Stanley Fields

List of Publications by Year
in descending order

56	7,337	159358 30	149479 56
papers	citations	h-index	g-index
66	66	66	8482
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Mapping functional regions of essential bacterial proteins with dominant-negative protein fragments. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	2
2	Balance between promiscuity and specificity in phage λ host range. ISME Journal, 2021, 15, 2195-2205.	4.4	8
3	Synthetic promoter designs enabled by a comprehensive analysis of plant core promoters. Nature Plants, 2021, 7, 842-855.	4.7	78
4	The regulatory landscape of Arabidopsis thaliana roots at single-cell resolution. Nature Communications, 2021, 12, 3334.	5.8	84
5	Expanding the binding specificity for RNA recognition by a PUF domain. Nature Communications, 2021, 12, 5107.	5.8	8
6	Effects of sequence motifs in the yeast 3′ untranslated region determined from massively parallel assays of random sequences. Genome Biology, 2021, 22, 293.	3.8	6
7	Identification of Plant Enhancers and Their Constituent Elements by STARR-seq in Tobacco Leaves. Plant Cell, 2020, 32, 2120-2131.	3.1	53
8	Dimensionality reduction by UMAP to visualize physical and genetic interactions. Nature Communications, 2020, 11, 1537.	5.8	126
9	Binding and Regulation of Transcription by Yeast Ste12 Variants To Drive Mating and Invasion Phenotypes. Genetics, 2020, 214, 397-407.	1.2	8
10	Distinct patterns of mutational sensitivity for λ resistance and maltodextrin transport in Escherichia coli LamB. Microbial Genomics, 2020, 6, .	1.0	9
11	Dynamics of Gene Expression in Single Root Cells of <i>Arabidopsis thaliana</i>. Plant Cell, 2019, 31, 993-1011.	3.1	279
12	High-throughput identification of dominant negative polypeptides in yeast. Nature Methods, 2019, 16, 413-416.	9.0	20
13	A Multiplex Homology-Directed DNA Repair Assay Reveals the Impact of More Than 1,000 BRCA1 Missense Substitution Variants on Protein Function. American Journal of Human Genetics, 2018, 103, 498-508.	2.6	99
14	Engineered Biosensors from Dimeric Ligand-Binding Domains. ACS Synthetic Biology, 2018, 7, 2457-2467.	1.9	21
15	Preferences in a trait decision determined by transcription factor variants. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7997-E8006.	3.3	15
16	Conditional accumulation of toxic tRNAs to cause amino acid misincorporation. Nucleic Acids Research, 2018, 46, 7831-7843.	6.5	25
17	Deep learning of the regulatory grammar of yeast 5′ untranslated regions from 500,000 random sequences. Genome Research, 2017, 27, 2015-2024.	2.4	166
18	Adjacent Codons Act in Concert to Modulate Translation Efficiency in Yeast. Cell, 2016, 166, 679-690.	13.5	180

#	Article	IF	Citations
19	Massively Parallel Genetics. Genetics, 2016, 203, 617-619.	1.2	24
20	Comprehensive Analysis of the *SUL1* Promoter of *Saccharomyces cerevisiae*. Genetics, 2016, 203, 191-202.	1.2	22
21	Engineering an allosteric transcription factor to respond to new ligands. Nature Methods, 2016, 13, 177-183.	9.0	274
22	Massively parallel single-amino-acid mutagenesis. Nature Methods, 2015, 12, 203-206.	9.0	153
23	Deep Mutational Scanning: Library Construction, Functional Selection, and High-Throughput Sequencing. Cold Spring Harbor Protocols, 2015, 2015, pdb.prot085225.	0.2	6
24	Deep Mutational Scanning: Calculating Enrichment Scores for Protein Variants from DNA Sequencing Output Files: Table 1.. Cold Spring Harbor Protocols, 2015, 2015, pdb.prot085233.	0.2	6
25	Deep Mutational Scanning: A Highly Parallel Method to Measure the Effects of Mutation on Protein Function. Cold Spring Harbor Protocols, 2015, 2015, pdb.top077503.	0.2	26
26	Combining Natural Sequence Variation with High Throughput Mutational Data to Reveal Protein Interaction Sites. PLoS Genetics, 2015, 11, e1004918.	1.5	26
27	Massively Parallel Functional Analysis of BRCA1 RING Domain Variants. Genetics, 2015, 200, 413-422.	1.2	272
28	A tetO Toolkit To Alter Expression of Genes in *Saccharomyces cerevisiae*. ACS Synthetic Biology, 2015, 4, 842-852.	1.9	18
29	The role of functional data in interpreting the effects of genetic variation. Molecular Biology of the Cell, 2015, 26, 3904-3908.	0.9	13
30	Measuring the activity of protein variants on a large scale using deep mutational scanning. Nature Protocols, 2014, 9, 2267-2284.	5.5	147
31	Would Fred Sanger Get Funded Today?. Genetics, 2014, 197, 435-439.	1.2	4
32	Identification of the determinants of tRNA function and susceptibility to rapid tRNA decay by high-throughput in vivo analysis. Genes and Development, 2014, 28, 1721-1732.	2.7	58
33	A homolog of lariat-debranching enzyme modulates turnover of branched RNA. Rna, 2014, 20, 1337-1348.	1.6	34
34	Engineering allostery. Trends in Genetics, 2014, 30, 521-528.	2.9	64
35	Deep mutational scanning: a new style of protein science. Nature Methods, 2014, 11, 801-807.	9.0	885
36	Global analysis of phosphorylation and ubiquitylation cross-talk in protein degradation. Nature Methods, 2013, 10, 676-682.	9.0	520

#	Article	IF	Citations
37	Deep mutational scanning of an RRM domain of the <i>Saccharomyces cerevisiae</i> poly(A)-binding protein. Rna, 2013, 19, 1537-1551.	1.6	207
38	A fundamental protein property, thermodynamic stability, revealed solely from large-scale measurements of protein function. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16858-16863.	3.3	226
39	High-resolution mapping of protein sequence-function relationships. Nature Methods, 2010, 7, 741-746.	9.0	482
40	Interactive learning: Lessons from two hybrids over two decades. Proteomics, 2009, 9, 5209-5213.	1.3	39
41	MOLECULAR BIOLOGY: Site-Seeing by Sequencing. Science, 2007, 316, 1441-1442.	6.0	29
42	High-throughput two-hybrid analysis. The promise and the peril. FEBS Journal, 2005, 272, 5391-5399.	2.2	163
43	CELL BIOLOGY: Whither Model Organism Research?. Science, 2005, 307, 1885-1886.	6.0	118
44	GENOMICS: A Crisis in Postgenomic Nomenclature. Science, 2002, 296, 671-672.	6.0	8
45	Approaches to Analyze Protein Interactions. Scientific World Journal, The, 2002, 2, 93-94.	0.8	0
46	Proteomics in Genomeland. Science, 2001, 291, 1221-1224.	6.0	226
47	A yeast sensor of ligand binding. Nature Biotechnology, 2001, 19, 1042-1046.	9.4	86
48	Constitutive activation of theSaccharomyces cerevisiae transcriptional regulator Ste12p by mutations at the amino-terminus. Yeast, 2000, 16, 1365-1375.	0.8	13
49	Grass-roots genomics. Nature Genetics, 2000, 24, 5-6.	9.4	10
50	A network of protein–protein interactions in yeast. Nature Biotechnology, 2000, 18, 1257-1261.	9.4	1,281
51	Identification of RNAs that bind to a specific protein using the yeast three-hybrid system. Rna, 1999, 5, 596-601.	1.6	63
52	The PDZ domain as you like it. Nature Biotechnology, 1999, 17, 132-133.	9.4	3
53	Caspase-3 inhibits growth inSaccharomyces cerevisiaewithout causing cell death1. FEBS Letters, 1999, 446, 9-14.	1.3	24
54	Mutation detection by a two-hybrid assay. Human Molecular Genetics, 1998, 7, 1029-1032.	1.4	30

#	ARTICLE	IF	CITATIONS
55	The future is function. Nature Genetics, 1997, 15, 325-327.	9.4	74
56	A conserved RNA-binding protein that regulates sexual fates in the C. elegans hermaphrodite germ line. Nature, 1997, 390, 477-484.	13.7	493