

Fan Yang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9489698/publications.pdf>

Version: 2024-02-01

15
papers

2,511
citations

759233

12
h-index

1125743

13
g-index

22
all docs

22
docs citations

22
times ranked

4929
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiple early factors anticipate post-acute COVID-19 sequelae. <i>Cell</i> , 2022, 185, 881-895.e20.	28.9	605
2	Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. <i>Cell</i> , 2015, 161, 647-660.	28.9	482
3	Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing. <i>Cell</i> , 2016, 164, 805-817.	28.9	479
4	Human B Cell Clonal Expansion and Convergent Antibody Responses to SARS-CoV-2. <i>Cell Host and Microbe</i> , 2020, 28, 516-525.e5.	11.0	219
5	A framework for exhaustively mapping functional missense variants. <i>Molecular Systems Biology</i> , 2017, 13, 957.	7.2	146
6	Modeling human adaptive immune responses with tonsil organoids. <i>Nature Medicine</i> , 2021, 27, 125-135.	30.7	133
7	An extended set of yeast-based functional assays accurately identifies human disease mutations. <i>Genome Research</i> , 2016, 26, 670-680.	5.5	116
8	Protein Domain-Level Landscape of Cancer-Type-Specific Somatic Mutations. <i>PLoS Computational Biology</i> , 2015, 11, e1004147.	3.2	59
9	Shared B cell memory to coronaviruses and other pathogens varies in human age groups and tissues. <i>Science</i> , 2021, 372, 738-741.	12.6	47
10	Impact of the Interaction between 3' UTR SNPs and microRNA on the Expression of Human Xenobiotic Metabolism Enzyme and Transporter Genes. <i>Frontiers in Genetics</i> , 2012, 3, 248.	2.3	38
11	Identifying pathogenicity of human variants via paralog-based yeast complementation. <i>PLoS Genetics</i> , 2017, 13, e1006779.	3.5	30
12	In situ demonstration and quantitative analysis of the intrinsic properties of glycoside hydrolases. <i>Electrophoresis</i> , 2012, 33, 280-287.	2.4	20
13	Quantifying immune-based counterselection of somatic mutations. <i>PLoS Genetics</i> , 2019, 15, e1008227.	3.5	14
14	Mechanisms classification for glycoside hydrolases by sequence and structure features using computational methods. <i>International Journal of Data Mining and Bioinformatics</i> , 2014, 9, 444.	0.1	0
15	Research on Classification Methods of Glycoside Hydrolases Mechanism. <i>Lecture Notes in Computer Science</i> , 2011, , 617-624.	1.3	0