

William F Flynn

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

2,322
citations

566801

15
h-index

839053

18
g-index

33
all docs

33
docs citations

33
times ranked

3646
citing authors

#	ARTICLE	IF	CITATIONS
1	Targeting p21Cip1 highly expressing cells in adipose tissue alleviates insulin resistance in obesity. <i>Cell Metabolism</i> , 2022, 34, 75-89.e8.	7.2	68
2	Single-cell analysis of human glioma and immune cells identifies S100A4 as an immunotherapy target. <i>Nature Communications</i> , 2022, 13, 767.	5.8	128
3	Somatostatin-expressing parafacial neurons are CO ₂ /H ⁺ sensitive and regulate baseline breathing. <i>ELife</i> , 2021, 10, .	2.8	9
4	Neurokinin B-expressing neurons of the central extended amygdala mediate inhibitory synaptic input onto melanin-concentrating hormone neuron subpopulations. <i>Journal of Neuroscience</i> , 2021, 41, JN-RM-2600-20.	1.7	3
5	CUP-AI-Dx: A tool for inferring cancer tissue of origin and molecular subtype using RNA gene-expression data and artificial intelligence. <i>EBioMedicine</i> , 2020, 61, 103030.	2.7	67
6	Mapping systemic lupus erythematosus heterogeneity at the single-cell level. <i>Nature Immunology</i> , 2020, 21, 1094-1106.	7.0	212
7	Cellular taxonomy and spatial organization of the murine ventral posterior hypothalamus. <i>ELife</i> , 2020, 9, .	2.8	45
8	Identification of a T follicular helper cell subset that drives anaphylactic IgE. <i>Science</i> , 2019, 365, .	6.0	304
9	Cross-Species Single-Cell Analysis of Pancreatic Ductal Adenocarcinoma Reveals Antigen-Presenting Cancer-Associated Fibroblasts. <i>Cancer Discovery</i> , 2019, 9, 1102-1123.	7.7	1,120
10	Identification of EOMES-expressing spermatogonial stem cells and their regulation by PLZF. <i>ELife</i> , 2019, 8, .	2.8	43
11	Coevolutionary Landscape of Kinase Family Proteins: Sequence Probabilities and Functional Motifs. <i>Biophysical Journal</i> , 2018, 114, 21-31.	0.2	19
12	Improving Prediction Accuracy of Binding Free Energies and Poses of HIV Integrase Complexes Using the Binding Energy Distribution Analysis Method with Flattening Potentials. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 1356-1371.	2.5	7
13	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
14	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
15	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
16	Large scale free energy calculations for blind predictions of protein-ligand binding: the D3R Grand Challenge 2015. <i>Journal of Computer-Aided Molecular Design</i> , 2016, 30, 743-751.	1.3	17
17	Large-scale asynchronous and distributed multidimensional replica exchange molecular simulations and efficiency analysis. <i>Journal of Computational Chemistry</i> , 2015, 36, 1772-1785.	1.5	19
18	Asynchronous replica exchange software for grid and heterogeneous computing. <i>Computer Physics Communications</i> , 2015, 196, 236-246.	3.0	35

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19	Deep Sequencing of Protease Inhibitor Resistant HIV Patient Isolates Reveals Patterns of Correlated Mutations in Gag and Protease. PLoS Computational Biology, 2015, 11, e1004249.	1.5	38