

Francesco Pappalardo

List of Publications by Year in descending order

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109
papers

2,025
citations

218677

26
h-index

276875

41
g-index

111
all docs

111
docs citations

111
times ranked

2065
citing authors

#	ARTICLE	IF	CITATIONS
1	In silico trials: Verification, validation and uncertainty quantification of predictive models used in the regulatory evaluation of biomedical products. <i>Methods</i> , 2021, 185, 120-127.	3.8	138
2	PETAL: a Python tool for deep analysis of biological pathways. <i>Bioinformatics</i> , 2021, 36, 5553-5555.	4.1	4
3	Possible Contexts of Use for <i>In Silico</i> Trials Methodologies: A Consensus-Based Review. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021, 25, 3977-3982.	6.3	21
4	Verification of an agent-based disease model of human <i>Mycobacterium tuberculosis</i> infection. <i>International Journal for Numerical Methods in Biomedical Engineering</i> , 2021, 37, e3470.	2.1	8
5	How can we accelerate COVID-19 vaccine discovery?. <i>Expert Opinion on Drug Discovery</i> , 2021, 16, 1081-1084.	5.0	2
6	Weighted multipolar Hardy inequalities and evolution problems with Kolmogorov operators perturbed by singular potentials. <i>Communications on Pure and Applied Analysis</i> , 2021, 20, 405-425.	0.8	7
7	A class of weighted Hardy inequalities and applications to evolution problems. <i>Annali Di Matematica Pura Ed Applicata</i> , 2020, 199, 1171-1181.	1.0	6
8	Credibility of <i>In Silico</i> Trial Technologies—A Theoretical Framing. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2020, 24, 4-13.	6.3	41
9	The combination of artificial intelligence and systems biology for intelligent vaccine design. <i>Expert Opinion on Drug Discovery</i> , 2020, 15, 1267-1281.	5.0	26
10	Moving forward through the in silico modeling of tuberculosis: a further step with UISS-TB. <i>BMC Bioinformatics</i> , 2020, 21, 458.	2.6	11
11	Generation of digital patients for the simulation of tuberculosis with UISS-TB. <i>BMC Bioinformatics</i> , 2020, 21, 449.	2.6	11
12	Computational modeling of the immune response in multiple sclerosis using epimod framework. <i>BMC Bioinformatics</i> , 2020, 21, 550.	2.6	9
13	Toward computational modelling on immune system function. <i>BMC Bioinformatics</i> , 2020, 21, 546.	2.6	3
14	In silico trial to test COVID-19 candidate vaccines: a case study with UISS platform. <i>BMC Bioinformatics</i> , 2020, 21, 527.	2.6	40
15	The Potential of Computational Modeling to Predict Disease Course and Treatment Response in Patients with Relapsing Multiple Sclerosis. <i>Cells</i> , 2020, 9, 586.	4.1	23
16	Gene Silencing of Transferrin-1 Receptor as a Potential Therapeutic Target for Human Follicular and Anaplastic Thyroid Cancer. <i>Molecular Therapy - Oncolytics</i> , 2020, 16, 197-206.	4.4	20
17	Efficient and Settings-Free Calibration of Detailed Kinetic Metabolic Models with Enzyme Isoforms Characterization. <i>Lecture Notes in Computer Science</i> , 2020, , 187-202.	1.3	3
18	Immune-checkpoint inhibitors from cancer to COVID-19: A promising avenue for the treatment of patients with COVID-19 (Review). <i>International Journal of Oncology</i> , 2020, 58, 145-157.	3.3	55

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19	Verify: a toolbox for deterministic verification of computational models. , 2020, , .		2
20	Modeling, simulation and prediction of protein structures for the design of oncolytic viruses. , 2020, , .		0
21	Evaluation of the predictive capability of PETAL tool: a retrospective study on potential tyrosine kinases drug resistance targets. , 2020, , .		0
22	Multiple Sclerosis Disease: A Computational Approach for Investigating Its Drug Interactions. Lecture Notes in Computer Science, 2020, , 299-308.	1.3	2
23	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
24	In silico clinical trials: concepts and early adoptions. Briefings in Bioinformatics, 2019, 20, 1699-1708.	6.5	156
25	Computational Immunogenetics. , 2019, , 906-930.		3
26	Design and optimization of PEGylated nanoparticles intended for Berberine Chloride delivery. Journal of Drug Delivery Science and Technology, 2019, 52, 521-530.	3.0	18
27	EpiMethEx: a tool for large-scale integrated analysis in methylation hotspots linked to genetic regulation. BMC Bioinformatics, 2019, 19, 385.	2.6	6
28	A MapReduce Based Tool for the Analysis and Discovery of Novel Therapeutic Targets. , 2019, , .		1
29	(2S)-N-2-methoxy-2-phenylethyl-6,7-benzomorphan compound (2S-LP2): Discovery of a biased mu/delta opioid receptor agonist. European Journal of Medicinal Chemistry, 2019, 168, 189-198.	5.5	17
30	Exploiting Stochastic Petri Net formalism to capture the Relapsing Remitting Multiple Sclerosis variability under Daclizumab administration. , 2019, , .		2
31	Gene expression and pathway bioinformatics analysis detect a potential predictive value of MAP3K8 in thyroid cancer progression. , 2019, , .		0
32	Evaluation of the efficacy of RUTI and ID93/GLA-SE vaccines in tuberculosis treatment: in silico trial through UISS-TB simulator. , 2019, , .		6
33	Generation of digital patients for the simulation of tuberculosis with UISS-TB. , 2019, , .		2
34	A MapReduce tool for in-depth analysis of KEGG pathways: identification and visualization of therapeutic target candidates. , 2019, , .		0
35	Toward computational modelling on immune system function. BMC Bioinformatics, 2019, 20, 622.	2.6	1
36	Predicting the artificial immunity induced by RUTI [®] vaccine against tuberculosis using universal immune system simulator (UISS). BMC Bioinformatics, 2019, 20, 504.	2.6	27

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37	Parallelisation strategies for agent based simulation of immune systems. BMC Bioinformatics, 2019, 20, 579.	2.6	12
38	A computational approach based on the colored Petri net formalism for studying multiple sclerosis. BMC Bioinformatics, 2019, 20, 623.	2.6	12
39	Computational modeling reveals MAP3K8 as mediator of resistance to vemurafenib in thyroid cancer stem cells. Bioinformatics, 2019, 35, 2267-2275.	4.1	28
40	GPU Accelerated Analysis of Treg-Teff Cross Regulation in Relapsing-Remitting Multiple Sclerosis. Lecture Notes in Computer Science, 2019, , 626-637.	1.3	4
41	Computational modeling of brain pathologies: the case of multiple sclerosis. Briefings in Bioinformatics, 2018, 19, bbw123.	6.5	4
42	Weighted Hardy inequalities and Ornstein-Uhlenbeck type operators perturbed by multipolar inverse square potentials. Journal of Mathematical Analysis and Applications, 2018, 463, 895-909.	1.0	8
43	Continuous Petri Nets and microRNA Analysis in Melanoma. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1492-1499.	3.0	12
44	An agent based modeling approach for the analysis of tuberculosis immune system dynamics. , 2018, , .		5
45	Agent based modeling of relapsing multiple sclerosis: a possible approach to predict treatment outcome. , 2018, , .		6
46	Parallel Pair-Wise Interaction for Multi-Agent Immune Systems Modelling. , 2018, , .		3
47	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
48	Combining Parallel Genetic Algorithms and Machine Learning to Improve the Research of Optimal Vaccination Protocols. , 2018, , .		1
49	Introducing scale factor adjustments on agent-based simulations of the immune system. , 2017, , .		0
50	Optimization and analysis of vaccination schedules using simulated annealing and agent based models. , 2017, , .		0
51	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
52	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
53	Modeling PI3K/PDK1/Akt and MAPK Signaling Pathways Using Continuous Petri Nets. Lecture Notes in Computer Science, 2017, , 169-175.	1.3	0
54	Computational Modeling of PI3K/AKT and MAPK Signaling Pathways in Melanoma Cancer. PLoS ONE, 2016, 11, e0152104.	2.5	50

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55	A methodological approach for using high-level Petri Nets to model the immune system response. BMC Bioinformatics, 2016, 17, 498.	2.6	20
56	Computational modeling in melanoma for novel drug discovery. Expert Opinion on Drug Discovery, 2016, 11, 609-621.	5.0	15
57	A computational model to predict the immune system activation by citrus-derived vaccine adjuvants. Bioinformatics, 2016, 32, 2672-2680.	4.1	41
58	Formal analysis of the surgical pathway and development of a new software tool to assist surgeons in the decision making in primary breast surgery. Breast, 2016, 29, 74-81.	2.2	10
59	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
60	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
61	Advances in Computational Immunology. Journal of Immunology Research, 2015, 2015, 1-3.	2.2	2
62	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
63	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
64	Computational modelling approaches to vaccinology. Pharmacological Research, 2015, 92, 40-45.	7.1	35
65	Targeting the Minimum Vertex Set Problem with an Enhanced Genetic Algorithm Improved with Local Search Strategies. Lecture Notes in Computer Science, 2015, , 177-188.	1.3	0
66	Computational and Bioinformatics Techniques for Immunology. BioMed Research International, 2014, 2014, 1-2.	1.9	7
67	Modeling Biology Spanning Different Scales: An Open Challenge. BioMed Research International, 2014, 2014, 1-9.	1.9	50
68	Agent-Based Modeling of the Immune System: NetLogo, a Promising Framework. BioMed Research International, 2014, 2014, 1-6.	1.9	74
69	In Silico Modeling of the Immune System: Cellular and Molecular Scale Approaches. BioMed Research International, 2014, 2014, 1-7.	1.9	7
70	Relapsing-remitting multiple sclerosis and the role of vitamin D. , 2014, , .		4
71	Induction of T-cell memory by a dendritic cell vaccine: a computational model. Bioinformatics, 2014, 30, 1884-1891.	4.1	35
72	OntoFast: Construct Ontology Rapidly. Communications in Computer and Information Science, 2014, , 237-241.	0.5	0

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73	Mathematical modeling of biological systems. Briefings in Bioinformatics, 2013, 14, 411-422.	6.5	93
74	Agent based modeling of Treg-Teff cross regulation in relapsing-remitting multiple sclerosis. BMC Bioinformatics, 2013, 14, S9.	2.6	33
75	iAtheroSim. , 2013, , .		0
76	Cancer Vaccines: State of the Art of the Computational Modeling Approaches. BioMed Research International, 2013, 2013, 1-6.	1.9	16
77	Modeling Cancer Vaccines. , 2012, , .		0
78	Immune System Modeling and Related Pathologies. Computational and Mathematical Methods in Medicine, 2012, 2012, 1-2.	1.3	1
79	Mathematical modeling of the immune system recognition to mammary carcinoma antigen. BMC Bioinformatics, 2012, 13, S21.	2.6	36
80	Optimal vaccination schedule search using genetic algorithm over MPI technology. BMC Medical Informatics and Decision Making, 2012, 12, 129.	3.0	5
81	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
82	Predicting Long-Term Vaccine Efficacy against Metastases Using Agents. Lecture Notes in Computer Science, 2012, , 97-106.	1.3	0
83	Computational Models as Novel Tools for Cancer Vaccines. SIMAI Springer Series, 2012, , 227-248.	0.4	0
84	SimB16: Modeling Induced Immune System Response against B16-Melanoma. PLoS ONE, 2011, 6, e26523.	2.5	56
85	A Model of Cytotoxic T Antitumor Activation Stimulated by Pulsed Dendritic Cells. , 2011, , .		1
86	Current Issues in Tumor Immunology. Current Bioinformatics, 2010, 5, 164-175.	1.5	0
87	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
88	Modeling the competition between lung metastases and the immune system using agents. BMC Bioinformatics, 2010, 11, S13.	2.6	44
89	Vaccine protocols optimization: In silico experiences. Biotechnology Advances, 2010, 28, 82-93.	11.7	44
90	Universal immune system simulator framework (UISS). , 2010, , .		12

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91	<i>In silico</i> Modeling and <i>In vivo</i> Efficacy of Cancer-Preventive Vaccinations. Cancer Research, 2010, 70, 7755-7763.	0.9	78
92	A novel paradigm for cell and molecule interaction ontology: from the CMM model to IMGT-ONTOLOGY. Immunome Research, 2010, 6, 1.	0.1	23
93	GRIDUISS â€“ A Grid Based Universal Immune System Simulator Framework. Lecture Notes in Computer Science, 2010, , 285-290.	1.3	0
94	The ImmunoGrid Simulator: How to Use It. Lecture Notes in Computer Science, 2010, , 1-19.	1.3	0
95	Cancer Immunoprevention: What Can We Learn from in Silico Models?. Communications in Computer and Information Science, 2010, , 111-118.	0.5	0
96	HAMFAST: Fast Hamming Distance Computation. , 2009, , .		6
97	SIMULATED ANNEALING AND OPTIMAL PROTOCOLS. Journal of Circuits, Systems and Computers, 2009, 18, 1565-1579.	1.5	4
98	Searching of optimal vaccination schedules. IEEE Engineering in Medicine and Biology Magazine, 2009, 28, 67-72.	0.8	9
99	The MWF method for kinetic equations system. Computers and Mathematics With Applications, 2009, 57, 831-840.	2.7	6
100	Agent Based Modeling of Lung Metastasis-Immune System Competition. Lecture Notes in Computer Science, 2009, , 1-3.	1.3	18
101	Agent Based Modeling of Atherosclerosis: A Concrete Help in Personalized Treatments. Lecture Notes in Computer Science, 2009, , 386-396.	1.3	7
102	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
103	Optimal vaccination schedules using simulated annealing. Bioinformatics, 2008, 24, 1740-1742.	4.1	34
104	Modeling immune system control of atherogenesis. Bioinformatics, 2008, 24, 1715-1721.	4.1	53
105	Computational Simulations of the Immune System for Personalized Medicine: State of the Art and Challenges. Current Pharmacogenomics and Personalized Medicine, 2008, 6, 260-271.	0.2	14
106	Predictive Models in Tumor Immunology. , 2008, , 1-22.		2
107	A Genetic Algorithm for Shortest Path Motion Problem in Three Dimensions. Lecture Notes in Computer Science, 2007, , 534-542.	1.3	0
108	Discovery of cancer vaccination protocols with a genetic algorithm driving an agent based simulator. BMC Bioinformatics, 2006, 7, 352.	2.6	59

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109	Using Viruses to Improve GAs. Lecture Notes in Computer Science, 2005, , 161-170.	1.3	1