Shawn M Gomez

List of Publications by Year
in descending order

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	Dynamic Reprogramming of the Kinome in Response to Targeted MEK Inhibition in Triple-Negative Breast Cancer. Cell, 2012, 149, 307-321.	28.9	637
2	The Genomic Sequence of the Accidental Pathogen *Legionella pneumophila*. Science, 2004, 305, 1966-1968.	12.6	452
3	Arp2/3 Is Critical for Lamellipodia and Response to Extracellular Matrix Cues but Is Dispensable for Chemotaxis. Cell, 2012, 148, 973-987.	28.9	409
4	Unexplored therapeutic opportunities in the human genome. Nature Reviews Drug Discovery, 2018, 17, 317-332.	46.4	263
5	Inhibition of Lapatinib-Induced Kinome Reprogramming in ERBB2-Positive Breast Cancer by Targeting BET Family Bromodomains. Cell Reports, 2015, 11, 390-404.	6.4	254
6	High-Resolution Quantification of Focal Adhesion Spatiotemporal Dynamics in Living Cells. PLoS ONE, 2011, 6, e22025.	2.5	145
7	Learning to predict protein-protein interactions from protein sequences. Bioinformatics, 2003, 19, 1875-1881.	4.1	140
8	The Focal Adhesion Analysis Server: a web tool for analyzing focal adhesion dynamics. F1000Research, 2013, 2, 68.	1.6	136
9	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
10	Coral: Clear and Customizable Visualization of Human Kinome Data. Cell Systems, 2018, 7, 347-350.e1.	6.2	118
11	MAP3K4/CBP-Regulated H2B Acetylation Controls Epithelial-Mesenchymal Transition in Trophoblast Stem Cells. Cell Stem Cell, 2011, 8, 525-537.	11.1	102
12	Mapping Protein Interactions between Dengue Virus and Its Human and Insect Hosts. PLoS Neglected Tropical Diseases, 2011, 5, e954.	3.0	93
13	The Dark Kinase Knowledgebase: an online compendium of knowledge and experimental results of understudied kinases. Nucleic Acids Research, 2021, 49, D529-D535.	14.5	75
14	Structural similarity-based predictions of protein interactions between HIV-1 and Homo sapiens. Virology Journal, 2010, 7, 82.	3.4	70
15	Two Functionally Distinct Sources of Actin Monomers Supply the Leading Edge of Lamellipodia. Cell Reports, 2015, 11, 433-445.	6.4	69
16	SAGE analysis of mosquito salivary gland transcriptomes during Plasmodium invasion. Cellular Microbiology, 2007, 9, 708-724.	2.1	53
17	MAP3K4 Controls the Chromatin Modifier HDAC6 during Trophoblast Stem Cell Epithelial-to-Mesenchymal Transition. Cell Reports, 2017, 18, 2387-2400.	6.4	49
18	Probabilistic Prediction of Unknown Metabolic and Signal-Transduction Networks. Genetics, 2001, 159, 1291-1298.	2.9	48

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19	Engineered kinase activation reveals unique morphodynamic phenotypes and associated trafficking for Src family isoforms. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12420-12425.	7.1	47
20	Dissecting motility signaling through activation of specific Src-effector complexes. Nature Chemical Biology, 2014, 10, 286-290.	8.0	44
21	Spatiotemporal organization of exocytosis emerges during neuronal shape change. Journal of Cell Biology, 2018, 217, 1113-1128.	5.2	44
22	Nck enables directional cell migration through the coordination of polarized membrane protrusion with adhesion dynamics. Journal of Cell Science, 2013, 126, 1637-49.	2.0	43
23	LKB1 loss in melanoma disrupts directional migration toward extracellular matrix cues. Journal of Cell Biology, 2014, 207, 299-315.	5.2	41
24	Of truth and pathways: chasing bits of information through myriads of articles. Bioinformatics, 2002, 18, S249-S257.	4.1	36
25	Transcriptome-wide identification and study of cancer-specific splicing events across multiple tumors. Oncotarget, 2015, 6, 6825-6839.	1.8	36
26	A Whole-Body Model for Glycogen Regulation Reveals a Critical Role for Substrate Cycling in Maintaining Blood Glucose Homeostasis. PLoS Computational Biology, 2011, 7, e1002272.	3.2	32
27	Differential expression and cellular localization of novel isoforms of the tendon biomarker tenomodulin. Journal of Applied Physiology, 2012, 113, 861-871.	2.5	32
28	Proteomic analysis defines kinase taxonomies specific for subtypes of breast cancer. Oncotarget, 2018, 9, 15480-15497.	1.8	24
29	Defining the expressed breast cancer kinome. Cell Research, 2012, 22, 620-623.	12.0	23
30	Pilot Anopheles gambiae full-length cDNA study: sequencing and initial characterization of 35,575 clones. Genome Biology, 2005, 6, R39.	9.6	21
31	The EXIT Strategy: an Approach for Identifying Bacterial Proteins Exported during Host Infection. MBio, 2017, 8, .	4.1	21
32	TOWARDS THE PREDICTION OF COMPLETE PROTEIN–PROTEIN INTERACTION NETWORKS. , 2001, , .		19
33	Anopheles gambiae genome reannotation through synthesis of ab initio and comparative gene prediction algorithms. Genome Biology, 2006, 7, R24.	9.6	18
34	Enhancing metabolomic data analysis with Progressive Consensus Alignment of NMR Spectra (PCANS). BMC Bioinformatics, 2010, 11, 123.	2.6	18
35	Analysis of sphingosine kinase activity in single natural killer cells from peripheral blood. Integrative Biology (United Kingdom), 2015, 7, 392-401.	1.3	17
36	Comparison of phylogenetic trees through alignment of embedded evolutionary distances. BMC Bioinformatics, 2009, 10, 423.	2.6	15

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37	Gleevec, an Abl Family Inhibitor, Produces a Profound Change in Cell Shape and Migration. PLoS ONE, 2013, 8, e52233.	2.5	15
38	EMBER: multi-label prediction of kinase-substrate phosphorylation events through deep learning. Bioinformatics, 2022, 38, 2119-2126.	4.1	11
39	Prevalent RNA recognition motif duplication in the human genome. Rna, 2014, 20, 702-712.	3.5	10
40	Recombination drives the evolution of mutational robustness. Current Opinion in Systems Biology, 2019, 13, 142-149.	2.6	9
41	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
42	Prediction of Protein–Protein Interaction Networks. Current Protocols in Bioinformatics, 2008, 22, Unit 8.2.	25.8	8
43	Capture of Rare Cells in Suspension with Antibody-Coated Polystyrene Beads. Biotechnology Progress, 1999, 15, 238-244.	2.6	6
44	Prediction of Protein-Protein Interaction Networks. Current Protocols in Bioinformatics, 2003, 1, 8.2.1-8.2.10.	25.8	6
45	Automated analysis of invadopodia dynamics in live cells. PeerJ, 2014, 2, e462.	2.0	4
46	Differential Performance of Machine Learning Models in Prediction of Procedure-Specific Outcomes. Journal of Gastrointestinal Surgery, 2022, 26, 1732-1742.	1.7	4
47	Stem/Proliferative and Differentiated Cells within Primary Murine Colonic Epithelium Display Distinct Intracellular Free Ca^{2+} Signal Codes. Advanced Healthcare Materials, 2021, 10, e2101318.	7.6	2
48	Sequence patches on MAPK surfaces define protein-protein interactions. Genome Biology, 2009, 10, 222.	9.6	1
49	Visinets: A Web-Based Pathway Modeling and Dynamic Visualization Tool. PLoS ONE, 2015, 10, e0123773.	2.5	1
50	LKB1 loss in melanoma disrupts directional migration toward extracellular matrix cues. Journal of Experimental Medicine, 2014, 211, 21112OIA68.	8.5	0
51	Direct Detection of Glutathione Biosynthesis, Conjugation, Depletion and Recovery in Intact Hepatoma Cells. International Journal of Molecular Sciences, 2022, 23, 4733.	4.1	0