

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	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
2	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
3	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
4	The dipeptide prolyl-hydroxyproline promotes cellular homeostasis and lamellipodia-driven motility via active β 1-integrin in adult tendon cells. <i>Journal of Biological Chemistry</i> , 2021, 297, 100819.	3.4	14
5	Systems analysis of miRNA biomarkers to inform drug safety. <i>Archives of Toxicology</i> , 2021, 95, 3475-3495.	4.2	14
6	Experimental and computational modeling for signature and biomarker discovery of renal cell carcinoma progression. <i>Molecular Cancer</i> , 2021, 20, 136.	19.2	17
7	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
8	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
9	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
10	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
11	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
12	The Sodium Channel β 4-Subunits are Dysregulated in Temporal Lobe Epilepsy Drug-Resistant Patients. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2955.	4.1	11
13	Deciphering the complex role of thrombospondin-1 in glioblastoma development. <i>Nature Communications</i> , 2019, 10, 1146.	12.8	143
14	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
15	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
16	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
17	In Silico Computational Transcriptomics Reveals Novel Endocrine Disruptors in Largemouth Bass (<i>Micropterus salmoides</i>). <i>Environmental Science & Technology</i> , 2018, 52, 7553-7565.	10.0	10
18	Transcriptional responses to hyperplastic MRL signalling in <i>Drosophila</i> . <i>Open Biology</i> , 2017, 7, 160306.	3.6	3

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19	How consistent are we? Interlaboratory comparison study in fathead minnows using the model estrogen 17 β -estradiol to develop recommendations for environmental transcriptomics. <i>Environmental Toxicology and Chemistry</i> , 2017, 36, 2614-2623.	4.3	16
20	Transcriptional mechanism of vascular endothelial growth factor-induced expression of protein kinase C β II in chronic lymphocytic leukaemia cells. <i>Scientific Reports</i> , 2017, 7, 43228.	3.3	6
21	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
22	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
23	NR4A orphan nuclear receptor family members, NR4A2 and NR4A3, regulate neutrophil number and survival. <i>Blood</i> , 2017, 130, 1014-1025.	1.4	46
24	ChainRank, a chain prioritisation method for contextualisation of biological networks. <i>BMC Bioinformatics</i> , 2016, 17, 17.	2.6	38
25	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
26	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
27	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
28	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
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 & Technology</i> , 2015, 49, 7400-7410.	10.0	54
30	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
31	Genomic and transcriptomic predictors of triglyceride response to regular exercise. <i>British Journal of Sports Medicine</i> , 2015, 49, 1524-1531.	6.7	14
32	Systems Biology Approach Reveals a Calcium-Dependent Mechanism for Basal Toxicity in <i>Daphnia magna</i> . <i>Environmental Science & Technology</i> , 2015, 49, 11132-11140.	10.0	28
33	Freshwater Conservation and Biomonitoring of Structure and Function. , 2015, , 241-271.		3
34	eIF6 coordinates insulin sensitivity and lipid metabolism by coupling translation to transcription. <i>Nature Communications</i> , 2015, 6, 8261.	12.8	73
35	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
36	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

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37	Stromal Transcriptional Profiles Reveal Hierarchies of Anatomical Site, Serum Response and Disease and Identify Disease Specific Pathways. PLoS ONE, 2015, 10, e0120917.	2.5	12
38	A systems biology approach reveals a link between systemic cytokines and skeletal muscle energy metabolism in a rodent smoking model and human COPD. Genome Medicine, 2014, 6, 59.	8.2	20
39	Systems Medicine: from molecular features and models to the clinic in COPD. Journal of Translational Medicine, 2014, 12, S4.	4.4	23
40	Chronic Obstructive Pulmonary Disease heterogeneity: challenges for health risk assessment, stratification and management. Journal of Translational Medicine, 2014, 12, S3.	4.4	34
41	The COPD Knowledge Base: enabling data analysis and computational simulation in translational COPD research. Journal of Translational Medicine, 2014, 12, S6.	4.4	26
42	A hierarchical Bayesian model for inference of copy number variants and their association to gene expression. Annals of Applied Statistics, 2014, 8, 148-175.	1.1	12
43	Silver Nanowire Exposure Results in Internalization and Toxicity to <i>Daphnia magna</i> . ACS Nano, 2013, 7, 10681-10694.	14.6	117
44	Molecular Toxicity Identification Evaluation (mTIE) Approach Predicts Chemical Exposure in <i>Daphnia magna</i> . Environmental Science & Technology, 2013, 47, 11747-11756.	10.0	29
45	The experimental renal cell carcinoma model in the chick embryo. Angiogenesis, 2013, 16, 181-194.	7.2	46
46	Gene Expression Networks Underlying Ovarian Development in Wild Largemouth Bass (<i>Micropterus</i>)	2.5	49
47	Muscle and blood redox status after exercise training in severe COPD patients. Free Radical Biology and Medicine, 2012, 52, 88-94.	2.9	89
48	COMPADRE: an R and web resource for pathway activity analysis by component decompositions. Bioinformatics, 2012, 28, 2701-2702.	4.1	9
49	Analysis of Normal-Tumour Tissue Interaction in Tumours: Prediction of Prostate Cancer Features from the Molecular Profile of Adjacent Normal Cells. PLoS ONE, 2011, 6, e16492.	2.5	17
50	Ribosomal proteins' association with transcription sites peaks at tRNA genes in <i>Schizosaccharomyces pombe</i> . Rna, 2011, 17, 1713-1726.	3.5	16
51	A computational framework for gene regulatory network inference that combines multiple methods and datasets. BMC Systems Biology, 2011, 5, 52.	3.0	29
52	Reverse engineering adverse outcome pathways. Environmental Toxicology and Chemistry, 2011, 30, 22-38.	4.3	72
53	A systems biology approach sheds new light on <i>Escherichia coli</i> acid resistance. Nucleic Acids Research, 2011, 39, 7512-7528.	14.5	86
54	Relative overexpression of X-linked genes in mouse embryonic stem cells is consistent with Ohno's hypothesis. Nature Genetics, 2011, 43, 1169-1170.	21.4	71

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55	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
56	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
57	Discovery of Metabolic Signatures for Predicting Whole Organism Toxicology. <i>Toxicological Sciences</i> , 2010, 115, 369-378.	3.1	74
58	Identifying Health Impacts of Exposure to Copper Using Transcriptomics and Metabolomics in a Fish Model. <i>Environmental Science & Technology</i> , 2010, 44, 820-826.	10.0	152
59	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
60	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
61	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
62	Hepatic Transcriptomic and Metabolomic Responses in the Stickleback (<i>Gasterosteus aculeatus</i>) Exposed to Environmentally Relevant Concentrations of Dibenzanthracene. <i>Environmental Science & Technology</i> , 2009, 43, 6341-6348.	10.0	71
63	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
64	Metabolomic analysis of human vitreous humor differentiates ocular inflammatory disease. <i>Molecular Vision</i> , 2009, 15, 1210-7.	1.1	47
65	Transcriptomic responses of European flounder (<i>Platichthys flesus</i>) to model toxicants. <i>Aquatic Toxicology</i> , 2008, 90, 83-91.	4.0	54
66	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
67	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
68	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
69	Dosage Compensation in the Mouse Balances Up-Regulation and Silencing of X-Linked Genes. <i>PLoS Biology</i> , 2007, 5, e326.	5.6	143
70	DNA Microarrays: a Powerful Genomic Tool for Biomedical and Clinical Research. <i>Molecular Medicine</i> , 2007, 13, 527-541.	4.4	205
71	GALGO: an R package for multivariate variable selection using genetic algorithms. <i>Bioinformatics</i> , 2006, 22, 1154-1156.	4.1	136
72	Multiplex Bead Immunoassay Analysis of Aqueous Humor Reveals Distinct Cytokine Profiles In Uveitis. , 2005, 46, 4251.		196

#	ARTICLE	IF	CITATIONS
73	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
74	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
75	Modeling T-cell activation using gene expression profiling and state-space models. <i>Bioinformatics</i> , 2004, 20, 1361-1372.	4.1	193
76	Bayesian Variable Selection in Multinomial Probit Models to Identify Molecular Signatures of Disease Stage. <i>Biometrics</i> , 2004, 60, 812-819.	1.4	110
77	Gene Selection in Arthritis Classification with Large-Scale Microarray Expression Profiles. <i>Comparative and Functional Genomics</i> , 2003, 4, 171-181.	2.0	19
78	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
79	Methods and approaches in the analysis of gene expression data. <i>Journal of Immunological Methods</i> , 2001, 250, 93-112.	1.4	76