Andrea Degasperi

List of Publications by Year
in descending order

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	Basal expression of RAD51 foci predicts olaparib response in patient-derived ovarian cancer xenografts. British Journal of Cancer, 2022, 126, 120-128.	6.4	21
2	Relationship Between Dimensionality and Convergence of Optimization Algorithms: A Comparison Between Data-Driven Normalization and Scaling Factor-Based Methods Using PEPSSBI. Methods in Molecular Biology, 2022, 2385, 91-115.	0.9	0
3	Preclinical <i>In Vivo</i> Validation of the RAD51 Test for Identification of Homologous Recombination-Deficient Tumors and Patient Stratification. Cancer Research, 2022, 82, 1646-1657.	0.9	40
4	Substitution mutational signatures in whole-genomeâ€"sequenced cancers in the UK population. Science, 2022, 376, .	12.6	104
5	Spectrum of mutational signatures in T-cell lymphoma reveals a key role for UV radiation in cutaneous T-cell lymphoma. Scientific Reports, 2021, 11, 3962.	3.3	33
6	A systematic CRISPR screen defines mutational mechanisms underpinning signatures caused by replication errors and endogenous DNA damage. Nature Cancer, 2021, 2, 643-657.	13.2	94
7	Mutational signatures: emerging concepts, caveats and clinical applications. Nature Reviews Cancer, 2021, 21, 619-637.	28.4	128
8	Homologous recombination DNA repair deficiency and PARP inhibition activity in primary triple negative breast cancer. Nature Communications, 2020, 11, 2662.	12.8	157
9	A practical framework and online tool for mutational signature analyses show intertissue variation and driver dependencies. Nature Cancer, 2020, 1, 249-263.	13.2	166
10	Abstract 4887: Direct mutational consequences of CRISPR-cas9 gene-edited DNA repair genes. , 2020, , .		0
11	A practical guide for mutational signature analysis in hematological malignancies. Nature Communications, 2019, 10, 2969.	12.8	145
12	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. Journal of Physical Education and Sports Management, 2019, 5, a004408.	1.2	34
13	Whole-genome sequencing reveals clinically relevant insights into the aetiology of familial breast cancers. Annals of Oncology, 2019, 30, 1071-1079.	1.2	64
14	A Compendium of Mutational Signatures of Environmental Agents. Cell, 2019, 177, 821-836.e16.	28.9	437
15	Whole-genome sequencing of triple-negative breast cancers in a population-based clinical study. Nature Medicine, 2019, 25, 1526-1533.	30.7	218
16	Abstract P5-10-01: Using whole genome sequencing and somatic mutation signatures to unravel insight into familial breast cancer aetiology. , 2019, , .		0
17	PO-339 Implications of organ-wise extraction of cancer mutational signatures using 2577 whole genomes. ESMO Open, 2018, 3, A154.	4.5	0
18	PO-340 Dysregulation of the TP53 network and PRC2 activity are independent poor prognostic factors in patients with malignant peripheral nerve sheath tumours. ESMO Open, 2018, 3, A154-A155.	4.5	0

#	Article	IF	Citations
19	Report from the 4th European Bone Sarcoma Networking meeting: focus on osteosarcoma. Clinical Sarcoma Research, 2018, 8, .	2.3	3
20	Improving machine learning in early drug discovery. Annals of Mathematics and Artificial Intelligence, 2017, 81, 155-166.	1.3	7
21	Performance of objective functions and optimisation procedures for parameter estimation in system biology models. Npj Systems Biology and Applications, 2017, 3, 20.	3.0	57
22	Bistability in the Rac1, PAK, and RhoA Signaling Network Drives Actin Cytoskeleton Dynamics and Cell Motility Switches. Cell Systems, 2016, 2, 38-48.	6.2	159
23	DYVIPAC: an integrated analysis and visualisation framework to probe multi-dimensional biological networks. Scientific Reports, 2015, 5, 12569.	3.3	23
24	Evaluating Strategies to Normalise Biological Replicates of Western Blot Data. PLoS ONE, 2014, 9, e87293.	2.5	174
25	A process algebra framework for multi-scale modelling of biological systems. Theoretical Computer Science, 2013, 488, 15-45.	0.9	1
26	Mitochondrial reactive oxygen species enhance AMP-activated protein kinase activation in the endothelium of patients with coronary artery disease and diabetes. Clinical Science, 2013, 124, 403-411.	4.3	61
27	Multi-scale modelling of biological systems in process algebra with multi-way synchronisation. , 2011, , .		5
28	Process Algebra with Hooks for Models of Pattern Formation. Electronic Notes in Theoretical Computer Science, 2010, 268, 31-47.	0.9	4
29	Relating PDEs in Cylindrical Coordinates and CTMCs with Levels of Concentration. Electronic Notes in Theoretical Computer Science, 2010, 268, 49-59.	0.9	1
30	From species to pathway and tissue as process. , 2010, , .		0
31	Modelling and Analysis of the NF-κB Pathway in Bio-PEPA. Lecture Notes in Computer Science, 2010, , 229-262.	1.3	9
32	Some Investigations Concerning the CTMC and the ODE Model Derived From Bio-PEPA. Electronic Notes in Theoretical Computer Science, 2009, 229, 145-163.	0.9	29
33	Modelling Biological Clocks with Bio-PEPA: Stochasticity and Robustness for the Neurospora crassa Circadian Network. Lecture Notes in Computer Science, 2009, , 52-67.	1.3	11
34	Sensitivity Analysis of Stochastic Models of Bistable Biochemical Reactions. , 2008, , 1-20.		18