Marzio Pennisi

List of Publications by Year
in descending order

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	Agent-Based Modeling of the Immune System: NetLogo, a Promising Framework. BioMed Research International, 2014, 2014, 1-6.	1.9	74
2	SimB16: Modeling Induced Immune System Response against B16-Melanoma. PLoS ONE, 2011, 6, e26523.	2.5	56
3	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
4	Computational Modeling of PI3K/AKT and MAPK Signaling Pathways in Melanoma Cancer. PLoS ONE, 2016, 11, e0152104.	2.5	50
5	Modeling the competition between lung metastases and the immune system using agents. BMC Bioinformatics, 2010, 11, S13.	2.6	44
6	Vaccine protocols optimization: In silico experiences. Biotechnology Advances, 2010, 28, 82-93.	11.7	44
7	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
8	A computational model to predict the immune system activation by citrus-derived vaccine adjuvants. Bioinformatics, 2016, 32, 2672-2680.	4.1	41
9	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
10	In silico trial to test COVID-19 candidate vaccines: a case study with UISS platform. BMC Bioinformatics, 2020, 21, 527.	2.6	40
11	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
12	Persistence analysis in a Kolmogorov-type model for cancer-immune system competition. , 2013, , .		39
13	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
14	Mathematical modeling of the immune system recognition to mammary carcinoma antigen. BMC Bioinformatics, 2012, 13, S21.	2.6	36
15	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
16	Mathematical and Computational Models in Tumor Immunology. Mathematical Modelling of Natural Phenomena, 2012, 7, 186-203.	2.4	35
17	Induction of T-cell memory by a dendritic cell vaccine: a computational model. Bioinformatics, 2014, 30, 1884-1891.	4.1	35
18	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

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19	Computational modelling approaches to vaccinology. Pharmacological Research, 2015, 92, 40-45.	7.1	35
20	Optimal vaccination schedules using simulated annealing. Bioinformatics, 2008, 24, 1740-1742.	4.1	34
21	Immune System Network and Cancer Vaccine. AIP Conference Proceedings, 2011, , .	0.4	33
22	Agent based modeling of Treg-Teff cross regulation in relapsing-remitting multiple sclerosis. BMC Bioinformatics, 2013, 14, S9.	2.6	33
23	Computational modeling reveals MAP3K8 as mediator of resistance to vemurafenib in thyroid cancer stem cells. Bioinformatics, 2019, 35, 2267-2275.	4.1	28
24	Predicting the artificial immunity induced by RUTIÂ® vaccine against tuberculosis using universal immune system simulator (UISS). BMC Bioinformatics, 2019, 20, 504.	2.6	27
25	The combination of artificial intelligence and systems biology for intelligent vaccine design. Expert Opinion on Drug Discovery, 2020, 15, 1267-1281.	5.0	26
26	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
27	Agent based modeling of the effects of potential treatments over the bloodâ€"brain barrier in multiple sclerosis. Journal of Immunological Methods, 2015, 427, 6-12.	1.4	22
28	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
29	A methodological approach for using high-level Petri Nets to model the immune system response. BMC Bioinformatics, 2016, 17, 498.	2.6	20
30	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
31	Agent Based Modeling of Lung Metastasis-Immune System Competition. Lecture Notes in Computer Science, 2009, , 1-3.	1.3	18
32	Computational modeling in melanoma for novel drug discovery. Expert Opinion on Drug Discovery, 2016, 11, 609-621.	5.0	15
33	<i>Harpagophytum procumbens</i> extract potentiates morphine antinociception in neuropathic rats. Natural Product Research, 2016, 30, 1248-1255.	1.8	15
34	Universal immune system simulator framework (UISS). , 2010, , .		12
35	Continuous Petri Nets and microRNA Analysis in Melanoma. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1492-1499.	3.0	12
36	Parallelisation strategies for agent based simulation of immune systems. BMC Bioinformatics, 2019, 20, 579.	2.6	12

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37	A computational approach based on the colored Petri net formalism for studying multiple sclerosis. BMC Bioinformatics, 2019, 20, 623.	2.6	12
38	A Mathematical Model of Immune-System-Melanoma Competition. Computational and Mathematical Methods in Medicine, 2012, 2012, 1-13.	1.3	11
39	Moving forward through the in silico modeling of tuberculosis: a further step with UISS-TB. BMC Bioinformatics, 2020, 21, 458.	2.6	11
40	Generation of digital patients for the simulation of tuberculosis with UISS-TB. BMC Bioinformatics, 2020, 21, 449.	2.6	11
41	Searching of optimal vaccination schedules. IEEE Engineering in Medicine and Biology Magazine, 2009, 28, 67-72.	0.8	9
42	Computational modeling of the immune response in multiple sclerosis using epimod framework. BMC Bioinformatics, 2020, 21, 550.	2.6	9
43	Verification of an <scp>agent€based</scp> disease model of human <scp><i>Mycobacterium tuberculosis</i></scp> infection. International Journal for Numerical Methods in Biomedical Engineering, 2021, 37, e3470.	2.1	8
44	In Silico Modeling of the Immune System: Cellular and Molecular Scale Approaches. BioMed Research International, 2014, 2014, 1-7.	1.9	7
45	Agent Based Modeling of Atherosclerosis: A Concrete Help in Personalized Treatments. Lecture Notes in Computer Science, 2009, , 386-396.	1.3	7
46	HAMFAST: Fast Hamming Distance Computation. , 2009, , .		6
47	A Modeling Framework For Immune-related Diseases. Mathematical Modelling of Natural Phenomena, 2012, 7, 40-48.	2.4	6
48	Agent based modeling of relapsing multiple sclerosis: a possible approach to predict treatment outcome. , 2018, , .		6
49	EpiMethEx: a tool for large-scale integrated analysis in methylation hotspots linked to genetic regulation. BMC Bioinformatics, 2019, 19, 385.	2.6	6
50	Evaluation of the efficacy of RUTI and ID93/GLA-SE vaccines in tuberculosis treatment: in silico trial through UISS-TB simulator. , 2019, , .		6
51	An agent based modeling approach for the analysis of tuberculosis â€" immune system dynamics. , 2018, , .		5
52	SIMULATED ANNEALING AND OPTIMAL PROTOCOLS. Journal of Circuits, Systems and Computers, 2009, 18, 1565-1579.	1.5	4
53	Relapsing-remitting multiple scleroris and the role of vitamin D. , 2014, , .		4
54	Fast numerical method for crack problem in the porous elastic material. Meccanica, 2014, 49, 2169-2179.	2.0	4

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55	GPU Accelerated Analysis of Treg-Teff Cross Regulation in Relapsing-Remitting Multiple Sclerosis. Lecture Notes in Computer Science, 2019, , 626-637.	1.3	4
56	Parallel Pair-Wise Interaction for Multi-Agent Immune Systems Modelling. , 2018, , .		3
57	Computational Immunogenetics. , 2019, , 906-930.		3
58	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
59	Advances in Computational Immunology. Journal of Immunology Research, 2015, 2015, 1-3.	2.2	2
60	Estimating Daclizumab effects in Multiple Sclerosis using Stochastic Symmetric Nets. , 2018, , .		2
61	Exploiting Stochastic Petri Net formalism to capture the Relapsing Remitting Multiple Sclerosis variability under Daclizumab administration. , 2019, , .		2
62	Generation of digital patients for the simulation of tuberculosis with UISS-TB. , 2019, , .		2
63	Verify: a toolbox for deterministic verification of computational models. , 2020, , .		2
64	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
65	A Model of Cytotoxic T Antitumor Activation Stimulated by Pulsed Dendritic Cells. , 2011, , .		1
66	On the Micromorphic Thermoelasticity without Energy Dissipation. Journal of Thermal Stresses, 2013, 36, 305-320.	2.0	1
67	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
68	A mathematical model to study breast cancer growth. , 2017, , .		1
69	Combining Parallel Genetic Algorithms and Machine Learning to Improve the Research of Optimal Vaccination Protocols. , 2018, , .		1
70	A MapReduce Based Tool for the Analysis and Discovery of Novel Therapeutic Targets. , 2019, , .		1
71	Toward computational modelling on immune system function. BMC Bioinformatics, 2019, 20, 622.	2.6	1
72	A Preliminary Analysis of Hospitalized Covid-19 Patients in Alessandria Area: a machine learning approach. , 2021, , .		1

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73	iAtheroSim. , 2013, , .		0
74	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
75	Introducing scale factor adjustments on agent-based simulations of the immune system. , 2017, , .		0
76	Optimization and analisys of vaccination schedules using simulated annealing and agent based models. , 2017, , .		0
77	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
78	Gene expression and pathway bioinformatics analysis detect a potential predictive value of MAP3K8 in thyroid cancer progression. , 2019, , .		0
79	A MapReduce tool for in-depth analysis of KEGG pathways: identification and visualization of therapeutic target candidates. , 2019, , .		0
80	THE STABILIZATION EFFECT OF THE TRIPLEX VACCINE. , 2006, , .		0
81	A Genetic Algorithm for Shortest Path Motion Problem in Three Dimensions. Lecture Notes in Computer Science, 2007, , 534-542.	1.3	0
82	GRIDUISS â€" A Grid Based Universal Immune System Simulator Framework. Lecture Notes in Computer Science, 2010, , 285-290.	1.3	0
83	The ImmunoGrid Simulator: How to Use It. Lecture Notes in Computer Science, 2010, , 1-19.	1.3	0
84	Cancer Immunoprevention: What Can We Learn from in Silico Models?. Communications in Computer and Information Science, 2010, , 111-118.	0.5	0
85	Predicting Long-Term Vaccine Efficacy against Metastases Using Agents. Lecture Notes in Computer Science, 2012, , 97-106.	1.3	0
86	Computational Models as Novel Tools for Cancer Vaccines. SIMAI Springer Series, 2012, , 227-248.	0.4	0
87	OntoFast: Construct Ontology Rapidly. Communications in Computer and Information Science, 2014, , 237-241.	0.5	0
88	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
89	Modeling PI3K/PDK1/Akt and MAPK Signaling Pathways Using Continuous Petri Nets. Lecture Notes in Computer Science, 2017, , 169-175.	1.3	0
90	Evaluation of the predictive capability of PETAL tool: a retrospective study on potential tyrosine kinases drug resistance targets. , 2020, , .		0

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91	Model verification tools: a computational framework for verification assessment of mechanistic agent-based models. BMC Bioinformatics, 2021, 22, 626.	2.6	0