

# Michael A Skinnider

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

40  
papers

1,191  
citations

16  
h-index

34  
g-index

46  
ext. papers

1,785  
ext. citations

13.6  
avg, IF

4.86  
L-index

#	Paper	IF	Citations
40	A deep generative model enables automated structure elucidation of novel psychoactive substances. <i>Nature Machine Intelligence</i> , <b>2021</b> , 3, 973-984	22.5	4
39	Prioritization of cell types responsive to biological perturbations in single-cell data with Augur. <i>Nature Protocols</i> , <b>2021</b> , 16, 3836-3873	18.8	4
38	Meta-analysis defines principles for the design and analysis of co-fractionation mass spectrometry experiments. <i>Nature Methods</i> , <b>2021</b> , 18, 806-815	21.6	6
37	Chemical language models enable navigation in sparsely populated chemical space. <i>Nature Machine Intelligence</i> , <b>2021</b> , 3, 759-770	22.5	8
36	Cell type prioritization in single-cell data. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 30-34	44.5	27
35	PrInCE: an R/bioconductor package for protein-protein interaction network inference from co-fractionation mass spectrometry data. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	3
34	Proteomic Portraits Reveal Evolutionarily Conserved and Divergent Responses to Spinal Cord Injury. <i>Molecular and Cellular Proteomics</i> , <b>2021</b> , 20, 100096	7.6	4
33	An atlas of protein-protein interactions across mouse tissues. <i>Cell</i> , <b>2021</b> , 184, 4073-4089.e17	56.2	7
32	Confronting false discoveries in single-cell differential expression. <i>Nature Communications</i> , <b>2021</b> , 12, 5692	17.4	21
31	Dynamic rewiring of the human interactome by interferon signaling. <i>Genome Biology</i> , <b>2020</b> , 21, 140	18.3	12
30	DeepRiPP integrates multiomics data to automate discovery of novel ribosomally synthesized natural products. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 371-380	11.5	44
29	Comprehensive prediction of secondary metabolite structure and biological activity from microbial genome sequences. <i>Nature Communications</i> , <b>2020</b> , 11, 6058	17.4	50
28	On the Robustness of Graph-Based Clustering to Random Network Alterations. <i>Molecular and Cellular Proteomics</i> , <b>2020</b> , 20, 100002	7.6	3
27	Evaluating measures of association for single-cell transcriptomics. <i>Nature Methods</i> , <b>2019</b> , 16, 381-386	21.6	46
26	Predictors of sustained research involvement among MD/PhD programme graduates. <i>Medical Education</i> , <b>2018</b> , 52, 536-545	3.7	16
25	Global analysis of prokaryotic tRNA-derived cyclodipeptide biosynthesis. <i>BMC Genomics</i> , <b>2018</b> , 19, 45	4.5	16
24	Context-specific interactions in literature-curated protein interaction databases. <i>BMC Genomics</i> , <b>2018</b> , 19, 758	4.5	13

23	Integrated systems analysis reveals conserved gene networks underlying response to spinal cord injury. <i>ELife</i> , <b>2018</b> , 7,	8.9	17
22	Genomic data integration systematically biases interactome mapping. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1006474	5	20
21	A Targeted Proteomics Analysis of Cerebrospinal Fluid after Acute Human Spinal Cord Injury. <i>Journal of Neurotrauma</i> , <b>2017</b> , 34, 2054-2068	5.4	20
20	Characteristics and outcomes of Canadian MD/PhD program graduates: a cross-sectional survey. <i>CMAJ Open</i> , <b>2017</b> , 5, E308-E314	2.5	11
19	Comparative analysis of chemical similarity methods for modular natural products with a hypothetical structure enumeration algorithm. <i>Journal of Cheminformatics</i> , <b>2017</b> , 9, 46	8.6	22
18	A rapid and accurate approach for prediction of interactomes from co-elution data (PrInCE). <i>BMC Bioinformatics</i> , <b>2017</b> , 18, 457	3.6	34
17	Statistical reanalysis of natural products reveals increasing chemical diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E6271-E6272	11.5	14
16	PRISM 3: expanded prediction of natural product chemical structures from microbial genomes. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, W49-W54	20.1	185
15	Cross-sectional-derived determinants of satisfaction with physician-scientist training among Canadian MD/PhD graduates. <i>PLoS ONE</i> , <b>2017</b> , 12, e0185218	3.7	4
14	Informatic search strategies to discover analogues and variants of natural product archetypes. <i>Journal of Industrial Microbiology and Biotechnology</i> , <b>2016</b> , 43, 293-8	4.2	8
13	Assembly and clustering of natural antibiotics guides target identification. <i>Nature Chemical Biology</i> , <b>2016</b> , 12, 233-9	11.7	65
12	Polyketide and nonribosomal peptide retro-biosynthesis and global gene cluster matching. <i>Nature Chemical Biology</i> , <b>2016</b> , 12, 1007-1014	11.7	92
11	Genomic charting of ribosomally synthesized natural product chemical space facilitates targeted mining. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, E6343-E6351	11.5	93
10	An automated Genomes-to-Natural Products platform (GNP) for the discovery of modular natural products. <i>Nature Communications</i> , <b>2015</b> , 6, 8421	17.4	94
9	Exploration of Nonribosomal Peptide Families with an Automated Informatic Search Algorithm. <i>Chemistry and Biology</i> , <b>2015</b> , 22, 1259-69		9
8	Automated identification of depsipeptide natural products by an informatic search algorithm. <i>ChemBioChem</i> , <b>2015</b> , 16, 223-7	3.8	8
7	Genomes to natural products PRediction Informatics for Secondary Metabolomes (PRISM). <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 9645-62	20.1	175
6	The Canadian clinician-scientist training program must be reinstated. <i>Journal of Clinical Investigation</i> , <b>2015</b> , 125, 4317-9	15.9	13

5	Cell type prioritization in single-cell data	2
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1	Proteomic portraits reveal evolutionarily conserved and divergent responses to spinal cord injury	1