Douglas M Fowler

List of Publications by Year
in descending order

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67	8,567	117625	102487
papers	citations	34 h-index	66 g-index

92	92	92	9468
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Measuring Pharmacogene Variant Function at Scale Using Multiplexed Assays. Annual Review of Pharmacology and Toxicology, 2022, 62, 531-550.	9.4	9
2	Environmental selection and epistasis in an empirical phenotypeâ€“environmentâ€“fitness landscape. Nature Ecology and Evolution, 2022, 6, 427-438.	7.8	10
3	Understanding the Origins of Loss of Protein Function by Analyzing the Effects of Thousands of Variants on Activity and Abundance. Molecular Biology and Evolution, 2021, 38, 3235-3246.	8.9	65
4	MaveRegistry: a collaboration platform for multiplexed assays of variant effect. Bioinformatics, 2021, 37, 3382-3383.	4.1	9
5	Massively parallel characterization of CYP2C9 variant enzyme activity and abundance. American Journal of Human Genetics, 2021, 108, 1735-1751.	6.2	53
6	Integrating thousands of PTEN variant activity and abundance measurements reveals variant subgroups and new dominant negatives in cancers. Genome Medicine, 2021, 13, 165.	8.2	14
7	Closing the gap: Systematic integration of multiplexed functional data resolves variants of uncertain significance in BRCA1, TP53, and PTEN. American Journal of Human Genetics, 2021, 108, 2248-2258.	6.2	42
8	Probing ion channel functional architecture and domain recombination compatibility by massively parallel domain insertion profiling. Nature Communications, 2021, 12, 7114.	12.8	19
9	An improved platform for functional assessment of large protein libraries in mammalian cells. Nucleic Acids Research, 2020, 48, e1.	14.5	51
10	Keeping up with the genomes: scaling genomic variant interpretation. Genome Medicine, 2020, 12, 5.	8.2	13
11	Temporal and rheostatic control of genome editing with a chemically-inducible Cas9. Methods in Enzymology, 2020, 633, 119-141.	1.0	3
12	Classifying disease-associated variants using measures of protein activity and stability. , 2020, , 91-107.		21
13	A Premalignant Cell-Based Model for Functionalization and Classification of PTEN Variants. Cancer Research, 2020, 80, 2775-2789.	0.9	11
14	Suppression of unwanted CRISPR-Cas9 editing by co-administration of catalytically inactivating truncated guide RNAs. Nature Communications, 2020, 11, 2697.	12.8	42
15	Parallel Chemoselective Profiling for Mapping Protein Structure. Cell Chemical Biology, 2020, 27, 1084-1096.e4.	5.2	6
16	High-throughput discovery of trafficking-deficient variants in the cardiac potassium channel KV11.1. Heart Rhythm, 2020, 17, 2180-2189.	0.7	42
17	Massively parallel variant characterization identifies NUDT15 alleles associated with thiopurine toxicity. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5394-5401.	7.1	95
18	Systematic misclassification of missense variants in BRCA1 and BRCA2 â€œcoldspotsâ€• Genetics in Medicine, 2020, 22, 825-830.	2.4	32

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19	Deep Mutational Scan of an SCN5A Voltage Sensor. Circulation Genomic and Precision Medicine, 2020, 13, e002786.	3.6	33
20	Highâ€throughput, microscopeâ€based sorting to dissect cellular heterogeneity. Molecular Systems Biology, 2020, 16, e9442.	7.2	46
21	Comprehensive exploration of the translocation, stability and substrate recognition requirements in VIM-2 lactamase. ELife, 2020, 9, .	6.0	26
22	Multiplexed measurement of variant abundance and activity reveals VKOR topology, active site and human variant impact. ELife, 2020, 9, .	6.0	58
23	Mutagenesis-based protein structure determination. Nature Genetics, 2019, 51, 1072-1073.	21.4	5
24	MaveDB: an open-source platform to distribute and interpret data from multiplexed assays of variant effect. Genome Biology, 2019, 20, 223.	8.8	130
25	The Impact of Genetic Variants on PTEN Molecular Functions and Cellular Phenotypes. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a036228.	6.2	9
26	Biophysical and Mechanistic Models for Disease-Causing Protein Variants. Trends in Biochemical Sciences, 2019, 44, 575-588.	7.5	143
27	Applying Multiplex Assays to Understand Variation in Pharmacogenes. Clinical Pharmacology and Therapeutics, 2019, 106, 290-294.	4.7	15
28	A Combined Approach Reveals a Regulatory Mechanism Coupling Srcâ€™s Kinase Activity, Localization, and Phosphotransferase-Independent Functions. Molecular Cell, 2019, 74, 393-408.e20.	9.7	45
29	Elucidating the Molecular Determinants of AÎ² Aggregation with Deep Mutational Scanning. G3: Genes, Genomes, Genetics, 2019, 9, 3683-3689.	1.8	32
30	Recommendations for the collection and use of multiplexed functional data for clinical variant interpretation. Genome Medicine, 2019, 11, 85.	8.2	47
31	Quantitative Missense Variant Effect Prediction Using Large-Scale Mutagenesis Data. Cell Systems, 2018, 6, 116-124.e3.	6.2	176
32	Rheostatic Control of Cas9-Mediated DNA Double Strand Break (DSB) Generation and Genome Editing. ACS Chemical Biology, 2018, 13, 438-442.	3.4	13
33	Multiplex assessment of protein variant abundance by massively parallel sequencing. Nature Genetics, 2018, 50, 874-882.	21.4	323
34	Pharmacogenomics of CYP2C9: Functional and Clinical Considerations. Journal of Personalized Medicine, 2018, 8, 1.	2.5	136
35	A platform for functional assessment of large variant libraries in mammalian cells. Nucleic Acids Research, 2017, 45, e102-e102.	14.5	80
36	Bedside Back to Bench: Building Bridges between Basic and Clinical Genomic Research. Cell, 2017, 169, 6-12.	28.9	103

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37	Expression and Functional Characterization of Breast Cancer-Associated Cytochrome P450 4Z1 inSaccharomyces cerevisiae. Drug Metabolism and Disposition, 2017, 45, 1364-1371.	3.3	35
38	Variant Interpretation: Functional Assays to the Rescue. American Journal of Human Genetics, 2017, 101, 315-325.	6.2	275
39	Rapidly inducible Cas9 and DSB-ddPCR to probe editing kinetics. Nature Methods, 2017, 14, 891-896.	19.0	88
40	New Pharmacogenomics Research Network: An Open Community Catalyzing Research and Translation in Precision Medicine. Clinical Pharmacology and Therapeutics, 2017, 102, 897-902.	4.7	34
41	Analysis of Large-Scale Mutagenesis Data To Assess the Impact of Single Amino Acid Substitutions. Genetics, 2017, 207, 53-61.	2.9	101
42	Early emergence of negative regulation of the tyrosine kinase Src by the C-terminal Src kinase. Journal of Biological Chemistry, 2017, 292, 18518-18529.	3.4	7
43	A framework for exhaustively mapping functional missense variants. Molecular Systems Biology, 2017, 13, 957.	7.2	146
44	A statistical framework for analyzing deep mutational scanning data. Genome Biology, 2017, 18, 150.	8.8	155
45	Novel Rhizosphere Soil Alleles for the Enzyme 1-Aminocyclopropane-1-Carboxylate Deaminase Queried for Function with an In Vivo Competition Assay. Applied and Environmental Microbiology, 2016, 82, 1050-1059.	3.1	13
46	Massively Parallel Functional Analysis of BRCA1 RING Domain Variants. Genetics, 2015, 200, 413-422.	2.9	272
47	Measuring the activity of protein variants on a large scale using deep mutational scanning. Nature Protocols, 2014, 9, 2267-2284.	12.0	147
48	Deep mutational scanning: a new style of protein science. Nature Methods, 2014, 11, 801-807.	19.0	885
49	Contemporary, yeast-based approaches to understanding human genetic variation. Current Opinion in Genetics and Development, 2013, 23, 658-664.	3.3	34
50	Engineering A-kinase Anchoring Protein (AKAP)-selective Regulatory Subunits of Protein Kinase A (PKA) through Structure-based Phage Selection. Journal of Biological Chemistry, 2013, 288, 17111-17121.	3.4	34
51	Activity-enhancing mutations in an E3 ubiquitin ligase identified by high-throughput mutagenesis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E1263-72.	7.1	158
52	Functional Amyloidogenesis and Cytotoxicityâ€"Insights into Biology and Pathology. PLoS Biology, 2012, 10, e1001459.	5.6	14
53	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.	7.1	226
54	Suppression of statin effectiveness by copper and zinc in yeast and human cells. Molecular BioSystems, 2011, 7, 533-544.	2.9	23

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55	Deep mutational scanning: assessing protein function on a massive scale. Trends in Biotechnology, 2011, 29, 435-442.	9.3	174
56	Enrich: software for analysis of protein function by enrichment and depletion of variants. Bioinformatics, 2011, 27, 3430-3431.	4.1	112
57	High-resolution mapping of protein sequence-function relationships. Nature Methods, 2010, 7, 741-746.	19.0	482
58	N-terminal Domains Elicit Formation of Functional Pmel17 Amyloid Fibrils. Journal of Biological Chemistry, 2009, 284, 35543-35555.	3.4	101
59	Aggregating Knowledge about Prions and Amyloid. Cell, 2009, 137, 20-22.	28.9	10
60	Partial Restoration of Mutant Enzyme Homeostasis in Three Distinct Lysosomal Storage Disease Cell Lines by Altering Calcium Homeostasis. PLoS Biology, 2008, 6, e26.	5.6	110
61	Semen-Derived Amyloid Fibrils Drastically Enhance HIV Infection. Cell, 2007, 131, 1059-1071.	28.9	510
62	The dynamin middle domain is critical for tetramerization and higher-order self-assembly. EMBO Journal, 2007, 26, 559-566.	7.8	164
63	Functional amyloid â€“ from bacteria to humans. Trends in Biochemical Sciences, 2007, 32, 217-224.	7.5	953
64	Elevated levels of oxidized cholesterol metabolites in Lewy body disease brains accelerate Î±-synuclein fibrilization. Nature Chemical Biology, 2006, 2, 249-253.	8.0	312
65	Structure of the Sec13/31 COPII coat cage. Nature, 2006, 439, 234-238.	27.8	286
66	Functional Amyloid Formation within Mammalian Tissue. PLoS Biology, 2005, 4, e6.	5.6	672
67	Protocol for rapidly inducible Cas9 and DSB-ddPCR. Protocol Exchange, 0, , .	0.3	2