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	BioSimulators: a central registry of simulation engines and services for recommending specific tools. Nucleic Acids Research, 2022, 50, W108-W114.	14.5	11
2	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
3	Agent Based Models of Polymicrobial Biofilms and the Microbiomeâ€"A Review. Microorganisms, 2021, 9, 417.	3.6	12
4	MYC dosage compensation is mediated by miRNA-transcription factor interactions in aneuploid cancer. IScience, 2021, 24, 103407.	4.1	6
5	Understanding Lactobacillus paracasei and Streptococcus oralis Biofilm Interactions through Agent-Based Modeling. MSphere, 2021, 6, e0087521.	2.9	2
6	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
7	<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
8	ModelBricksâ€"modules for reproducible modeling improving model annotation and provenance. Npj Systems Biology and Applications, 2019, 5, 37.	3.0	13
9	Gastrointestinal iron excretion and reversal of iron excess in a mouse model of inherited iron excess. Haematologica, 2019, 104, 678-689.	3.5	15
10	A computational model to understand mouse iron physiology and disease. PLoS Computational Biology, 2019, 15, e1006680.	3.2	8
11	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
12	Reproducible Research Using Biomodels. Bulletin of Mathematical Biology, 2018, 80, 3081-3087.	1.9	13
13	An important role for periplasmic storage in Pseudomonas aeruginosa copper homeostasis revealed by a combined experimental and computational modeling study. Molecular Microbiology, 2018, 110, 357-369.	2.5	13
14	An Overview of Network-Based and -Free Approaches for Stochastic Simulation of Biochemical Systems. Computation, 2018, 6, 9.	2.0	14
15	Translation initiation events on structured eukaryotic mRNAs generate gene expression noise. Nucleic Acids Research, 2017, 45, 6981-6992.	14.5	18
16	COPASI and its applications in biotechnology. Journal of Biotechnology, 2017, 261, 215-220.	3.8	78
17	Modeling the dynamics of mouse iron body distribution: hepcidin is necessary but not sufficient. BMC Systems Biology, 2017, 11, 57.	3.0	10
18	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

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19	biochem4j: Integrated and extensible biochemical knowledge through graph databases. PLoS ONE, 2017, 12, e0179130.	2.5	31
20	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
21	Toward Community Standards and Software for Whole-Cell Modeling. IEEE Transactions on Biomedical Engineering, 2016, 63, 2007-2014.	4.2	51
22	Response to â€˜The Need for Speedâ€™, by Matsson et al .. Trends in Pharmacological Sciences, 2016, 37, 245-246.	8.7	2
23	Recon 2.2: from reconstruction to model of human metabolism. Metabolomics, 2016, 12, 109.	3.0	243
24	COMODI: an ontology to characterise differences in versions of computational models in biology. Journal of Biomedical Semantics, 2016, 7, 46.	1.6	15
25	libChEBI: an API for accessing the ChEBI database. Journal of Cheminformatics, 2016, 8, 11.	6.1	19
26	ChEBI in 2016: Improved services and an expanding collection of metabolites. Nucleic Acids Research, 2016, 44, D1214-D1219.	14.5	752
27	Impact of kinetic isotope effects in isotopic studies of metabolic systems. BMC Systems Biology, 2015, 9, 64.	3.0	29
28	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
29	BioPreDyn-bench: a suite of benchmark problems for dynamic modelling in systems biology. BMC Systems Biology, 2015, 9, 8.	3.0	61
30	Silence on the relevant literature and errors in implementation. Nature Biotechnology, 2015, 33, 336-339.	17.5	14
31	Top-Down Dynamical Modeling of Molecular Regulatory Networks. , 2014, , 223-239.		0
32	Bridging the gaps in systems biology. Molecular Genetics and Genomics, 2014, 289, 727-734.	2.1	38
33	An analysis of a â€˜community-drivenâ€™ reconstruction of the human metabolic network. Metabolomics, 2013, 9, 757-764.	3.0	30
34	A new regulatory principle for in vivo biochemistry: Pleiotropic low affinity regulation by the adenine nucleotides â€“ Illustrated for the glycolytic enzymes of Saccharomyces cerevisiae. FEBS Letters, 2013, 587, 2860-2867.	2.8	14
35	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
36	Path2Models: large-scale generation of computational models from biochemical pathway maps. BMC Systems Biology, 2013, 7, 116.	3.0	145

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37	A model of yeast glycolysis based on a consistent kinetic characterisation of all its enzymes. FEBS Letters, 2013, 587, 2832-2841.	2.8	113
38	An in vivo control map for the eukaryotic mRNA translation machinery. Molecular Systems Biology, 2013, 9, 635.	7.2	89
39	A community-driven global reconstruction of human metabolism. Nature Biotechnology, 2013, 31, 419-425.	17.5	920
40	A Computational Model of Liver Iron Metabolism. PLoS Computational Biology, 2013, 9, e1003299.	3.2	33
41	Large-Scale Metabolic Models: From Reconstruction to Differential Equations. Industrial Biotechnology, 2013, 9, 179-184.	0.8	58
42	The Genome-Wide Early Temporal Response of Saccharomyces cerevisiae to Oxidative Stress Induced by Cumene Hydroperoxide. PLoS ONE, 2013, 8, e74939.	2.5	29
43	Systematic Construction of Kinetic Models from Genome-Scale Metabolic Networks. PLoS ONE, 2013, 8, e79195.	2.5	102
44	What Can We Learn from Global Sensitivity Analysis of Biochemical Systems?. PLoS ONE, 2013, 8, e79244.	2.5	40
45	A Method for Comparing Multivariate Time Series with Different Dimensions. PLoS ONE, 2013, 8, e54201.	2.5	17
46	Yeast 5 â€“ an expanded reconstruction of the Saccharomyces cerevisiae metabolic network. BMC Systems Biology, 2012, 6, 55.	3.0	118
47	Improving metabolic flux predictions using absolute gene expression data. BMC Systems Biology, 2012, 6, 73.	3.0	126
48	Biochemical fluctuations, optimisation and the linear noise approximation. BMC Systems Biology, 2012, 6, 86.	3.0	25
49	Condor-COPASI: high-throughput computing for biochemical networks. BMC Systems Biology, 2012, 6, 91.	3.0	44
50	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
51	Multi-scale modelling and simulation in systems biology. Integrative Biology (United Kingdom), 2011, 3, 86.	1.3	162
52	Plant Metabolomics by GC-MS and Differential Analysis. Methods in Molecular Biology, 2011, 678, 229-246.	0.9	18
53	The SuBliMinaL Toolbox: automating steps in the reconstruction of metabolic networks. Journal of Integrative Bioinformatics, 2011, 8, 187-203.	1.5	67
54	Mining metabolites: extracting the yeast metabolome from the literature. Metabolomics, 2011, 7, 94-101.	3.0	37

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55	Bioinformatics tools for cancer metabolomics. Metabolomics, 2011, 7, 329-343.	3.0	106
56	Controlled vocabularies and semantics in systems biology. Molecular Systems Biology, 2011, 7, 543.	7.2	246
57	Efficient discovery of anti-inflammatory small-molecule combinations using evolutionary computing. Nature Chemical Biology, 2011, 7, 902-908.	8.0	61
58	Kinetic modelling of large-scale metabolic networks. , 2011, , .		2
59	The SuBliMinaL Toolbox: automating steps in the reconstruction of metabolic networks. Journal of Integrative Bioinformatics, 2011, 8, 186.	1.5	51
60	Systematic integration of experimental data and models in systems biology. BMC Bioinformatics, 2010, 11, 582.	2.6	28
61	Towards a genome-scale kinetic model of cellular metabolism. BMC Systems Biology, 2010, 4, 6.	3.0	132
62	Enzyme kinetics informatics: from instrument to browser. FEBS Journal, 2010, 277, 3769-3779.	4.7	20
63	SBRML: a markup language for associating systems biology data with models. Bioinformatics, 2010, 26, 932-938.	4.1	54
64	Further developments towards a genome-scale metabolic model of yeast. BMC Systems Biology, 2010, 4, 145.	3.0	95
65	Integrative Information Management for Systems Biology. Lecture Notes in Computer Science, 2010, , 164-178.	1.3	6
66	libAnnotationSBML: a library for exploiting SBML annotations. Bioinformatics, 2009, 25, 2292-2293.	4.1	28
67	A systems biology view of cancer. Biochimica Et Biophysica Acta: Reviews on Cancer, 2009, 1796, 129-139.	7.4	55
68	Design and Architecture of Web Services for Simulation of Biochemical Systems. Lecture Notes in Computer Science, 2009, , 182-195.	1.3	7
69	Computational Modeling of Biochemical Networks Using COPASI. Methods in Molecular Biology, 2009, 500, 17-59.	0.9	163
70	A general map of iron metabolism and tissue-specific subnetworks. Molecular BioSystems, 2009, 5, 422.	2.9	74
71	Chapter 22 Enzyme Kinetics and Computational Modeling for Systems Biology. Methods in Enzymology, 2009, 467, 583-599.	1.0	23
72	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

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73	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. Nature Biotechnology, 2008, 26, 1155-1160.	17.5	530
74	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
75	ModelMage: A TOOL FOR AUTOMATIC MODEL GENERATION, SELECTION AND MANAGEMENT. , 2008, , .		6
76	ModelMage: a tool for automatic model generation, selection and management. Genome Informatics, 2008, 20, 52-63.	0.4	11
77	Comparison of sampling techniques for parallel analysis of transcript and metabolite levels inSaccharomyces cerevisiae. Yeast, 2007, 24, 181-188.	1.7	15
78	Metabolic Footprinting:Â 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
79	The Metabolomics Standards Initiative. Nature Biotechnology, 2007, 25, 846-848.	17.5	328
80	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
81	The metabolomics standards initiative (MSI). Metabolomics, 2007, 3, 175-178.	3.0	396
82	COPASI--a COmplex PAthway SImulator. Bioinformatics, 2006, 22, 3067-3074.	4.1	2,265
83	A hybrid approach for efficient and robust parameter estimation in biochemical pathways. BioSystems, 2006, 83, 248-265.	2.0	251
84	Metabolomics and the challenges ahead. Briefings in Bioinformatics, 2006, 7, 127-127.	6.5	13
85	Simulation of Biochemical Networks using Copasi - A Complex Pathway Simulator. , 2006, , .		9
86	Challenges for Modeling and Simulation Methods in Systems Biology. , 2006, , .		13
87	Minimum information requested in the annotation of biochemical models (MIRIAM). Nature Biotechnology, 2005, 23, 1509-1515.	17.5	553
88	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
89	The origin of correlations in metabolomics data. Metabolomics, 2005, 1, 53-63.	3.0	248
90	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

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91	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
92	Modelling and simulation for metabolomics data analysis. Biochemical Society Transactions, 2005, 33, 1427.	3.4	28
93	Discovery of meaningful associations in genomic data using partial correlation coefficients. Bioinformatics, 2004, 20, 3565-3574.	4.1	476
94	A proposed framework for the description of plant metabolomics experiments and their results. Nature Biotechnology, 2004, 22, 1601-1606.	17.5	283
95	myo-Inositol Oxygenase Offers a Possible Entry Point into Plant Ascorbate Biosynthesis. Plant Physiology, 2004, 134, 1200-1205.	4.8	423
96	Potential of metabolomics as a functional genomics tool. Trends in Plant Science, 2004, 9, 418-425.	8.8	685
97	Plant Metabolomics: Large-Scale Phytochemistry in the Functional Genomics Era.. ChemInform, 2003, 34, no.	0.0	1
98	Plant metabolomics: large-scale phytochemistry in the functional genomics era. Phytochemistry, 2003, 62, 817-836.	2.9	1,010
99	Artificial gene networks for objective comparison of analysis algorithms. Bioinformatics, 2003, 19, ii122-ii129.	4.1	148
100	Parameter Estimation in Biochemical Pathways: A Comparison of Global Optimization Methods. Genome Research, 2003, 13, 2467-2474.	5.5	706
101	Databases and Visualization for Metabolomics. , 2003, , 293-309.		6
102	Integrative modelling of gene expression and cell metabolism. Applied Bioinformatics, 2003, 2, 79-90.	1.6	3
103	Emerging bioinformatics for the metabolome. Briefings in Bioinformatics, 2002, 3, 134-145.	6.5	104
104	Gene networks: how to put the function in genomics. Trends in Biotechnology, 2002, 20, 467-472.	9.3	241
105	Linking the genes: inferring quantitative gene networks from microarray data. Trends in Genetics, 2002, 18, 395-398.	6.7	149
106	Metabolic control in integrated biochemical systems. FEBS Journal, 2002, 269, 4399-4408.	0.2	19
107	Quantifying gene networks with regulatory strengths. Molecular Biology Reports, 2002, 29, 73-77.	2.3	13
108	In situkinetic analysis of glyoxalase I and glyoxalase II inSaccharomyces cerevisiae. FEBS Journal, 2001, 268, 3930-3936.	0.2	51

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109	Snapshots of Systems. , 2000, , 3-25.		29
110	On the analysis of the inverse problem of metabolic pathways using artificial neural networks. BioSystems, 1996, 38, 15-28.	2.0	23
111	Metabolic Channeling in Organized Enzyme Systems: Experiments and Models. Advances in Molecular and Cell Biology, 1995, , 1-19.	0.1	21
112	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
113	GEPASI: A User Oriented Metabolic Simulator. , 1993, , 463-466.		0
114	Control Analysis of Metabolic Channeling. , 1993, , 211-216.		0
115	Channelling can decrease pool size. FEBS Journal, 1992, 204, 257-266.	0.2	62