

# Francesco Falciani

## List of Publications by Year in descending order

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Version: 2024-02-01

79  
papers

4,801  
citations

117625

34  
h-index

102487

66  
g-index

82  
all docs

82  
docs citations

82  
times ranked

7532  
citing authors

#	ARTICLE	IF	CITATIONS
1	Early rheumatoid arthritis is characterized by a distinct and transient synovial fluid cytokine profile of T cell and stromal cell origin. <i>Arthritis Research and Therapy</i> , 2005, 7, R784-95.	3.5	425
2	Global gene expression profiles in fibroblasts from synovial, skin and lymphoid tissue reveals distinct cytokine and chemokine expression patterns. <i>Thrombosis and Haemostasis</i> , 2003, 90, 688-697.	3.4	283
3	Future water quality monitoring – Adapting tools to deal with mixtures of pollutants in water resource management. <i>Science of the Total Environment</i> , 2015, 512-513, 540-551.	8.0	243
4	DNA Microarrays: a Powerful Genomic Tool for Biomedical and Clinical Research. <i>Molecular Medicine</i> , 2007, 13, 527-541.	4.4	205
5	Multiplex Bead Immunoassay Analysis of Aqueous Humor Reveals Distinct Cytokine Profiles In Uveitis. , 2005, 46, 4251.		196
6	Modeling T-cell activation using gene expression profiling and state-space models. <i>Bioinformatics</i> , 2004, 20, 1361-1372.	4.1	193
7	The SOLUTIONS project: Challenges and responses for present and future emerging pollutants in land and water resources management. <i>Science of the Total Environment</i> , 2015, 503-504, 22-31.	8.0	163
8	The Role of Omics in the Application of Adverse Outcome Pathways for Chemical Risk Assessment. <i>Toxicological Sciences</i> , 2017, 158, 252-262.	3.1	161
9	Identifying Health Impacts of Exposure to Copper Using Transcriptomics and Metabolomics in a Fish Model. <i>Environmental Science &amp; Technology</i> , 2010, 44, 820-826.	10.0	152
10	Dosage Compensation in the Mouse Balances Up-Regulation and Silencing of X-Linked Genes. <i>PLoS Biology</i> , 2007, 5, e326.	5.6	143
11	Deciphering the complex role of thrombospondin-1 in glioblastoma development. <i>Nature Communications</i> , 2019, 10, 1146.	12.8	143
12	GALGO: an R package for multivariate variable selection using genetic algorithms. <i>Bioinformatics</i> , 2006, 22, 1154-1156.	4.1	136
13	Silver Nanowire Exposure Results in Internalization and Toxicity to <i>Daphnia magna</i> . <i>ACS Nano</i> , 2013, 7, 10681-10694.	14.6	117
14	Bayesian Variable Selection in Multinomial Probit Models to Identify Molecular Signatures of Disease Stage. <i>Biometrics</i> , 2004, 60, 812-819.	1.4	110
15	Muscle and blood redox status after exercise training in severe COPD patients. <i>Free Radical Biology and Medicine</i> , 2012, 52, 88-94.	2.9	89
16	A systems biology approach sheds new light on <i>Escherichia coli</i> acid resistance. <i>Nucleic Acids Research</i> , 2011, 39, 7512-7528.	14.5	86
17	Towards a System Level Understanding of Non-Model Organisms Sampled from the Environment: A Network Biology Approach. <i>PLoS Computational Biology</i> , 2011, 7, e1002126.	3.2	83
18	Adverse Outcome Pathways for Regulatory Applications: Examination of Four Case Studies With Different Degrees of Completeness and Scientific Confidence. <i>Toxicological Sciences</i> , 2015, 148, 14-25.	3.1	81

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19	Methods and approaches in the analysis of gene expression data. <i>Journal of Immunological Methods</i> , 2001, 250, 93-112.	1.4	76
20	Deletion of Hexose-6-phosphate Dehydrogenase Activates the Unfolded Protein Response Pathway and Induces Skeletal Myopathy. <i>Journal of Biological Chemistry</i> , 2008, 283, 8453-8461.	3.4	75
21	Discovery of Metabolic Signatures for Predicting Whole Organism Toxicology. <i>Toxicological Sciences</i> , 2010, 115, 369-378.	3.1	74
22	eIF6 coordinates insulin sensitivity and lipid metabolism by coupling translation to transcription. <i>Nature Communications</i> , 2015, 6, 8261.	12.8	73
23	Reverse engineering adverse outcome pathways. <i>Environmental Toxicology and Chemistry</i> , 2011, 30, 22-38.	4.3	72
24	Hepatic Transcriptomic and Metabolomic Responses in the Stickleback ( <i>Gasterosteus aculeatus</i> ) Exposed to Environmentally Relevant Concentrations of Dibenzanthracene. <i>Environmental Science &amp; Technology</i> , 2009, 43, 6341-6348.	10.0	71
25	Hepatic transcriptomic and metabolomic responses in the Stickleback ( <i>Gasterosteus aculeatus</i> ) exposed to ethinyl-estradiol. <i>Aquatic Toxicology</i> , 2010, 97, 174-187.	4.0	71
26	Relative overexpression of X-linked genes in mouse embryonic stem cells is consistent with Ohno's hypothesis. <i>Nature Genetics</i> , 2011, 43, 1169-1170.	21.4	71
27	A Systems Biology Approach Identifies Molecular Networks Defining Skeletal Muscle Abnormalities in Chronic Obstructive Pulmonary Disease. <i>PLoS Computational Biology</i> , 2011, 7, e1002129.	3.2	66
28	Transcriptomic responses of European flounder ( <i>Platichthys flesus</i> ) to model toxicants. <i>Aquatic Toxicology</i> , 2008, 90, 83-91.	4.0	54
29	Gene Transcription, Metabolite and Lipid Profiling in Eco-Indicator <i>Daphnia magna</i> Indicate Diverse Mechanisms of Toxicity by Legacy and Emerging Flame-Retardants. <i>Environmental Science &amp; Technology</i> , 2015, 49, 7400-7410.	10.0	54
30	Gene Expression Networks Underlying Ovarian Development in Wild Largemouth Bass ( <i>Micropterus</i> ) Tj ETQqO 0 0 rBT /Overlock 10 Tf	2.5	49
31	Metabolomic analysis of human vitreous humor differentiates ocular inflammatory disease. <i>Molecular Vision</i> , 2009, 15, 1210-7.	1.1	47
32	The experimental renal cell carcinoma model in the chick embryo. <i>Angiogenesis</i> , 2013, 16, 181-194.	7.2	46
33	NR4A orphan nuclear receptor family members, NR4A2 and NR4A3, regulate neutrophil number and survival. <i>Blood</i> , 2017, 130, 1014-1025.	1.4	46
34	ChainRank, a chain prioritisation method for contextualisation of biological networks. <i>BMC Bioinformatics</i> , 2016, 17, 17.	2.6	38
35	Chronic Obstructive Pulmonary Disease heterogeneity: challenges for health risk assessment, stratification and management. <i>Journal of Translational Medicine</i> , 2014, 12, S3.	4.4	34
36	Vision of a near future: Bridging the human health–environment divide. Toward an integrated strategy to understand mechanisms across species for chemical safety assessment. <i>Toxicology in Vitro</i> , 2020, 62, 104692.	2.4	33

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37	A computational framework for gene regulatory network inference that combines multiple methods and datasets. <i>BMC Systems Biology</i> , 2011, 5, 52.	3.0	29
38	Molecular Toxicity Identification Evaluation (mTIE) Approach Predicts Chemical Exposure in <i>Daphnia magna</i> . <i>Environmental Science &amp; Technology</i> , 2013, 47, 11747-11756.	10.0	29
39	Systems Biology Approach Reveals a Calcium-Dependent Mechanism for Basal Toxicity in <i>Daphnia magna</i> . <i>Environmental Science &amp; Technology</i> , 2015, 49, 11132-11140.	10.0	28
40	The COPD Knowledge Base: enabling data analysis and computational simulation in translational COPD research. <i>Journal of Translational Medicine</i> , 2014, 12, S6.	4.4	26
41	Systems Medicine: from molecular features and models to the clinic in COPD. <i>Journal of Translational Medicine</i> , 2014, 12, S4.	4.4	23
42	The Role of Eif6 in Skeletal Muscle Homeostasis Revealed by Endurance Training Co-expression Networks. <i>Cell Reports</i> , 2017, 21, 1507-1520.	6.4	22
43	Comparative toxicity of three phenolic compounds on the embryo of fathead minnow, <i>Pimephales promelas</i> . <i>Aquatic Toxicology</i> , 2018, 201, 66-72.	4.0	22
44	Computationally predicted gene regulatory networks in molluscan biomineralization identify extracellular matrix production and ion transportation pathways. <i>Bioinformatics</i> , 2020, 36, 1326-1332.	4.1	21
45	A systems biology approach reveals a link between systemic cytokines and skeletal muscle energy metabolism in a rodent smoking model and human COPD. <i>Genome Medicine</i> , 2014, 6, 59.	8.2	20
46	Gene Selection in Arthritis Classification with Large-Scale Microarray Expression Profiles. <i>Comparative and Functional Genomics</i> , 2003, 4, 171-181.	2.0	19
47	Stratification of pediatric ALL by in vitro cellular responses to DNA double-strand breaks provides insight into the molecular mechanisms underlying clinical response. <i>Blood</i> , 2009, 113, 117-126.	1.4	18
48	Analysis of Normal-Tumour Tissue Interaction in Tumours: Prediction of Prostate Cancer Features from the Molecular Profile of Adjacent Normal Cells. <i>PLoS ONE</i> , 2011, 6, e16492.	2.5	17
49	Experimental and computational modeling for signature and biomarker discovery of renal cell carcinoma progression. <i>Molecular Cancer</i> , 2021, 20, 136.	19.2	17
50	Ribosomal proteins' association with transcription sites peaks at tRNA genes in <i>Schizosaccharomyces pombe</i> . <i>Rna</i> , 2011, 17, 1713-1726.	3.5	16
51	How consistent are we? Interlaboratory comparison study in fathead minnows using the model estrogen 17 $\beta$ -estradiol to develop recommendations for environmental transcriptomics. <i>Environmental Toxicology and Chemistry</i> , 2017, 36, 2614-2623.	4.3	16
52	MMP13 and TIMP1 are functional markers for two different potential modes of action by mesenchymal stem/stromal cells when treating osteoarthritis. <i>Stem Cells</i> , 2020, 38, 1438-1453.	3.2	15
53	Genomic and transcriptomic predictors of triglyceride response to regular exercise. <i>British Journal of Sports Medicine</i> , 2015, 49, 1524-1531.	6.7	14
54	A novel panel of differentially-expressed microRNAs in breast cancer brain metastasis may predict patient survival. <i>Scientific Reports</i> , 2019, 9, 18518.	3.3	14

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55	The dipeptide prolyl-hydroxyproline promotes cellular homeostasis and lamellipodia-driven motility via active $\beta$ 1-integrin in adult tendon cells. <i>Journal of Biological Chemistry</i> , 2021, 297, 100819.	3.4	14
56	Systems analysis of miRNA biomarkers to inform drug safety. <i>Archives of Toxicology</i> , 2021, 95, 3475-3495.	4.2	14
57	Inference of Low and High-Grade Glioma Gene Regulatory Networks Delineates the Role of Rnd3 in Establishing Multiple Hallmarks of Cancer. <i>PLoS Genetics</i> , 2015, 11, e1005325.	3.5	14
58	Mapping Drug Physico-Chemical Features to Pathway Activity Reveals Molecular Networks Linked to Toxicity Outcome. <i>PLoS ONE</i> , 2010, 5, e12385.	2.5	14
59	Functional modules integrating essential cellular functions are predictive of the response of leukaemia cells to DNA damage. <i>Bioinformatics</i> , 2008, 24, 2602-2607.	4.1	12
60	A hierarchical Bayesian model for inference of copy number variants and their association to gene expression. <i>Annals of Applied Statistics</i> , 2014, 8, 148-175.	1.1	12
61	Stromal Transcriptional Profiles Reveal Hierarchies of Anatomical Site, Serum Response and Disease and Identify Disease Specific Pathways. <i>PLoS ONE</i> , 2015, 10, e0120917.	2.5	12
62	Models and computational strategies linking physiological response to molecular networks from large-scale data. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2008, 366, 3067-3089.	3.4	11
63	Kinome-wide transcriptional profiling of uveal melanoma reveals new vulnerabilities to targeted therapeutics. <i>Pigment Cell and Melanoma Research</i> , 2018, 31, 253-266.	3.3	11
64	The Sodium Channel $\beta$ 4-Subunits are Dysregulated in Temporal Lobe Epilepsy Drug-Resistant Patients. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2955.	4.1	11
65	Infection of bovine dendritic cells by rinderpest or measles viruses induces different changes in host transcription. <i>Virology</i> , 2009, 395, 223-231.	2.4	10
66	Multilevel functional genomics data integration as a tool for understanding physiology: a network biology perspective. <i>Journal of Applied Physiology</i> , 2016, 120, 297-309.	2.5	10
67	In Silico Computational Transcriptomics Reveals Novel Endocrine Disruptors in Largemouth Bass ( <i>Micropterus salmoides</i> ). <i>Environmental Science &amp; Technology</i> , 2018, 52, 7553-7565.	10.0	10
68	COMPADRE: an R and web resource for pathway activity analysis by component decompositions. <i>Bioinformatics</i> , 2012, 28, 2701-2702.	4.1	9
69	Analysis of host response to bacterial infection using error model based gene expression microarray experiments. <i>Nucleic Acids Research</i> , 2005, 33, e53-e53.	14.5	8
70	Transcriptional mechanism of vascular endothelial growth factor-induced expression of protein kinase $\text{C}\beta$ II in chronic lymphocytic leukaemia cells. <i>Scientific Reports</i> , 2017, 7, 43228.	3.3	6
71	Assessing technical and biological variation in SWATH-MS-based proteomic analysis of chronic lymphocytic leukaemia cells. <i>Scientific Reports</i> , 2021, 11, 2932.	3.3	5
72	A Network Biology Approach Identifies Molecular Cross-Talk between Normal Prostate Epithelial and Prostate Carcinoma Cells. <i>PLoS Computational Biology</i> , 2016, 12, e1004884.	3.2	5

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73	Mapping the Transcriptional and Fitness Landscapes of a Pathogenic <i>E. coli</i> Strain: The Effects of Organic Acid Stress under Aerobic and Anaerobic Conditions. <i>Genes</i> , 2021, 12, 53.	2.4	5
74	Genome-wide chromosomal association of Upf1 is linked to Pol II transcription in <i>Schizosaccharomyces pombe</i> . <i>Nucleic Acids Research</i> , 2022, 50, 350-367.	14.5	4
75	A Bayesian model for the identification of differentially expressed genes in <i>Daphnia magna</i> exposed to munition pollutants. <i>Biometrics</i> , 2015, 71, 803-811.	1.4	3
76	Freshwater Conservation and Biomonitoring of Structure and Function. , 2015, , 241-271.		3
77	Transcriptional responses to hyperplastic MRL signalling in <i>Drosophila</i> . <i>Open Biology</i> , 2017, 7, 160306.	3.6	3
78	Modeling the metabolic profile of <i>Mytilus edulis</i> reveals molecular signatures linked to gonadal development, sex and environmental site. <i>Scientific Reports</i> , 2021, 11, 12882.	3.3	3
79	Genomics and transcriptomics landscapes associated to changes in insulin sensitivity in response to endurance exercise training. <i>Scientific Reports</i> , 2021, 11, 23314.	3.3	3