Michael A Skinnider

List of Publications by Year
in descending order

36 papers	2,365 citations	331642 21 h-index	345203 36 g-index
46 all docs	46 docs citations	46 times ranked	2806 citing authors

#	Article	IF	Citations
1	Confronting false discoveries in single-cell differential expression. Nature Communications, 2021, 12, 5692.	12.8	332
2	PRISM 3: expanded prediction of natural product chemical structures from microbial genomes. Nucleic Acids Research, 2017, 45, W49-W54.	14.5	273
3	Genomes to natural products PRediction Informatics for Secondary Metabolomes (PRISM). Nucleic Acids Research, 2015, 43, gkv1012.	14.5	210
4	Comprehensive prediction of secondary metabolite structure and biological activity from microbial genome sequences. Nature Communications, 2020, 11, 6058.	12.8	174
5	Genomic charting of ribosomally synthesized natural product chemical space facilitates targeted mining. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6343-E6351.	7.1	127
6	An automated Genomes-to-Natural Products platform (GNP) for the discovery of modular natural products. Nature Communications, 2015, 6, 8421.	12.8	123
7	Polyketide and nonribosomal peptide retro-biosynthesis and global gene cluster matching. Nature Chemical Biology, 2016, 12, 1007-1014.	8.0	117
8	Evaluating measures of association for single-cell transcriptomics. Nature Methods, 2019, 16, 381-386.	19.0	109
9	Cell type prioritization in single-cell data. Nature Biotechnology, 2021, 39, 30-34.	17.5	96
10	DeepRiPP integrates multiomics data to automate discovery of novel ribosomally synthesized natural products. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 371-380.	7.1	89
11	Assembly and clustering of natural antibiotics guides target identification. Nature Chemical Biology, 2016, 12, 233-239.	8.0	86
12	An atlas of protein-protein interactions across mouse tissues. Cell, 2021, 184, 4073-4089.e17.	28.9	59
13	A rapid and accurate approach for prediction of interactomes from co-elution data (PrInCE). BMC Bioinformatics, 2017, 18, 457.	2.6	54
14	Chemical language models enable navigation in sparsely populated chemical space. Nature Machine Intelligence, 2021, 3, 759-770.	16.0	48
15	Meta-analysis defines principles for the design and analysis of co-fractionation mass spectrometry experiments. Nature Methods, 2021, 18, 806-815.	19.0	40
16	Global analysis of prokaryotic tRNA-derived cyclodipeptide biosynthesis. BMC Genomics, 2018, 19, 45.	2.8	35
17	Comparative analysis of chemical similarity methods for modular natural products with a hypothetical structure enumeration algorithm. Journal of Cheminformatics, 2017, 9, 46.	6.1	33
18	Genomic data integration systematically biases interactome mapping. PLoS Computational Biology, 2018, 14, e1006474.	3.2	33

#	Article	IF	Citations
19	A Targeted Proteomics Analysis of Cerebrospinal Fluid after Acute Human Spinal Cord Injury. Journal of Neurotrauma, 2017, 34, 2054-2068.	3.4	30
20	Integrated systems analysis reveals conserved gene networks underlying response to spinal cord injury. ELife, 2018, 7, .	6.0	29
21	A deep generative model enables automated structure elucidation of novel psychoactive substances. Nature Machine Intelligence, 2021, 3, 973-984.	16.0	28
22	Dynamic rewiring of the human interactome by interferon signaling. Genome Biology, 2020, 21, 140.	8.8	25
23	Context-specific interactions in literature-curated protein interaction databases. BMC Genomics, 2018, 19, 758.	2.8	22
24	Prioritization of cell types responsive to biological perturbations in single-cell data with Augur. Nature Protocols, 2021, 16, 3836-3873.	12.0	22
25	Predictors of sustained research involvement among MD/PhD programme graduates. Medical Education, 2018, 52, 536-545.	2.1	18
26	The Canadian clinician-scientist training program must be reinstated. Journal of Clinical Investigation, 2015, 125, 4317-4319.	8.2	16
27	Characteristics and outcomes of Canadian MD/PhD program graduates: a cross-sectional survey. CMAJ Open, 2017, 5, E308-E314.	2.4	15
28	Statistical reanalysis of natural products reveals increasing chemical diversity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6271-E6272.	7.1	15
29	Proteomic Portraits Reveal Evolutionarily Conserved and Divergent Responses to Spinal Cord Injury. Molecular and Cellular Proteomics, 2021, 20, 100096.	3.8	14
30	PrInCE: an R/Bioconductor package for protein–protein interaction network inference from co-fractionation mass spectrometry data. Bioinformatics, 2021, 37, 2775-2777.	4.1	11
31	Exploration of Nonribosomal Peptide Families with an Automated Informatic Search Algorithm. Chemistry and Biology, 2015, 22, 1259-1269.	6.0	10
32	Automated Identification of Depsipeptide Natural Products by an Informatic Search Algorithm. ChemBioChem, 2015, 16, 223-227.	2.6	9
33	Enabling reproducible re-analysis of single-cell data. Genome Biology, 2021, 22, 215.	8.8	9
34	Informatic search strategies to discover analogues and variants of natural product archetypes. Journal of Industrial Microbiology and Biotechnology, 2016, 43, 293-298.	3.0	8
35	On the Robustness of Graph-Based Clustering to Random Network Alterations. Molecular and Cellular Proteomics, 2021, 20, 100002.	3.8	8
36	Cross-sectional-derived determinants of satisfaction with physician-scientist training among Canadian MD/PhD graduates. PLoS ONE, 2017, 12, e0185218.	2.5	6