

# Samuel A Danziger

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5109753/publications.pdf>

Version: 2024-02-01

25  
papers

534  
citations

759233

12  
h-index

794594

19  
g-index

28  
all docs

28  
docs citations

28  
times ranked

989  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Linking EPCR-Binding PfEMP1 to Brain Swelling in Pediatric Cerebral Malaria. <i>Cell Host and Microbe</i> , 2017, 22, 601-614.e5.  | 11.0 | 92        |
| 2  | Severe adult malaria is associated with specific PfEMP1 adhesion types and high parasite biomass. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3270-9.     | 7.1  | 87        |
| 3  | Predicting Positive p53 Cancer Rescue Regions Using Most Informative Positive (MIP) Active Learning. <i>PLoS Computational Biology</i> , 2009, 5, e1000498.  | 3.2  | 49        |
| 4  | Combining inferred regulatory and reconstructed metabolic networks enhances phenotype prediction in yeast. <i>PLoS Computational Biology</i> , 2017, 13, e1005489.   | 3.2  | 46        |
| 5  | Predicting Antidisease Immunity Using Proteome Arrays and Sera from Children Naturally Exposed to Malaria. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2646-2660.   | 3.8  | 36        |
| 6  | Multiple Myeloma DREAM Challenge reveals epigenetic regulator PHF19 as marker of aggressive disease. <i>Leukemia</i> , 2020, 34, 1866-1874.  | 7.2  | 36        |
| 7  | Bone marrow microenvironments that contribute to patient outcomes in newly diagnosed multiple myeloma: A cohort study of patients in the Total Therapy clinical trials. <i>PLoS Medicine</i> , 2020, 17, e1003323. | 8.4  | 33        |
| 8  | Functional Census of Mutation Sequence Spaces: The Example of p53 Cancer Rescue Mutants. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2006, 3, 114-125.                              | 3.0  | 28        |
| 9  | Molecular mechanisms of system responses to novel stimuli are predictable from public data. <i>Nucleic Acids Research</i> , 2014, 42, 1442-1460.   | 14.5 | 28        |
| 10 | A generalizable data-driven multicellular model of pancreatic ductal adenocarcinoma. <i>GigaScience</i> , 2020, 9, .   | 6.4  | 20        |
| 11 | ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. <i>PLoS ONE</i> , 2019, 14, e0224693.  | 2.5  | 19        |
| 12 | All-codon scanning identifies p53 cancer rescue mutations. <i>Nucleic Acids Research</i> , 2010, 38, 7079-7088.  | 14.5 | 17        |
| 13 | The Promise of Systems Biology Approaches for Revealing Host Pathogen Interactions in Malaria. <i>Frontiers in Microbiology</i> , 2017, 8, 2183.   | 3.5  | 17        |
| 14 | The functional role of SUMO E3 ligase Mms21p in the maintenance of subtelomeric silencing in budding yeast. <i>Biochemical and Biophysical Research Communications</i> , 2013, 438, 746-752.                       | 2.1  | 5         |
| 15 | Genetic program activity delineates risk, relapse, and therapy responsiveness in multiple myeloma. <i>Npj Precision Oncology</i> , 2021, 5, 60.  | 5.4  | 5         |
| 16 | Bicluster Sampled Coherence Metric (BSCM) provides an accurate environmental context for phenotype predictions. <i>BMC Systems Biology</i> , 2015, 9, S1.  | 3.0  | 4         |
| 17 | Baseline and on-Treatment Bone Marrow Microenvironments Predict Myeloma Patient Outcomes and Inform Potential Intervention Strategies. <i>Blood</i> , 2018, 132, 1882-1882.  | 1.4  | 3         |
| 18 | Systematic Analysis of Yeast Proteome Reveals Peptide Detectability Factors for Mass Spectrometry. <i>Journal of Proteomics and Bioinformatics</i> , 2015, 8, 231-239.   | 0.4  | 3         |

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|----|---|------|-----------|
| 19 | A systems-level gene regulatory network model for <i>Plasmodium falciparum</i> . Nucleic Acids Research, 2021, 49, 4891-4906.             | 14.5 | 2         |
| 20 | P3179: Development of an Indicator Cell Assay for Blood-Based Diagnosis of Alzheimer's Disease. Alzheimer's and Dementia, 2016, 12, P889. | 0.8  | 0         |
| 21 | An indicator cell assay for blood-based diagnostics. PLoS ONE, 2017, 12, e0178608.  | 2.5  | 0         |
| 22 | ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. , 2019, 14, e0224693.                                 |      | 0         |
| 23 | ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. , 2019, 14, e0224693.                                 |      | 0         |
| 24 | ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. , 2019, 14, e0224693.                                 |      | 0         |
| 25 | ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. , 2019, 14, e0224693.                                 |      | 0         |