

Allan Haldane

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6387824/publications.pdf>

Version: 2024-02-01

13
papers

10,479
citations

932766

10
h-index

1125271

13
g-index

16
all docs

16
docs citations

16
times ranked

14127
citing authors

#	ARTICLE	IF	CITATIONS
1	Array programming with NumPy. <i>Nature</i> , 2020, 585, 357-362.	13.7	10,143
2	Potts Hamiltonian models of protein co-variation, free energy landscapes, and evolutionary fitness. <i>Current Opinion in Structural Biology</i> , 2017, 43, 55-62.	2.6	73
3	Inference of Epistatic Effects Leading to Entrenchment and Drug Resistance in HIV-1 Protease. <i>Molecular Biology and Evolution</i> , 2017, 34, 1291-1306.	3.5	51
4	Structural propensities of kinase family proteins from a Potts model of residue co-variation. <i>Protein Science</i> , 2016, 25, 1378-1384.	3.1	50
5	Biophysical Fitness Landscapes for Transcription Factor Binding Sites. <i>PLoS Computational Biology</i> , 2014, 10, e1003683.	1.5	32
6	The generative capacity of probabilistic protein sequence models. <i>Nature Communications</i> , 2021, 12, 6302.	5.8	28
7	Epistasis and entrenchment of drug resistance in HIV-1 subtype B. <i>ELife</i> , 2019, 8, .	2.8	25
8	Coevolutionary Landscape of Kinase Family Proteins: Sequence Probabilities and Functional Motifs. <i>Biophysical Journal</i> , 2018, 114, 21-31.	0.2	19
9	Influence of multiple-sequence-alignment depth on Potts statistical models of protein covariation. <i>Physical Review E</i> , 2019, 99, 032405.	0.8	17
10	Mi3-GPU: MCMC-based inverse Ising inference on GPUs for protein covariation analysis. <i>Computer Physics Communications</i> , 2021, 260, 107312.	3.0	17
11	A universal scaling law determines time reversibility and steady state of substitutions under selection. <i>Theoretical Population Biology</i> , 2012, 82, 66-76.	0.5	13
12	Limits to detecting epistasis in the fitness landscape of HIV. <i>PLoS ONE</i> , 2022, 17, e0262314.	1.1	6
13	Unique features of different classes of <scp>G“protein”coupled</scp> receptors revealed from sequence coevolutionary and structural analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 601-614.	1.5	4