# Douglas M Fowler

List of Publications by Year
in descending order



| 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 | Functional amyloid â€“ from bacteria to humans. Trends in Biochemical Sciences, 2007, 32, 217-224. | 7.5 | 953 |
| 2 | Deep mutational scanning: a new style of protein science. Nature Methods, 2014, 11, 801-807. | 19.0 | 885 |
| 3 | Functional Amyloid Formation within Mammalian Tissue. PLoS Biology, 2005, 4, e6. | 5.6 | 672 |
| 4 | Semen-Derived Amyloid Fibrils Drastically Enhance HIV Infection. Cell, 2007, 131, 1059-1071. | 28.9 | 510 |
| 5 | High-resolution mapping of protein sequence-function relationships. Nature Methods, 2010, 7, 741-746. | 19.0 | 482 |
| 6 | Multiplex assessment of protein variant abundance by massively parallel sequencing. Nature Genetics, 2018, 50, 874-882. | 21.4 | 323 |
| 7 | 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 |
| 8 | Structure of the Sec13/31 COPII coat cage. Nature, 2006, 439, 234-238. | 27.8 | 286 |
| 9 | Variant Interpretation: Functional Assays to the Rescue. American Journal of Human Genetics, 2017, 101, 315-325. | 6.2 | 275 |
| 10 | Massively Parallel Functional Analysis of BRCA1 RING Domain Variants. Genetics, 2015, 200, 413-422. | 2.9 | 272 |
| 11 | 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 |
| 12 | Quantitative Missense Variant Effect Prediction Using Large-Scale Mutagenesis Data. Cell Systems, 2018, 6, 116-124.e3. | 6.2 | 176 |
| 13 | Deep mutational scanning: assessing protein function on a massive scale. Trends in Biotechnology, 2011, 29, 435-442. | 9.3 | 174 |
| 14 | The dynamin middle domain is critical for tetramerization and higher-order self-assembly. EMBO Journal, 2007, 26, 559-566. | 7.8 | 164 |
| 15 | 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 |
| 16 | A statistical framework for analyzing deep mutational scanning data. Genome Biology, 2017, 18, 150. | 8.8 | 155 |
| 17 | Measuring the activity of protein variants on a large scale using deep mutational scanning. Nature Protocols, 2014, 9, 2267-2284. | 12.0 | 147 |
| 18 | A framework for exhaustively mapping functional missense variants. Molecular Systems Biology, 2017, 13, 957. | 7.2 | 146 |

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|---|---|---|---|
| 19 | Biophysical and Mechanistic Models for Disease-Causing Protein Variants. Trends in Biochemical Sciences, 2019, 44, 575-588. | 7.5 | 143 |
| 20 | Pharmacogenomics of CYP2C9: Functional and Clinical Considerations. Journal of Personalized Medicine, 2018, 8, 1. | 2.5 | 136 |
| 21 | MaveDB: an open-source platform to distribute and interpret data from multiplexed assays of variant effect. Genome Biology, 2019, 20, 223. | 8.8 | 130 |
| 22 | Enrich: software for analysis of protein function by enrichment and depletion of variants. Bioinformatics, 2011, 27, 3430-3431. | 4.1 | 112 |
| 23 | 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 |
| 24 | Bedside Back to Bench: Building Bridges between Basic and Clinical Genomic Research. Cell, 2017, 169, 6-12. | 28.9 | 103 |
| 25 | N-terminal Domains Elicit Formation of Functional Pmel17 Amyloid Fibrils. Journal of Biological Chemistry, 2009, 284, 35543-35555. | 3.4 | 101 |
| 26 | Analysis of Large-Scale Mutagenesis Data To Assess the Impact of Single Amino Acid Substitutions. Genetics, 2017, 207, 53-61. | 2.9 | 101 |
| 27 | 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 |
| 28 | Rapidly inducible Cas9 and DSB-ddPCR to probe editing kinetics. Nature Methods, 2017, 14, 891-896. | 19.0 | 88 |
| 29 | A platform for functional assessment of large variant libraries in mammalian cells. Nucleic Acids Research, 2017, 45, e102-e102. | 14.5 | 80 |
| 30 | 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 |
| 31 | Multiplexed measurement of variant abundance and activity reveals VKOR topology, active site and human variant impact. ELife, 2020, 9, . | 6.0 | 58 |
| 32 | Massively parallel characterization of CYP2C9 variant enzyme activity and abundance. American Journal of Human Genetics, 2021, 108, 1735-1751. | 6.2 | 53 |
| 33 | An improved platform for functional assessment of large protein libraries in mammalian cells. Nucleic Acids Research, 2020, 48, e1. | 14.5 | 51 |
| 34 | Recommendations for the collection and use of multiplexed functional data for clinical variant interpretation. Genome Medicine, 2019, 11, 85. | 8.2 | 47 |
| 35 | Highâ€throughput, microscopeâ€based sorting to dissect cellular heterogeneity. Molecular Systems Biology, 2020, 16, e9442. | 7.2 | 46 |
| 36 | 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 |

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|---|---|---|---|
| 37 | Suppression of unwanted CRISPR-Cas9 editing by co-administration of catalytically inactivating truncated guide RNAs. Nature Communications, 2020, 11, 2697. | 12.8 | 42 |
| 38 | High-throughput discovery of trafficking-deficient variants in the cardiac potassium channel KV11.1. Heart Rhythm, 2020, 17, 2180-2189. | 0.7 | 42 |
| 39 | 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 |
| 40 | Expression and Functional Characterization of Breast Cancer-Associated Cytochrome P450 4Z1 inSaccharomyces cerevisiae. Drug Metabolism and Disposition, 2017, 45, 1364-1371. | 3.3 | 35 |
| 41 | Contemporary, yeast-based approaches to understanding human genetic variation. Current Opinion in Genetics and Development, 2013, 23, 658-664. | 3.3 | 34 |
| 42 | 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 |
| 43 | 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 |
| 44 | Deep Mutational Scan of an SCN5A Voltage Sensor. Circulation Genomic and Precision Medicine, 2020, 13, e002786. | 3.6 | 33 |
| 45 | Elucidating the Molecular Determinants of AÎ² Aggregation with Deep Mutational Scanning. G3: Genes, Genomes, Genetics, 2019, 9, 3683-3689. | 1.8 | 32 |
| 46 | Systematic misclassification of missense variants in BRCA1 and BRCA2 â€œcoldspotsâ€• Genetics in Medicine, 2020, 22, 825-830. | 2.4 | 32 |
| 47 | Comprehensive exploration of the translocation, stability and substrate recognition requirements in VIM-2 lactamase. ELife, 2020, 9, . | 6.0 | 26 |
| 48 | Suppression of statin effectiveness by copper and zinc in yeast and human cells. Molecular BioSystems, 2011, 7, 533-544. | 2.9 | 23 |
| 49 | Classifying disease-associated variants using measures of protein activity and stability. , 2020, , 91-107. | | 21 |
| 50 | Probing ion channel functional architecture and domain recombination compatibility by massively parallel domain insertion profiling. Nature Communications, 2021, 12, 7114. | 12.8 | 19 |
| 51 | Applying Multiplex Assays to Understand Variation in Pharmacogenes. Clinical Pharmacology and Therapeutics, 2019, 106, 290-294. | 4.7 | 15 |
| 52 | Functional Amyloidogenesis and Cytotoxicityâ€”Insights into Biology and Pathology. PLoS Biology, 2012, 10, e1001459. | 5.6 | 14 |
| 53 | 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 |
| 54 | 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 |

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|---|---|---|---|
| 55 | Rheostatic Control of Cas9-Mediated DNA Double Strand Break (DSB) Generation and Genome Editing. ACS Chemical Biology, 2018, 13, 438-442. | 3.4 | 13 |
| 56 | Keeping up with the genomes: scaling genomic variant interpretation. Genome Medicine, 2020, 12, 5. | 8.2 | 13 |
| 57 | A Premalignant Cell-Based Model for Functionalization and Classification of PTEN Variants. Cancer Research, 2020, 80, 2775-2789. | 0.9 | 11 |
| 58 | Aggregating Knowledge about Prions and Amyloid. Cell, 2009, 137, 20-22. | 28.9 | 10 |
| 59 | Environmental selection and epistasis in an empirical phenotypeâ€“environmentâ€“fitness landscape. Nature Ecology and Evolution, 2022, 6, 427-438. | 7.8 | 10 |
| 60 | The Impact of Genetic Variants on PTEN Molecular Functions and Cellular Phenotypes. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a036228. | 6.2 | 9 |
| 61 | MaveRegistry: a collaboration platform for multiplexed assays of variant effect. Bioinformatics, 2021, 37, 3382-3383. | 4.1 | 9 |
| 62 | Measuring Pharmacogene Variant Function at Scale Using Multiplexed Assays. Annual Review of Pharmacology and Toxicology, 2022, 62, 531-550. | 9.4 | 9 |
| 63 | 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 |
| 64 | Parallel Chemoselective Profiling for Mapping Protein Structure. Cell Chemical Biology, 2020, 27, 1084-1096.e4. | 5.2 | 6 |
| 65 | Mutagenesis-based protein structure determination. Nature Genetics, 2019, 51, 1072-1073. | 21.4 | 5 |
| 66 | Temporal and rheostatic control of genome editing with a chemically-inducible Cas9. Methods in Enzymology, 2020, 633, 119-141. | 1.0 | 3 |
| 67 | Protocol for rapidly inducible Cas9 and DSB-ddPCR. Protocol Exchange, 0, , . | 0.3 | 2 |