Allan Haldane

List of Publications by Year
in descending order

13 papers	10,479 citations	933447 10 h-index	1125743 13 g-index
16 all docs	16 docs citations	16 times ranked	14127 citing authors

#	Article	IF	Citations
1	Array programming with NumPy. Nature, 2020, 585, 357-362.	27.8	10,143
2	Potts Hamiltonian models of protein co-variation, free energy landscapes, and evolutionary fitness. Current Opinion in Structural Biology, 2017, 43, 55-62.	5.7	73
3	Inference of Epistatic Effects Leading to Entrenchment and Drug Resistance in HIV-1 Protease. Molecular Biology and Evolution, 2017, 34, 1291-1306.	8.9	51
4	Structural propensities of kinase family proteins from a Potts model of residue coâ€variation. Protein Science, 2016, 25, 1378-1384.	7.6	50
5	Biophysical Fitness Landscapes for Transcription Factor Binding Sites. PLoS Computational Biology, 2014, 10, e1003683.	3.2	32
6	The generative capacity of probabilistic protein sequence models. Nature Communications, 2021, 12, 6302.	12.8	28
7	Epistasis and entrenchment of drug resistance in HIV-1 subtype B. ELife, 2019, 8, .	6.0	25
8	Coevolutionary Landscape of Kinase Family Proteins: Sequence Probabilities and Functional Motifs. Biophysical Journal, 2018, 114, 21-31.	0.5	19
9	Influence of multiple-sequence-alignment depth on Potts statistical models of protein covariation. Physical Review E, 2019, 99, 032405.	2.1	17
10	Mi3-GPU: MCMC-based inverse Ising inference on GPUs for protein covariation analysis. Computer Physics Communications, 2021, 260, 107312.	7.5	17
11	A universal scaling law determines time reversibility and steady state of substitutions under selection. Theoretical Population Biology, 2012, 82, 66-76.	1.1	13
12	Limits to detecting epistasis in the fitness landscape of HIV. PLoS ONE, 2022, 17, e0262314.	2.5	6
13	Unique features of different classes of <scp>Gâ€proteinâ€coupled</scp> receptors revealed from sequence coevolutionary and structural analysis. Proteins: Structure, Function and Bioinformatics, 2022, 90, 601-614.	2.6	4