Pedro Mendes

List of Publications by Year
in descending order

115 papers	15,468 citations	41344 49 h-index	27406 106 g-index
131 all docs	131 docs citations	131 times ranked	17654 citing authors

#	Article	IF	Citations
1	COPASI--a COmplex PAthway SImulator. Bioinformatics, 2006, 22, 3067-3074.	4.1	2,265
2	Plant metabolomics: large-scale phytochemistry in the functional genomics era. Phytochemistry, 2003, 62, 817-836.	2.9	1,010
3	A community-driven global reconstruction of human metabolism. Nature Biotechnology, 2013, 31, 419-425.	17.5	920
4	ChEBI in 2016: Improved services and an expanding collection of metabolites. Nucleic Acids Research, 2016, 44, D1214-D1219.	14.5	752
5	Parameter Estimation in Biochemical Pathways: A Comparison of Global Optimization Methods. Genome Research, 2003, 13, 2467-2474.	5.5	706
6	Potential of metabolomics as a functional genomics tool. Trends in Plant Science, 2004, 9, 418-425.	8.8	685
7	Minimum information requested in the annotation of biochemical models (MIRIAM). Nature Biotechnology, 2005, 23, 1509-1515.	17.5	553
8	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. Nature Biotechnology, 2008, 26, 1155-1160.	17.5	530
9	Discovery of meaningful associations in genomic data using partial correlation coefficients. Bioinformatics, 2004, 20, 3565-3574.	4.1	476
10	myo-Inositol Oxygenase Offers a Possible Entry Point into Plant Ascorbate Biosynthesis. Plant Physiology, 2004, 134, 1200-1205.	4.8	423
11	The metabolomics standards initiative (MSI). Metabolomics, 2007, 3, 175-178.	3.0	396
12	Metabolic profiling of Medicago truncatula cell cultures reveals the effects of biotic and abiotic elicitors on metabolism. Journal of Experimental Botany, 2005, 56, 323-336.	4.8	347
13	The Metabolomics Standards Initiative. Nature Biotechnology, 2007, 25, 846-848.	17.5	328
14	A proposed framework for the description of plant metabolomics experiments and their results. Nature Biotechnology, 2004, 22, 1601-1606.	17.5	283
15	A hybrid approach for efficient and robust parameter estimation in biochemical pathways. BioSystems, 2006, 83, 248-265.	2.0	251
16	The origin of correlations in metabolomics data. Metabolomics, 2005, 1, 53-63.	3.0	248
17	Controlled vocabularies and semantics in systems biology. Molecular Systems Biology, 2011, 7, 543.	7.2	246
18	GEPASI: a software package for modelling the dynamics, steady states and control of biochemical and other systems. Bioinformatics, 1993, 9, 563-571.	4.1	245

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19	Recon 2.2: from reconstruction to model of human metabolism. Metabolomics, 2016, 12, 109.	3.0	243
20	Gene networks: how to put the function in genomics. Trends in Biotechnology, 2002, 20, 467-472.	9.3	241
21	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
22	Methyl jasmonate and yeast elicitor induce differential transcriptional and metabolic re-programming in cell suspension cultures of the model legume Medicago truncatula. Planta, 2005, 220, 696-707.	3.2	175
23	Computational Modeling of Biochemical Networks Using COPASI. Methods in Molecular Biology, 2009, 500, 17-59.	0.9	163
24	Multi-scale modelling and simulation in systems biology. Integrative Biology (United Kingdom), 2011, 3, 86.	1.3	162
25	Linking the genes: inferring quantitative gene networks from microarray data. Trends in Genetics, 2002, 18, 395-398.	6.7	149
26	Artificial gene networks for objective comparison of analysis algorithms. Bioinformatics, 2003, 19, ii122-ii129.	4.1	148
27	Path2Models: large-scale generation of computational models from biochemical pathway maps. BMC Systems Biology, 2013, 7, 116.	3.0	145
28	Towards a genome-scale kinetic model of cellular metabolism. BMC Systems Biology, 2010, 4, 6.	3.0	132
29	Improving metabolic flux predictions using absolute gene expression data. BMC Systems Biology, 2012, 6, 73.	3.0	126
30	Yeast 5 â€" an expanded reconstruction of the Saccharomyces cerevisiae metabolic network. BMC Systems Biology, 2012, 6, 55.	3.0	118
31	A model of yeast glycolysis based on a consistent kinetic characterisation of all its enzymes. FEBS Letters, 2013, 587, 2832-2841.	2.8	113
32	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. Briefings in Bioinformatics, 2021, 22, 642-663.	6.5	110
33	A Two-dimensional Electrophoresis Proteomic Reference Map and Systematic Identification of 1367 Proteins from a Cell Suspension Culture of the Model Legume Medicago truncatula. Molecular and Cellular Proteomics, 2005, 4, 1812-1825.	3.8	108
34	Bioinformatics tools for cancer metabolomics. Metabolomics, 2011, 7, 329-343.	3.0	106
35	Emerging bioinformatics for the metabolome. Briefings in Bioinformatics, 2002, 3, 134-145.	6.5	104
36	Systematic Construction of Kinetic Models from Genome-Scale Metabolic Networks. PLoS ONE, 2013, 8, e79195.	2.5	102

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37	Further developments towards a genome-scale metabolic model of yeast. BMC Systems Biology, 2010, 4, 145.	3.0	95
38	An <i>in vivo</i> control map for the eukaryotic mRNA translation machinery. Molecular Systems Biology, 2013, 9, 635.	7.2	89
39	Metabolic regulation is sufficient for global and robust coordination of glucose uptake, catabolism, energy production and growth in Escherichia coli. PLoS Computational Biology, 2017, 13, e1005396.	3.2	85
40	COPASI and its applications in biotechnology. Journal of Biotechnology, 2017, 261, 215-220.	3.8	78
41	A general map of iron metabolism and tissue-specific subnetworks. Molecular BioSystems, 2009, 5, 422.	2.9	74
42	Elevating vitamin C content via overexpression of myo-inositol oxygenase and l-gulono-1,4-lactone oxidase in Arabidopsis leads to enhanced biomass and tolerance to abiotic stresses. In Vitro Cellular and Developmental Biology - Plant, 2013, 49, 643-655.	2.1	70
43	The SuBliMinaL Toolbox: automating steps in the reconstruction of metabolic networks. Journal of Integrative Bioinformatics, 2011, 8, 187-203.	1.5	67
44	Channelling can decrease pool size. FEBS Journal, 1992, 204, 257-266.	0.2	62
45	Efficient discovery of anti-inflammatory small-molecule combinations using evolutionary computing. Nature Chemical Biology, 2011, 7, 902-908.	8.0	61
46	BioPreDyn-bench: a suite of benchmark problems for dynamic modelling in systems biology. BMC Systems Biology, 2015, 9, 8.	3.0	61
47	Large-Scale Metabolic Models: From Reconstruction to Differential Equations. Industrial Biotechnology, 2013, 9, 179-184.	0.8	58
48	A systems biology view of cancer. Biochimica Et Biophysica Acta: Reviews on Cancer, 2009, 1796, 129-139.	7.4	55
49	SBRML: a markup language for associating systems biology data with models. Bioinformatics, 2010, 26, 932-938.	4.1	54
50	In situkinetic analysis of glyoxalase I and glyoxalase II inSaccharomyces cerevisiae. FEBS Journal, 2001, 268, 3930-3936.	0.2	51
51	Toward Community Standards and Software for Whole-Cell Modeling. IEEE Transactions on Biomedical Engineering, 2016, 63, 2007-2014.	4.2	51
52	The SuBliMinaL Toolbox: automating steps in the reconstruction of metabolic networks. Journal of Integrative Bioinformatics, 2011, 8, 186.	1.5	51
53	Condor-COPASI: high-throughput computing for biochemical networks. BMC Systems Biology, 2012, 6, 91.	3.0	44
54	What Can We Learn from Global Sensitivity Analysis of Biochemical Systems?. PLoS ONE, 2013, 8, e79244.	2.5	40

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55	Bridging the gaps in systems biology. Molecular Genetics and Genomics, 2014, 289, 727-734.	2.1	38
56	A new strategy for assessing sensitivities in biochemical models. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2008, 366, 3619-3631.	3.4	37
57	Mining metabolites: extracting the yeast metabolome from the literature. Metabolomics, 2011, 7, 94-101.	3.0	37
58	Comparison of Reverse-Engineering Methods Using an in Silico Network. Annals of the New York Academy of Sciences, 2007, 1115, 73-89.	3.8	36
59	A Computational Model of Liver Iron Metabolism. PLoS Computational Biology, 2013, 9, e1003299.	3.2	33
60	biochem4j: Integrated and extensible biochemical knowledge through graph databases. PLoS ONE, 2017, 12, e0179130.	2.5	31
61	Metabolic Footprinting: A New Approach to Identify Physiological Changes in Complex Microbial Communities upon Exposure to Toxic Chemicals. Environmental Science & Technology, 2007, 41, 3945-3951.	10.0	30
62	An analysis of a â€˜community-drivenâ€™ reconstruction of the human metabolic network. Metabolomics, 2013, 9, 757-764.	3.0	30
63	The Genome-Wide Early Temporal Response of Saccharomyces cerevisiae to Oxidative Stress Induced by Cumene Hydroperoxide. PLoS ONE, 2013, 8, e74939.	2.5	29
64	Impact of kinetic isotope effects in isotopic studies of metabolic systems. BMC Systems Biology, 2015, 9, 64.	3.0	29
65	Snapshots of Systems. , 2000, , 3-25.		29
66	Modelling and simulation for metabolomics data analysis. Biochemical Society Transactions, 2005, 33, 1427.	3.4	28
67	libAnnotationSBML: a library for exploiting SBML annotations. Bioinformatics, 2009, 25, 2292-2293.	4.1	28
68	Systematic integration of experimental data and models in systems biology. BMC Bioinformatics, 2010, 11, 582.	2.6	28
69	Biochemical fluctuations, optimisation and the linear noise approximation. BMC Systems Biology, 2012, 6, 86.	3.0	25
70	The markup is the model: Reasoning about systems biology models in the Semantic Web era. Journal of Theoretical Biology, 2008, 252, 538-543.	1.7	24
71	Fitting Transporter Activities to Cellular Drug Concentrations and Fluxes: Why the Bumblebee Can Fly. Trends in Pharmacological Sciences, 2015, 36, 710-723.	8.7	24
72	On the analysis of the inverse problem of metabolic pathways using artificial neural networks. BioSystems, 1996, 38, 15-28.	2.0	23

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73	Chapter 22 Enzyme Kinetics and Computational Modeling for Systems Biology. Methods in Enzymology, 2009, 467, 583-599.	1.0	23
74	Characterisation of multiple substrate-specific (d)ITP/(d)XTPase and modelling of deaminated purine nucleotide metabolism. BMB Reports, 2012, 45, 259-264.	2.4	23
75	Metabolic Channeling in Organized Enzyme Systems: Experiments and Models. Advances in Molecular and Cell Biology, 1995, , 1-19.	0.1	21
76	Enzyme kinetics informatics: from instrument to browser. FEBS Journal, 2010, 277, 3769-3779.	4.7	20
77	Metabolic control in integrated biochemical systems. FEBS Journal, 2002, 269, 4399-4408.	0.2	19
78	libChEBI: an API for accessing the ChEBI database. Journal of Cheminformatics, 2016, 8, 11.	6.1	19
79	Plant Metabolomics by GC-MS and Differential Analysis. Methods in Molecular Biology, 2011, 678, 229-246.	0.9	18
80	Translation initiation events on structured eukaryotic mRNAs generate gene expression noise. Nucleic Acids Research, 2017, 45, 6981-6992.	14.5	18
81	A Method for Comparing Multivariate Time Series with Different Dimensions. PLoS ONE, 2013, 8, e54201.	2.5	17
82	Minimum-noise production of translation factor eIF4G maps to a mechanistically determined optimal rate control window for protein synthesis. Nucleic Acids Research, 2017, 45, 1015-1025.	14.5	16
83	Comparison of sampling techniques for parallel analysis of transcript and metabolite levels inSaccharomyces cerevisiae. Yeast, 2007, 24, 181-188.	1.7	15
84	COMODI: an ontology to characterise differences in versions of computational models in biology. Journal of Biomedical Semantics, 2016, 7, 46.	1.6	15
85	Gastrointestinal iron excretion and reversal of iron excess in a mouse model of inherited iron excess. Haematologica, 2019, 104, 678-689.	3.5	15
86	A new regulatory principle for in vivo biochemistry: Pleiotropic low affinity regulation by the adenine nucleotides â€" Illustrated for the glycolytic enzymes of <i>Saccharomyces cerevisiae</i>. FEBS Letters, 2013, 587, 2860-2867.	2.8	14
87	Silence on the relevant literature and errors in implementation. Nature Biotechnology, 2015, 33, 336-339.	17.5	14
88	An Overview of Network-Based and -Free Approaches for Stochastic Simulation of Biochemical Systems. Computation, 2018, 6, 9.	2.0	14
89	Quantifying gene networks with regulatory strengths. Molecular Biology Reports, 2002, 29, 73-77.	2.3	13
90	Metabolomics and the challenges ahead. Briefings in Bioinformatics, 2006, 7, 127-127.	6.5	13

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91	Challenges for Modeling and Simulation Methods in Systems Biology. , 2006, , .		13
92	Reproducible Research Using Biomodels. Bulletin of Mathematical Biology, 2018, 80, 3081-3087.	1.9	13
93	An important role for periplasmic storage in <i>Pseudomonas aeruginosa</i> copper homeostasis revealed by a combined experimental and computational modeling study. Molecular Microbiology, 2018, 110, 357-369.	2.5	13
94	ModelBricksâ€"modules for reproducible modeling improving model annotation and provenance. Npj Systems Biology and Applications, 2019, 5, 37.	3.0	13
95	Agent Based Models of Polymicrobial Biofilms and the Microbiomeâ€"A Review. Microorganisms, 2021, 9, 417.	3.6	12
96	ModelMage: a tool for automatic model generation, selection and management. Genome Informatics, 2008, 20, 52-63.	0.4	11
97	BioSimulators: a central registry of simulation engines and services for recommending specific tools. Nucleic Acids Research, 2022, 50, W108-W114.	14.5	11
98	Modeling the dynamics of mouse iron body distribution: hepcidin is necessary but not sufficient. BMC Systems Biology, 2017, 11, 57.	3.0	10
99	Simulation of Biochemical Networks using Copasi - A Complex Pathway Simulator. , 2006, , .		9
100	A computational model to understand mouse iron physiology and disease. PLoS Computational Biology, 2019, 15, e1006680.	3.2	8
101	Design and Architecture of Web Services for Simulation of Biochemical Systems. Lecture Notes in Computer Science, 2009, , 182-195.	1.3	7
102	ModelMage: A TOOL FOR AUTOMATIC MODEL GENERATION, SELECTION AND MANAGEMENT. , 2008, , .		6
103	Databases and Visualization for Metabolomics. , 2003, , 293-309.		6
104	Integrative Information Management for Systems Biology. Lecture Notes in Computer Science, 2010, , 164-178.	1.3	6
105	MYC dosage compensation is mediated by miRNA-transcription factor interactions in aneuploid cancer. IScience, 2021, 24, 103407.	4.1	6
106	Data Management in Computational Systems Biology: Exploring Standards, Tools, Databases, and Packaging Best Practices. Methods in Molecular Biology, 2019, 2049, 285-314.	0.9	3
107	Integrative modelling of gene expression and cell metabolism. Applied Bioinformatics, 2003, 2, 79-90.	1.6	3
108	Kinetic modelling of large-scale metabolic networks. , 2011, , .		2

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109	Response to â€˜The Need for Speedâ€™, by Matsson et al .. Trends in Pharmacological Sciences, 2016, 37, 245-246.	8.7	2
110	Understanding Lactobacillus paracasei and Streptococcus oralis Biofilm Interactions through Agent-Based Modeling. MSphere, 2021, 6, e0087521.	2.9	2
111	Plant Metabolomics: Large-Scale Phytochemistry in the Functional Genomics Era.. ChemInform, 2003, 34, no.	0.0	1
112	Top-Down Dynamical Modeling of Molecular Regulatory Networks. , 2014, , 223-239.		0
113	Multisite rate control analysis identifies ribosomal scanning as the sole highâ€‌capacity/lowâ€‌fluxâ€‌control step in mRNA translation. FEBS Journal, 2020, 287, 925-940.	4.7	0
114	GEPASI: A User Oriented Metabolic Simulator. , 1993, , 463-466.		0
115	Control Analysis of Metabolic Channeling. , 1993, , 211-216.		0