# Stanley Fields

## List of Publications by Year
in descending order

| 56 | 7,337 | 159358 | 149479 |
|:---:|:---:|:---:|:---:|
| papers | citations | 30 | 56 |
| | | h-index | g-index |

| 66 | 66 | 66 | 8482 |
|:---:|:---:|:---:|:---:|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 1 | A network of protein–protein interactions in yeast. Nature Biotechnology, 2000, 18, 1257-1261. | 9.4 | 1,281 |
| 2 | Deep mutational scanning: a new style of protein science. Nature Methods, 2014, 11, 801-807. | 9.0 | 885 |
| 3 | Global analysis of phosphorylation and ubiquitylation cross-talk in protein degradation. Nature Methods, 2013, 10, 676-682. | 9.0 | 520 |
| 4 | A conserved RNA-binding protein that regulates sexual fates in the C. elegans hermaphrodite germ line. Nature, 1997, 390, 477-484. | 13.7 | 493 |
| 5 | High-resolution mapping of protein sequence-function relationships. Nature Methods, 2010, 7, 741-746. | 9.0 | 482 |
| 6 | Dynamics of Gene Expression in Single Root Cells of *Arabidopsis thaliana*. Plant Cell, 2019, 31, 993-1011. | 3.1 | 279 |
| 7 | Engineering an allosteric transcription factor to respond to new ligands. Nature Methods, 2016, 13, 177-183. | 9.0 | 274 |
| 8 | Massively Parallel Functional Analysis of BRCA1 RING Domain Variants. Genetics, 2015, 200, 413-422. | 1.2 | 272 |
| 9 | Proteomics in Genomeland. Science, 2001, 291, 1221-1224. | 6.0 | 226 |
| 10 | 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 |
| 11 | Deep mutational scanning of an RRM domain of the *Saccharomyces cerevisiae* poly(A)-binding protein. Rna, 2013, 19, 1537-1551. | 1.6 | 207 |
| 12 | Adjacent Codons Act in Concert to Modulate Translation Efficiency in Yeast. Cell, 2016, 166, 679-690. | 13.5 | 180 |
| 13 | 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 |
| 14 | High-throughput two-hybrid analysis. The promise and the peril. FEBS Journal, 2005, 272, 5391-5399. | 2.2 | 163 |
| 15 | Massively parallel single-amino-acid mutagenesis. Nature Methods, 2015, 12, 203-206. | 9.0 | 153 |
| 16 | Measuring the activity of protein variants on a large scale using deep mutational scanning. Nature Protocols, 2014, 9, 2267-2284. | 5.5 | 147 |
| 17 | Dimensionality reduction by UMAP to visualize physical and genetic interactions. Nature Communications, 2020, 11, 1537. | 5.8 | 126 |
| 18 | CELL BIOLOGY: Whither Model Organism Research?. Science, 2005, 307, 1885-1886. | 6.0 | 118 |

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|---|---------|-----|-----------|
| 19 | 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 |
| 20 | A yeast sensor of ligand binding. Nature Biotechnology, 2001, 19, 1042-1046. | 9.4 | 86 |
| 21 | The regulatory landscape of Arabidopsis thaliana roots at single-cell resolution. Nature Communications, 2021, 12, 3334. | 5.8 | 84 |
| 22 | Synthetic promoter designs enabled by a comprehensive analysis of plant core promoters. Nature Plants, 2021, 7, 842-855. | 4.7 | 78 |
| 23 | The future is function. Nature Genetics, 1997, 15, 325-327. | 9.4 | 74 |
| 24 | Engineering allostery. Trends in Genetics, 2014, 30, 521-528. | 2.9 | 64 |
| 25 | Identification of RNAs that bind to a specific protein using the yeast three-hybrid system. Rna, 1999, 5, 596-601. | 1.6 | 63 |
| 26 | 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 |
| 27 | Identification of Plant Enhancers and Their Constituent Elements by STARR-seq in Tobacco Leaves. Plant Cell, 2020, 32, 2120-2131. | 3.1 | 53 |
| 28 | Interactive learning: Lessons from two hybrids over two decades. Proteomics, 2009, 9, 5209-5213. | 1.3 | 39 |
| 29 | A homolog of lariat-debranching enzyme modulates turnover of branched RNA. Rna, 2014, 20, 1337-1348. | 1.6 | 34 |
| 30 | Mutation detection by a two-hybrid assay. Human Molecular Genetics, 1998, 7, 1029-1032. | 1.4 | 30 |
| 31 | MOLECULAR BIOLOGY: Site-Seeing by Sequencing. Science, 2007, 316, 1441-1442. | 6.0 | 29 |
| 32 | 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 |
| 33 | Combining Natural Sequence Variation with High Throughput Mutational Data to Reveal Protein Interaction Sites. PLoS Genetics, 2015, 11, e1004918. | 1.5 | 26 |
| 34 | Conditional accumulation of toxic tRNAs to cause amino acid misincorporation. Nucleic Acids Research, 2018, 46, 7831-7843. | 6.5 | 25 |
| 35 | Caspase-3 inhibits growth inSaccharomyces cerevisiaewithout causing cell death1. FEBS Letters, 1999, 446, 9-14. | 1.3 | 24 |
| 36 | Massively Parallel Genetics. Genetics, 2016, 203, 617-619. | 1.2 | 24 |

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|---|---------|-----|-----------|
| 37 | Comprehensive Analysis of the *SUL1* Promoter of *Saccharomyces cerevisiae*. Genetics, 2016, 203, 191-202. | 1.2 | 22 |
| 38 | Engineered Biosensors from Dimeric Ligand-Binding Domains. ACS Synthetic Biology, 2018, 7, 2457-2467. | 1.9 | 21 |
| 39 | High-throughput identification of dominant negative polypeptides in yeast. Nature Methods, 2019, 16, 413-416. | 9.0 | 20 |
| 40 | A tetO Toolkit To Alter Expression of Genes in *Saccharomyces cerevisiae*. ACS Synthetic Biology, 2015, 4, 842-852. | 1.9 | 18 |
| 41 | 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 |
| 42 | Constitutive activation of theSaccharomyces cerevisiae transcriptional regulator Ste12p by mutations at the amino-terminus. Yeast, 2000, 16, 1365-1375. | 0.8 | 13 |
| 43 | The role of functional data in interpreting the effects of genetic variation. Molecular Biology of the Cell, 2015, 26, 3904-3908. | 0.9 | 13 |
| 44 | Grass-roots genomics. Nature Genetics, 2000, 24, 5-6. | 9.4 | 10 |
| 45 | Distinct patterns of mutational sensitivity for Î» resistance and maltodextrin transport in Escherichia coli LamB. Microbial Genomics, 2020, 6, . | 1.0 | 9 |
| 46 | GENOMICS: A Crisis in Postgenomic Nomenclature. Science, 2002, 296, 671-672. | 6.0 | 8 |
| 47 | Binding and Regulation of Transcription by Yeast Ste12 Variants To Drive Mating and Invasion Phenotypes. Genetics, 2020, 214, 397-407. | 1.2 | 8 |
| 48 | Balance between promiscuity and specificity in phage Î» host range. ISME Journal, 2021, 15, 2195-2205. | 4.4 | 8 |
| 49 | Expanding the binding specificity for RNA recognition by a PUF domain. Nature Communications, 2021, 12, 5107. | 5.8 | 8 |
| 50 | Deep Mutational Scanning: Library Construction, Functional Selection, and High-Throughput Sequencing. Cold Spring Harbor Protocols, 2015, 2015, pdb.prot085225. | 0.2 | 6 |
| 51 | 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 |
| 52 | Effects of sequence motifs in the yeast 3â€² untranslated region determined from massively parallel assays of random sequences. Genome Biology, 2021, 22, 293. | 3.8 | 6 |
| 53 | Would Fred Sanger Get Funded Today?. Genetics, 2014, 197, 435-439. | 1.2 | 4 |
| 54 | The PDZ domain as you like it. Nature Biotechnology, 1999, 17, 132-133. | 9.4 | 3 |

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|---|---------|-----|-----------|
| 55 | 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 |
| 56 | Approaches to Analyze Protein Interactions. Scientific World Journal, The, 2002, 2, 93-94. | 0.8 | 0 |