## Stephano Monti

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6881718/publications.pdf

Version: 2024-02-01

99 papers 14,712 citations

50276 46 h-index 100 g-index

118 all docs

 $\frac{118}{\text{docs citations}}$ 

118 times ranked 22428 citing authors

#	Article	IF	CITATIONS
1	Title is missing!. Machine Learning, 2003, 52, 91-118.	5.4	1,613
2	Initial genome sequencing and analysis of multiple myeloma. Nature, 2011, 471, 467-472.	27.8	1,288
3	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. Nature Medicine, 2018, 24, 679-690.	30.7	1,224
4	Integrative analysis reveals selective 9p24.1 amplification, increased PD-1 ligand expression, and further induction via JAK2 in nodular sclerosing Hodgkin lymphoma and primary mediastinal large B-cell lymphoma. Blood, 2010, 116, 3268-3277.	1.4	1,122
5	The molecular signature of mediastinal large B-cell lymphoma differs from that of other diffuse large B-cell lymphomas and shares features with classical Hodgkin lymphoma. Blood, 2003, 102, 3871-3879.	1.4	793
6	Molecular profiling of diffuse large B-cell lymphoma identifies robust subtypes including one characterized by host inflammatory response. Blood, 2005, 105, 1851-1861.	1.4	778
7	Discovery and Characterization of Super-Enhancer-Associated Dependencies in Diffuse Large B Cell Lymphoma. Cancer Cell, 2013, 24, 777-790.	16.8	635
8	Prevalence and clinical significance of antineutrophil cytoplasmic antibodies in Churg-Strauss syndrome. Arthritis and Rheumatism, 2005, 52, 2926-2935.	6.7	592
9	Targetable genetic features of primary testicular and primary central nervous system lymphomas. Blood, 2016, 127, 869-881.	1.4	429
10	Metabolic Signatures Uncover Distinct Targets in Molecular Subsets of Diffuse Large B Cell Lymphoma. Cancer Cell, 2012, 22, 547-560.	16.8	422
11	Genome-wide Translocation Sequencing Reveals Mechanisms of Chromosome Breaks and Rearrangements in B Cells. Cell, 2011, 147, 107-119.	28.9	411
12	Inactivation of the PRDM1/BLIMP1 gene in diffuse large B cell lymphoma. Journal of Experimental Medicine, 2006, 203, 311-317.	8.5	326
13	The AP1-dependent secretion of galectin-1 by Reed–Sternberg cells fosters immune privilege in classical Hodgkin lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 13134-13139.	7.1	299
14	SYK-dependent tonic B-cell receptor signaling is a rational treatment target in diffuse large B-cell lymphoma. Blood, 2008, 111, 2230-2237.	1.4	289
15	Gene Expression Profiling Reveals Reproducible Human Lung Adenocarcinoma Subtypes in Multiple Independent Patient Cohorts. Journal of Clinical Oncology, 2006, 24, 5079-5090.	1.6	263
16	NFÂB activity, function, and target-gene signatures in primary mediastinal large B-cell lymphoma and diffuse large B-cell lymphoma subtypes. Blood, 2005, 106, 1392-1399.	1.4	229
17	Integrative Analysis Reveals an Outcome-Associated and Targetable Pattern of p53 and Cell Cycle Deregulation in Diffuse Large B Cell Lymphoma. Cancer Cell, 2012, 22, 359-372.	16.8	179
18	Renal Involvement in Churg-Strauss Syndrome. American Journal of Kidney Diseases, 2006, 47, 770-779.	1.9	169

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19	Nonlinear partial differential equations and applications: Identification of endoglin as a functional marker that defines long-term repopulating hematopoietic stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 15468-15473.	7.1	156
20	SYK Inhibition Modulates Distinct PI3K/AKT- Dependent Survival Pathways and Cholesterol Biosynthesis in Diffuse Large B Cell Lymphomas. Cancer Cell, 2013, 23, 826-838.	16.8	152
21	Immunohistochemical Detection of MYC-driven Diffuse Large B-Cell Lymphomas. PLoS ONE, 2012, 7, e33813.	2.5	137
22	Transcriptional signature with differential expression of BCL6 target genes accurately identifies BCL6-dependent diffuse large B cell lymphomas. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3207-3212.	7.1	130
23	An Aryl Hydrocarbon Receptor-Mediated Amplification Loop That Enforces Cell Migration in ER <sup>â°'</sup> /PR <sup>â°'</sup> /Her2 <sup>â°'</sup> Human Breast Cancer Cells. Molecular Pharmacology, 2016, 90, 674-688.	2.3	124
24	Comparative gene marker selection suite. Bioinformatics, 2006, 22, 1924-1925.	4.1	123
25	The aryl hydrocarbon receptor directs hematopoietic progenitor cell expansion and differentiation. Blood, 2013, 122, 376-385.	1.4	119
26	hypeR: an R package for geneset enrichment workflows. Bioinformatics, 2020, 36, 1307-1308.	4.1	117
27	Lesional gene expression profiling in cutaneous T-cell lymphoma reveals natural clusters associated with disease outcome. Blood, 2007, 110, 3015-3027.	1.4	115
28	Selective JAK2 Inhibition Specifically Decreases Hodgkin Lymphoma and Mediastinal Large B-cell Lymphoma Growth <i>In Vitro</i> and <i>In Vivo</i> Clinical Cancer Research, 2014, 20, 2674-2683.	7.0	114
29	Transcriptional Profiling Identifies Cyclin D1 as a Critical Downstream Effector of Mutant Epidermal Growth Factor Receptor Signaling. Cancer Research, 2006, 66, 11389-11398.	0.9	112
30	A YAP/TAZ-Regulated Molecular Signature Is Associated with Oral Squamous Cell Carcinoma. Molecular Cancer Research, 2015, 13, 957-968.	3.4	107
31	The role of the aryl hydrocarbon receptor in the development of cells with the molecular and functional characteristics of cancer stem-like cells. BMC Biology, 2016, 14, 20.	3.8	80
32	Altered RNA editing in $3\hat{a}\in^2$ UTR perturbs microRNA-mediated regulation of oncogenes and tumor-suppressors. Scientific Reports, 2016, 6, 23226.	3.3	77
33	Viral induction and targeted inhibition of galectin-1 in EBV+ posttransplant lymphoproliferative disorders. Blood, 2011, 117, 4315-4322.	1.4	75
34	Pathways of Toxicity. ALTEX: Alternatives To Animal Experimentation, 2014, 31, 53-61.	1.5	75
35	Genomic Models of Short-Term Exposure Accurately Predict Long-Term Chemical Carcinogenicity and Identify Putative Mechanisms of Action. PLoS ONE, 2014, 9, e102579.	2.5	72
36	Glutamineâ€utilizing transaminases are a metabolic vulnerability of TAZ/YAPâ€activated cancer cells. EMBO Reports, 2018, 19, .	4.5	70

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37	Diffuse large B-cell lymphoma patient-derived xenograft models capture the molecular and biological heterogeneity of the disease. Blood, 2016, 127, 2203-2213.	1.4	68
38	RNA Binding and Core Complexes Constitute the U-Insertion/Deletion Editosome. Molecular and Cellular Biology, 2014, 34, 4329-4342.	2.3	67
39	Role for the Aryl Hydrocarbon Receptor and Diverse Ligands in Oral Squamous Cell Carcinoma Migration and Tumorigenesis. Molecular Cancer Research, 2016, 14, 696-706.	3.4	67
40	A Transcriptional Profiling Study of CCAAT/Enhancer Binding Protein Targets Identifies Hepatocyte Nuclear Factor 3Î <sup>2</sup> as a Novel Tumor Suppressor in Lung Cancer. Cancer Research, 2004, 64, 4137-4147.	0.9	66
41	The role of the aryl hydrocarbon receptor in normal and malignant B cell development. Seminars in Immunopathology, 2013, 35, 705-716.	6.1	63
42	Respiratory Failure Due to Differentiation Arrest and Expansion of Alveolar Cells following Lung-Specific Loss of the Transcription Factor C/EBPα in Mice. Molecular and Cellular Biology, 2006, 26, 1109-1123.	2.3	61
43	Yap suppresses T-cell function and infiltration in the tumor microenvironment. PLoS Biology, 2020, 18, e3000591.	5.6	58
44	How the AHR Became Important in Cancer: The Role of Chronically Active AHR in Cancer Aggression. International Journal of Molecular Sciences, 2021, 22, 387.	4.1	54
45	ld1 is a common downstream target of oncogenic tyrosine kinases in leukemic cells. Blood, 2008, 112, 1981-1992.	1.4	51
46	Predicting dire outcomes of patients with community acquired pneumonia. Journal of Biomedical Informatics, 2005, 38, 347-366.	4.3	50
47	Signatures of murine B-cell development implicate Yy1 as a regulator of the germinal center-specific program. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2873-2878.	7.1	49
48	Cancer cell responses to Hsp70 inhibitor JG-98: Comparison with Hsp90 inhibitors and finding synergistic drug combinations. Scientific Reports, 2018, 8, 3010.	3.3	48
49	Towards Resolving the Pro- and Anti-Tumor Effects of the Aryl Hydrocarbon Receptor. International Journal of Molecular Sciences, 2018, 19, 1388.	4.1	45
50	Thyroid Progenitors Are Robustly Derived from Embryonic Stem Cells through Transient, Developmental Stage-Specific Overexpression of Nkx2-1. Stem Cell Reports, 2017, 8, 216-225.	4.8	44
51	Functional and genomic analyses reveal therapeutic potential of targeting $\hat{l}^2$ -catenin/CBP activity in head and neck cancer. Genome Medicine, 2018, 10, 54.	8.2	43
52	Inhibition of LSD1 epigenetically attenuates oral cancer growth and metastasis. Oncotarget, 2017, 8, 73372-73386.	1.8	43
53	Induced Pluripotent Stem Cell Modeling of Multisystemic, Hereditary Transthyretin Amyloidosis. Stem Cell Reports, 2013, 1, 451-463.	4.8	42
54	15-Hydroxyprostaglandin Dehydrogenase is a Target of Hepatocyte Nuclear Factor $3\hat{l}^2$ and a Tumor Suppressor in Lung Cancer. Cancer Research, 2008, 68, 5040-5048.	0.9	40

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55	FAS Death Domain Deletions and Cellular FADD-like Interleukin $1\hat{l}^2$ Converting Enzyme Inhibitory Protein (Long) Overexpression: Alternative Mechanisms for Deregulating the Extrinsic Apoptotic Pathway in Diffuse Large B-Cell Lymphoma Subtypes. Clinical Cancer Research, 2006, 12, 3265-3271.	7.0	37
56	Antisense Transcripts Delimit Exonucleolytic Activity of the Mitochondrial 3′ Processome to Generate Guide RNAs. Molecular Cell, 2016, 61, 364-378.	9.7	35
57	Oncogenic ALK regulates EMT in non-small cell lung carcinoma through repression of the epithelial splicing regulatory protein 1. Oncotarget, 2016, 7, 33316-33330.	1.8	35
58	Assessment of microRNA differential expression and detection in multiplexed small RNA sequencing data. Rna, 2015, 21, 164-171.	3.5	31
59	PDGFRÎ <sup>2</sup> Is a Novel Marker of Stromal Activation in Oral Squamous Cell Carcinomas. PLoS ONE, 2016, 11, e0154645.	2.5	31
60	Inhibition of Ubc13-mediated Ubiquitination by GPS2 Regulates Multiple Stages of B Cell Development. Journal of Biological Chemistry, 2017, 292, 2754-2772.	3.4	30
61	Bayesian Methods for Multivariate Modeling of Pleiotropic SNP Associations and Genetic Risk Prediction. Frontiers in Genetics, 2012, 3, 176.	2.3	28
62	ASSIGN: context-specific genomic profiling of multiple heterogeneous biological pathways. Bioinformatics, 2015, 31, 1745-1753.	4.1	28
63	Pipeliner: A Nextflow-Based Framework for the Definition of Sequencing Data Processing Pipelines. Frontiers in Genetics, 2019, 10, 614.	2.3	28
64	A serum protein signature of <i>APOE</i> genotypes in centenarians. Aging Cell, 2019, 18, e13023.	6.7	27
65	Molecular Classification of MYC-Driven B-Cell Lymphomas by Targeted Gene Expression Profiling of Fixed Biopsy Specimens. Journal of Molecular Diagnostics, 2015, 17, 19-30.	2.8	25
66	Yap/Taz inhibit goblet cell fate to maintain lung epithelial homeostasis. Cell Reports, 2021, 36, 109347.	6.4	24
67	Tributyltin induces a transcriptional response without a brite adipocyte signature in adipocyte models. Archives of Toxicology, 2018, 92, 2859-2874.	4.2	23
68	CXCR4 upregulation is an indicator of sensitivity to B-cell receptor/PI3K blockade and a potential resistance mechanism in B-cell receptor-dependent diffuse large B-cell lymphomas. Haematologica, 2020, 105, 1361-1368.	3.5	23
69	<scp>PPR</scp> polyadenylation factor defines mitochondrial <scp>mRNA</scp> identity and stability in trypanosomes. EMBO Journal, 2017, 36, 2435-2454.	7.8	20
70	The Carcinogenome Project: <i>In Vitro</i> Gene Expression Profiling of Chemical Perturbations to Predict Long-Term Carcinogenicity. Environmental Health Perspectives, 2019, 127, 47002.	6.0	20
71	Naturally occurring hotspot cancer mutations in $\widehat{Gl}\pm 13$ promote oncogenic signaling. Journal of Biological Chemistry, 2020, 295, 16897-16904.	3.4	19
72	animalcules: interactive microbiome analytics and visualization in R. Microbiome, 2021, 9, 76.	11.1	18

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73	Lack of IKBA coding region mutations in primary mediastinal large B-cell lymphoma and the host response subtype of diffuse large B-cell lymphoma. Blood, 2006, 107, 844-845.	1.4	17
74	Network-based analysis of transcriptional profiles from chemical perturbations experiments. BMC Bioinformatics, 2017, 18, 130.	2.6	17
75	Learning Bayesian Networks from Correlated Data. Scientific Reports, 2016, 6, 25156.	3.3	16
76	The diverse and important contributions of the AHR to cancer and cancer immunity. Current Opinion in Toxicology, 2017, 2, 93-102.	5.0	14
77	$\hat{l}^2$ -Catenin/CBP inhibition alters epidermal growth factor receptor fucosylation status in oral squamous cell carcinoma. Molecular Omics, 2020, 16, 195-209.	2.8	14
78	Effect of longevity genetic variants on the molecular aging rate. GeroScience, 2021, 43, 1237-1251.	4.6	12
79	Inhibition of LSD1 Attenuates Oral Cancer Development and Promotes Therapeutic Efficacy of Immune Checkpoint Blockade and YAP/TAZ Inhibition. Molecular Cancer Research, 2022, 20, 712-721.	3.4	12
80	Loss of G-Protein Pathway Suppressor 2 Promotes Tumor Growth Through Activation of AKT Signaling. Frontiers in Cell and Developmental Biology, 2020, 8, 608044.	3.7	10
81	Bounded recursive decomposition: a search-based method for belief-network inference under limited resources. International Journal of Approximate Reasoning, 1996, 15, 49-75.	3.3	9
82	Gene expression alterations in salivary gland epithelia of Sjögren's syndrome patients are associated with clinical and histopathological manifestations. Scientific Reports, 2021, 11, 11154.	3.3	9
83	Contextualized Protein-Protein Interactions. Patterns, 2021, 2, 100153.	5.9	8
84	A Data-Driven Transcriptional Taxonomy of Adipogenic Chemicals to Identify White and Brite Adipogens. Environmental Health Perspectives, 2021, 129, 77006.	6.0	7
85	CaDrA: A Computational Framework for Performing Candidate Driver Analyses Using Genomic Features. Frontiers in Genetics, 2019, 10, 121.	2.3	6
86	Diffuse Large B-Cell Lymphoma Patient-Derived Xenograft Models Capture Molecular and Biologic Heterogeneity and Inform Therapy. Blood, 2015, 126, 817-817.	1.4	5
87	Serum Orotidine: A Novel Biomarker of Increased CVD Risk in Type 2 Diabetes Discovered Through Metabolomics Studies. Diabetes Care, 2022, 45, 1882-1892.	8.6	5
88	Assessment of a Highly Multiplexed RNA Sequencing Platform and Comparison to Existing High-Throughput Gene Expression Profiling Techniques. Frontiers in Genetics, 2019, 10, 150.	2.3	4
89	Identification of candidate cancer drivers by integrative Epi-DNA and Gene Expression (iEDGE) data analysis. Scientific Reports, 2019, 9, 16904.	3.3	4
90	Multi-resolution characterization of molecular taxonomies in bulk and single-cell transcriptomics data. Nucleic Acids Research, 2021, 49, e98-e98.	14.5	4

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91	SimFuse: A Novel Fusion Simulator for RNA Sequencing (RNA-Seq) Data. BioMed Research International, 2015, 2015, 1-5.	1.9	3
92	PopCluster: an algorithm to identify genetic variants with ethnicity-dependent effects. Bioinformatics, 2019, 35, 3046-3054.	4.1	3
93	Actionable Genetic Features of Primary Testicular and Primary Central Nervous System Lymphomas. Blood, 2014, 124, 74-74.	1.4	2
94	An information-based bayesian approach to history taking. Lecture Notes in Computer Science, 1995, , 127-138.	1.3	2
95	Disruption Of Super Enhancer-Driven Cancer Dependencies In Diffuse Large B-Cell Lymphoma. Blood, 2013, 122, 3021-3021.	1.4	1
96	Preclinical Analyses Of The Chemical JAK2 Inhibitor, SAR302503, In Classical Hodgkin Lymphoma and Primary Mediastinal Large B-Cell Lymphoma. Blood, 2013, 122, 4230-4230.	1.4	1
97	CXCR4 Upregulation Is a Biomarker Of Sensitivity To Targeted Inhibition Of B-Cell Receptor Signaling In Diffuse Large B-Cell Lymphoma. Blood, 2013, 122, 631-631.	1.4	1
98	Resolving the Biological Heterogeneity of B-Cell Lymphoma, Unclassifiable, with Features Intermediate Between DLBCL and BL (BCL-U) Using Quantitative Profiles of Oncogenic Signaling Networks. Blood, 2015, 126, 3903-3903.	1.4	0
99	Comprehensive Analyses of Genetic Features Identify Coordinate Signatures in Diffuse Large B-Cell Lymphoma. Blood, 2015, 126, 3922-3922.	1.4	O