Alex N Nguyen Ba

List of Publications by Year
in descending order

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	Barcoded bulk QTL mapping reveals highly polygenic and epistatic architecture of complex traits in yeast. ELife, 2022, 11, .	6.0	33
2	Bulk-Fitness Measurements Using Barcode Sequencing Analysis in Yeast. Methods in Molecular Biology, 2022, 2477, 399-415.	0.9	1
3	Idiosyncratic epistasis leads to global fitness€"correlated trends. Science, 2022, 376, 630-635.	12.6	36
4	Microbial experimental evolution in a massively multiplexed and high-throughput era. Current Opinion in Genetics and Development, 2022, 75, 101943.	3.3	9
5	Phenotypic and molecular evolution across 10,000 generations in laboratory budding yeast populations. ELife, 2021, 10, .	6.0	60
6	The genetic basis of differential autodiploidization in evolving yeast populations. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	7
7	Dynamics and variability in the pleiotropic effects of adaptation in laboratory budding yeast populations. ELife, 2021, 10, .	6.0	18
8	Chance and necessity in the pleiotropic consequences of adaptation for budding yeast. Nature Ecology and Evolution, 2020, 4, 601-611.	7.8	45
9	Exploring whole-genome duplicate gene retention with complex genetic interaction analysis. Science, 2020, 368, .	12.6	79
10	Microwave-Generated Steam Decontamination of N95 Respirators Utilizing Universally Accessible Materials. MBio, 2020, 11, .	4.1	52
11	Experimental evolution for niche breadth in bacteriophage T4 highlights the importance of structural genes. MicrobiologyOpen, 2020, 9, e968.	3.0	2
12	High-resolution lineage tracking reveals travelling wave of adaptation in laboratory yeast. Nature, 2019, 575, 494-499.	27.8	119
13	Evolthon: A community endeavor to evolve lab evolution. PLoS Biology, 2019, 17, e3000182.	5.6	10
14	Modular epistasis and the compensatory evolution of gene deletion mutants. PLoS Genetics, 2019, 15, e1007958.	3.5	47
15	Proteome-wide signatures of function in highly diverged intrinsically disordered regions. ELife, 2019, 8, .	6.0	131
16	Experimental Studies of Evolutionary Dynamics in Microbes. Trends in Genetics, 2018, 34, 693-703.	6.7	34
17	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
18	Functional Analysis of Kinases and Transcription Factors in <i>Saccharomyces cerevisiae</i> Using an Integrated Overexpression Library. G3: Genes, Genomes, Genetics, 2017, 7, 911-921.	1.8	19

#	Article	IF	Citations
19	Parallel reorganization of protein function in the spindle checkpoint pathway through evolutionary paths in the fitness landscape that appear neutral in laboratory experiments. PLoS Genetics, 2017, 13, e1006735.	3.5	9
20	The Structure of an NDR/LATS Kinase–Mob Complex Reveals a Novel Kinase–Coactivator System and Substrate Docking Mechanism. PLoS Biology, 2015, 13, e1002146.	5.6	45
21	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
22	Detecting Functional Divergence after Gene Duplication through Evolutionary Changes in Posttranslational Regulatory Sequences. PLoS Computational Biology, 2014, 10, e1003977.	3.2	39
23	Proteome-Wide Discovery of Evolutionary Conserved Sequences in Disordered Regions. Science Signaling, 2012, 5, rs1.	3.6	109
24	A quantitative literature-curated gold standard for kinase-substrate pairs. Genome Biology, 2011, 12, R39.	9.6	56
25	Evolution of Characterized Phosphorylation Sites in Budding Yeast. Molecular Biology and Evolution, 2010, 27, 2027-2037.	8.9	62
26	NLStradamus: a simple Hidden Markov Model for nuclear localization signal prediction. BMC Bioinformatics, 2009, 10, 202.	2.6	526