

# John A Bachman

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/524065/publications.pdf>

Version: 2024-02-01

19  
papers

1,078  
citations

687363

13  
h-index

752698

20  
g-index

31  
all docs

31  
docs citations

31  
times ranked

2061  
citing authors

#	ARTICLE	IF	CITATIONS
1	STonKGs: a sophisticated transformer trained on biomedical text and knowledge graphs. <i>Bioinformatics</i> , 2022, 38, 1648-1656.	4.1	11
2	Automated Network Assembly of Mechanistic Literature for Informed Evidence Identification to Support Cancer Risk Assessment. <i>Environmental Health Perspectives</i> , 2022, 130, 37002.	6.0	3
3	shinyDepMap, a tool to identify targetable cancer genes and their functional connections from Cancer Dependency Map data. <i>ELife</i> , 2021, 10, .	6.0	45
4	GeneWalk identifies relevant gene functions for a biological context using network representation learning. <i>Genome Biology</i> , 2021, 22, 55.	8.8	28
5	From knowledge to models: Automated modeling in systems and synthetic biology. <i>Current Opinion in Systems Biology</i> , 2021, 28, 100362.	2.6	4
6	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	7.2	53
7	Author-sourced capture of pathway knowledge in computable form using Biofactoid. <i>ELife</i> , 2021, 10, .	6.0	11
8	Adept: Acromine-based Disambiguation of Entities from Text with applications to the biomedical literature. <i>Journal of Open Source Software</i> , 2020, 5, 1708.	4.6	6
9	Synthetic Lethal Interaction of SHOC2 Depletion with MEK Inhibition in RAS-Driven Cancers. <i>Cell Reports</i> , 2019, 29, 118-134.e8.	6.4	63
10	Re-curation and rational enrichment of knowledge graphs in Biological Expression Language. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	20
11	INDRA-IPM: interactive pathway modeling using natural language with automated assembly. <i>Bioinformatics</i> , 2019, 35, 4501-4503.	4.1	18
12	FamPlex: a resource for entity recognition and relationship resolution of human protein families and complexes in biomedical text mining. <i>BMC Bioinformatics</i> , 2018, 19, 248.	2.6	29
13	Fundamental trade-offs between information flow in single cells and cellular populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5755-5760.	7.1	106
14	From word models to executable models of signaling networks using automated assembly. <i>Molecular Systems Biology</i> , 2017, 13, 954.	7.2	137
15	BID Preferentially Activates BAK while BIM Preferentially Activates BAX, Affecting Chemotherapy Response. <i>Molecular Cell</i> , 2013, 51, 751-765.	9.7	200
16	Programming biological models in Python using PySB. <i>Molecular Systems Biology</i> , 2013, 9, 646.	7.2	216
17	Optimizing ring assembly reveals the strength of weak interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2348-2353.	7.1	41
18	MEASURING AND MODELING LIFE-DEATH DECISIONS IN SINGLE CELLS. <i>FASEB Journal</i> , 2012, 26, 228.1.	0.5	1

#	ARTICLE	IF	CITATIONS
19	New approaches to modeling complex biochemistry. Nature Methods, 2011, 8, 130-131.	19.0	31