

Alex N Nguyen Ba

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7830757/publications.pdf>

Version: 2024-02-01

26
papers

1,644
citations

471509

17
h-index

552781

26
g-index

32
all docs

32
docs citations

32
times ranked

2766
citing authors

#	ARTICLE	IF	CITATIONS
1	NLStradamus: a simple Hidden Markov Model for nuclear localization signal prediction. BMC Bioinformatics, 2009, 10, 202.	2.6	526
2	Proteome-wide signatures of function in highly diverged intrinsically disordered regions. ELife, 2019, 8, .	6.0	131
3	High-resolution lineage tracking reveals travelling wave of adaptation in laboratory yeast. Nature, 2019, 575, 494-499.	27.8	119
4	Proteome-Wide Discovery of Evolutionary Conserved Sequences in Disordered Regions. Science Signaling, 2012, 5, rs1.	3.6	109
5	Exploring whole-genome duplicate gene retention with complex genetic interaction analysis. Science, 2020, 368, .	12.6	79
6	Selection maintains signaling function of a highly diverged intrinsically disordered region. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1450-E1459.	7.1	65
7	Evolution of Characterized Phosphorylation Sites in Budding Yeast. Molecular Biology and Evolution, 2010, 27, 2027-2037.	8.9	62
8	Phenotypic and molecular evolution across 10,000 generations in laboratory budding yeast populations. ELife, 2021, 10, .	6.0	60
9	A quantitative literature-curated gold standard for kinase-substrate pairs. Genome Biology, 2011, 12, R39.	9.6	56
10	Microwave-Generated Steam Decontamination of N95 Respirators Utilizing Universally Accessible Materials. MBio, 2020, 11, .	4.1	52
11	Modular epistasis and the compensatory evolution of gene deletion mutants. PLoS Genetics, 2019, 15, e1007958.	3.5	47
12	The Structure of an NDR/LATS Kinaseâ€‘Mob Complex Reveals a Novel Kinaseâ€‘Coactivator System and Substrate Docking Mechanism. PLoS Biology, 2015, 13, e1002146.	5.6	45
13	Chance and necessity in the pleiotropic consequences of adaptation for budding yeast. Nature Ecology and Evolution, 2020, 4, 601-611.	7.8	45
14	Detecting Functional Divergence after Gene Duplication through Evolutionary Changes in Posttranslational Regulatory Sequences. PLoS Computational Biology, 2014, 10, e1003977.	3.2	39
15	Idiosyncratic epistasis leads to global fitnessâ€‘correlated trends. Science, 2022, 376, 630-635.	12.6	36
16	Experimental Studies of Evolutionary Dynamics in Microbes. Trends in Genetics, 2018, 34, 693-703.	6.7	34
17	Barcoded bulk QTL mapping reveals highly polygenic and epistatic architecture of complex traits in yeast. ELife, 2022, 11, .	6.0	33
18	Polymorphism Analysis Reveals Reduced Negative Selection and Elevated Rate of Insertions and Deletions in Intrinsically Disordered Protein Regions. Genome Biology and Evolution, 2015, 7, 1815-1826.	2.5	27

#	ARTICLE	IF	CITATIONS
19	Functional Analysis of Kinases and Transcription Factors in <i>Saccharomyces cerevisiae</i> Using an Integrated Overexpression Library. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 911-921.	1.8	19
20	Dynamics and variability in the pleiotropic effects of adaptation in laboratory budding yeast populations. <i>ELife</i> , 2021, 10, .	6.0	18
21	Evolthon: A community endeavor to evolve lab evolution. <i>PLoS Biology</i> , 2019, 17, e3000182.	5.6	10
22	Parallel reorganization of protein function in the spindle checkpoint pathway through evolutionary paths in the fitness landscape that appear neutral in laboratory experiments. <i>PLoS Genetics</i> , 2017, 13, e1006735.	3.5	9
23	Microbial experimental evolution in a massively multiplexed and high-throughput era. <i>Current Opinion in Genetics and Development</i> , 2022, 75, 101943.	3.3	9
24	The genetic basis of differential autodiploidization in evolving yeast populations. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	7
25	Experimental evolution for niche breadth in bacteriophage T4 highlights the importance of structural genes. <i>MicrobiologyOpen</i> , 2020, 9, e968.	3.0	2
26	Bulk-Fitness Measurements Using Barcode Sequencing Analysis in Yeast. <i>Methods in Molecular Biology</i> , 2022, 2477, 399-415.	0.9	1