

# Shawn M Gomez

## List of Publications by Year in descending order

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Version: 2024-02-01

51  
papers

4,040  
citations

201674

27  
h-index

197818

49  
g-index

60  
all docs

60  
docs citations

60  
times ranked

7115  
citing authors

#	ARTICLE	IF	CITATIONS
1	EMBER: multi-label prediction of kinase-substrate phosphorylation events through deep learning. <i>Bioinformatics</i> , 2022, 38, 2119-2126.	4.1	11
2	Direct Detection of Glutathione Biosynthesis, Conjugation, Depletion and Recovery in Intact Hepatoma Cells. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4733.	4.1	0
3	Differential Performance of Machine Learning Models in Prediction of Procedure-Specific Outcomes. <i>Journal of Gastrointestinal Surgery</i> , 2022, 26, 1732-1742.	1.7	4
4	The Dark Kinase Knowledgebase: an online compendium of knowledge and experimental results of understudied kinases. <i>Nucleic Acids Research</i> , 2021, 49, D529-D535.	14.5	75
5	Stem/Proliferative and Differentiated Cells within Primary Murine Colonic Epithelium Display Distinct Intracellular Free Ca <sup>2+</sup> Signal Codes. <i>Advanced Healthcare Materials</i> , 2021, 10, e2101318.	7.6	2
6	Recombination drives the evolution of mutational robustness. <i>Current Opinion in Systems Biology</i> , 2019, 13, 142-149.	2.6	9
7	Unexplored therapeutic opportunities in the human genome. <i>Nature Reviews Drug Discovery</i> , 2018, 17, 317-332.	46.4	263
8	Spatiotemporal organization of exocytosis emerges during neuronal shape change. <i>Journal of Cell Biology</i> , 2018, 217, 1113-1128.	5.2	44
9	Proteomic analysis defines kinase taxonomies specific for subtypes of breast cancer. <i>Oncotarget</i> , 2018, 9, 15480-15497.	1.8	24
10	Coral: Clear and Customizable Visualization of Human Kinome Data. <i>Cell Systems</i> , 2018, 7, 347-350.e1.	6.2	118
11	MAP3K4 Controls the Chromatin Modifier HDAC6 during Trophoblast Stem Cell Epithelial-to-Mesenchymal Transition. <i>Cell Reports</i> , 2017, 18, 2387-2400.	6.4	49
12	The EXIT Strategy: an Approach for Identifying Bacterial Proteins Exported during Host Infection. <i>MBio</i> , 2017, 8, .	4.1	21
13	Two Functionally Distinct Sources of Actin Monomers Supply the Leading Edge of Lamellipodia. <i>Cell Reports</i> , 2015, 11, 433-445.	6.4	69
14	Analysis of sphingosine kinase activity in single natural killer cells from peripheral blood. <i>Integrative Biology (United Kingdom)</i> , 2015, 7, 392-401.	1.3	17
15	Inhibition of Lapatinib-Induced Kinome Reprogramming in ERBB2-Positive Breast Cancer by Targeting BET Family Bromodomains. <i>Cell Reports</i> , 2015, 11, 390-404.	6.4	254
16	Transcriptome-wide identification and study of cancer-specific splicing events across multiple tumors. <i>Oncotarget</i> , 2015, 6, 6825-6839.	1.8	36
17	Visinets: A Web-Based Pathway Modeling and Dynamic Visualization Tool. <i>PLoS ONE</i> , 2015, 10, e0123773.	2.5	1
18	Prevalent RNA recognition motif duplication in the human genome. <i>Rna</i> , 2014, 20, 702-712.	3.5	10

#	ARTICLE	IF	CITATIONS
19	Dissecting motility signaling through activation of specific Src-effector complexes. <i>Nature Chemical Biology</i> , 2014, 10, 286-290.	8.0	44
20	LKB1 loss in melanoma disrupts directional migration toward extracellular matrix cues. <i>Journal of Cell Biology</i> , 2014, 207, 299-315.	5.2	41
21	Engineered kinase activation reveals unique morphodynamic phenotypes and associated trafficking for Src family isoforms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12420-12425.	7.1	47
22	Automated analysis of invadopodia dynamics in live cells. <i>PeerJ</i> , 2014, 2, e462.	2.0	4
23	LKB1 loss in melanoma disrupts directional migration toward extracellular matrix cues. <i>Journal of Experimental Medicine</i> , 2014, 211, 211120IA68.	8.5	0
24	Nck enables directional cell migration through the coordination of polarized membrane protrusion with adhesion dynamics. <i>Journal of Cell Science</i> , 2013, 126, 1637-49.	2.0	43
25	The Focal Adhesion Analysis Server: a web tool for analyzing focal adhesion dynamics. <i>F1000Research</i> , 2013, 2, 68.	1.6	136
26	Gleevec, an Abl Family Inhibitor, Produces a Profound Change in Cell Shape and Migration. <i>PLoS ONE</i> , 2013, 8, e52233.	2.5	15
27	Differential expression and cellular localization of novel isoforms of the tendon biomarker tenomodulin. <i>Journal of Applied Physiology</i> , 2012, 113, 861-871.	2.5	32
28	Arp2/3 Is Critical for Lamellipodia and Response to Extracellular Matrix Cues but Is Dispensable for Chemotaxis. <i>Cell</i> , 2012, 148, 973-987.	28.9	409
29	Dynamic Reprogramming of the Kinome in Response to Targeted MEK Inhibition in Triple-Negative Breast Cancer. <i>Cell</i> , 2012, 149, 307-321.	28.9	637
30	Defining the expressed breast cancer kinome. <i>Cell Research</i> , 2012, 22, 620-623.	12.0	23
31	MAP3K4/CBP-Regulated H2B Acetylation Controls Epithelial-Mesenchymal Transition in Trophoblast Stem Cells. <i>Cell Stem Cell</i> , 2011, 8, 525-537.	11.1	102
32	Mapping Protein Interactions between Dengue Virus and Its Human and Insect Hosts. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e954.	3.0	93
33	A Whole-Body Model for Glycogen Regulation Reveals a Critical Role for Substrate Cycling in Maintaining Blood Glucose Homeostasis. <i>PLoS Computational Biology</i> , 2011, 7, e1002272.	3.2	32
34	High-Resolution Quantification of Focal Adhesion Spatiotemporal Dynamics in Living Cells. <i>PLoS ONE</i> , 2011, 6, e22025.	2.5	145
35	Enhancing metabolomic data analysis with Progressive Consensus Alignment of NMR Spectra (PCANS). <i>BMC Bioinformatics</i> , 2010, 11, 123.	2.6	18
36	Structural similarity-based predictions of protein interactions between HIV-1 and Homo sapiens. <i>Virology Journal</i> , 2010, 7, 82.	3.4	70

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37	Comparison of phylogenetic trees through alignment of embedded evolutionary distances. BMC Bioinformatics, 2009, 10, 423.	2.6	15
38	Sequence patches on MAPK surfaces define protein-protein interactions. Genome Biology, 2009, 10, 222.	9.6	1
39	Data-driven modeling of cellular stimulation, signaling and output response in RAW 264.7 cells. Journal of Molecular Signaling, 2008, 3, 11.	0.5	8
40	Prediction of Protein-Protein Interaction Networks. Current Protocols in Bioinformatics, 2008, 22, Unit 8.2.	25.8	8
41	SAGE analysis of mosquito salivary gland transcriptomes during Plasmodium invasion. Cellular Microbiology, 2007, 9, 708-724.	2.1	53
42	Anopheles gambiae genome reannotation through synthesis of ab initio and comparative gene prediction algorithms. Genome Biology, 2006, 7, R24.	9.6	18
43	Pilot Anopheles gambiae full-length cDNA study: sequencing and initial characterization of 35,575 clones. Genome Biology, 2005, 6, R39.	9.6	21
44	The Genomic Sequence of the Accidental Pathogen <i>Legionella pneumophila</i> . Science, 2004, 305, 1966-1968.	12.6	452
45	Prediction of Protein-Protein Interaction Networks. Current Protocols in Bioinformatics, 2003, 1, 8.2.1-8.2.10.	25.8	6
46	Learning to predict protein-protein interactions from protein sequences. Bioinformatics, 2003, 19, 1875-1881.	4.1	140
47	Of truth and pathways: chasing bits of information through myriads of articles. Bioinformatics, 2002, 18, S249-S257.	4.1	36
48	Birth of scale-free molecular networks and the number of distinct DNA and protein domains per genome. Bioinformatics, 2001, 17, 988-996.	4.1	130
49	Probabilistic Prediction of Unknown Metabolic and Signal-Transduction Networks. Genetics, 2001, 159, 1291-1298.	2.9	48
50	TOWARDS THE PREDICTION OF COMPLETE PROTEIN-PROTEIN INTERACTION NETWORKS. , 2001, , .		19
51	Capture of Rare Cells in Suspension with Antibody-Coated Polystyrene Beads. Biotechnology Progress, 1999, 15, 238-244.	2.6	6