

# Kevin A Janes

## List of Publications by Year in descending order

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Version: 2024-02-01

61  
papers

5,829  
citations

172457

29  
h-index

149698

56  
g-index

71  
all docs

71  
docs citations

71  
times ranked

8145  
citing authors

#	ARTICLE	IF	CITATIONS
1	Chitosan-DNA nanoparticles as gene carriers: synthesis, characterization and transfection efficiency. <i>Journal of Controlled Release</i> , 2001, 70, 399-421.	9.9	1,140
2	Chitosan nanoparticles as delivery systems for doxorubicin. <i>Journal of Controlled Release</i> , 2001, 73, 255-267.	9.9	639
3	A Systems Model of Signaling Identifies a Molecular Basis Set for Cytokine-Induced Apoptosis. <i>Science</i> , 2005, 310, 1646-1653.	12.6	506
4	Low molecular weight chitosan nanoparticles as new carriers for nasal vaccine delivery in mice. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2004, 57, 123-131.	4.3	408
5	Data-driven modelling of signal-transduction networks. <i>Nature Reviews Molecular Cell Biology</i> , 2006, 7, 820-828.	37.0	347
6	A multiplexed homogeneous fluorescence-based assay for protein kinase activity in cell lysates. <i>Nature Methods</i> , 2005, 2, 277-284.	19.0	202
7	The Response of Human Epithelial Cells to TNF Involves an Inducible Autocrine Cascade. <i>Cell</i> , 2006, 124, 1225-1239.	28.9	188
8	Common effector processing mediates cell-specific responses to stimuli. <i>Nature</i> , 2007, 448, 604-608.	27.8	183
9	An analysis of critical factors for quantitative immunoblotting. <i>Science Signaling</i> , 2015, 8, rs2.	3.6	167
10	A Compendium of Signals and Responses Triggered by Prodeath and Prosurvival Cytokines. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1569-1590.	3.8	134
11	Applying computational modeling to drug discovery and development. <i>Drug Discovery Today</i> , 2006, 11, 806-811.	6.4	115
12	Identifying single-cell molecular programs by stochastic profiling. <i>Nature Methods</i> , 2010, 7, 311-317.	19.0	112
13	A biological approach to computational models of proteomic networks. <i>Current Opinion in Chemical Biology</i> , 2006, 10, 73-80.	6.1	111
14	Intersection of FOXO- and RUNX1-mediated gene expression programs in single breast epithelial cells during morphogenesis and tumor progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E803-12.	7.1	108
15	Cue-Signal-Response Analysis of TNF-Induced Apoptosis by Partial Least Squares Regression of Dynamic Multivariate Data. <i>Journal of Computational Biology</i> , 2004, 11, 544-561.	1.6	106
16	Astrocytic trans-Differentiation Completes a Multicellular Paracrine Feedback Loop Required for Medulloblastoma Tumor Growth. <i>Cell</i> , 2020, 180, 502-520.e19.	28.9	99
17	Cytokine-Induced Signaling Networks Prioritize Dynamic Range over Signal Strength. <i>Cell</i> , 2008, 135, 343-354.	28.9	96
18	Automated brightfield morphometry of 3D organoid populations by OrganoSeg. <i>Scientific Reports</i> , 2018, 8, 5319.	3.3	92

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19	A High-throughput Quantitative Multiplex Kinase Assay for Monitoring Information Flow in Signaling Networks. <i>Molecular and Cellular Proteomics</i> , 2003, 2, 463-473.	3.8	89
20	Small Molecule Inhibitor of CBF $\beta$ -RUNX Binding for RUNX Transcription Factor Driven Cancers. <i>EBioMedicine</i> , 2016, 8, 117-131.	6.1	84
21	Models of signalling networks – what cell biologists can gain from them and give to them. <i>Journal of Cell Science</i> , 2013, 126, 1913-1921.	2.0	78
22	A time- and matrix-dependent TGFBR3 $\beta$ -JUND $\beta$ -KRT5 regulatory circuit in single breast epithelial cells and basal-like premalignancies. <i>Nature Cell Biology</i> , 2014, 16, 345-356.	10.3	70
23	RUNX1 and its understudied role in breast cancer. <i>Cell Cycle</i> , 2011, 10, 3461-3465.	2.6	62
24	Tumor-Suppressor Inactivation of GDF11 Occurs by Precursor Sequestration in Triple-Negative Breast Cancer. <i>Developmental Cell</i> , 2017, 43, 418-435.e13.	7.0	62
25	Pairwise network mechanisms in the host signaling response to coxsackievirus B3 infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17053-17058.	7.1	42
26	Normal morphogenesis of epithelial tissues and progression of epithelial tumors. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2012, 4, 51-78.	6.6	42
27	An ERK-p38 Subnetwork Coordinates Host Cell Apoptosis and Necrosis during Coxsackievirus B3 Infection. <i>Cell Host and Microbe</i> , 2013, 13, 67-76.	11.0	39
28	Parameterizing cell-to-cell regulatory heterogeneities via stochastic transcriptional profiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E626-35.	7.1	37
29	Computational Models of Reactive Oxygen Species as Metabolic Byproducts and Signal-Transduction Modulators. <i>Frontiers in Pharmacology</i> , 2016, 7, 457.	3.5	34
30	Stochastic profiling of transcriptional regulatory heterogeneities in tissues, tumors and cultured cells. <i>Nature Protocols</i> , 2013, 8, 282-301.	12.0	32
31	Simultaneous Profiling of 194 Distinct Receptor Transcripts in Human Cells. <i>Science Signaling</i> , 2013, 6, rs13.	3.6	30
32	TNF-insulin crosstalk at the transcription factor GATA6 is revealed by a model that links signaling and transcriptomic data tensors. <i>Science Signaling</i> , 2016, 9, ra59.	3.6	25
33	Sporadic activation of an oxidative stress $\beta$ -dependent NRF2-p53 signaling network in breast epithelial spheroids and premalignancies. <i>Science Signaling</i> , 2020, 13, .	3.6	25
34	The receptor tyrosine kinase Ror is required for dendrite regeneration in <i>Drosophila</i> neurons. <i>PLoS Biology</i> , 2020, 18, e3000657.	5.6	24
35	Single-cell states versus single-cell atlases – two classes of heterogeneity that differ in meaning and method. <i>Current Opinion in Biotechnology</i> , 2016, 39, 120-125.	6.6	23
36	In situ 10-cell RNA sequencing in tissue and tumor biopsy samples. <i>Scientific Reports</i> , 2019, 9, 4836.	3.3	23

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37	A High-throughput Assay for Phosphoprotein-specific Phosphatase Activity in Cellular Extracts. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 797-806.	3.8	22
38	An engineering design approach to systems biology. <i>Integrative Biology (United Kingdom)</i> , 2017, 9, 574-583.	1.3	22
39	Adenoviral vector saturates Akt pro-survival signaling and blocks insulin-mediated rescue of tumor-necrosis-factor-induced apoptosis. <i>Journal of Cell Science</i> , 2006, 119, 3788-3798.	2.0	21
40	Network Architecture Predisposes an Enzyme to Either Pharmacologic or Genetic Targeting. <i>Cell Systems</i> , 2016, 2, 112-121.	6.2	21
41	A cell-nonautonomous mechanism of yeast chronological aging regulated by caloric restriction and one-carbon metabolism. <i>Journal of Biological Chemistry</i> , 2021, 296, 100125.	3.4	17
42	Modeling the latent dimensions of multivariate signaling datasets. <i>Physical Biology</i> , 2012, 9, 045004.	1.8	16
43	Multiscale Models of Cell Signaling. <i>Annals of Biomedical Engineering</i> , 2012, 40, 2319-2327.	2.5	16
44	Profiling Subcellular Protein Phosphatase Responses to Coxsackievirus B3 Infection of Cardiomyocytes. <i>Molecular and Cellular Proteomics</i> , 2017, 16, S244-S262.	3.8	13
45	Distinct MUNC lncRNA structural domains regulate transcription of different promyogenic factors. <i>Cell Reports</i> , 2022, 38, 110361.	6.4	13
46	Modeling the complete kinetics of coxsackievirus B3 reveals human determinants of host-cell feedback. <i>Cell Systems</i> , 2021, 12, 304-323.e13.	6.2	12
47	Fragile epitopesâ€™ Antibodyâ€™s guess is as good as yours. <i>Science Signaling</i> , 2020, 13, .	3.6	11
48	Premalignant Oligodendrocyte Precursor Cells Stall in a Heterogeneous State of Replication Stress Prior to Gliomagenesis. <i>Cancer Research</i> , 2021, 81, 1868-1882.	0.9	11
49	Pan-Cancer Drivers Are Recurrent Transcriptional Regulatory Heterogeneities in Early-Stage Luminal Breast Cancer. <i>Cancer Research</i> , 2021, 81, 1840-1852.	0.9	10
50	Fragmentation of Small-Cell Lung Cancer Regulatory States in Heterotypic Microenvironments. <i>Cancer Research</i> , 2021, 81, 1853-1867.	0.9	9
51	Paring down signaling complexity. <i>Nature Biotechnology</i> , 2010, 28, 681-682.	17.5	8
52	Cell-to-Cell Transcript Variability: Seeing Signal in the Noise. <i>Cell</i> , 2015, 163, 1566-1568.	28.9	7
53	CIRCOAST: a statistical hypothesis test for cellular colocalization with network structures. <i>Bioinformatics</i> , 2019, 35, 506-514.	4.1	4
54	Non-genetic heterogeneity caused by differential single-cell adhesion. <i>Cell Cycle</i> , 2014, 13, 2149-2150.	2.6	3

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55	Robust latent-variable interpretation of in vivo regression models by nested resampling. <i>Scientific Reports</i> , 2019, 9, 19671.	3.3	3
56	An ultrasensitive fiveplex activity assay for cellular kinases. <i>Scientific Reports</i> , 2019, 9, 19409.	3.3	3
57	Simulating coxsackievirus B3 infection with an accessible computational model of its complete kinetics. <i>STAR Protocols</i> , 2021, 2, 100940.	1.2	1
58	When microarrays Met epidermal cell migration. <i>Molecular Systems Biology</i> , 2008, 4, 200.	7.2	0
59	Ten simple rules for being a faculty advocate of first-year graduate students. <i>PLoS Computational Biology</i> , 2021, 17, e1009379.	3.2	0
60	Systems-Engineering Principles in Signal Transduction and Cell-Fate Choice. , 2012, , 1-14.		0
61	<i>Science Signaling</i> Podcast for 7 June 2016: Modeling signal integration. <i>Science Signaling</i> , 2016, 9, pc13.	3.6	0