Jean-Marc Schwartz

List of Publications by Year
in descending order

94 papers	2,602 citations	218592 26 h-index	214721 47 g-index
105 all docs	105 docs citations	105 times ranked	3739 citing authors

#	Article	IF	Citations
1	Microfilament dynamics during cell movement and chemotaxis monitored using a GFP–actin fusion protein. Current Biology, 1997, 7, 176-183.	1.8	238
2	Modelling liver tissue properties using a non-linear visco-elastic model for surgery simulation. Medical Image Analysis, 2005, 9, 103-112.	7.0	139
3	G Protein β Subunit–null Mutants Are Impaired in Phagocytosis and Chemotaxis Due to Inappropriate Regulation of the Actin Cytoskeleton. Journal of Cell Biology, 1998, 141, 1529-1537.	2.3	113
4	Membrane Tension Orchestrates Rear Retraction in Matrix-Directed Cell Migration. Developmental Cell, 2019, 51, 460-475.e10.	3.1	112
5	Dynein motor regulation stabilizes interphase microtubule arrays and determines centrosome position. EMBO Journal, 1999, 18, 6786-6792.	3.5	110
6	Cytokinesis mediated through the recruitment of cortexillins into the cleavage furrow. EMBO Journal, 1999, 18, 586-594.	3.5	98
7	Gene expression changes in damaged osteoarthritic cartilage identify a signature of non-chondrogenic and mechanical responses. Osteoarthritis and Cartilage, 2016, 24, 1431-1440.	0.6	93
8	Stratification of knee osteoarthritis: two major patient subgroups identified by genome-wide expression analysis of articular cartilage. Annals of the Rheumatic Diseases, 2018, 77, 423-423.	0.5	89
9	A global view of drug-therapy interactions. BMC Pharmacology, 2008, 8, 5.	0.4	81
10	Integration of metabolic databases for the reconstruction of genome-scale metabolic networks. BMC Systems Biology, 2010, 4, 114.	3.0	79
11	Environmental systems biology of cold–tolerant phenotype in <i>Saccharomyces</i> species adapted to grow at different temperatures. Molecular Ecology, 2014, 23, 5241-5257.	2.0	79
12	A quantitative brain map of experimental cerebral malaria pathology. PLoS Pathogens, 2017, 13, e1006267.	2.1	73
13	Three-dimensional Patterns and Redistribution of Myosin II and Actin in Mitotic Dictyostelium Cells. Journal of Cell Biology, 1997, 139, 1793-1804.	2.3	68
14	The chaperone activity of 4PBA ameliorates the skeletal phenotype of Chihuahua, a zebrafish model for dominant osteogenesis imperfecta. Human Molecular Genetics, 2017, 26, 2897-2911.	1.4	68
15	Quantitative elementary mode analysis of metabolic pathways: the example of yeast glycolysis. BMC Bioinformatics, 2006, 7, 186.	1.2	66
16	Flux sampling is a powerful tool to study metabolism under changing environmental conditions. Npj Systems Biology and Applications, 2019, 5, 32.	1.4	62
17	Flux balance analysis reveals acetate metabolism modulates cyclic electron flow and alternative glycolytic pathways in Chlamydomonas reinhardtii. Frontiers in Plant Science, 2015, 6, 474.	1.7	59
18	Observing metabolic functions at the genome scale. Genome Biology, 2007, 8, R123.	13.9	54

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19	From empirical to theoretical models of light response curves - linking photosynthetic and metabolic acclimation. Photosynthesis Research, 2020, 145, 5-14.	1.6	45
20	Golvesin-GFP fusions as distinct markers for Golgi and post-Golgi vesicles in Dictyostelium cells. Biology of the Cell, 2000, 92, 495-511.	0.7	41
21	Modularity in Protein Complex and Drug Interactions Reveals New Polypharmacological Properties. PLoS ONE, 2012, 7, e30028.	1.1	40
22	A quadratic programming approach for decomposing steady-state metabolic flux distributions onto elementary modes. Bioinformatics, 2005, 21, ii204-ii205.	1.8	39
23	Metabolic acclimation—a key to enhancing photosynthesis in changing environments?. Journal of Experimental Botany, 2019, 70, 3043-3056.	2.4	37
24	A MAPK-Driven Feedback Loop Suppresses Rac Activity to Promote RhoA-Driven Cancer Cell Invasion. PLoS Computational Biology, 2016, 12, e1004909.	1.5	36
25	Erg and AP-1 as determinants of glucocorticoid response in acute lymphoblastic leukemia. Oncogene, 2013, 32, 3039-3048.	2.6	31
26	Comprehensive Modelling of the Neurospora Circadian Clock and Its Temperature Compensation. PLoS Computational Biology, 2012, 8, e1002437.	1.5	29
27	Why COVID-19 models should incorporate the network of social interactions. Physical Biology, 2020, 17, 065008.	0.8	29
28	Calcium activated nucleotidase 1 (CANT1) is critical for glycosaminoglycan biosynthesis in cartilage and endochondral ossification. Matrix Biology, 2019, 81, 70-90.	1.5	27
29	PhenomeExpress: A refined network analysis of expression datasets by inclusion of known disease phenotypes. Scientific Reports, 2015, 5, 8117.	1.6	25
30	Dynamics of DNA Damage Induced Pathways to Cancer. PLoS ONE, 2013, 8, e72303.	1.1	23
31	A logical model of HIV-1 interactions with the T-cell activation signalling pathway. Bioinformatics, 2015, 31, 1075-1083.	1.8	23
32	Deterministic mathematical models of the cAMP pathway in Saccharomyces cerevisiae. BMC Systems Biology, 2009, 3, 70.	3.0	22
33	Mapping biological process relationships and disease perturbations within a pathway network. Npj Systems Biology and Applications, 2018, 4, 22.	1.4	21
34	A Holistic Approach to Study Photosynthetic Acclimation Responses of Plants to Fluctuating Light. Frontiers in Plant Science, 2021, 12, 668512.	1.7	21
35	Using set theory to reduce redundancy in pathway sets. BMC Bioinformatics, 2018, 19, 386.	1.2	20
36	Network controllability analysis of intracellular signalling reveals viruses are actively controlling molecular systems. Scientific Reports, 2019, 9, 2066.	1.6	19

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37	PathNER: a tool for systematic identification of biological pathway mentions in the literature. BMC Systems Biology, 2013, 7, S2.	3.0	18
38	SkeletalVis: an exploration and meta-analysis data portal of cross-species skeletal transcriptomics data. Bioinformatics, 2019, 35, 2283-2290.	1.8	18
39	Streamlining the construction of large-scale dynamic models using generic kinetic equations. Bioinformatics, 2010, 26, 1324-1331.	1.8	16
40	XBP1 signalling is essential for alleviating mutant protein aggregation in ER-stress related skeletal disease. PLoS Genetics, 2019, 15, e1008215.	1.5	16
41	Probabilistic controllability approach to metabolic fluxes in normal and cancer tissues. Nature Communications, 2019, 10, 2725.	5.8	15
42	Transcriptional Profile of the Industrial Hybrid *Saccharomyces pastorianus* Reveals Temperature-Dependent Allele Expression Bias and Preferential Orthologous Protein Assemblies. Molecular Biology and Evolution, 2021, 38, 5437-5452.	3.5	15
43	Mechanical loading activates the YAP/TAZ pathway and chemokine expression in the MLO-Y4 osteocyte-like cell line. Laboratory Investigation, 2021, 101, 1597-1604.	1.7	14
44	PhenomeScape: a cytoscape app to identify differentially regulated sub-networks using known disease associations. Bioinformatics, 2016, 32, 3847-3849.	1.8	13
45	Quantitative analysis and modeling of glucocorticoid-controlled gene expression. Pharmacogenomics, 2010, 11, 1545-1560.	0.6	12
46	Exploring the genetic control of glycolytic oscillations in Saccharomyces Cerevisiae. BMC Systems Biology, 2012, 6, 108.	3.0	12
47	Quantitative proteomics and network analysis of SSA1 and SSB1 deletion mutants reveals robustness of chaperone HSP70 network in *Saccharomyces cerevisiae*. Proteomics, 2015, 15, 3126-3139.	1.3	12
48	Rationalizing Rac1 and RhoA GTPase signaling: A mathematical approach. Small GTPases, 2018, 9, 224-229.	0.7	12
49	p53 modeling as a route to mesothelioma patients stratification and novel therapeutic identification. Journal of Translational Medicine, 2018, 16, 282.	1.8	11
50	The chloroplast genome of the marine microalga *Tisochrysis lutea*. Mitochondrial DNA Part B: Resources, 2019, 4, 253-255.	0.2	11
51	Molecular profiling of thyroid cancer subtypes using large-scale text mining. BMC Medical Genomics, 2014, 7, S3.	0.7	10
52	Organising metabolic networks: Cycles in flux distributions. Journal of Theoretical Biology, 2010, 265, 250-260.	0.8	9
53	Constructing a molecular interaction network for thyroid cancer via large-scale text mining of gene and pathway events. BMC Systems Biology, 2015, 9, S5.	3.0	9
54	Disentangling the multigenic and pleiotropic nature of molecular function. BMC Systems Biology, 2015, 9, S3.	3.0	9

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55	Regulation of dual specificity phosphatases in breast cancer during initial treatment with Herceptin: a Boolean model analysis. BMC Systems Biology, 2018, 12, 11.	3.0	9
56	Metabolic flux from the chloroplast provides signals controlling photosynthetic acclimation to cold in <scp><i>Arabidopsis thaliana</i></scp>. Plant, Cell and Environment, 2021, 44, 171-185.	2.8	9
57	Local and global modes of drug action in biochemical networks. BMC Chemical Biology, 2009, 9, 4.	1.6	8
58	Metabolic flux prediction in cancer cells with altered substrate uptake. Biochemical Society Transactions, 2015, 43, 1177-1181.	1.6	8
59	Modelling GTPase dynamics to understand RhoA-driven cancer cell invasion. Biochemical Society Transactions, 2016, 44, 1695-1700.	1.6	8
60	HybridMine: A Pipeline for Allele Inheritance and Gene Copy Number Prediction in Hybrid Genomes and Its Application to Industrial Yeasts. Microorganisms, 2020, 8, 1554.	1.6	8
61	Integrating Geometric and Biomechanical Models of a Liver Tumour for Cryosurgery Simulation. Lecture Notes in Computer Science, 2003, , 121-131.	1.0	7
62	Insight into glucocorticoid receptor signalling through interactome model analysis. PLoS Computational Biology, 2017, 13, e1005825.	1.5	7
63	COVID-19 vaccination strategies depend on the underlying network of social interactions. Scientific Reports, 2021, 11, 24051.	1.6	7
64	SubcellulaRVis: a web-based tool to simplify and visualise subcellular compartment enrichment. Nucleic Acids Research, 2022, 50, W718-W725.	6.5	7
65	Modelling liver tissue properties using a non-linear viscoelastic model ror surgery simulation. ESAIM: Proceedings and Surveys, 2002, 12, 146-153.	0.4	6
66	Network medicine analysis of chondrocyte proteins towards new treatments of osteoarthritis. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20132907.	1.2	6
67	Data integration and mechanistic modelling for breast cancer biology: current state and future directions. Current Opinion in Endocrine and Metabolic Research, 2022, , 100350.	0.6	6
68	Construction of a Genome-Scale Kinetic Model of Mycobacterium Tuberculosis Using Generic Rate Equations. Metabolites, 2012, 2, 382-397.	1.3	5
69	Combinatorial mathematical modelling approaches to interrogate rear retraction dynamics in 3D cell migration. PLoS Computational Biology, 2021, 17, e1008213.	1.5	5
70	Non-linear Soft Tissue Deformations for the Simulation of Percutaneous Surgeries. Lecture Notes in Computer Science, 2001, , 1271-1272.	1.0	5
71	Identification of metabolic units induced by environmental signals. Bioinformatics, 2006, 22, e375-e383.	1.8	4
72	Cyclic decomposition explains a photosynthetic down regulation for Chlamydomonas reinhardtii. BioSystems, 2017, 162, 119-127.	0.9	4

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73	Modelling the role of dual specificity phosphatases in herceptin resistant breast cancer cell lines. Computational Biology and Chemistry, 2019, 80, 138-146.	1.1	4
74	Using Multilayer Heterogeneous Networks to Infer Functions of Phosphorylated Sites. Journal of Proteome Research, 2021, 20, 3532-3548.	1.8	4
75	Genome-Scale Integrative Data Analysis and Modeling of Dynamic Processes in Yeast. Methods in Molecular Biology, 2011, 759, 427-443.	0.4	4
76	Differential regulation of cell death pathways by the microenvironment correlates with chemoresistance and survival in leukaemia. PLoS ONE, 2017, 12, e0178606.	1.1	4
77	Modeling the Mechanism of GR/c-Jun/Erg Crosstalk in Apoptosis of Acute Lymphoblastic Leukemia. Frontiers in Physiology, 2012, 3, 410.	1.3	3
78	The Expanded p53 Interactome as a Predictive Model for Cancer Therapy. Genomics and Computational Biology, 2015, 1, 20.	0.7	3
79	Cytosolic fumarase acts as a metabolic fail-safe for both high and low temperature acclimation of <i>Arabidopsis thaliana</i>. Journal of Experimental Botany, 2022, 73, 2112-2124.	2.4	3
80	Kinetic Modeling of DUSP Regulation in Herceptin-Resistant HER2-Positive Breast Cancer. Genes, 2019, 10, 568.	1.0	2
81	Effect of IAPP on the proteome of cultured Rin-5F cells. BMC Biochemistry, 2018, 19, 9.	4.4	1
82	Modeling Rho GTPase Dynamics Using Boolean Logic. Methods in Molecular Biology, 2018, 1821, 37-46.	0.4	1
83	Model Parameterization with Quantitative Proteomics: Case Study with Trehalose Metabolism in Saccharomyces cerevisiae. Processes, 2021, 9, 139.	1.3	1
84	Transgenic inhibition of interleukin-6 trans-signaling does not prevent skeletal pathologies in mucolipidosis type II mice. Scientific Reports, 2021, 11, 3556.	1.6	1
85	Membrane Tension Orchestrates Rear Retraction in Matrix Directed Cell Migration. SSRN Electronic Journal, 0, , .	0.4	1
86	Local and global modes of drug action in biochemical networks. Nature Precedings, 2008, , .	0.1	0
87	A meta-analysis portal for human breast cancer transcriptomics data: BreastCancerVis. , 2018, , .		0
88	Metabolic Models. , 2019, , 438-444.		0
89	Exploring the Interactions of Physical, Chemical and Biological Variables of an Urban River Using Network Analysis. Water (Switzerland), 2020, 12, 2578.	1.2	0
90	MODELING TECHNIQUES FOR LIVER TISSUE PROPERTIES AND THEIR APPLICATION IN SURGICAL TREATMENT OF LIVER CANCER. , 2007, , 45-81.		0

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91	Systems Pharmacology, Drug-Target Networks. , 2013, , 2106-2108.		0
92	Drug Scope, Metabolic. , 2013, , 618-618.		0
93	Systems Pharmacology, Drug Disease Interactions. , 2013, , 2103-2106.		0
94	Opportunities and Challenges Provided by Boolean Modelling of Cancer Signalling Pathways. Computational Biology, 2020, , 199-216.	0.1	0