

# Marzio Pennisi

## List of Publications by Year in descending order

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Version: 2024-02-01

91  
papers

1,351  
citations

279798

23  
h-index

395702

33  
g-index

93  
all docs

93  
docs citations

93  
times ranked

1301  
citing authors

#	ARTICLE	IF	CITATIONS
1	Verification of an agent-based disease model of human <i>Mycobacterium tuberculosis</i> infection. International Journal for Numerical Methods in Biomedical Engineering, 2021, 37, e3470.	2.1	8
2	A Preliminary Analysis of Hospitalized Covid-19 Patients in Alessandria Area: a machine learning approach. , 2021, , .		1
3	Model verification tools: a computational framework for verification assessment of mechanistic agent-based models. BMC Bioinformatics, 2021, 22, 626.	2.6	0
4	Credibility of <i>In Silico</i> Trial Technologies – A Theoretical Framing. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 4-13.	6.3	41
5	The combination of artificial intelligence and systems biology for intelligent vaccine design. Expert Opinion on Drug Discovery, 2020, 15, 1267-1281.	5.0	26
6	Moving forward through the in silico modeling of tuberculosis: a further step with UISS-TB. BMC Bioinformatics, 2020, 21, 458.	2.6	11
7	Generation of digital patients for the simulation of tuberculosis with UISS-TB. BMC Bioinformatics, 2020, 21, 449.	2.6	11
8	Computational modeling of the immune response in multiple sclerosis using epimod framework. BMC Bioinformatics, 2020, 21, 550.	2.6	9
9	In silico trial to test COVID-19 candidate vaccines: a case study with UISS platform. BMC Bioinformatics, 2020, 21, 527.	2.6	40
10	The Potential of Computational Modeling to Predict Disease Course and Treatment Response in Patients with Relapsing Multiple Sclerosis. Cells, 2020, 9, 586.	4.1	23
11	Gene Silencing of Transferrin-1 Receptor as a Potential Therapeutic Target for Human Follicular and Anaplastic Thyroid Cancer. Molecular Therapy - Oncolytics, 2020, 16, 197-206.	4.4	20
12	Efficient and Settings-Free Calibration of Detailed Kinetic Metabolic Models with Enzyme Isoforms Characterization. Lecture Notes in Computer Science, 2020, , 187-202.	1.3	3
13	Verify: a toolbox for deterministic verification of computational models. , 2020, , .		2
14	Evaluation of the predictive capability of PETAL tool: a retrospective study on potential tyrosine kinases drug resistance targets. , 2020, , .		0
15	In Silico Evaluation of Daclizumab and Vitamin D Effects in Multiple Sclerosis Using Agent Based Models. Lecture Notes in Computer Science, 2020, , 285-298.	1.3	2
16	Computational Immunogenetics. , 2019, , 906-930.		3
17	EpiMethEx: a tool for large-scale integrated analysis in methylation hotspots linked to genetic regulation. BMC Bioinformatics, 2019, 19, 385.	2.6	6
18	A MapReduce Based Tool for the Analysis and Discovery of Novel Therapeutic Targets. , 2019, , .		1

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19	Exploiting Stochastic Petri Net formalism to capture the Relapsing Remitting Multiple Sclerosis variability under Daclizumab administration. , 2019, , .		2
20	Gene expression and pathway bioinformatics analysis detect a potential predictive value of MAP3K8 in thyroid cancer progression. , 2019, , .		0
21	Evaluation of the efficacy of RUTI and ID93/GLA-SE vaccines in tuberculosis treatment: in silico trial through UISS-TB simulator. , 2019, , .		6
22	Generation of digital patients for the simulation of tuberculosis with UISS-TB. , 2019, , .		2
23	A MapReduce tool for in-depth analysis of KEGG pathways: identification and visualization of therapeutic target candidates. , 2019, , .		0
24	Toward computational modelling on immune system function. BMC Bioinformatics, 2019, 20, 622.	2.6	1
25	Predicting the artificial immunity induced by RUTIÂ® vaccine against tuberculosis using universal immune system simulator (UISS). BMC Bioinformatics, 2019, 20, 504.	2.6	27
26	Parallelisation strategies for agent based simulation of immune systems. BMC Bioinformatics, 2019, 20, 579.	2.6	12
27	A computational approach based on the colored Petri net formalism for studying multiple sclerosis. BMC Bioinformatics, 2019, 20, 623.	2.6	12
28	Computational modeling reveals MAP3K8 as mediator of resistance to vemurafenib in thyroid cancer stem cells. Bioinformatics, 2019, 35, 2267-2275.	4.1	28
29	GPU Accelerated Analysis of Treg-Teff Cross Regulation in Relapsing-Remitting Multiple Sclerosis. Lecture Notes in Computer Science, 2019, , 626-637.	1.3	4
30	Continuous Petri Nets and microRNA Analysis in Melanoma. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1492-1499.	3.0	12
31	An agent based modeling approach for the analysis of tuberculosis “ immune system dynamics. , 2018, , .		5
32	Agent based modeling of relapsing multiple sclerosis: a possible approach to predict treatment outcome. , 2018, , .		6
33	Parallel Pair-Wise Interaction for Multi-Agent Immune Systems Modelling. , 2018, , .		3
34	Estimating Daclizumab effects in Multiple Sclerosis using Stochastic Symmetric Nets. , 2018, , .		2
35	BIOESOnet: A Tool for the Generation of Personalized Human Metabolic Pathways from 23andMe Exome Data. Lecture Notes in Computer Science, 2018, , 345-352.	1.3	0
36	Combining Parallel Genetic Algorithms and Machine Learning to Improve the Research of Optimal Vaccination Protocols. , 2018, , .		1

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37	A mathematical model to study breast cancer growth. , 2017, , .		1
38	Introducing scale factor adjustments on agent-based simulations of the immune system. , 2017, , .		0
39	Optimization and analysis of vaccination schedules using simulated annealing and agent based models. , 2017, , .		0
40	Combining agent based-models and virtual screening techniques to predict the best citrus-derived vaccine adjuvants against human papilloma virus. BMC Bioinformatics, 2017, 18, 544.	2.6	21
41	2DIs: A SBML Compliant Web Platform for the Design and Modeling of Immune System Interactions. Lecture Notes in Computer Science, 2017, , 145-154.	1.3	0
42	Modeling PI3K/PDK1/Akt and MAPK Signaling Pathways Using Continuous Petri Nets. Lecture Notes in Computer Science, 2017, , 169-175.	1.3	0
43	Computational Modeling of PI3K/AKT and MAPK Signaling Pathways in Melanoma Cancer. PLoS ONE, 2016, 11, e0152104.	2.5	50
44	A methodological approach for using high-level Petri Nets to model the immune system response. BMC Bioinformatics, 2016, 17, 498.	2.6	20
45	Computational modeling in melanoma for novel drug discovery. Expert Opinion on Drug Discovery, 2016, 11, 609-621.	5.0	15
46	A computational model to predict the immune system activation by citrus-derived vaccine adjuvants. Bioinformatics, 2016, 32, 2672-2680.	4.1	41
47	Agent based simulations in disease modeling Comment on "Towards a unified approach in the modeling of fibrosis: A review with research perspectives" by Martine Ben Amar and Carlo Bianca. Physics of Life Reviews, 2016, 17, 110-111.	2.8	1
48	SHyFTA, a Stochastic Hybrid Fault Tree Automaton for the modelling and simulation of dynamic reliability problems. Expert Systems With Applications, 2016, 47, 42-57.	7.6	44
49	<i>Harpagophytum procumbens</i> extract potentiates morphine antinociception in neuropathic rats. Natural Product Research, 2016, 30, 1248-1255.	1.8	15
50	Advances in Computational Immunology. Journal of Immunology Research, 2015, 2015, 1-3.	2.2	2
51	Computational modeling of the expansion of human cord blood CD133+ hematopoietic stem/progenitor cells with different cytokine combinations. Bioinformatics, 2015, 31, 2514-2522.	4.1	35
52	Agent based modeling of the effects of potential treatments over the blood-brain barrier in multiple sclerosis. Journal of Immunological Methods, 2015, 427, 6-12.	1.4	22
53	Computational modelling approaches to vaccinology. Pharmacological Research, 2015, 92, 40-45.	7.1	35
54	Agent-Based Modeling of the Immune System: NetLogo, a Promising Framework. BioMed Research International, 2014, 2014, 1-6.	1.9	74

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55	In Silico Modeling of the Immune System: Cellular and Molecular Scale Approaches. BioMed Research International, 2014, 2014, 1-7.	1.9	7
56	Relapsing-remitting multiple sclerosis and the role of vitamin D. , 2014, , .		4
57	Fast numerical method for crack problem in the porous elastic material. Meccanica, 2014, 49, 2169-2179.	2.0	4
58	Induction of T-cell memory by a dendritic cell vaccine: a computational model. Bioinformatics, 2014, 30, 1884-1891.	4.1	35
59	OntoFast: Construct Ontology Rapidly. Communications in Computer and Information Science, 2014, , 237-241.	0.5	0
60	Agent based modeling of Treg-Teff cross regulation in relapsing-remitting multiple sclerosis. BMC Bioinformatics, 2013, 14, S9.	2.6	33
61	On the Micromorphic Thermoelasticity without Energy Dissipation. Journal of Thermal Stresses, 2013, 36, 305-320.	2.0	1
62	iAtheroSim. , 2013, , .		0
63	FAST ITERATION ALGORITHM FOR INTEGRAL EQUATIONS OF THE FIRST KIND ARISING IN 2D DIFFRACTION BY SOFT OBSTACLES. Journal of Computational Acoustics, 2013, 21, 1350007.	1.0	0
64	Persistence analysis in a Kolmogorov-type model for cancer-immune system competition. , 2013, , .		39
65	A Mathematical Model of Immune-System-Melanoma Competition. Computational and Mathematical Methods in Medicine, 2012, 2012, 1-13.	1.3	11
66	Mathematical and Computational Models in Tumor Immunology. Mathematical Modelling of Natural Phenomena, 2012, 7, 186-203.	2.4	35
67	A Modeling Framework For Immune-related Diseases. Mathematical Modelling of Natural Phenomena, 2012, 7, 40-48.	2.4	6
68	Mathematical modeling of the immune system recognition to mammary carcinoma antigen. BMC Bioinformatics, 2012, 13, S21.	2.6	36
69	The triplex vaccine effects in mammary carcinoma: A nonlinear model in tune with SimTriplex. Nonlinear Analysis: Real World Applications, 2012, 13, 1913-1940.	1.7	36
70	Combining cellular automata and lattice Boltzmann method to model multiscale avascular tumor growth coupled with nutrient diffusion and immune competition. Journal of Immunological Methods, 2012, 376, 55-68.	1.4	53
71	Predicting Long-Term Vaccine Efficacy against Metastases Using Agents. Lecture Notes in Computer Science, 2012, , 97-106.	1.3	0
72	Computational Models as Novel Tools for Cancer Vaccines. SIMAI Springer Series, 2012, , 227-248.	0.4	0

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73	SimB16: Modeling Induced Immune System Response against B16-Melanoma. PLoS ONE, 2011, 6, e26523.	2.5	56
74	A Model of Cytotoxic T Antitumor Activation Stimulated by Pulsed Dendritic Cells. , 2011, , .		1
75	Immune System Network and Cancer Vaccine. AIP Conference Proceedings, 2011, , .	0.4	33
76	ImmunoGrid: towards agent-based simulations of the human immune system at a natural scale <sup />. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2010, 368, 2799-2815.	3.4	39
77	Modeling the competition between lung metastases and the immune system using agents. BMC Bioinformatics, 2010, 11, S13.	2.6	44
78	Vaccine protocols optimization: In silico experiences. Biotechnology Advances, 2010, 28, 82-93.	11.7	44
79	Universal immune system simulator framework (UISS). , 2010, , .		12
80	GRIDUISS â€“ A Grid Based Universal Immune System Simulator Framework. Lecture Notes in Computer Science, 2010, , 285-290.	1.3	0
81	The ImmunoGrid Simulator: How to Use It. Lecture Notes in Computer Science, 2010, , 1-19.	1.3	0
82	Cancer Immunoprevention: What Can We Learn from in Silico Models?. Communications in Computer and Information Science, 2010, , 111-118.	0.5	0
83	HAMFAST: Fast Hamming Distance Computation. , 2009, , .		6
84	SIMULATED ANNEALING AND OPTIMAL PROTOCOLS. Journal of Circuits, Systems and Computers, 2009, 18, 1565-1579.	1.5	4
85	Searching of optimal vaccination schedules. IEEE Engineering in Medicine and Biology Magazine, 2009, 28, 67-72.	0.8	9
86	Agent Based Modeling of Lung Metastasis-Immune System Competition. Lecture Notes in Computer Science, 2009, , 1-3.	1.3	18
87	Agent Based Modeling of Atherosclerosis: A Concrete Help in Personalized Treatments. Lecture Notes in Computer Science, 2009, , 386-396.	1.3	7
88	ImmunoGrid, an integrative environment for large-scale simulation of the immune system for vaccine discovery, design and optimization. Briefings in Bioinformatics, 2008, 10, 330-340.	6.5	36
89	Optimal vaccination schedules using simulated annealing. Bioinformatics, 2008, 24, 1740-1742.	4.1	34
90	A Genetic Algorithm for Shortest Path Motion Problem in Three Dimensions. Lecture Notes in Computer Science, 2007, , 534-542.	1.3	0

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91	THE STABILIZATION EFFECT OF THE TRIPLEX VACCINE. , 2006, , .		0