

# Andrea Degasperi

## List of Publications by Year in descending order

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Version: 2024-02-01

34  
papers

2,218  
citations

430874

18  
h-index

501196

28  
g-index

39  
all docs

39  
docs citations

39  
times ranked

3878  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Compendium of Mutational Signatures of Environmental Agents. <i>Cell</i> , 2019, 177, 821-836.e16.	28.9	437
2	Whole-genome sequencing of triple-negative breast cancers in a population-based clinical study. <i>Nature Medicine</i> , 2019, 25, 1526-1533.	30.7	218
3	Evaluating Strategies to Normalise Biological Replicates of Western Blot Data. <i>PLoS ONE</i> , 2014, 9, e87293.	2.5	174
4	A practical framework and online tool for mutational signature analyses show intertissue variation and driver dependencies. <i>Nature Cancer</i> , 2020, 1, 249-263.	13.2	166
5	Bistability in the Rac1, PAK, and RhoA Signaling Network Drives Actin Cytoskeleton Dynamics and Cell Motility Switches. <i>Cell Systems</i> , 2016, 2, 38-48.	6.2	159
6	Homologous recombination DNA repair deficiency and PARP inhibition activity in primary triple negative breast cancer. <i>Nature Communications</i> , 2020, 11, 2662.	12.8	157
7	A practical guide for mutational signature analysis in hematological malignancies. <i>Nature Communications</i> , 2019, 10, 2969.	12.8	145
8	Mutational signatures: emerging concepts, caveats and clinical applications. <i>Nature Reviews Cancer</i> , 2021, 21, 619-637.	28.4	128
9	Substitution mutational signatures in whole-genome-sequenced cancers in the UK population. <i>Science</i> , 2022, 376, .	12.6	104
10	A systematic CRISPR screen defines mutational mechanisms underpinning signatures caused by replication errors and endogenous DNA damage. <i>Nature Cancer</i> , 2021, 2, 643-657.	13.2	94
11	Whole-genome sequencing reveals clinically relevant insights into the aetiology of familial breast cancers. <i>Annals of Oncology</i> , 2019, 30, 1071-1079.	1.2	64
12	Mitochondrial reactive oxygen species enhance AMP-activated protein kinase activation in the endothelium of patients with coronary artery disease and diabetes. <i>Clinical Science</i> , 2013, 124, 403-411.	4.3	61
13	Performance of objective functions and optimisation procedures for parameter estimation in system biology models. <i>Npj Systems Biology and Applications</i> , 2017, 3, 20.	3.0	57
14	Preclinical <i>In Vivo</i> Validation of the RAD51 Test for Identification of Homologous Recombination-Deficient Tumors and Patient Stratification. <i>Cancer Research</i> , 2022, 82, 1646-1657.	0.9	40
15	Dramatic response of metastatic cutaneous angiosarcoma to an immune checkpoint inhibitor in a patient with xeroderma pigmentosum: whole-genome sequencing aids treatment decision in end-stage disease. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a004408.	1.2	34
16	Spectrum of mutational signatures in T-cell lymphoma reveals a key role for UV radiation in cutaneous T-cell lymphoma. <i>Scientific Reports</i> , 2021, 11, 3962.	3.3	33
17	Some Investigations Concerning the CTMC and the ODE Model Derived From Bio-PEPA. <i>Electronic Notes in Theoretical Computer Science</i> , 2009, 229, 145-163.	0.9	29
18	DYVIPAC: an integrated analysis and visualisation framework to probe multi-dimensional biological networks. <i>Scientific Reports</i> , 2015, 5, 12569.	3.3	23

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19	Basal expression of RAD51 foci predicts olaparib response in patient-derived ovarian cancer xenografts. <i>British Journal of Cancer</i> , 2022, 126, 120-128.	6.4	21
20	Sensitivity Analysis of Stochastic Models of Bistable Biochemical Reactions. , 2008, , 1-20.		18
21	Modelling Biological Clocks with Bio-PEPA: Stochasticity and Robustness for the <i>Neurospora crassa</i> Circadian Network. <i>Lecture Notes in Computer Science</i> , 2009, , 52-67.	1.3	11
22	Modelling and Analysis of the NF- $\kappa$ B Pathway in Bio-PEPA. <i>Lecture Notes in Computer Science</i> , 2010, , 229-262.	1.3	9
23	Improving machine learning in early drug discovery. <i>Annals of Mathematics and Artificial Intelligence</i> , 2017, 81, 155-166.	1.3	7
24	Multi-scale modelling of biological systems in process algebra with multi-way synchronisation. , 2011, , .		5
25	Process Algebra with Hooks for Models of Pattern Formation. <i>Electronic Notes in Theoretical Computer Science</i> , 2010, 268, 31-47.	0.9	4
26	Report from the 4th European Bone Sarcoma Networking meeting: focus on osteosarcoma. <i>Clinical Sarcoma Research</i> , 2018, 8, .	2.3	3
27	Relating PDEs in Cylindrical Coordinates and CTMCs with Levels of Concentration. <i>Electronic Notes in Theoretical Computer Science</i> , 2010, 268, 49-59.	0.9	1
28	A process algebra framework for multi-scale modelling of biological systems. <i>Theoretical Computer Science</i> , 2013, 488, 15-45.	0.9	1
29	From species to pathway and tissue as process. , 2010, , .		0
30	PO-339 Implications of organ-wise extraction of cancer mutational signatures using 2577 whole genomes. <i>ESMO Open</i> , 2018, 3, A154.	4.5	0
31	PO-340 Dysregulation of the TP53 network and PRC2 activity are independent poor prognostic factors in patients with malignant peripheral nerve sheath tumours. <i>ESMO Open</i> , 2018, 3, A154-A155.	4.5	0
32	Abstract P5-10-01: Using whole genome sequencing and somatic mutation signatures to unravel insight into familial breast cancer aetiology. , 2019, , .		0
33	Abstract 4887: Direct mutational consequences of CRISPR-cas9 gene-edited DNA repair genes. , 2020, , .		0
34	Relationship Between Dimensionality and Convergence of Optimization Algorithms: A Comparison Between Data-Driven Normalization and Scaling Factor-Based Methods Using PEPSSBI. <i>Methods in Molecular Biology</i> , 2022, 2385, 91-115.	0.9	0