Aleksej Zelezniak

List of Publications by Year
in descending order

30 papers	2,892 citations	304602 22 h-index	501076 28 g-index
46 all docs	46 docs citations	46 times ranked	4932 citing authors

#	ARTICLE	IF	CITATIONS
1	Metabolic dependencies drive species co-occurrence in diverse microbial communities. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6449-6454.	3.3	588
2	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. Cell Systems, 2020, 11, 11-24.e4.	2.9	439
3	Nutritional preferences of human gut bacteria reveal their metabolic idiosyncrasies. Nature Microbiology, 2018, 3, 514-522.	5.9	196
4	Ultra-fast proteomics with Scanning SWATH. Nature Biotechnology, 2021, 39, 846-854.	9.4	173
5	Expanding functional protein sequence spaces using generative adversarial networks. Nature Machine Intelligence, 2021, 3, 324-333.	8.3	165
6	Functional Metabolomics Describes the Yeast Biosynthetic Regulome. Cell, 2016, 167, 553-565.e12.	13.5	137
7	A time-resolved proteomic and prognostic map of COVID-19. Cell Systems, 2021, 12, 780-794.e7.	2.9	125
8	The self-inhibitory nature of metabolic networks and its alleviation through compartmentalization. Nature Communications, 2017, 8, 16018.	5.8	95
9	Deep learning suggests that gene expression is encoded in all parts of a co-evolving interacting gene regulatory structure. Nature Communications, 2020, 11, 6141.	5.8	83
10	Designing and interpreting 'multi-omic' experiments that may change our understanding of biology. Current Opinion in Systems Biology, 2017, 6, 37-45.	1.3	81
11	Machine Learning Predicts the Yeast Metabolome from the Quantitative Proteome of Kinase Knockouts. Cell Systems, 2018, 7, 269-283.e6.	2.9	80
12	The metabolic background is a global player in Saccharomyces gene expression epistasis. Nature Microbiology, 2016, 1, 15030.	5.9	76
13	Metabolic Network Topology Reveals Transcriptional Regulatory Signatures of Type 2 Diabetes. PLoS Computational Biology, 2010, 6, e1000729.	1.5	75
14	Cost-effective generation of precise label-free quantitative proteomes in high-throughput by microLC and data-independent acquisition. Scientific Reports, 2018, 8, 4346.	1.6	66
15	Contribution of Network Connectivity in Determining the Relationship between Gene Expression and Metabolite Concentration Changes. PLoS Computational Biology, 2014, 10, e1003572.	1.5	64
16	Flux coupling and transcriptional regulation within the metabolic network of the photosynthetic bacterium *Synechocystis* sp. PCC6803. Biotechnology Journal, 2011, 6, 330-342.	1.8	51
17	Plastic-Degrading Potential across the Global Microbiome Correlates with Recent Pollution Trends. MBio, 2021, 12, e0215521.	1.8	51
18	metaGEM: reconstruction of genome scale metabolic models directly from metagenomes. Nucleic Acids Research, 2021, 49, e126-e126.	6.5	50

#	ARTICLE	IF	CITATIONS
19	Prediction and identification of sequences coding for orphan enzymes using genomic and metagenomic neighbours. Molecular Systems Biology, 2012, 8, 581.	3.2	29
20	Biochemical principles enabling metabolic cooperativity and phenotypic heterogeneity at the single cell level. Current Opinion in Systems Biology, 2018, 8, 97-108.	1.3	29
21	Data mining of Saccharomyces cerevisiae mutants engineered for increased tolerance towards inhibitors in lignocellulosic hydrolysates. Biotechnology Advances, 2022, 57, 107947.	6.0	29
22	A proteomic survival predictor for COVID-19 patients in intensive care. , 2022, 1, e0000007.		28
23	Ice-Age Climate Adaptations Trap the Alpine Marmot in a State of Low Genetic Diversity. Current Biology, 2019, 29, 1712-1720.e7.	1.8	27
24	Bayesian genome scale modelling identifies thermal determinants of yeast metabolism. Nature Communications, 2021, 12, 190.	5.8	25
25	Learning the Regulatory Code of Gene Expression. Frontiers in Molecular Biosciences, 2021, 8, 673363.	1.6	17
26	Benchmarking accuracy and precision of intensity€based absolute quantification of protein abundances in <i>Saccharomyces cerevisiae</i>. Proteomics, 2021, 21, e2000093.	1.3	13
27	Performance of Regression Models as a Function of Experiment Noise. Bioinformatics and Biology Insights, 2021, 15, 117793222110203.	1.0	9
28	Potential for improved retention rate by personalized antiseizure medication selection: A register€based analysis. Epilepsia, 2021, 62, 2123-2132.	2.6	7
29	Parallel Factor Analysis Enables Quantification and Identification of Highly Convolved Data-Independent-Acquired Protein Spectra. Patterns, 2020, 1, 100137.	3.1	2
30	Learning the regulatory grammar of DNA for gene expression engineering. , 2020, , .		0