

Jean-Marc Schwartz

List of Publications by Year in descending order

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Version: 2024-02-01

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	Data integration and mechanistic modelling for breast cancer biology: current state and future directions. <i>Current Opinion in Endocrine and Metabolic Research</i> , 2022, , 100350.	0.6	6
2	Cytosolic fumarase acts as a metabolic fail-safe for both high and low temperature acclimation of <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2022, 73, 2112-2124.	2.4	3
3	SubcellularRVis: a web-based tool to simplify and visualise subcellular compartment enrichment. <i>Nucleic Acids Research</i> , 2022, 50, W718-W725.	6.5	7
4	Metabolic flux from the chloroplast provides signals controlling photosynthetic acclimation to cold in <i>Arabidopsis thaliana</i> . <i>Plant, Cell and Environment</i> , 2021, 44, 171-185.	2.8	9
5	Model Parameterization with Quantitative Proteomics: Case Study with Trehalose Metabolism in <i>Saccharomyces cerevisiae</i> . <i>Processes</i> , 2021, 9, 139.	1.3	1
6	Transgenic inhibition of interleukin-6 trans-signaling does not prevent skeletal pathologies in mucopolidosis type II mice. <i>Scientific Reports</i> , 2021, 11, 3556.	1.6	1
7	Combinatorial mathematical modelling approaches to interrogate rear retraction dynamics in 3D cell migration. <i>PLoS Computational Biology</i> , 2021, 17, e1008213.	1.5	5
8	A Holistic Approach to Study Photosynthetic Acclimation Responses of Plants to Fluctuating Light. <i>Frontiers in Plant Science</i> , 2021, 12, 668512.	1.7	21
9	Using Multilayer Heterogeneous Networks to Infer Functions of Phosphorylated Sites. <i>Journal of Proteome Research</i> , 2021, 20, 3532-3548.	1.8	4
10	Transcriptional Profile of the Industrial Hybrid <i>Saccharomyces pastorianus</i> Reveals Temperature-Dependent Allele Expression Bias and Preferential Orthologous Protein Assemblies. <i>Molecular Biology and Evolution</i> , 2021, 38, 5437-5452.	3.5	15
11	Mechanical loading activates the YAP/TAZ pathway and chemokine expression in the MLO-Y4 osteocyte-like cell line. <i>Laboratory Investigation</i> , 2021, 101, 1597-1604.	1.7	14
12	COVID-19 vaccination strategies depend on the underlying network of social interactions. <i>Scientific Reports</i> , 2021, 11, 24051.	1.6	7
13	From empirical to theoretical models of light response curves - linking photosynthetic and metabolic acclimation. <i>Photosynthesis Research</i> , 2020, 145, 5-14.	1.6	45
14	HybridMine: A Pipeline for Allele Inheritance and Gene Copy Number Prediction in Hybrid Genomes and Its Application to Industrial Yeasts. <i>Microorganisms</i> , 2020, 8, 1554.	1.6	8
15	Exploring the Interactions of Physical, Chemical and Biological Variables of an Urban River Using Network Analysis. <i>Water (Switzerland)</i> , 2020, 12, 2578.	1.2	0
16	Why COVID-19 models should incorporate the network of social interactions. <i>Physical Biology</i> , 2020, 17, 065008.	0.8	29
17	Opportunities and Challenges Provided by Boolean Modelling of Cancer Signalling Pathways. <i>Computational Biology</i> , 2020, , 199-216.	0.1	0
18	<i>Metabolic Models.</i> , 2019, , 438-444.		0

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19	Kinetic Modeling of DUSP Regulation in Herceptin-Resistant HER2-Positive Breast Cancer. <i>Genes</i> , 2019, 10, 568.	1.0	2
20	XBP1 signalling is essential for alleviating mutant protein aggregation in ER-stress related skeletal disease. <i>PLoS Genetics</i> , 2019, 15, e1008215.	1.5	16
21	Membrane Tension Orchestrates Rear Retraction in Matrix-Directed Cell Migration. <i>Developmental Cell</i> , 2019, 51, 460-475.e10.	3.1	112
22	Flux sampling is a powerful tool to study metabolism under changing environmental conditions. <i>Npj Systems Biology and Applications</i> , 2019, 5, 32.	1.4	62
23	Probabilistic controllability approach to metabolic fluxes in normal and cancer tissues. <i>Nature Communications</i> , 2019, 10, 2725.	5.8	15
24	Metabolic acclimation—a key to enhancing photosynthesis in changing environments?. <i>Journal of Experimental Botany</i> , 2019, 70, 3043-3056.	2.4	37
25	Modelling the role of dual specificity phosphatases in herceptin resistant breast cancer cell lines. <i>Computational Biology and Chemistry</i> , 2019, 80, 138-146.	1.1	4
26	The chloroplast genome of the marine microalga <i>Tisochrysis lutea</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 253-255.	0.2	11
27	Network controllability analysis of intracellular signalling reveals viruses are actively controlling molecular systems. <i>Scientific Reports</i> , 2019, 9, 2066.	1.6	19
28	SkeletalVis: an exploration and meta-analysis data portal of cross-species skeletal transcriptomics data. <i>Bioinformatics</i> , 2019, 35, 2283-2290.	1.8	18
29	Calcium activated nucleotidase 1 (CANT1) is critical for glycosaminoglycan biosynthesis in cartilage and endochondral ossification. <i>Matrix Biology</i> , 2019, 81, 70-90.	1.5	27
30	Stratification of knee osteoarthritis: two major patient subgroups identified by genome-wide expression analysis of articular cartilage. <i>Annals of the Rheumatic Diseases</i> , 2018, 77, 423-423.	0.5	89
31	Rationalizing Rac1 and RhoA GTPase signaling: A mathematical approach. <i>Small GTPases</i> , 2018, 9, 224-229.	0.7	12
32	A meta-analysis portal for human breast cancer transcriptomics data: BreastCancerVis. , 2018, , .		0
33	Using set theory to reduce redundancy in pathway sets. <i>BMC Bioinformatics</i> , 2018, 19, 386.	1.2	20
34	Effect of IAPP on the proteome of cultured Rin-5F cells. <i>BMC Biochemistry</i> , 2018, 19, 9.	4.4	1
35	p53 modeling as a route to mesothelioma patients stratification and novel therapeutic identification. <i>Journal of Translational Medicine</i> , 2018, 16, 282.	1.8	11
36	Modeling Rho GTPase Dynamics Using Boolean Logic. <i>Methods in Molecular Biology</i> , 2018, 1821, 37-46.	0.4	1

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37	Regulation of dual specificity phosphatases in breast cancer during initial treatment with Herceptin: a Boolean model analysis. <i>BMC Systems Biology</i> , 2018, 12, 11.	3.0	9
38	Mapping biological process relationships and disease perturbations within a pathway network. <i>Npj Systems Biology and Applications</i> , 2018, 4, 22.	1.4	21
39	The chaperone activity of 4PBA ameliorates the skeletal phenotype of Chihuahua, a zebrafish model for dominant osteogenesis imperfecta. <i>Human Molecular Genetics</i> , 2017, 26, 2897-2911.	1.4	68
40	Cyclic decomposition explains a photosynthetic down regulation for <i>Chlamydomonas reinhardtii</i> . <i>BioSystems</i> , 2017, 162, 119-127.	0.9	4
41	A quantitative brain map of experimental cerebral malaria pathology. <i>PLoS Pathogens</i> , 2017, 13, e1006267.	2.1	73
42	Insight into glucocorticoid receptor signalling through interactome model analysis. <i>PLoS Computational Biology</i> , 2017, 13, e1005825.	1.5	7
43	Differential regulation of cell death pathways by the microenvironment correlates with chemoresistance and survival in leukaemia. <i>PLoS ONE</i> , 2017, 12, e0178606.	1.1	4
44	A MAPK-Driven Feedback Loop Suppresses Rac Activity to Promote RhoA-Driven Cancer Cell Invasion. <i>PLoS Computational Biology</i> , 2016, 12, e1004909.	1.5	36
45	Modelling GTPase dynamics to understand RhoA-driven cancer cell invasion. <i>Biochemical Society Transactions</i> , 2016, 44, 1695-1700.	1.6	8
46	Gene expression changes in damaged osteoarthritic cartilage identify a signature of non-chondrogenic and mechanical responses. <i>Osteoarthritis and Cartilage</i> , 2016, 24, 1431-1440.	0.6	93
47	PhenomeScape: a cytoscape app to identify differentially regulated sub-networks using known disease associations. <i>Bioinformatics</i> , 2016, 32, 3847-3849.	1.8	13
48	Quantitative proteomics and network analysis of SSA1 and SSB1 deletion mutants reveals robustness of chaperone HSP70 network in <i>Saccharomyces cerevisiae</i> . <i>Proteomics</i> , 2015, 15, 3126-3139.	1.3	12
49	Constructing a molecular interaction network for thyroid cancer via large-scale text mining of gene and pathway events. <i>BMC Systems Biology</i> , 2015, 9, S5.	3.0	9
50	Metabolic flux prediction in cancer cells with altered substrate uptake. <i>Biochemical Society Transactions</i> , 2015, 43, 1177-1181.	1.6	8
51	Disentangling the multigenic and pleiotropic nature of molecular function. <i>BMC Systems Biology</i> , 2015, 9, S3.	3.0	9
52	Flux balance analysis reveals acetate metabolism modulates cyclic electron flow and alternative glycolytic pathways in <i>Chlamydomonas reinhardtii</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 474.	1.7	59
53	PhenomeExpress: A refined network analysis of expression datasets by inclusion of known disease phenotypes. <i>Scientific Reports</i> , 2015, 5, 8117.	1.6	25
54	A logical model of HIV-1 interactions with the T-cell activation signalling pathway. <i>Bioinformatics</i> , 2015, 31, 1075-1083.	1.8	23

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55	The Expanded p53 Interactome as a Predictive Model for Cancer Therapy. <i>Genomics and Computational Biology</i> , 2015, 1, 20.	0.7	3
56	Network medicine analysis of chondrocyte proteins towards new treatments of osteoarthritis. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20132907.	1.2	6
57	Environmental systems biology of cold-tolerant phenotype in <i>Saccharomyces</i> species adapted to grow at different temperatures. <i>Molecular Ecology</i> , 2014, 23, 5241-5257.	2.0	79
58	Molecular profiling of thyroid cancer subtypes using large-scale text mining. <i>BMC Medical Genomics</i> , 2014, 7, S3.	0.7	10
59	Erg and AP-1 as determinants of glucocorticoid response in acute lymphoblastic leukemia. <i>Oncogene</i> , 2013, 32, 3039-3048.	2.6	31
60	PathNER: a tool for systematic identification of biological pathway mentions in the literature. <i>BMC Systems Biology</i> , 2013, 7, S2.	3.0	18
61	Dynamics of DNA Damage Induced Pathways to Cancer. <i>PLoS ONE</i> , 2013, 8, e72303.	1.1	23
62	<i>Systems Pharmacology, Drug-Target Networks.</i> , 2013, , 2106-2108.		0
63	<i>Drug Scope, Metabolic.</i> , 2013, , 618-618.		0
64	<i>Systems Pharmacology, Drug Disease Interactions.</i> , 2013, , 2103-2106.		0
65	Modeling the Mechanism of GR/c-Jun/Erg Crosstalk in Apoptosis of Acute Lymphoblastic Leukemia. <i>Frontiers in Physiology</i> , 2012, 3, 410.	1.3	3
66	Comprehensive Modelling of the Neurospora Circadian Clock and Its Temperature Compensation. <i>PLoS Computational Biology</i> , 2012, 8, e1002437.	1.5	29
67	Exploring the genetic control of glycolytic oscillations in <i>Saccharomyces Cerevisiae</i> . <i>BMC Systems Biology</i> , 2012, 6, 108.	3.0	12
68	Modularity in Protein Complex and Drug Interactions Reveals New Polypharmacological Properties. <i>PLoS ONE</i> , 2012, 7, e30028.	1.1	40
69	Construction of a Genome-Scale Kinetic Model of <i>Mycobacterium Tuberculosis</i> Using Generic Rate Equations. <i>Metabolites</i> , 2012, 2, 382-397.	1.3	5
70	Genome-Scale Integrative Data Analysis and Modeling of Dynamic Processes in Yeast. <i>Methods in Molecular Biology</i> , 2011, 759, 427-443.	0.4	4
71	Organising metabolic networks: Cycles in flux distributions. <i>Journal of Theoretical Biology</i> , 2010, 265, 250-260.	0.8	9
72	Integration of metabolic databases for the reconstruction of genome-scale metabolic networks. <i>BMC Systems Biology</i> , 2010, 4, 114.	3.0	79

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73	Streamlining the construction of large-scale dynamic models using generic kinetic equations. <i>Bioinformatics</i> , 2010, 26, 1324-1331.	1.8	16
74	Quantitative analysis and modeling of glucocorticoid-controlled gene expression. <i>Pharmacogenomics</i> , 2010, 11, 1545-1560.	0.6	12
75	Deterministic mathematical models of the cAMP pathway in <i>Saccharomyces cerevisiae</i> . <i>BMC Systems Biology</i> , 2009, 3, 70.	3.0	22
76	Local and global modes of drug action in biochemical networks. <i>BMC Chemical Biology</i> , 2009, 9, 4.	1.6	8
77	A global view of drug-therapy interactions. <i>BMC Pharmacology</i> , 2008, 8, 5.	0.4	81
78	Local and global modes of drug action in biochemical networks. <i>Nature Precedings</i> , 2008, , .	0.1	0
79	Observing metabolic functions at the genome scale. <i>Genome Biology</i> , 2007, 8, R123.	13.9	54
80	MODELING TECHNIQUES FOR LIVER TISSUE PROPERTIES AND THEIR APPLICATION IN SURGICAL TREATMENT OF LIVER CANCER. , 2007, , 45-81.		0
81	Quantitative elementary mode analysis of metabolic pathways: the example of yeast glycolysis. <i>BMC Bioinformatics</i> , 2006, 7, 186.	1.2	66
82	Identification of metabolic units induced by environmental signals. <i>Bioinformatics</i> , 2006, 22, e375-e383.	1.8	4
83	Modelling liver tissue properties using a non-linear visco-elastic model for surgery simulation. <i>Medical Image Analysis</i> , 2005, 9, 103-112.	7.0	139
84	A quadratic programming approach for decomposing steady-state metabolic flux distributions onto elementary modes. <i>Bioinformatics</i> , 2005, 21, ii204-ii205.	1.8	39
85	Integrating Geometric and Biomechanical Models of a Liver Tumour for Cryosurgery Simulation. <i>Lecture Notes in Computer Science</i> , 2003, , 121-131.	1.0	7
86	Modelling liver tissue properties using a non-linear viscoelastic model for surgery simulation. <i>ESAIM: Proceedings and Surveys</i> , 2002, 12, 146-153.	0.4	6
87	Non-linear Soft Tissue Deformations for the Simulation of Percutaneous Surgeries. <i>Lecture Notes in Computer Science</i> , 2001, , 1271-1272.	1.0	5
88	Golgesin-GFP fusions as distinct markers for Golgi and post-Golgi vesicles in <i>Dictyostelium</i> cells. <i>Biology of the Cell</i> , 2000, 92, 495-511.	0.7	41
89	Dynein motor regulation stabilizes interphase microtubule arrays and determines centrosome position. <i>EMBO Journal</i> , 1999, 18, 6786-6792.	3.5	110
90	Cytokinesis mediated through the recruitment of cortexillins into the cleavage furrow. <i>EMBO Journal</i> , 1999, 18, 586-594.	3.5	98

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91	G Protein β^2 Subunit ² null Mutants Are Impaired in Phagocytosis and Chemotaxis Due to Inappropriate Regulation of the Actin Cytoskeleton. <i>Journal of Cell Biology</i> , 1998, 141, 1529-1537.	2.3	113
92	Three-dimensional Patterns and Redistribution of Myosin II and Actin in Mitotic Dictyostelium Cells. <i>Journal of Cell Biology</i> , 1997, 139, 1793-1804.	2.3	68
93	Microfilament dynamics during cell movement and chemotaxis monitored using a GFP ² actin fusion protein. <i>Current Biology</i> , 1997, 7, 176-183.	1.8	238
94	Membrane Tension Orchestrates Rear Retraction in Matrix Directed Cell Migration. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1