Edoardo Saccenti

List of Publications by Year
in descending order

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	NMR Spectroscopy for Metabolomics Research. Metabolites, 2019, 9, 123.	1.3	627
2	Double-check: validation of diagnostic statistics for PLS-DA models in metabolomics studies. Metabolomics, 2012, 8, 3-16.	1.4	622
3	Reflections on univariate and multivariate analysis of metabolomics data. Metabolomics, 2014, 10, 361-374.	1.4	406
4	The Metabonomic Signature of Celiac Disease. Journal of Proteome Research, 2009, 8, 170-177.	1.8	160
5	From correlation to causation: analysis of metabolomics data using systems biology approaches. Metabolomics, 2018, 14, 37.	1.4	151
6	Individual Human Phenotypes in Metabolic Space and Time. Journal of Proteome Research, 2009, 8, 4264-4271.	1.8	143
7	Recommended strategies for spectral processing and post-processing of 1D 1H-NMR data of biofluids with a particular focus on urine. Metabolomics, 2018, 14, 31.	1.4	107
8	Corruption of the Pearson correlation coefficient by measurement error and its estimation, bias, and correction under different error models. Scientific Reports, 2020, 10, 438.	1.6	87
9	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. Annals of Oncology, 2011, 22, 1295-1301.	0.6	83
10	Correlating Infant Fecal Microbiota Composition and Human Milk Oligosaccharide Consumption by Microbiota of 1‐Month‐Old Breastfed Infants. Molecular Nutrition and Food Research, 2019, 63, e1801214.	1.5	83
11	Patient's characteristics and outcomes in necrotising soft-tissue infections: results from a Scandinavian, multicentre, prospective cohort study. Intensive Care Medicine, 2019, 45, 1241-1251.	3.9	82
12	Impact of a wastewater treatment plant on microbial community composition and function in a hyporheic zone of a eutrophic river. Scientific Reports, 2015, 5, 17284.	1.6	70
13	The association between breastmilk oligosaccharides and faecal microbiota in healthy breastfed infants at two, six, and twelve weeks of age. Scientific Reports, 2020, 10, 4270.	1.6	70
14	Approaches to Sample Size Determination for Multivariate Data: Applications to PCA and PLS-DA of Omics Data. Journal of Proteome Research, 2016, 15, 2379-2393.	1.8	68
15	Diurnal Dynamics of Gaseous and Dissolved Metabolites and Microbiota Composition in the Bovine Rumen. Frontiers in Microbiology, 2017, 8, 425.	1.5	67
16	Age and Sex Effects on Plasma Metabolite Association Networks in Healthy Subjects. Journal of Proteome Research, 2018, 17, 97-107.	1.8	66
17	Allostasis and Resilience of the Human Individual Metabolic Phenotype. Journal of Proteome Research, 2015, 14, 2951-2962.	1.8	58
18	Association between Psychosocial Stress and Fecal Microbiota in Pregnant Women. Scientific Reports, 2019, 9, 4463.	1.6	55

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19	Comparison of 432 Pseudomonas strains through integration of genomic, functional, metabolic and expression data. Scientific Reports, 2016, 6, 38699.	1.6	53
20	Geochemical and microbial community determinants of reductive dechlorination at a site biostimulated with glycerol. Environmental Microbiology, 2017, 19, 968-981.	1.8	47
21	The Effect of DNA Extraction Methods on Observed Microbial Communities from Fibrous and Liquid Rumen Fractions of Dairy Cows. Frontiers in Microbiology, 2018, 9, 92.	1.5	46
22	Probabilistic Networks of Blood Metabolites in Healthy Subjects As Indicators of Latent Cardiovascular Risk. Journal of Proteome Research, 2015, 14, 1101-1111.	1.8	45
23	SAPP: functional genome annotation and analysis through a semantic framework using FAIR principles. Bioinformatics, 2018, 34, 1401-1403.	1.8	44
24	The Power of Microbiome Studies: Some Considerations on Which Alpha and Beta Metrics to Use and How to Report Results. Frontiers in Microbiology, 2021, 12, 796025.	1.5	44
25	Plasma and Serum Metabolite Association Networks: Comparability within and between Studies Using NMR and MS Profiling. Journal of Proteome Research, 2017, 16, 2547-2559.	1.8	43
26	Correlation Patterns in Experimental Data Are Affected by Normalization Procedures: Consequences for Data Analysis and Network Inference. Journal of Proteome Research, 2017, 16, 619-634.	1.8	42
27	Determining the number of components in principal components analysis: A comparison of statistical, crossvalidation and approximated methods. Chemometrics and Intelligent Laboratory Systems, 2015, 149, 99-116.	1.8	39
28	Milk Metabolomics Data Reveal the Energy Balance of Individual Dairy Cows in Early Lactation. Scientific Reports, 2018, 8, 15828.	1.6	39
29	Prediction of metabolic status of dairy cows in early lactation with on-farm cow data and machine learning algorithms. Journal of Dairy Science, 2019, 102, 10186-10201.	1.4	39
30	Relationship between energy balance and metabolic profiles in plasma and milk of dairy cows in early lactation. Journal of Dairy Science, 2020, 103, 4795-4805.	1.4	33
31	Beethoven's deafness and his three styles. BMJ, The, 2011, 343, d7589-d7589.	3.0	32
32	Semi-Supervised Multivariate Statistical Network Monitoring for Learning Security Threats. IEEE Transactions on Information Forensics and Security, 2019, 14, 2179-2189.	4.5	31
33	Metabolomics of Milk Reflects a Negative Energy Balance in Cows. Journal of Proteome Research, 2020, 19, 2942-2949.	1.8	29
34	Necrotizing soft tissue infections â€" a multicentre, prospective observational study (<scp>INFECT</scp>): protocol and statistical analysis plan. Acta Anaesthesiologica Scandinavica, 2018, 62, 272-279.	0.7	28
35	Consistency, Inconsistency, and Ambiguity of Metabolite Names in Biochemical Databases Used for Genome-Scale Metabolic Modelling. Metabolites, 2019, 9, 28.	1.3	28
36	Weight loss predictability by plasma metabolic signatures in adults with obesity and morbid obesity of the <scp>D</scp>i<scp>O</scp><scp>G</scp>enes study. Obesity, 2016, 24, 379-388.	1.5	27

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37	Group-Wise Principal Component Analysis for Exploratory Data Analysis. Journal of Computational and Graphical Statistics, 2017, 26, 501-512.	0.9	27
38	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. Journal of Proteome Research, 2020, 19, 949-961.	1.8	27
39	A Metabolomic Perspective on Coeliac Disease. Autoimmune Diseases, 2014, 2014, 1-13.	2.7	26
40	All sparse PCA models are wrong, but some are useful. Part I: Computation of scores, residuals and explained variance. Chemometrics and Intelligent Laboratory Systems, 2020, 196, 103907.	1.8	26
41	Disease Activity Patterns of Crohn's Disease in the First Ten Years After Diagnosis in the Population-based IBD South Limburg Cohort. Journal of Crohn's and Colitis, 2021, 15, 391-400.	0.6	25
42	Comparative transcriptomics reveal developmental turning points during embryogenesis of a hemimetabolous insect, the damselfly Ischnura elegans. Scientific Reports, 2017, 7, 13547.	1.6	24
43	Entropy-Based Network Representation of the Individual Metabolic Phenotype. Journal of Proteome Research, 2016, 15, 3298-3307.	1.8	23
44	In silico-guided engineering of Pseudomonas putida towards growth under micro-oxic conditions. Microbial Cell Factories, 2019, 18, 179.	1.9	23
45	Of Monkeys and Men: A Metabolomic Analysis of Static and Dynamic Urinary Metabolic Phenotypes in Two Species. PLoS ONE, 2014, 9, e106077.	1.1	22
46	The war of tools: how can NMR spectroscopists detect errors in their structures?. Journal of Biomolecular NMR, 2008, 40, 251-261.	1.6	21
47	On the use of the observation-wise k-fold operation in PCA cross-validation. Journal of Chemometrics, 2015, 29, 467-478.	0.7	20
48	Effects of Sample Size and Dimensionality on the Performance of Four Algorithms for Inference of Association Networks in Metabonomics. Journal of Proteome Research, 2015, 14, 5119-5130.	1.8	20
49	On the Use of Correlation and MI as a Measure of Metabolite—Metabolite Association for Network Differential Connectivity Analysis. Metabolites, 2020, 10, 171.	1.3	20
50	Protein domain architectures provide a fast, efficient and scalable alternative to sequence-based methods for comparative functional genomics. F1000Research, 2016, 5, 1987.	0.8	20
51	Domesticated equine species and their derived hybrids differ in their fecal microbiota. Animal Microbiome, 2020, 2, 8.	1.5	19
52	Group-wise ANOVA simultaneous component analysis for designed omics experiments. Metabolomics, 2018, 14, 73.	1.4	18
53	Simulation and Reconstruction of Metabolite—Metabolite Association Networks Using a Metabolic Dynamic Model and Correlation Based Algorithms. Journal of Proteome Research, 2019, 18, 1099-1113.	1.8	18
54	Protein domain architectures provide a fast, efficient and scalable alternative to sequence-based methods for comparative functional genomics. F1000Research, 2016, 5, 1987.	0.8	18

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55	Tracy–Widom statistic for the largest eigenvalue of autoscaled real matrices. Journal of Chemometrics, 2011, 25, 644-652.	0.7	17
56	Considering Horn's Parallel Analysis from a Random Matrix Theory Point of View. Psychometrika, 2017, 82, 186-209.	1.2	17
57	Microbial Community Response of an Organohalide Respiring Enrichment Culture to Permanganate Oxidation. PLoS ONE, 2015, 10, e0134615.	1.1	17
58	Integrated Univariate, Multivariate, and Correlation-Based Network Analyses Reveal Metabolite-Specific Effects on Bacterial Growth and Biofilm Formation in Necrotizing Soft Tissue Infections. Journal of Proteome Research, 2020, 19, 688-698.	1.8	16
59	Covariances Simultaneous Component Analysis: a new method within a framework for modeling covariances. Journal of Chemometrics, 2015, 29, 277-288.	0.7	15
60	In-Pero: Exploiting Deep Learning Embeddings of Protein Sequences to Predict the Localisation of Peroxisomal Proteins. International Journal of Molecular Sciences, 2021, 22, 6409.	1.8	14
61	Simplivariate Models: Uncovering the Underlying Biology in Functional Genomics Data. PLoS ONE, 2011, 6, e20747.	1.1	13
62	Age- and Sex-Dependent Changes of Free Circulating Blood Metabolite and Lipid Abundances, Correlations, and Ratios. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2022, 77, 918-926.	1.7	13
63	Read all about it!? Public accountability, fragmented global climate governance and the media. Climate Policy, 2017, 17, 982-997.	2.6	12
64	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
65	Evaluation of Single Sample Network Inference Methods for Metabolomics-Based Systems Medicine. Journal of Proteome Research, 2021, 20, 932-949.	1.8	11
66	Monomorphism of human cytochrome c. Genomics, 2006, 88, 669-672.	1.3	10
67	Group–wise partial least square regression. Journal of Chemometrics, 2018, 32, e2964.	0.7	10
68	Metabolomics in systems medicine: an overview of methods and applications. Current Opinion in Systems Biology, 2019, 15, 91-99.	1.3	9
69	Assessing the Metabolic Diversity of Streptococcus from a Protein Domain Point of View. PLoS ONE, 2015, 10, e0137908.	1.1	8
70	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. Journal of Proteome Research, 2021, 20, 4758-4770.	1.8	8
71	Use of Microarray Datasets to generate Caco-2-dedicated Networks and to identify Reporter Genes of Specific Pathway Activity. Scientific Reports, 2017, 7, 6778.	1.6	7
72	Comparison of dimensionality assessment methods in Principal Component Analysis based on permutation tests. Chemometrics and Intelligent Laboratory Systems, 2018, 181, 79-94.	1.8	7

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73	All sparse PCA models are wrong, but some are useful. Part II: Limitations and problems of deflation. Chemometrics and Intelligent Laboratory Systems, 2021, 208, 104212.	1.8	7
74	Discriminatory plasma biomarkers predict specific clinical phenotypes of necrotizing soft-tissue infections. Journal of Clinical Investigation, 2021, 131, .	3.9	7
75	Strategies for Individual Phenotyping of Linoleic and Arachidonic Acid Metabolism Using an Oral Glucose Tolerance Test. PLoS ONE, 2015, 10, e0119856.	1.1	6
76	Phenotype and multi-omics comparison of Staphylococcus and Streptococcus uncovers pathogenic traits and predicts zoonotic potential. BMC Genomics, 2021, 22, 102.	1.2	6
77	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. Metabolites, 2021, 11, 326.	1.3	5
78	Phenotyping metabolic status of dairy cows using clustering of time profiles of energy balance peripartum. Journal of Dairy Science, 2022, 105, 4565-4580.	1.4	5
79	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. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2022, 1865, 194826.	0.9	5
80	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. Journal of Dairy Science, 2020, 103, 6576-6582.	1.4	4
81	Cancers in Agreement? Exploring the Cross-Talk of Cancer Metabolomic and Transcriptomic Landscapes Using Publicly Available Data. Cancers, 2021, 13, 393.	1.7	4
82	Systems Biology and Biomarkers in Necrotizing Soft Tissue Infections. Advances in Experimental Medicine and Biology, 2020, 1294, 167-186.	0.8	4
83	Diabetes and necrotizing soft tissue infections—A prospective observational cohort study: Statistical analysis plan. Acta Anaesthesiologica Scandinavica, 2018, 62, 1171-1177.	0.7	3
84	Differential Network Analysis Reveals Molecular Determinants Associated with Blood Pressure and Heart Rate in Healthy Subjects. Journal of Proteome Research, 2021, 20, 1040-1051.	1.8	3
85	Analysis of host-pathogen gene association networks reveals patient-specific response to streptococcal and polymicrobial necrotising soft tissue infections. BMC Medicine, 2022, 20, 173.	2.3	3
86	Multivariate modeling of the collaboration between Luigi Illica and Giuseppe Giacosa for the librettos of three operas by Giacomo Puccini. Digital Scholarship in the Humanities, 2015, 30, 405-422.	0.4	2
87	Multivariate Exploratory Data Analysis Using Component Models. , 2021, , 241-268.		2
88	Lipid and metabolite correlation networks specific to clinical and biochemical covariate show differences associated with sexual dimorphism in a cohort of nonagenarians. GeroScience, 2021, , 1.	2.1	2
89	Nuclear magnetic resonance in metabolomics. , 2022, , 149-218.		2
90	Hypothesis: The Sound of the Individual Metabolic Phenotype? Acoustic Detection of NMR Experiments. OMICS A Journal of Integrative Biology, 2015, 19, 147-156.	1.0	1

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91	Chemometrics Analysis of Big Data. , 2020, , 437-458.		1
92	Transcriptome-based identification of the beneficial role of blackcurrant, strawberry and yellow onion to attenuate the cytopathic effects of Clostridium difficile toxins. Journal of Berry Research, 2021, 11, 231-248.	0.7	1
93	Systems and Precision Medicine in Necrotizing Soft Tissue Infections. Advances in Experimental Medicine and Biology, 2020, 1294, 187-207.	0.8	1
94	Specialty Grand Challenge: Data and Model Integration in Systems Biology. Frontiers in Systems Biology, 2021, 1, .	0.5	1
95	Metabolomics as a tool for precision medicine. , 2022, , 605-624.		0