

Samuel A Danziger

List of Publications by Year in descending order

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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	A systems-level gene regulatory network model for <i>Plasmodium falciparum</i> . <i>Nucleic Acids Research</i> , 2021, 49, 4891-4906.	14.5	2
2	Genetic program activity delineates risk, relapse, and therapy responsiveness in multiple myeloma. <i>Npj Precision Oncology</i> , 2021, 5, 60.	5.4	5
3	A generalizable data-driven multicellular model of pancreatic ductal adenocarcinoma. <i>GigaScience</i> , 2020, 9, .	6.4	20
4	Multiple Myeloma DREAM Challenge reveals epigenetic regulator PHF19 as marker of aggressive disease. <i>Leukemia</i> , 2020, 34, 1866-1874.	7.2	36
5	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
6	ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. <i>PLoS ONE</i> , 2019, 14, e0224693.	2.5	19
7	ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. , 2019, 14, e0224693.		0
8	ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. , 2019, 14, e0224693.		0
9	ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. , 2019, 14, e0224693.		0
10	ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. , 2019, 14, e0224693.		0
11	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
12	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
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	Combining inferred regulatory and reconstructed metabolic networks enhances phenotype prediction in yeast. <i>PLoS Computational Biology</i> , 2017, 13, e1005489.	3.2	46
15	An indicator cell assay for blood-based diagnostics. <i>PLoS ONE</i> , 2017, 12, e0178608.	2.5	0
16	P3179: Development of an Indicator Cell Assay for Blood-Based Diagnosis of Alzheimer's Disease. <i>Alzheimer's and Dementia</i> , 2016, 12, P889.	0.8	0
17	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
18	Bicluster Sampled Coherence Metric (BSCM) provides an accurate environmental context for phenotype predictions. <i>BMC Systems Biology</i> , 2015, 9, S1.	3.0	4

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19	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
20	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
21	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
22	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
23	All-codon scanning identifies p53 cancer rescue mutations. <i>Nucleic Acids Research</i> , 2010, 38, 7079-7088.	14.5	17
24	Predicting Positive p53 Cancer Rescue Regions Using Most Informative Positive (MIP) Active Learning. <i>PLoS Computational Biology</i> , 2009, 5, e1000498.	3.2	49
25	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