

Stanley Fields

List of Publications by Year in Descending Order

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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.

56

papers

5,156

citations

26

h-index

66

g-index

66

ext. papers

6,442

ext. citations

15.6

avg, IF

5.95

L-index

#	Paper	IF	Citations
56	Effects of sequence motifs in the yeast 3' untranslated region determined from massively parallel assays of random sequences. <i>Genome Biology</i> , 2021 , 22, 293	18.3	0
55	Synthetic promoter designs enabled by a comprehensive analysis of plant core promoters. <i>Nature Plants</i> , 2021 , 7, 842-855	11.5	7
54	The regulatory landscape of <i>Arabidopsis thaliana</i> roots at single-cell resolution. <i>Nature Communications</i> , 2021 , 12, 3334	17.4	23
53	Balance between promiscuity and specificity in phage host range. <i>ISME Journal</i> , 2021 , 15, 2195-2205	11.9	2
52	Expanding the binding specificity for RNA recognition by a PUF domain. <i>Nature Communications</i> , 2021 , 12, 5107	17.4	0
51	Identification of Plant Enhancers and Their Constituent Elements by STARR-seq in Tobacco Leaves. <i>Plant Cell</i> , 2020 , 32, 2120-2131	11.6	15
50	Dimensionality reduction by UMAP to visualize physical and genetic interactions. <i>Nature Communications</i> , 2020 , 11, 1537	17.4	43
49	Distinct patterns of mutational sensitivity for resistance and maltodextrin transport in LamB. <i>Microbial Genomics</i> , 2020 , 6,	4.4	4
48	Binding and Regulation of Transcription by Yeast Ste12 Variants To Drive Mating and Invasion Phenotypes. <i>Genetics</i> , 2020 , 214, 397-407	4	3
47	Dynamics of Gene Expression in Single Root Cells of. <i>Plant Cell</i> , 2019 , 31, 993-1011	11.6	133
46	High-throughput identification of dominant negative polypeptides in yeast. <i>Nature Methods</i> , 2019 , 16, 413-416	21.6	9
45	Preferences in a trait decision determined by transcription factor variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E7997-E8006	11.5	7
44	Conditional accumulation of toxic tRNAs to cause amino acid misincorporation. <i>Nucleic Acids Research</i> , 2018 , 46, 7831-7843	20.1	14
43	A Multiplex Homology-Directed DNA Repair Assay Reveals the Impact of More Than 1,000 BRCA1 Missense Substitution Variants on Protein Function. <i>American Journal of Human Genetics</i> , 2018 , 103, 498-508	11	62
42	Engineered Biosensors from Dimeric Ligand-Binding Domains. <i>ACS Synthetic Biology</i> , 2018 , 7, 2457-2467	5.7	15
41	Deep learning of the regulatory grammar of yeast 5' untranslated regions from 500,000 random sequences. <i>Genome Research</i> , 2017 , 27, 2015-2024	9.7	96
40	Massively Parallel Genetics. <i>Genetics</i> , 2016 , 203, 617-9	4	21

39	Comprehensive Analysis of the SUL1 Promoter of <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2016 , 203, 191-204		13
38	Engineering an allosteric transcription factor to respond to new ligands. <i>Nature Methods</i> , 2016 , 13, 177-81.6		184
37	Adjacent Codons Act in Concert to Modulate Translation Efficiency in Yeast. <i>Cell</i> , 2016 , 166, 679-690	56.2	122
36	Deep Mutational Scanning: Library Construction, Functional Selection, and High-Throughput Sequencing. <i>Cold Spring Harbor Protocols</i> , 2015 , 2015, 777-80	1.2	2
35	Deep Mutational Scanning: Calculating Enrichment Scores for Protein Variants from DNA Sequencing Output Files. <i>Cold Spring Harbor Protocols</i> , 2015 , 2015, 781-3	1.2	5
34	Deep Mutational Scanning: A Highly Parallel Method to Measure the Effects of Mutation on Protein Function. <i>Cold Spring Harbor Protocols</i> , 2015 , 2015, 711-4	1.2	15
33	Combining natural sequence variation with high throughput mutational data to reveal protein interaction sites. <i>PLoS Genetics</i> , 2015 , 11, e1004918	6	18
32	Massively Parallel Functional Analysis of BRCA1 RING Domain Variants. <i>Genetics</i> , 2015 , 200, 413-22	4	190
31	A tetO Toolkit To Alter Expression of Genes in <i>Saccharomyces cerevisiae</i> . <i>ACS Synthetic Biology</i> , 2015 , 4, 842-52	5.7	13
30	The role of functional data in interpreting the effects of genetic variation. <i>Molecular Biology of the Cell</i> , 2015 , 26, 3904-8	3.5	10
29	Massively parallel single-amino-acid mutagenesis. <i>Nature Methods</i> , 2015 , 12, 203-6, 4 p following 206	21.6	101
28	Identification of the determinants of tRNA function and susceptibility to rapid tRNA decay by high-throughput in vivo analysis. <i>Genes and Development</i> , 2014 , 28, 1721-32	12.6	45
27	A homolog of lariat-debranching enzyme modulates turnover of branched RNA. <i>Rna</i> , 2014 , 20, 1337-48	5.8	22
26	Engineering allostery. <i>Trends in Genetics</i> , 2014 , 30, 521-8	8.5	50
25	Deep mutational scanning: a new style of protein science. <i>Nature Methods</i> , 2014 , 11, 801-7	21.6	520
24	Measuring the activity of protein variants on a large scale using deep mutational scanning. <i>Nature Protocols</i> , 2014 , 9, 2267-84	18.8	97
23	Would Fred Sanger get funded today?. <i>Genetics</i> , 2014 , 197, 435-9	4	1
22	Global analysis of phosphorylation and ubiquitylation cross-talk in protein degradation. <i>Nature Methods</i> , 2013 , 10, 676-82	21.6	381

21	Deep mutational scanning of an RRM domain of the <i>Saccharomyces cerevisiae</i> poly(A)-binding protein. <i>Rna</i> , 2013 , 19, 1537-51	5.8	136
20	A fundamental protein property, thermodynamic stability, revealed solely from large-scale measurements of protein function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 16858-63	11.5	146
19	High-resolution mapping of protein sequence-function relationships. <i>Nature Methods</i> , 2010 , 7, 741-6	21.6	350
18	Interactive learning: lessons from two hybrids over two decades. <i>Proteomics</i> , 2009 , 9, 5209-13	4.8	31
17	Molecular biology. Site-seeing by sequencing. <i>Science</i> , 2007 , 316, 1441-2	33.3	26
16	Cell biology. Whither model organism research?. <i>Science</i> , 2005 , 307, 1885-6	33.3	90
15	High-throughput two-hybrid analysis. The promise and the peril. <i>FEBS Journal</i> , 2005 , 272, 5391-9	5.7	151
14	Approaches to Analyze Protein Interactions. <i>Scientific World Journal, The</i> , 2002 , 2, 93-94	2.2	
13	Genomics. A crisis in postgenomic nomenclature. <i>Science</i> , 2002 , 296, 671-2	33.3	6
12	A yeast sensor of ligand binding. <i>Nature Biotechnology</i> , 2001 , 19, 1042-6	44.5	74
11	Proteomics. Proteomics in genomeland. <i>Science</i> , 2001 , 291, 1221-4	33.3	196
10	Constitutive activation of the <i>Saccharomyces cerevisiae</i> transcriptional regulator Ste12p by mutations at the amino-terminus. <i>Yeast</i> , 2000 , 16, 1365-75	3.4	11
9	A network of protein-protein interactions in yeast. <i>Nature Biotechnology</i> , 2000 , 18, 1257-61	44.5	1066
8	Identification of RNAs that bind to a specific protein using the yeast three-hybrid system. <i>Rna</i> , 1999 , 5, 596-601	5.8	58
7	Caspase-3 inhibits growth in <i>Saccharomyces cerevisiae</i> without causing cell death. <i>FEBS Letters</i> , 1999 , 446, 9-14	3.8	21
6	Mutation detection by a two-hybrid assay. <i>Human Molecular Genetics</i> , 1998 , 7, 1029-32	5.6	19
5	A conserved RNA-binding protein that regulates sexual fates in the <i>C. elegans</i> hermaphrodite germ line. <i>Nature</i> , 1997 , 390, 477-84	50.4	443
4	The regulatory landscape of <i>Arabidopsis thaliana</i> roots at single-cell resolution		7

3	Dynamics of gene expression in single root cells of <i>A. thaliana</i>	4
2	Dimensionality reduction by UMAP to visualize physical and genetic interactions	1
1	Synthetic Promoter Designs Enabled by a Comprehensive Analysis of Plant Core Promoters	1