

Paolo Magni

List of Publications by Year in descending order

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109
papers

2,554
citations

257101

24
h-index

223531

46
g-index

115
all docs

115
docs citations

115
times ranked

2715
citing authors

#	ARTICLE	IF	CITATIONS
1	Predictive Pharmacokinetic-Pharmacodynamic Modeling of Tumor Growth Kinetics in Xenograft Models after Administration of Anticancer Agents. <i>Cancer Research</i> , 2004, 64, 1094-1101.	0.4	432
2	2 month evening and night closed-loop glucose control in patients with type 1 diabetes under free-living conditions: a randomised crossover trial. <i>Lancet Diabetes and Endocrinology</i> , 2015, 3, 939-947.	5.5	189
3	A Review of Mixed-Effects Models of Tumor Growth and Effects of Anticancer Drug Treatment Used in Population Analysis. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2014, 3, 1-10.	1.3	137
4	Day-and-Night Closed-Loop Glucose Control in Patients With Type 1 Diabetes Under Free-Living Conditions: Results of a Single-Arm 1-Month Experience Compared With a Previously Reported Feasibility Study of Evening and Night at Home. <i>Diabetes Care</i> , 2016, 39, 1151-1160.	4.3	98
5	Temporal data mining for the quality assessment of hemodialysis services. <i>Artificial Intelligence in Medicine</i> , 2005, 34, 25-39.	3.8	93
6	A mathematical model to study the effects of drugs administration on tumor growth dynamics. <i>Mathematical Biosciences</i> , 2006, 200, 127-151.	0.9	74
7	Intelligent analysis of clinical time series: an application in the diabetes mellitus domain. <i>Artificial Intelligence in Medicine</i> , 2000, 20, 37-57.	3.8	63
8	Integrating model-based decision support in a multi-modal reasoning system for managing type 1 diabetic patients. <i>Artificial Intelligence in Medicine</i> , 2003, 29, 131-151.	3.8	56
9	Integration of enzymatic data in <i>Bacillus subtilis</i> genome-scale metabolic model improves phenotype predictions and enables in silico design of poly- β -glutamic acid production strains. <i>Microbial Cell Factories</i> , 2019, 18, 3.	1.9	56
10	A hierarchical Naïve Bayes Model for handling sample heterogeneity in classification problems: an application to tissue microarrays. <i>BMC Bioinformatics</i> , 2006, 7, 514.	1.2	54
11	Bayesian function learning using MCMC methods. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 1998, 20, 1319-1331.	9.7	50
12	TimeClust: a clustering tool for gene expression time series. <i>Bioinformatics</i> , 2008, 24, 430-432.	1.8	50
13	Minimal model $S_{I₁}=0$ problem in NIDDM subjects: nonzero Bayesian estimates with credible confidence intervals. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2002, 282, E564-E573.	1.8	42
14	Fermentation of lactose to ethanol in cheese whey permeate and concentrated permeate by engineered <i>Escherichia coli</i> . <i>BMC Biotechnology</i> , 2017, 17, 48.	1.7	42
15	Deciding when to intervene: a Markov decision process approach. <i>International Journal of Medical Informatics</i> , 2000, 60, 237-253.	1.6	40
16	Pharmacometrics Markup Language (PharmML): Opening New Perspectives for Model Exchange in Drug Development. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2015, 4, 316-319.	1.3	37
17	Modeling of human tumor xenografts and dose rationale in oncology. <i>Drug Discovery Today: Technologies</i> , 2013, 10, e365-e372.	4.0	36
18	Testing additivity of anticancer agents in pre-clinical studies: A PK/PD modelling approach. <i>European Journal of Cancer</i> , 2009, 45, 3336-3346.	1.3	32

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19	A predictive pharmacokineticâ€“pharmacodynamic model of tumor growth kinetics in xenograft mice after administration of anticancer agents given in combination. <i>Cancer Chemotherapy and Pharmacology</i> , 2013, 72, 471-482.	1.1	32
20	Predictive pharmacokineticâ€“pharmacodynamic modeling of tumor growth after administration of an anti-angiogenic agent, bevacizumab, as single-agent and combination therapy in tumor xenografts. <i>Cancer Chemotherapy and Pharmacology</i> , 2013, 71, 1147-1157.	1.1	30
21	Half-life measurements of chemical inducers for recombinant gene expression. <i>Journal of Biological Engineering</i> , 2014, 8, 5.	2.0	30
22	Bottom-Up Engineering of Biological Systems through Standard Bricks: A Modularity Study on Basic Parts and Devices. <i>PLoS ONE</i> , 2012, 7, e39407.	1.1	29
23	Multiplexing and demultiplexing logic functions for computing signal processing tasks in synthetic biology. <i>Biotechnology Journal</i> , 2011, 6, 784-795.	1.8	28
24	A standard vector for the chromosomal integration and characterization of BioBrickâ„¢ parts in <i>Escherichia coli</i> . <i>Journal of Biological Engineering</i> , 2013, 7, 12.	2.0	28
25	A Minimal Model of Tumor Growth Inhibition. <i>IEEE Transactions on Biomedical Engineering</i> , 2008, 55, 2683-2690.	2.5	26
26	Characterization of a synthetic bacterial self-destruction device for programmed cell death and for recombinant proteins release. <i>Journal of Biological Engineering</i> , 2011, 5, 8.	2.0	26
27	Characterization of an inducible promoter in different DNA copy number conditions. <i>BMC Bioinformatics</i> , 2012, 13, S11.	1.2	26
28	A machine learning approach based on ACMG/AMP guidelines for genomic variant classification and prioritization. <i>Scientific Reports</i> , 2022, 12, 2517.	1.6	26
29	Mouse embryonic stem cells that survive γ rays exposure maintain pluripotent differentiation potential and genome stability. <i>Journal of Cellular Physiology</i> , 2012, 227, 1242-1249.	2.0	24
30	Bayesian analysis of blood glucose time series from diabetes home monitoring. <i>IEEE Transactions on Biomedical Engineering</i> , 2000, 47, 971-975.	2.5	23
31	Nonparametric AUC estimation in population studies with incomplete sampling: a Bayesian approach. <i>Journal of Pharmacokinetics and Pharmacodynamics</i> , 2002, 29, 445-471.	0.8	23
32	Three Thiamine Analogues Differently Alter Thiamine Transport and Metabolism in Nervous Tissue: An In Vivo Kinetic Study Using Rats. <i>Metabolic Brain Disease</i> , 2003, 18, 245-263.	1.4	22
33	TA-clustering: Cluster analysis of gene expression profiles through Temporal Abstractions. <i>International Journal of Medical Informatics</i> , 2005, 74, 505-517.	1.6	22
34	dCas9 regulator to neutralize competition in CRISPRi circuits. <i>Nature Communications</i> , 2021, 12, 1692.	5.8	22
35	A model-based approach to the in vitro evaluation of anticancer activity. <i>Cancer Chemotherapy and Pharmacology</i> , 2009, 63, 827-836.	1.1	21
36	Multi-Faceted Characterization of a Novel LuxR-Repressible Promoter Library for <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2015, 10, e0126264.	1.1	19

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37	Pharmacokinetic/pharmacodynamic modeling of etoposide tumor growth inhibitory effect in Walker-256 tumor-bearing rat model using free intratumoral drug concentrations. <i>European Journal of Pharmaceutical Sciences</i> , 2017, 97, 70-78.	1.9	16
38	Accounting for inter-correlation between enzyme abundance: a simulation study to assess implications on global sensitivity analysis within physiologically-based pharmacokinetics. <i>Journal of Pharmacokinetics and Pharmacodynamics</i> , 2019, 46, 137-154.	0.8	16
39	Insulin Minimal Model Indexes and Secretion: Proper Handling of Uncertainty by a Bayesian Approach. <i>Annals of Biomedical Engineering</i> , 2004, 32, 1027-1037.	1.3	15
40	Current mathematical models for cancer drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2017, 12, 1-15.	2.5	15
41	Model Description Language (MDL): A Standard for Modeling and Simulation. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2017, 6, 647-650.	1.3	15
42	Random Walk Models for Bayesian Clustering of Gene Expression Profiles. <i>Applied Bioinformatics</i> , 2005, 4, 263-276.	1.7	14
43	Reduced sampling schedule for the glucose minimal model: importance of Bayesian estimation. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2006, 290, E177-E184.	1.8	14
44	Bayesian Identification of a Population Compartmental Model of C-Peptide Kinetics. <i>Annals of Biomedical Engineering</i> , 2000, 28, 812-823.	1.3	13
45	DT-Planner: an environment for managing dynamic decision problems. <i>Computer Methods and Programs in Biomedicine</i> , 1997, 54, 183-200.	2.6	12
46	Precedence Temporal Networks to represent temporal relationships in gene expression data. <i>Journal of Biomedical Informatics</i> , 2007, 40, 761-774.	2.5	12
47	Analysis of amplicon-based NGS data from neurological disease gene panels: a new method for allele drop-out management. <i>BMC Bioinformatics</i> , 2016, 17, 339.	1.2	12
48	Application of Artificial Neural Networks to Predict the Intrinsic Solubility of Drug-Like Molecules. <i>Pharmaceutics</i> , 2021, 13, 1101.	2.0	12
49	Experimental measurements and mathematical modeling of biological noise arising from transcriptional and translational regulation of basic synthetic gene circuits. <i>Journal of Theoretical Biology</i> , 2016, 395, 153-160.	0.8	11
50	Accurate peak list extraction from proteomic mass spectra for identification and profiling studies. <i>BMC Bioinformatics</i> , 2010, 11, 518.	1.2	10
51	Re-using biological devices: a model-aided analysis of interconnected transcriptional cascades designed from the bottom-up. <i>Journal of Biological Engineering</i> , 2017, 11, 50.	2.0	10
52	Variance based global sensitivity analysis of physiologically based pharmacokinetic absorption models for BCS I-IV drugs. <i>Journal of Pharmacokinetics and Pharmacodynamics</i> , 2019, 46, 27-42.	0.8	10
53	A Population Dynamic Energy Budget-Based Tumor Growth Inhibition Model for Etoposide Effects on Wistar Rats. <i>Pharmaceutical Research</i> , 2019, 36, 38.	1.7	10
54	A Tumor-in-Host DEB-Based Approach for Modeling Cachexia and Bevacizumab Resistance. <i>Cancer Research</i> , 2020, 80, 820-831.	0.4	10

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55	Dynamic Probabilistic Networks for Modelling and Identifying Dynamic Systems: A MCMC Approach. Intelligent Data Analysis, 1997, 1, 245-262.	0.4	9
56	Compartmental model identification based on an empirical Bayesian approach: The case of thiamine kinetics in rats. Medical and Biological Engineering and Computing, 2001, 39, 700-706.	1.6	9
57	In vitro cell growth pharmacodynamic studies: a new nonparametric approach to determining the relative importance of drug concentration and treatment time. Cancer Chemotherapy and Pharmacology, 2003, 52, 507-513.	1.1	9
58	Optimal Design for Informative Protocols in Xenograft Tumor Growth Inhibition Experiments in Mice. AAPS Journal, 2016, 18, 1233-1243.	2.2	9
59	Model-Based Assessment of Alternative Study Designs in Pediatric Trials. Part II: Bayesian Approaches. CPT: Pharmacometrics and Systems Pharmacology, 2016, 5, 402-410.	1.3	9
60	Modeling tumor growth inhibition and toxicity outcome after administration of anticancer agents in xenograft mice: A Dynamic Energy Budget (DEB) approach. Journal of Theoretical Biology, 2018, 450, 1-14.	0.8	9
61	A Bioinformatics Approach to Explore MicroRNAs as Tools to Bridge Pathways Between Plants and Animals. Is DNA Damage Response (DDR) a Potential Target Process?. Frontiers in Plant Science, 2019, 10, 1535.	1.7	9
62	Engineering endogenous fermentative routes in ethanologenic Escherichia coli W for bioethanol production from concentrated whey permeate. New Biotechnology, 2020, 57, 55-66.	2.4	9
63	Quantification of the gene silencing performances of rationally-designed synthetic small RNAs. Systems and Synthetic Biology, 2015, 9, 107-123.	1.0	8
64	Building in-house PBPK modelling tools for oral drug administration from literature information. ADMET and DMPK, 2019, 7, 4-21.	1.1	8
65	Learning Rules with Complex Temporal Patterns in Biomedical Domains. Lecture Notes in Computer Science, 2005, , 23-32.	1.0	8
66	Dynamic probabilistic networks for modelling and identifying dynamic systems: a MCMC approach. Intelligent Data Analysis, 1997, 1, 245-262.	0.4	7
67	Inferring gene regulatory networks by integrating static and dynamic data. International Journal of Medical Informatics, 2007, 76, S462-S475.	1.6	7
68	TGI-Simulator: A visual tool to support the preclinical phase of the drug discovery process by assessing in silico the effect of an anticancer drug. Computer Methods and Programs in Biomedicine, 2012, 105, 162-174.	2.6	7
69	A Minimal Model of Tumor Growth Inhibition in Combination Regimens Under the Hypothesis of No Interaction Between Drugs. IEEE Transactions on Biomedical Engineering, 2012, 59, 2161-2170.	2.5	7
70	Population Pharmacokinetic Modeling of Etoposide Free Concentrations in Solid Tumor. Pharmaceutical Research, 2016, 33, 1657-1670.	1.7	7
71	Mathematical modeling of efficacy and safety for anticancer drugs clinical development. Expert Opinion on Drug Discovery, 2018, 13, 5-21.	2.5	7
72	A synthetic close-loop controller circuit for the regulation of an extracellular molecule by engineered bacteria. IEEE Transactions on Biomedical Circuits and Systems, 2018, 13, 1-1.	2.7	7

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73	Modeling approaches for reducing safety-related attrition in drug discovery and development: a review on myelotoxicity, immunotoxicity, cardiovascular toxicity, and liver toxicity. <i>Expert Opinion on Drug Discovery</i> , 2021, 16, 1365-1390.	2.5	7
74	A Dynamic Energy Budget (DEB) based modeling framework to describe tumor-in-host growth inhibition and cachexia onset during anticancer treatment in in vivo xenograft studies. <i>Oncotarget</i> , 2021, 12, 1434-1441.	0.8	7
75	Modeling restoration of gefitinib efficacy by co-administration of MET inhibitors in an EGFR inhibitor-resistant NSCLC xenograft model: A tumor-in-host DEB-based approach. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2021, 10, 1396-1411.	1.3	7
76	Determining the maximum periodic inspection interval for medium voltage motors using a Markov model. <i>Production Planning and Control</i> , 2008, 19, 356-364.	5.8	6
77	A Perl procedure for protein identification by Peptide Mass Fingerprinting. <i>BMC Bioinformatics</i> , 2009, 10, S11.	1.2	6
78	PhosphoHunter: An Efficient Software Tool for Phosphopeptide Identification. <i>Advances in Bioinformatics</i> , 2015, 2015, 1-12.	5.7	6
79	Model-Based Assessment of Alternative Study Designs in Pediatric Trials. Part I: Frequentist Approaches. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2016, 5, 305-312.	1.3	6
80	In Vitro-In Vivo Correlation (IVIVC) Population Modeling for the In Silico Bioequivalence of a Long-Acting Release Formulation of Progesterone. <i>Pharmaceutics</i> , 2021, 13, 255.	2.0	6
81	Inter-compound and Intra-compound Global Sensitivity Analysis of a Physiological Model for Pulmonary Absorption of Inhaled Compounds. <i>AAPS Journal</i> , 2020, 22, 116.	2.2	6
82	A procedure to decompose high resolution mass spectra. <i>BMC Bioinformatics</i> , 2007, 8, .	1.2	5
83	Modelling the effects of cell-to-cell variability on the output of interconnected gene networks in bacterial populations. <i>BMC Systems Biology</i> , 2015, 9, S6.	3.0	5
84	Mechanistic Models of Inducible Synthetic Circuits for Joint Description of DNA Copy Number, Regulatory Protein Level, and Cell Load. <i>Processes</i> , 2019, 7, 119.	1.3	5
85	Quality Assessment of Hemodialysis Services through Temporal Data Mining. <i>Lecture Notes in Computer Science</i> , 2003, , 11-20.	1.0	5
86	Intelligent Analysis of Clinical Time Series by Combining Structural Filtering and Temporal Abstractions. <i>Lecture Notes in Computer Science</i> , 1999, , 261-270.	1.0	4
87	Use of prior knowledge and extrapolation in paediatric drug development: A case study with deferasirox. <i>European Journal of Pharmaceutical Sciences</i> , 2019, 136, 104931.	1.9	4
88	A translational model-based approach to inform the choice of the dose in phase 1 oncology trials: the case study of erdafitinib. <i>Cancer Chemotherapy and Pharmacology</i> , 2022, 89, 117-128.	1.1	4
89	Characterisation of individual ferritin response in patients receiving chelation therapy. <i>British Journal of Clinical Pharmacology</i> , 2022, 88, 3683-3694.	1.1	4
90	Analysing Italian voluntary abortion data using a Bayesian approach to the time series decomposition. <i>Statistics in Medicine</i> , 2004, 23, 105-123.	0.8	3

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91	Modelling for Synthetic Biology. , 2014, , 545-564.		3
92	A BioBrickâ„¢-Compatible Vector for Allelic Replacement Using the Xyle Gene as Selection Marker. Biological Procedures Online, 2016, 18, 6.	1.4	3
93	Complex Bayesian Modeling Workflows Encoding and Execution Made Easy With a Novel WinBUGS Plugin of the Drug Disease Model Resources Interoperability Framework. CPT: Pharmacometrics and Systems Pharmacology, 2018, 7, 298-308.	1.3	3
94	Ethambutol disposition in humans: Challenges and limitations of whole-body physiologically-based pharmacokinetic modelling in early drug development. European Journal of Pharmaceutical Sciences, 2020, 150, 105359.	1.9	3
95	Functional genomics meta-analysis to identify gene set enrichment networks in cardiac hypertrophy. Biological Chemistry, 2021, 402, 953-972.	1.2	3
96	Inferring gene expression networks via static and dynamic data integration. Studies in Health Technology and Informatics, 2006, 124, 119-24.	0.2	3
97	A minimal model describing the effect of drug administration on tumor growth dynamics. , 2006, ,		2
98	Population Modelling. , 2014, , 131-158.		2
99	Online Microreactor Titanium Dioxide RPLC-LTQ-Orbitrap MS Automated Platform for Shotgun Analysis of (Phospho) Proteins in Human Amniotic Fluid. Chromatographia, 2014, 77, 39-50.	0.7	2
100	Mathematical modeling of growth and death dynamics of mouse embryonic stem cells irradiated with β -rays. Journal of Theoretical Biology, 2014, 363, 374-380.	0.8	2
101	Methods for genetic optimization of biocatalysts for biofuel production from dairy waste through synthetic biology. , 2015, 2015, 953-6.		2
102	Mechanistic Multiscale Pharmacokinetic Model for the Anticancer Drug 2â€™,2â€™-difluorodeoxycytidine (Gemcitabine) in Pancreatic Cancer. Clinical and Translational Science, 2020, 13, 608-617.	1.5	2
103	A Population Pharmacokinetic Model of Macitentan and Its Active Metabolite Aprocitentan in Healthy Volunteers and Patients with Pulmonary Arterial Hypertension. Clinical Pharmacokinetics, 2021, 60, 1605-1619.	1.6	2
104	CRISPR Interference Modules as Low-Burden Logic Inverters in Synthetic Circuits. Frontiers in Bioengineering and Biotechnology, 2021, 9, 743950.	2.0	2
105	Summarizing Probe Intensities of Affymetrix GeneChip 3' Expression Arrays Taking into Account Day-to-Day Variability. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1425-1430.	1.9	1
106	Comprehensive kinome NGS targeted expression profiling by KING-REX. BMC Genomics, 2019, 20, 307.	1.2	1
107	A new approach to optimal dynamic therapy planning. Proceedings, 1998, , 936-40.	0.6	1
108	A Bayesian Nonparametric Approach to AUC Determination in Population Studies. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2000, 33, 249-254.	0.4	0

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109	Tumor Growth Modelling for Drug Development. , 2014, , 449-477.		0