

Edoardo Saccenti

List of Publications by Year in descending order

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Version: 2024-02-01

95
papers

4,390
citations

147566

31
h-index

114278

63
g-index

102
all docs

102
docs citations

102
times ranked

6654
citing authors

#	ARTICLE	IF	CITATIONS
1	Age- and Sex-Dependent Changes of Free Circulating Blood Metabolite and Lipid Abundances, Correlations, and Ratios. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2022, 77, 918-926.	1.7	13
2	Metabolomics as a tool for precision medicine. , 2022, , 605-624.		0
3	Nuclear magnetic resonance in metabolomics. , 2022, , 149-218.		2
4	Phenotyping metabolic status of dairy cows using clustering of time profiles of energy balance peripartum. <i>Journal of Dairy Science</i> , 2022, 105, 4565-4580.	1.4	5
5	Analysis of host-pathogen gene association networks reveals patient-specific response to streptococcal and polymicrobial necrotising soft tissue infections. <i>BMC Medicine</i> , 2022, 20, 173.	2.3	3
6	A large-scale analysis of codon usage bias in 4868 bacterial genomes shows association of codon adaptation index with GC content, protein functional domains and bacterial phenotypes. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2022, 1865, 194826.	0.9	5
7	Multivariate Exploratory Data Analysis Using Component Models. , 2021, , 241-268.		2
8	Evaluation of Single Sample Network Inference Methods for Metabolomics-Based Systems Medicine. <i>Journal of Proteome Research</i> , 2021, 20, 932-949.	1.8	11
9	All sparse PCA models are wrong, but some are useful. Part II: Limitations and problems of deflation. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2021, 208, 104212.	1.8	7
10	Differential Network Analysis Reveals Molecular Determinants Associated with Blood Pressure and Heart Rate in Healthy Subjects. <i>Journal of Proteome Research</i> , 2021, 20, 1040-1051.	1.8	3
11	Disease Activity Patterns of Crohn's Disease in the First Ten Years After Diagnosis in the Population-based IBD South Limburg Cohort. <i>Journal of Crohn's and Colitis</i> , 2021, 15, 391-400.	0.6	25
12	Cancers in Agreement? Exploring the Cross-Talk of Cancer Metabolomic and Transcriptomic Landscapes Using Publicly Available Data. <i>Cancers</i> , 2021, 13, 393.	1.7	4
13	Phenotype and multi-omics comparison of <i>Staphylococcus</i> and <i>Streptococcus</i> uncovers pathogenic traits and predicts zoonotic potential. <i>BMC Genomics</i> , 2021, 22, 102.	1.2	6
14	Exploration of Blood Lipoprotein and Lipid Fraction Profiles in Healthy Subjects through Integrated Univariate, Multivariate, and Network Analysis Reveals Association of Lipase Activity and Cholesterol Esterification with Sex and Age. <i>Metabolites</i> , 2021, 11, 326.	1.3	5
15	Transcriptome-based identification of the beneficial role of blackcurrant, strawberry and yellow onion to attenuate the cytopathic effects of <i>Clostridium difficile</i> toxins. <i>Journal of Berry Research</i> , 2021, 11, 231-248.	0.7	1
16	In-Pero: Exploiting Deep Learning Embeddings of Protein Sequences to Predict the Localisation of Peroxisomal Proteins. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6409.	1.8	14
17	Discriminatory plasma biomarkers predict specific clinical phenotypes of necrotizing soft-tissue infections. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	7
18	Lipid and metabolite correlation networks specific to clinical and biochemical covariate show differences associated with sexual dimorphism in a cohort of nonagenarians. <i>GeroScience</i> , 2021, , 1.	2.1	2

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19	Analysis of Metabolite and Lipid Association Networks Reveals Molecular Mechanisms Associated with 3-Month Mortality and Poor Functional Outcomes in Patients with Acute Ischemic Stroke after Thrombolytic Treatment with Recombinant Tissue Plasminogen Activator. <i>Journal of Proteome Research</i> , 2021, 20, 4758-4770.	1.8	8
20	Specialty Grand Challenge: Data and Model Integration in Systems Biology. <i>Frontiers in Systems Biology</i> , 2021, 1, .	0.5	1
21	The Power of Microbiome Studies: Some Considerations on Which Alpha and Beta Metrics to Use and How to Report Results. <i>Frontiers in Microbiology</i> , 2021, 12, 796025.	1.5	44
22	Integrated Univariate, Multivariate, and Correlation-Based Network Analyses Reveal Metabolite-Specific Effects on Bacterial Growth and Biofilm Formation in Necrotizing Soft Tissue Infections. <i>Journal of Proteome Research</i> , 2020, 19, 688-698.	1.8	16
23	All sparse PCA models are wrong, but some are useful. Part I: Computation of scores, residuals and explained variance. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2020, 196, 103907.	1.8	26
24	Differential Network Analysis Reveals Metabolic Determinants Associated with Mortality in Acute Myocardial Infarction Patients and Suggests Potential Mechanisms Underlying Different Clinical Scores Used To Predict Death. <i>Journal of Proteome Research</i> , 2020, 19, 949-961.	1.8	27
25	Chemometrics Analysis of Big Data. , 2020, , 437-458.		1
26	Relationship between energy balance and metabolic profiles in plasma and milk of dairy cows in early lactation. <i>Journal of Dairy Science</i> , 2020, 103, 4795-4805.	1.4	33
27	The association between breastmilk oligosaccharides and faecal microbiota in healthy breastfed infants at two, six, and twelve weeks of age. <i>Scientific Reports</i> , 2020, 10, 4270.	1.6	70
28	Short communication: Prediction of hyperketonemia in dairy cows in early lactation using on-farm cow data and net energy intake by partial least square discriminant analysis. <i>Journal of Dairy Science</i> , 2020, 103, 6576-6582.	1.4	4
29	Metabolomics of Milk Reflects a Negative Energy Balance in Cows. <i>Journal of Proteome Research</i> , 2020, 19, 2942-2949.	1.8	29
30	Corruption of the Pearson correlation coefficient by measurement error and its estimation, bias, and correction under different error models. <i>Scientific Reports</i> , 2020, 10, 438.	1.6	87
31	On the Use of Correlation and MI as a Measure of Metaboliteâ€™s Metabolite Association for Network Differential Connectivity Analysis. <i>Metabolites</i> , 2020, 10, 171.	1.3	20
32	Domesticated equine species and their derived hybrids differ in their fecal microbiota. <i>Animal Microbiome</i> , 2020, 2, 8.	1.5	19
33	Systems and Precision Medicine in Necrotizing Soft Tissue Infections. <i>Advances in Experimental Medicine and Biology</i> , 2020, 1294, 187-207.	0.8	1
34	Systems Biology and Biomarkers in Necrotizing Soft Tissue Infections. <i>Advances in Experimental Medicine and Biology</i> , 2020, 1294, 167-186.	0.8	4
35	Patientâ€™s characteristics and outcomes in necrotising soft-tissue infections: results from a Scandinavian, multicentre, prospective cohort study. <i>Intensive Care Medicine</i> , 2019, 45, 1241-1251.	3.9	82
36	NMR Spectroscopy for Metabolomics Research. <i>Metabolites</i> , 2019, 9, 123.	1.3	627

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37	Prediction of metabolic status of dairy cows in early lactation with on-farm cow data and machine learning algorithms. <i>Journal of Dairy Science</i> , 2019, 102, 10186-10201.	1.4	39
38	Semi-Supervised Multivariate Statistical Network Monitoring for Learning Security Threats. <i>IEEE Transactions on Information Forensics and Security</i> , 2019, 14, 2179-2189.	4.5	31
39	Simulation and Reconstruction of Metabolite Association Networks Using a Metabolic Dynamic Model and Correlation Based Algorithms. <i>Journal of Proteome Research</i> , 2019, 18, 1099-1113.	1.8	18
40	Correlating Infant Fecal Microbiota Composition and Human Milk Oligosaccharide Consumption by Microbiota of 1-Month-Old Breastfed Infants. <i>Molecular Nutrition and Food Research</i> , 2019, 63, e1801214.	1.5	83
41	Metabolomics in systems medicine: an overview of methods and applications. <i>Current Opinion in Systems Biology</i> , 2019, 15, 91-99.	1.3	9
42	Consistency, Inconsistency, and Ambiguity of Metabolite Names in Biochemical Databases Used for Genome-Scale Metabolic Modelling. <i>Metabolites</i> , 2019, 9, 28.	1.3	28
43	Association between Psychosocial Stress and Fecal Microbiota in Pregnant Women. <i>Scientific Reports</i> , 2019, 9, 4463.	1.6	55
44	In silico-guided engineering of <i>Pseudomonas putida</i> towards growth under micro-oxic conditions. <i>Microbial Cell Factories</i> , 2019, 18, 179.	1.9	23
45	From correlation to causation: analysis of metabolomics data using systems biology approaches. <i>Metabolomics</i> , 2018, 14, 37.	1.4	151
46	Recommended strategies for spectral processing and post-processing of 1D 1H-NMR data of biofluids with a particular focus on urine. <i>Metabolomics</i> , 2018, 14, 31.	1.4	107
47	Diabetes and necrotizing soft tissue infections—A prospective observational cohort study: Statistical analysis plan. <i>Acta Anaesthesiologica Scandinavica</i> , 2018, 62, 1171-1177.	0.7	3
48	Age and Sex Effects on Plasma Metabolite Association Networks in Healthy Subjects. <i>Journal of Proteome Research</i> , 2018, 17, 97-107.	1.8	66
49	Necrotizing soft tissue infections— a multicentre, prospective observational study (<sc>INFECT</sc>): protocol and statistical analysis plan. <i>Acta Anaesthesiologica Scandinavica</i> , 2018, 62, 272-279.	0.7	28
50	Group-wise partial least square regression. <i>Journal of Chemometrics</i> , 2018, 32, e2964.	0.7	10
51	Milk Metabolomics Data Reveal the Energy Balance of Individual Dairy Cows in Early Lactation. <i>Scientific Reports</i> , 2018, 8, 15828.	1.6	39
52	The Effect of DNA Extraction Methods on Observed Microbial Communities from Fibrous and Liquid Rumen Fractions of Dairy Cows. <i>Frontiers in Microbiology</i> , 2018, 9, 92.	1.5	46
53	SAPP: functional genome annotation and analysis through a semantic framework using FAIR principles. <i>Bioinformatics</i> , 2018, 34, 1401-1403.	1.8	44
54	Comparison of dimensionality assessment methods in Principal Component Analysis based on permutation tests. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2018, 181, 79-94.	1.8	7

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55	Group-wise ANOVA simultaneous component analysis for designed omics experiments. <i>Metabolomics</i> , 2018, 14, 73.	1.4	18
56	Plasma and Serum Metabolite Association Networks: Comparability within and between Studies Using NMR and MS Profiling. <i>Journal of Proteome Research</i> , 2017, 16, 2547-2559.	1.8	43
57	Group-Wise Principal Component Analysis for Exploratory Data Analysis. <i>Journal of Computational and Graphical Statistics</i> , 2017, 26, 501-512.	0.9	27
58	Comparative transcriptomics reveal developmental turning points during embryogenesis of a hemimetabolous insect, the damselfly <i>Ischnura elegans</i> . <i>Scientific Reports</i> , 2017, 7, 13547.	1.6	24
59	Use of Microarray Datasets to generate Caco-2-dedicated Networks and to identify Reporter Genes of Specific Pathway Activity. <i>Scientific Reports</i> , 2017, 7, 6778.	1.6	7
60	Considering Horn's Parallel Analysis from a Random Matrix Theory Point of View. <i>Psychometrika</i> , 2017, 82, 186-209.	1.2	17
61	Read all about it!? Public accountability, fragmented global climate governance and the media. <i>Climate Policy</i> , 2017, 17, 982-997.	2.6	12
62	Geochemical and microbial community determinants of reductive dechlorination at a site biostimulated with glycerol. <i>Environmental Microbiology</i> , 2017, 19, 968-981.	1.8	47
63	Correlation Patterns in Experimental Data Are Affected by Normalization Procedures: Consequences for Data Analysis and Network Inference. <i>Journal of Proteome Research</i> , 2017, 16, 619-634.	1.8	42
64	Diurnal Dynamics of Gaseous and Dissolved Metabolites and Microbiota Composition in the Bovine Rumen. <i>Frontiers in Microbiology</i> , 2017, 8, 425.	1.5	67
65	Weight loss predictability by plasma metabolic signatures in adults with obesity and morbid obesity of the D.O.G. study. <i>Obesity</i> , 2016, 24, 379-388.	1.5	27
66	Comparison of 432 <i>Pseudomonas</i> strains through integration of genomic, functional, metabolic and expression data. <i>Scientific Reports</i> , 2016, 6, 38699.	1.6	53
67	Entropy-Based Network Representation of the Individual Metabolic Phenotype. <i>Journal of Proteome Research</i> , 2016, 15, 3298-3307.	1.8	23
68	Approaches to Sample Size Determination for Multivariate Data: Applications to PCA and PLS-DA of Omics Data. <i>Journal of Proteome Research</i> , 2016, 15, 2379-2393.	1.8	68
69	Protein domain architectures provide a fast, efficient and scalable alternative to sequence-based methods for comparative functional genomics. <i>F1000Research</i> , 2016, 5, 1987.	0.8	20
70	Protein domain architectures provide a fast, efficient and scalable alternative to sequence-based methods for comparative functional genomics. <i>F1000Research</i> , 2016, 5, 1987.	0.8	18
71	Impact of a wastewater treatment plant on microbial community composition and function in a hyporheic zone of a eutrophic river. <i>Scientific Reports</i> , 2015, 5, 17284.	1.6	70
72	On the use of the observation-wise k -fold operation in PCA cross-validation. <i>Journal of Chemometrics</i> , 2015, 29, 467-478.	0.7	20

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73	Covariances Simultaneous Component Analysis: a new method within a framework for modeling covariances. <i>Journal of Chemometrics</i> , 2015, 29, 277-288.	0.7	15
74	Strategies for Individual Phenotyping of Linoleic and Arachidonic Acid Metabolism Using an Oral Glucose Tolerance Test. <i>PLoS ONE</i> , 2015, 10, e0119856.	1.1	6
75	Assessing the Metabolic Diversity of <i>Streptococcus</i> from a Protein Domain Point of View. <i>PLoS ONE</i> , 2015, 10, e0137908.	1.1	8
76	Multivariate modeling of the collaboration between Luigi Illica and Giuseppe Giacosa for the librettos of three operas by Giacomo Puccini. <i>Digital Scholarship in the Humanities</i> , 2015, 30, 405-422.	0.4	2
77	Probabilistic Networks of Blood Metabolites in Healthy Subjects As Indicators of Latent Cardiovascular Risk. <i>Journal of Proteome Research</i> , 2015, 14, 1101-1111.	1.8	45
78	Allotaxis and Resilience of the Human Individual Metabolic Phenotype. <i>Journal of Proteome Research</i> , 2015, 14, 2951-2962.	1.8	58
79	Effects of Sample Size and Dimensionality on the Performance of Four Algorithms for Inference of Association Networks in Metabonomics. <i>Journal of Proteome Research</i> , 2015, 14, 5119-5130.	1.8	20
80	Determining the number of components in principal components analysis: A comparison of statistical, crossvalidation and approximated methods. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2015, 149, 99-116.	1.8	39
81	Hypothesis: The Sound of the Individual Metabolic Phenotype? Acoustic Detection of NMR Experiments. <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 147-156.	1.0	1
82	Microbial Community Response of an Organohalide Respiring Enrichment Culture to Permanganate Oxidation. <i>PLoS ONE</i> , 2015, 10, e0134615.	1.1	17
83	Of Monkeys and Men: A Metabolomic Analysis of Static and Dynamic Urinary Metabolic Phenotypes in Two Species. <i>PLoS ONE</i> , 2014, 9, e106077.	1.1	22
84	A Metabolomic Perspective on Coeliac Disease. <i>Autoimmune Diseases</i> , 2014, 2014, 1-13.	2.7	26
85	Reflections on univariate and multivariate analysis of metabolomics data. <i>Metabolomics</i> , 2014, 10, 361-374.	1.4	406
86	Double-check: validation of diagnostic statistics for PLS-DA models in metabolomics studies. <i>Metabolomics</i> , 2012, 8, 3-16.	1.4	622
87	Beethoven's deafness and his three styles. <i>BMJ, The</i> , 2011, 343, d7589-d7589.	3.0	32
88	Simplivariate Models: Uncovering the Underlying Biology in Functional Genomics Data. <i>PLoS ONE</i> , 2011, 6, e20747.	1.1	13
89	Tracy's "Widom statistic for the largest eigenvalue of autoscaled real matrices. <i>Journal of Chemometrics</i> , 2011, 25, 644-652.	0.7	17
90	Identification of a serum-detectable metabolomic fingerprint potentially correlated with the presence of micrometastatic disease in early breast cancer patients at varying risks of disease relapse by traditional prognostic methods. <i>Annals of Oncology</i> , 2011, 22, 1295-1301.	0.6	83

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91	Individual Human Phenotypes in Metabolic Space and Time. Journal of Proteome Research, 2009, 8, 4264-4271.	1.8	143
92	The Metabonomic Signature of Celiac Disease. Journal of Proteome Research, 2009, 8, 170-177.	1.8	160
93	The war of tools: how can NMR spectroscopists detect errors in their structures?. Journal of Biomolecular NMR, 2008, 40, 251-261.	1.6	21
94	Monomorphism of human cytochrome c. Genomics, 2006, 88, 669-672.	1.3	10
95	Protein domain architectures provide a fast, efficient and scalable alternative to sequence-based methods for comparative functional genomics. F1000Research, 0, 5, 1987.	0.8	12