast-based functional assays accurately identifies human disease mutations. <i>Genome Research</i> , 2016, 26, 670-680.	5.5	116
26	Survey of variation in human transcription factors reveals prevalent DNA binding changes. <i>Science</i> , 2016, 351, 1450-1454.	12.6	114
27	Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing. <i>Cell</i> , 2016, 164, 805-817.	28.9	479
28	Comparative analysis of protein interactome networks prioritizes candidate genes with cancer signatures. <i>Oncotarget</i> , 2016, 7, 78841-78849.	1.8	14
29	Human Gene-Centered Transcription Factor Networks for Enhancers and Disease Variants. <i>Cell</i> , 2015, 161, 661-673.	28.9	111
30	Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. <i>Cell</i> , 2015, 161, 647-660.	28.9	482
31	Computational Advances in Cancer Informatics (A). <i>Cancer Informatics</i> , 2014, 13s1, CIN.S19243.	1.9	0
32	Protein interaction network of alternatively spliced isoforms from brain links genetic risk factors for autism. <i>Nature Communications</i> , 2014, 5, 3650.	12.8	131
33	A Proteome-Scale Map of the Human Interactome Network. <i>Cell</i> , 2014, 159, 1212-1226.	28.9	1,199
34	Edgotype: a fundamental link between genotype and phenotype. <i>Current Opinion in Genetics and Development</i> , 2013, 23, 649-657.	3.3	129
35	Nonsex Genes in the Mating Type Locus of <i>Candida albicans</i> Play Roles in $\alpha$ ± Biofilm Formation, Including Impermeability and Fluconazole Resistance. <i>PLoS Pathogens</i> , 2012, 8, e1002476.	4.7	27
36	Utilization of the Mating Scaffold Protein in the Evolution of a New Signal Transduction Pathway for Biofilm Development. <i>MBio</i> , 2011, 2, e00237-10.	4.1	24

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37	Self-Induction of <i>Candida albicans</i> or <i>Candida glabrata</i> Biofilms in <i>Candida albicans</i> Is a Pheromone-Based Paracrine System Requiring Switching. <i>Eukaryotic Cell</i> , 2011, 10, 753-760.	3.4	22
38	Alternative Mating Type Configurations (a/α versus a/a or α/α) of <i>Candida albicans</i> Result in Alternative Biofilms Regulated by Different Pathways. <i>PLoS Biology</i> , 2011, 9, e1001117.	5.6	73
39	Tec1 Mediates the Pheromone Response of the White Phenotype of <i>Candida albicans</i> : Insights into the Evolution of New Signal Transduction Pathways. <i>PLoS Biology</i> , 2010, 8, e1000363.	5.6	85
40	N-Acetylglucosamine Induces White to Opaque Switching, a Mating Prerequisite in <i>Candida albicans</i> . <i>PLoS Pathogens</i> , 2010, 6, e1000806.	4.7	180
41	The White Cell Response to Pheromone Is a General Characteristic of <i>Candida albicans</i> Strains. <i>Eukaryotic Cell</i> , 2009, 8, 251-256.	3.4	23
42	Genes Selectively Up-Regulated by Pheromone in White Cells Are Involved in Biofilm Formation in <i>Candida albicans</i> . <i>PLoS Pathogens</i> , 2009, 5, e1000601.	4.7	59
43	CO2 Regulates White-to-Opaque Switching in <i>Candida albicans</i> . <i>Current Biology</i> , 2009, 19, 330-334.	3.9	160
44	A <i>Candida albicans</i> -specific region of the α-pheromone receptor plays a selective role in the white cell pheromone response. <i>Molecular Microbiology</i> , 2009, 71, 925-947.	2.5	37
45	Dark brown is the more virulent of the switch phenotypes of <i>Candida glabrata</i> . <i>Microbiology (United Kingdom)</i> 151: 1078-1088 (2007)	1.8	28
46	The Same Receptor, G Protein, and Mitogen-activated Protein Kinase Pathway Activate Different Downstream Regulators in the Alternative White and Opaque Pheromone Responses of <i>Candida albicans</i> . <i>Molecular Biology of the Cell</i> , 2008, 19, 957-970.	2.1	60
47	The Shwachman-Bodian-Diamond syndrome gene encodes an RNA-binding protein that localizes to the pseudopod of <i>Dictyostelium amoebae</i> during chemotaxis. <i>Journal of Cell Science</i> , 2006, 119, 370-379.	2.0	51
48	TOS9 Regulates White-Opaque Switching in <i>Candida albicans</i> . <i>Eukaryotic Cell</i> , 2006, 5, 1674-1687.	3.4	207