

Anastasia Baryshnikova

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

6,402
citations

201674

27
h-index

254184

43
g-index

51
all docs

51
docs citations

51
times ranked

7730
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genetic Landscape of a Cell. <i>Science</i> , 2010, 327, 425-431.	12.6	1,937
2	A global genetic interaction network maps a wiring diagram of cellular function. <i>Science</i> , 2016, 353, .	12.6	979
3	Systematic exploration of essential yeast gene function with temperature-sensitive mutants. <i>Nature Biotechnology</i> , 2011, 29, 361-367.	17.5	352
4	Quantitative analysis of fitness and genetic interactions in yeast on a genome scale. <i>Nature Methods</i> , 2010, 7, 1017-1024.	19.0	319
5	Systematic exploration of synergistic drug pairs. <i>Molecular Systems Biology</i> , 2011, 7, 544.	7.2	284
6	Systematic Mapping of Genetic Interaction Networks. <i>Annual Review of Genetics</i> , 2009, 43, 601-625.	7.6	250
7	An integrated approach to characterize genetic interaction networks in yeast metabolism. <i>Nature Genetics</i> , 2011, 43, 656-662.	21.4	194
8	Global Gene Deletion Analysis Exploring Yeast Filamentous Growth. <i>Science</i> , 2012, 337, 1353-1356.	12.6	186
9	Synthetic Genetic Array (SGA) Analysis in <i>Saccharomyces cerevisiae</i> and <i>Schizosaccharomyces pombe</i> . <i>Methods in Enzymology</i> , 2010, 470, 145-179.	1.0	175
10	Exploring genetic suppression interactions on a global scale. <i>Science</i> , 2016, 354, .	12.6	157
11	Systematic Functional Annotation and Visualization of Biological Networks. <i>Cell Systems</i> , 2016, 2, 412-421.	6.2	142
12	SGAtools: one-stop analysis and visualization of array-based genetic interaction screens. <i>Nucleic Acids Research</i> , 2013, 41, W591-W596.	14.5	141
13	Genetic Interaction Networks: Toward an Understanding of Heritability. <i>Annual Review of Genomics and Human Genetics</i> , 2013, 14, 111-133.	6.2	105
14	Charting the genetic interaction map of a cell. <i>Current Opinion in Biotechnology</i> , 2011, 22, 66-74.	6.6	103
15	Genetic interactions reveal the evolutionary trajectories of duplicate genes. <i>Molecular Systems Biology</i> , 2010, 6, 429.	7.2	97
16	Dosage suppression genetic interaction networks enhance functional wiring diagrams of the cell. <i>Nature Biotechnology</i> , 2011, 29, 505-511.	17.5	90
17	A negative genetic interaction map in isogenic cancer cell lines reveals cancer cell vulnerabilities. <i>Molecular Systems Biology</i> , 2013, 9, 696.	7.2	90
18	Functional annotation of chemical libraries across diverse biological processes. <i>Nature Chemical Biology</i> , 2017, 13, 982-993.	8.0	76

#	ARTICLE	IF	CITATIONS
19	DRYGIN: a database of quantitative genetic interaction networks in yeast. <i>Nucleic Acids Research</i> , 2010, 38, D502-D507.	14.5	75
20	Combining functional genomics and chemical biology to identify targets of bioactive compounds. <i>Current Opinion in Chemical Biology</i> , 2011, 15, 66-78.	6.1	72
21	Functional wiring of the yeast kinome revealed by global analysis of genetic network motifs. <i>Genome Research</i> , 2012, 22, 791-801.	5.5	65
22	Exploring the Yeast Acetylome Using Functional Genomics. <i>Cell</i> , 2012, 149, 936-948.	28.9	63
23	Protein Complexes are Central in the Yeast Genetic Landscape. <i>PLoS Computational Biology</i> , 2011, 7, e1001092.	3.2	57
24	Chromosome-Specific and Global Effects of Aneuploidy in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2016, 202, 1395-1409.	2.9	37
25	A genome-scale yeast library with inducible expression of individual genes. <i>Molecular Systems Biology</i> , 2021, 17, e10207.	7.2	37
26	<i>trappc11</i> is required for protein glycosylation in zebrafish and humans. <i>Molecular Biology of the Cell</i> , 2016, 27, 1220-1234.	2.1	36
27	Exploratory Analysis of Biological Networks through Visualization, Clustering, and Functional Annotation in Cytoscape. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot077644.	0.3	31
28	Synthetic Genetic Array Analysis for Global Mapping of Genetic Networks in Yeast. <i>Methods in Molecular Biology</i> , 2014, 1205, 143-168.	0.9	30
29	<i>Skp</i> , Cullin, F-box (SCF)- <i>Met30</i> and SCF- <i>Cdc4</i> -Mediated Proteolysis of CENP-A Prevents Mislocalization of CENP-A for Chromosomal Stability in Budding Yeast. <i>PLoS Genetics</i> , 2020, 16, e1008597.	3.5	28
30	Genome Rearrangements Caused by Depletion of Essential DNA Replication Proteins in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2012, 192, 147-160.	2.9	25
31	A Systems Biology Approach Reveals the Role of a Novel Methyltransferase in Response to Chemical Stress and Lipid Homeostasis. <i>PLoS Genetics</i> , 2011, 7, e1002332.	3.5	21
32	A Genome-Wide Screen Reveals a Role for the HIR Histone Chaperone Complex in Preventing Mislocalization of Budding Yeast CENP-A. <i>Genetics</i> , 2018, 210, 203-218.	2.9	20
33	Identifying <i>Pseudomonas syringae</i> Type III Secreted Effector Function via a Yeast Genomic Screen. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 535-547.	1.8	20
34	Spatial Analysis of Functional Enrichment (SAFE) in Large Biological Networks. <i>Methods in Molecular Biology</i> , 2018, 1819, 249-268.	0.9	18
35	ER-associated retrograde SNAREs and the <i>Dsl1</i> complex mediate an alternative, <i>Sey1p</i> -independent homotypic ER fusion pathway. <i>Molecular Biology of the Cell</i> , 2014, 25, 3401-3412.	2.1	16
36	Neighboring-gene effect: a genetic uncertainty principle. <i>Nature Methods</i> , 2012, 9, 341-343.	19.0	15

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37	Global Linkage Map Connects Meiotic Centromere Function to Chromosome Size in Budding Yeast. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1741-1751.	1.8	12
38	Dbf4-Dependent Kinase (DDK)-Mediated Proteolysis of CENP-A Prevents Mislocalization of CENP-A in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2057-2068.	1.8	11
39	The promise and reality of therapeutic discovery from large cohorts. <i>Journal of Clinical Investigation</i> , 2020, 130, 575-581.	8.2	9
40	<i>VID22</i> counteracts G-quadruplex-induced genome instability. <i>Nucleic Acids Research</i> , 2021, 49, 12785-12804.	14.5	5
41	You too can play with an edge. <i>Nature Methods</i> , 2009, 6, 797-798.	19.0	3
42	Data libraries – the missing element for modeling biological systems. <i>FEBS Journal</i> , 2020, 287, 4594-4601.	4.7	3
43	Genetic Networks. , 2013, , 115-135.		1