

Aleksej Zelezniak

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3879392/publications.pdf>

Version: 2024-02-01

30
papers

2,892
citations

304743

22
h-index

501196

28
g-index

46
all docs

46
docs citations

46
times ranked

4932
citing authors

#	ARTICLE	IF	CITATIONS
1	A proteomic survival predictor for COVID-19 patients in intensive care. , 2022, 1, e0000007.		28
2	Data mining of <i>Saccharomyces cerevisiae</i> mutants engineered for increased tolerance towards inhibitors in lignocellulosic hydrolysates. <i>Biotechnology Advances</i> , 2022, 57, 107947.	11.7	29
3	Performance of Regression Models as a Function of Experiment Noise. <i>Bioinformatics and Biology Insights</i> , 2021, 15, 117793222110203.	2.0	9
4	metaGEM: reconstruction of genome scale metabolic models directly from metagenomes. <i>Nucleic Acids Research</i> , 2021, 49, e126-e126.	14.5	50
5	Bayesian genome scale modelling identifies thermal determinants of yeast metabolism. <i>Nature Communications</i> , 2021, 12, 190.	12.8	25
6	Benchmarking accuracy and precision of intensity-based absolute quantification of protein abundances in <i>Saccharomyces cerevisiae</i> . <i>Proteomics</i> , 2021, 21, e2000093.	2.2	13
7	Expanding functional protein sequence spaces using generative adversarial networks. <i>Nature Machine Intelligence</i> , 2021, 3, 324-333.	16.0	165
8	Ultra-fast proteomics with Scanning SWATH. <i>Nature Biotechnology</i> , 2021, 39, 846-854.	17.5	173
9	Learning the Regulatory Code of Gene Expression. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 673363.	3.5	17
10	Potential for improved retention rate by personalized antiseizure medication selection: A register-based analysis. <i>Epilepsia</i> , 2021, 62, 2123-2132.	5.1	7
11	A time-resolved proteomic and prognostic map of COVID-19. <i>Cell Systems</i> , 2021, 12, 780-794.e7.	6.2	125
12	Plastic-Degrading Potential across the Global Microbiome Correlates with Recent Pollution Trends. <i>MBio</i> , 2021, 12, e0215521.	4.1	51
13	Deep learning suggests that gene expression is encoded in all parts of a co-evolving interacting gene regulatory structure. <i>Nature Communications</i> , 2020, 11, 6141.	12.8	83
14	Parallel Factor Analysis Enables Quantification and Identification of Highly Convolved Data-Independent-Acquired Protein Spectra. <i>Patterns</i> , 2020, 1, 100137.	5.9	2
15	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. <i>Cell Systems</i> , 2020, 11, 11-24.e4.	6.2	439
16	Learning the regulatory grammar of DNA for gene expression engineering. , 2020, , .		0
17	Ice-Age Climate Adaptations Trap the Alpine Marmot in a State of Low Genetic Diversity. <i>Current Biology</i> , 2019, 29, 1712-1720.e7.	3.9	27
18	Biochemical principles enabling metabolic cooperativity and phenotypic heterogeneity at the single cell level. <i>Current Opinion in Systems Biology</i> , 2018, 8, 97-108.	2.6	29

#	ARTICLE	IF	CITATIONS
19	Cost-effective generation of precise label-free quantitative proteomes in high-throughput by microLC and data-independent acquisition. <i>Scientific Reports</i> , 2018, 8, 4346.	3.3	66
20	Nutritional preferences of human gut bacteria reveal their metabolic idiosyncrasies. <i>Nature Microbiology</i> , 2018, 3, 514-522.	13.3	196
21	Machine Learning Predicts the Yeast Metabolome from the Quantitative Proteome of Kinase Knockouts. <i>Cell Systems</i> , 2018, 7, 269-283.e6.	6.2	80
22	Designing and interpreting "multi-omic"™ experiments that may change our understanding of biology. <i>Current Opinion in Systems Biology</i> , 2017, 6, 37-45.	2.6	81
23	The self-inhibitory nature of metabolic networks and its alleviation through compartmentalization. <i>Nature Communications</i> , 2017, 8, 16018.	12.8	95
24	Functional Metabolomics Describes the Yeast Biosynthetic Regulome. <i>Cell</i> , 2016, 167, 553-565.e12.	28.9	137
25	The metabolic background is a global player in <i>Saccharomyces</i> gene expression epistasis. <i>Nature Microbiology</i> , 2016, 1, 15030.	13.3	76
26	Metabolic dependencies drive species co-occurrence in diverse microbial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6449-6454.	7.1	588
27	Contribution of Network Connectivity in Determining the Relationship between Gene Expression and Metabolite Concentration Changes. <i>PLoS Computational Biology</i> , 2014, 10, e1003572.	3.2	64
28	Prediction and identification of sequences coding for orphan enzymes using genomic and metagenomic neighbours. <i>Molecular Systems Biology</i> , 2012, 8, 581.	7.2	29
29	Flux coupling and transcriptional regulation within the metabolic network of the photosynthetic bacterium <i>Synechocystis</i> sp. PCC6803. <i>Biotechnology Journal</i> , 2011, 6, 330-342.	3.5	51
30	Metabolic Network Topology Reveals Transcriptional Regulatory Signatures of Type 2 Diabetes. <i>PLoS Computational Biology</i> , 2010, 6, e1000729.	3.2	75