Marc-Emmanuel Dumas

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

10,612 46 103 105 h-index g-index citations papers 5.83 12.5 114 13,339 L-index avg, IF ext. citations ext. papers

#	Paper	IF	Citations
105	SARS-CoV-2 Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses <i>Cell</i> , 2022 ,	56.2	154
104	ITCH E3 Ubiquitin Ligase downregulation compromises hepatic degradation of branched-chain amino acids <i>Molecular Metabolism</i> , 2022 , 101454	8.8	O
103	Impairment of gut microbial biotin metabolism and host biotin status in severe obesity: effect of biotin and prebiotic supplementation on improved metabolism <i>Gut</i> , 2022 ,	19.2	5
102	Metabolomic and microbiome profiling reveals personalized risk factors for coronary artery disease <i>Nature Medicine</i> , 2022 ,	50.5	7
101	Microbiome and metabolome features of the cardiometabolic disease spectrum <i>Nature Medicine</i> , 2022 ,	50.5	4
100	Implementation of corticosteroids in treatment of COVID-19 in the ISARIC WHO Clinical Characterisation Protocol UK: prospective, cohort study <i>The Lancet Digital Health</i> , 2022 , 4, e220-e234	14.4	1
99	Combinatorial, additive and dose-dependent drug-microbiome associations. <i>Nature</i> , 2021 ,	50.4	11
98	An integrated workflow for enhanced taxonomic and functional coverage of the mouse fecal metaproteome. <i>Gut Microbes</i> , 2021 , 13, 1994836	8.8	0
97	Human and preclinical studies of the host-gut microbiome co-metabolite hippurate as a marker and mediator of metabolic health. <i>Gut</i> , 2021 , 70, 2105-2114	19.2	13
96	Iron status influences non-alcoholic fatty liver disease in obesity through the gut microbiome. <i>Microbiome</i> , 2021 , 9, 104	16.6	15
95	Characterisation of in-hospital complications associated with COVID-19 using the ISARIC WHO Clinical Characterisation Protocol UK: a prospective, multicentre cohort study. <i>Lancet, The</i> , 2021 , 398, 223-237	40	39
94	The microbial metabolite p-Cresol induces autistic-like behaviors in mice by remodeling the gut microbiota. <i>Microbiome</i> , 2021 , 9, 157	16.6	21
93	A targeted ultra performance liquid chromatography - Tandem mass spectrometric assay for tyrosine and metabolites in urine and plasma: Application to the effects of antibiotics on mice. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2021,	3.2	1
92	Accuracy of citrulline, I-FABP and D-lactate in the diagnosis of acute mesenteric ischemia. <i>Scientific Reports</i> , 2021 , 11, 18929	4.9	2
91	A prenylated dsRNA sensor protects against severe COVID-19. <i>Science</i> , 2021 , 374, eabj3624	33.3	26
90	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. <i>Nature</i> , 2020 , 581, 310-3	1 55 0.4	100
89	Dominant gut Prevotella copri in gastrectomised non-obese diabetic Goto-Kakizaki rats improves glucose homeostasis through enhanced FXR signalling. <i>Diabetologia</i> , 2020 , 63, 1223-1235	10.3	17

(2017-2020)

88	The APOA1bp-SREBF-NOTCH axis is associated with reduced atherosclerosis risk in morbidly obese patients. <i>Clinical Nutrition</i> , 2020 , 39, 3408-3418	5.9	5
87	The Natural Metabolite 4-Cresol Improves Glucose Homeostasis and Enhances Ecell Function. <i>Cell Reports</i> , 2020 , 30, 2306-2320.e5	10.6	18
86	Imidazole propionate is increased in diabetes and associated with dietary patterns and altered microbial ecology. <i>Nature Communications</i> , 2020 , 11, 5881	17.4	29
85	The translational regulator FMRP controls lipid and glucose metabolism in mice and humans. <i>Molecular Metabolism</i> , 2019 , 21, 22-35	8.8	16
84	Diet-induced metabolic changes of the human gut microbiome: importance of short-chain fatty acids, methylamines and indoles. <i>Acta Diabetologica</i> , 2019 , 56, 493-500	3.9	47
83	Systems Genetics of Hepatic Metabolome Reveals Octopamine as a Target for Non-Alcoholic Fatty Liver Disease Treatment. <i>Scientific Reports</i> , 2019 , 9, 3656	4.9	9
82	Untargeted Mass Spectrometry Lipidomics identifies correlation between serum sphingomyelins and plasma cholesterol. <i>Lipids in Health and Disease</i> , 2019 , 18, 38	4.4	12
81	pJRES Binning Algorithm (JBA): a new method to facilitate the recovery of metabolic information from pJRES 1H NMR spectra. <i>Bioinformatics</i> , 2019 , 35, 1916-1922	7.2	6
80	A Data Integration Multi-Omics Approach to Study Calorie Restriction-Induced Changes in Insulin Sensitivity. <i>Frontiers in Physiology</i> , 2018 , 9, 1958	4.6	24
79	Exploring the Genetic Landscape of Metabolic Phenotypes with MetaboSignal. <i>Current Protocols in Bioinformatics</i> , 2018 , 61, 14.14.1-14.14.13	24.2	5
78	MWASTools: an R/bioconductor package for metabolome-wide association studies. <i>Bioinformatics</i> , 2018 , 34, 890-892	7.2	13
77	Metabolic retroconversion of trimethylamine N-oxide and the gut microbiota. <i>Microbiome</i> , 2018 , 6, 73	16.6	82
76	Implication of gut microbiota metabolites in cardiovascular and metabolic diseases. <i>Cellular and Molecular Life Sciences</i> , 2018 , 75, 3977-3990	10.3	84
75	2-hydroxycaproate predicts cardiovascular mortality in patients with atherosclerotic disease. <i>Atherosclerosis</i> , 2018 , 277, 179-185	3.1	6
74	CHAPTER 12:Advances in Computational Analysis of Metabolomic NMR Data. <i>New Developments in NMR</i> , 2018 , 310-323	0.9	1
73	Gut Microbiota Interacts with Markers of Adipose Tissue Browning, Insulin Action and Plasma Acetate in Morbid Obesity. <i>Molecular Nutrition and Food Research</i> , 2018 , 62, 1700721	5.9	46
72	Molecular phenomics and metagenomics of hepatic steatosis in non-diabetic obese women. <i>Nature Medicine</i> , 2018 , 24, 1070-1080	50.5	276
71	Are Gut Microbes Responsible for Post-dieting Weight Rebound?. <i>Cell Metabolism</i> , 2017 , 25, 6-7	24.6	5

70	Circulating MicroRNAs to Predict the Risk for Metabolic Diseases in the General Population?. <i>Diabetes</i> , 2017 , 66, 565-567	0.9	7
69	Genomic regulation of type 2 diabetes endophenotypes: Contribution from genetic studies in the Goto-Kakizaki rat. <i>Biochimie</i> , 2017 , 143, 56-65	4.6	7
68	J-Resolved H NMR 1D-Projections for Large-Scale Metabolic Phenotyping Studies: Application to Blood Plasma Analysis. <i>Analytical Chemistry</i> , 2017 , 89, 11405-11412	7.8	13
67	Microbial-Host Co-metabolites Are Prodromal Markers Predicting Phenotypic Heterogeneity in Behavior, Obesity, and Impaired Glucose Tolerance. <i>Cell Reports</i> , 2017 , 20, 136-148	10.6	57
66	A purified membrane protein from Akkermansia muciniphila or the pasteurized bacterium improves metabolism in obese and diabetic mice. <i>Nature Medicine</i> , 2017 , 23, 107-113	50.5	896
65	MetaboSignal: a network-based approach for topological analysis of metabotype regulation via metabolic and signaling pathways. <i>Bioinformatics</i> , 2017 , 33, 773-775	7.2	9
64	Akkermansia muciniphila and improved metabolic health during a dietary intervention in obesity: relationship with gut microbiome richness and ecology. <i>Gut</i> , 2016 , 65, 426-36	19.2	938
63	The microbial-mammalian metabolic axis: a critical symbiotic relationship. <i>Current Opinion in Clinical Nutrition and Metabolic Care</i> , 2016 , 19, 250-256	3.8	12
62	Is the way welke dieting wrong?. <i>Genome Medicine</i> , 2016 , 8, 7	14.4	2
61	A multiplexed targeted assay for high-throughput quantitative analysis of serum methylamines by ultra performance liquid chromatography coupled to high resolution mass spectrometry. <i>Archives of Biochemistry and Biophysics</i> , 2016 , 597, 12-20	4.1	11
60	Impact of the gut microbiota on inflammation, obesity, and metabolic disease. <i>Genome Medicine</i> , 2016 , 8, 42	14.4	669
59	Topological analysis of metabolic networks integrating co-segregating transcriptomes and metabolomes in type 2 diabetic rat congenic series. <i>Genome Medicine</i> , 2016 , 8, 101	14.4	14
58	Quantifying Diet-Induced Metabolic Changes of the Human Gut Microbiome. <i>Cell Metabolism</i> , 2015 , 22, 320-31	24.6	275
57	mQTL.NMR: an integrated suite for genetic mapping of quantitative variations of (1)H NMR-based metabolic profiles. <i>Analytical Chemistry</i> , 2015 , 87, 4377-84	7.8	24
56	Bile acid profiling and quantification in biofluids using ultra-performance liquid chromatography tandem mass spectrometry. <i>Analytical Chemistry</i> , 2015 , 87, 9662-70	7.8	120
55	The microbiome and its pharmacological targets: therapeutic avenues in cardiometabolic diseases. <i>Current Opinion in Pharmacology</i> , 2015 , 25, 36-44	5.1	19
54	Metabolic Profiling and Phenotyping of Central Nervous System Diseases: Metabolites Bring Insights into Brain Dysfunctions. <i>Journal of NeuroImmune Pharmacology</i> , 2015 , 10, 402-24	6.9	28
53	Metabolic phenotyping and systems biology approaches to understanding metabolic syndrome and fatty liver disease. <i>Gastroenterology</i> , 2014 , 146, 46-62	13.3	124

(2011-2014)

52	Objective set of criteria for optimization of sample preparation procedures for ultra-high throughput untargeted blood plasma lipid profiling by ultra performance liquid chromatography-mass spectrometry. <i>Analytical Chemistry</i> , 2014 , 86, 5766-74	7.8	153
51	Symbiotic bacterial metabolites regulate gastrointestinal barrier function via the xenobiotic sensor PXR and Toll-like receptor 4. <i>Immunity</i> , 2014 , 41, 296-310	32.3	47°
50	Colonic bacterial metabolites and human health. Current Opinion in Microbiology, 2013, 16, 246-54	7.9	243
49	Early metabolic adaptation in C57BL/6 mice resistant to high fat diet induced weight gain involves an activation of mitochondrial oxidative pathways. <i>Journal of Proteome Research</i> , 2013 , 12, 1956-68	5.6	47
48	Metabolomics-on-a-chip of hepatotoxicity induced by anticancer drug flutamide and Its active metabolite hydroxyflutamide using HepG2/C3a microfluidic biochips. <i>Toxicological Sciences</i> , 2013 , 132, 8-20	4.4	67
47	Weaning diet induces sustained metabolic phenotype shift in the pig and influences host response to Bifidobacterium lactis NCC2818. <i>Gut</i> , 2013 , 62, 842-51	19.2	17
46	Metabolic phenotyping and systems biology approaches to understanding neurological disorders. <i>F1000prime Reports</i> , 2013 , 5, 18		12
45	Predictive toxicology using systemic biology and liver microfluidic "on chip" approaches: application to acetaminophen injury. <i>Toxicology and Applied Pharmacology</i> , 2012 , 259, 270-80	4.6	49
44	Gut microbiota modulate the metabolism of brown adipose tissue in mice. <i>Journal of Proteome Research</i> , 2012 , 11, 620-30	5.6	73
43	Genetic determinants of metabolism in health and disease: from biochemical genetics to genome-wide associations. <i>Genome Medicine</i> , 2012 , 4, 30	14.4	25
42	Untargeted metabolome quantitative trait locus mapping associates variation in urine glycerate to mutant glycerate kinase. <i>Journal of Proteome Research</i> , 2012 , 11, 631-42	5.6	23
41	Metabolomics-on-a-chip and metabolic flux analysis for label-free modeling of the internal metabolism of HepG2/C3A cells. <i>Molecular BioSystems</i> , 2012 , 8, 1908-20		34
40	Metabolome 2.0: quantitative genetics and network biology of metabolic phenotypes. <i>Molecular BioSystems</i> , 2012 , 8, 2494-502		46
39	Metabolomics-on-a-chip and predictive systems toxicology in microfluidic bioartificial organs. <i>Analytical Chemistry</i> , 2012 , 84, 1840-8	7.8	82
38	Mapping Metabolomic Quantitative Trait Loci (mQTL): A Link Between Metabolome-Wide Association Studies and Systems Biology 2012 , 233-254		1
37	Broad-ranging natural metabotype variation drives physiological plasticity in healthy control inbred rat strains. <i>Journal of Proteome Research</i> , 2011 , 10, 1675-89	5.6	17
36	The microbial-mammalian metabolic axis: beyond simple metabolism. <i>Cell Metabolism</i> , 2011 , 13, 489-90	24.6	28
35	Pyruvate imbalance mediates metabolic reprogramming and mimics lifespan extension by dietary restriction in Caenorhabditis elegans. <i>Aging Cell</i> , 2011 , 10, 39-54	9.9	58

34	Colonization-induced host-gut microbial metabolic interaction. <i>MBio</i> , 2011 , 2, e00271-10	7.8	281
33	A metabolic system-wide characterisation of the pig: a model for human physiology. <i>Molecular BioSystems</i> , 2011 , 7, 2577-88		89
32	Bacterial adaptation to the gut environment favors successful colonization: microbial and metabonomic characterization of a simplified microbiota mouse model. <i>Gut Microbes</i> , 2011 , 2, 307-18	8.8	14
31	A metabolomic and systems biology perspective on the brain of the fragile X syndrome mouse model. <i>Genome Research</i> , 2011 , 21, 2190-202	9.7	84
30	Human metabolic profiles are stably controlled by genetic and environmental variation. <i>Molecular Systems Biology</i> , 2011 , 7, 525	12.2	119
29	A genome-wide metabolic QTL analysis in Europeans implicates two loci shaped by recent positive selection. <i>PLoS Genetics</i> , 2011 , 7, e1002270	6	109
28	Metabolic profiling strategy for discovery of nutritional biomarkers: proline betaine as a marker of citrus consumption. <i>American Journal of Clinical Nutrition</i> , 2010 , 92, 436-43	7	201
27	Two-dimensional statistical recoupling for the identification of perturbed metabolic networks from NMR spectroscopy. <i>Journal of Proteome Research</i> , 2010 , 9, 4513-20	5.6	40
26	The evolution of partial least squares models and related chemometric approaches in metabonomics and metabolic phenotyping. <i>Journal of Chemometrics</i> , 2010 , 24, 636-649	1.6	104
25	Intra- and inter-omic fusion of metabolic profiling data in a systems biology framework. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2010 , 104, 121-131	3.8	48
24	Statistical recoupling prior to significance testing in nuclear magnetic resonance based metabonomics. <i>Analytical Chemistry</i> , 2009 , 81, 6242-51	7.8	80
23	Metabolic profiling strategy of Caenorhabditis elegans by whole-organism nuclear magnetic resonance. <i>Journal of Proteome Research</i> , 2009 , 8, 2542-50	5.6	48
22	Phylometabonomic patterns of adaptation to high fat diet feeding in inbred mice. <i>PLoS ONE</i> , 2008 , 3, e1668	3.7	83
21	Direct quantitative trait locus mapping of mammalian metabolic phenotypes in diabetic and normoglycemic rat models. <i>Nature Genetics</i> , 2007 , 39, 666-72	36.3	132
20	Subtle metabolic and liver gene transcriptional changes underlie diet-induced fatty liver susceptibility in insulin-resistant mice. <i>Diabetologia</i> , 2007 , 50, 1867-1879	10.3	94
19	Metabotyping of Caenorhabditis elegans reveals latent phenotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 19808-12	11.5	102
18	A top-down systems biology view of microbiome-mammalian metabolic interactions in a mouse model. <i>Molecular Systems Biology</i> , 2007 , 3, 112	12.2	374
17	Metabonomics in diabetes research. <i>Journal of Diabetes Science and Technology</i> , 2007 , 1, 549-57	4.1	21

LIST OF PUBLICATIONS

16	Metabolic profiling reveals a contribution of gut microbiota to fatty liver phenotype in insulin-resistant mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 12511-6	11.5	854
15	Transgenomic metabolic interactions in a mouse disease model: interactions of Trichinella spiralis infection with dietary Lactobacillus paracasei supplementation. <i>Journal of Proteome Research</i> , 2006 , 5, 2185-93	5.6	72
14	Assessment of analytical reproducibility of 1H NMR spectroscopy based metabonomics for large-scale epidemiological research: the INTERMAP Study. <i>Analytical Chemistry</i> , 2006 , 78, 2199-208	7.8	304
13	Evaluation of the orthogonal projection on latent structure model limitations caused by chemical shift variability and improved visualization of biomarker changes in 1H NMR spectroscopic metabonomic studies. <i>Analytical Chemistry</i> , 2005 , 77, 517-26	7.8	508
12	Homeostatic signature of anabolic steroids in cattle using 1H-13C HMBC NMR metabonomics. Journal of Proteome Research, 2005 , 4, 1493-502	5.6	35
11	Selection of biomarkers by a multivariate statistical processing of composite metabonomic data sets using multiple factor analysis. <i>Journal of Proteome Research</i> , 2005 , 4, 1485-92	5.6	31
10	Signature biologique du dopage : un avenir pour la dtection ?. Science and Sports, 2005, 20, 222-225	0.8	2
9	Statistical total correlation spectroscopy: an exploratory approach for latent biomarker identification from metabolic 1H NMR data sets. <i>Analytical Chemistry</i> , 2005 , 77, 1282-9	7.8	729
8	Multiple parasite infections and their relationship to self-reported morbidity in a community of rural CEe dRvoire. <i>International Journal of Epidemiology</i> , 2004 , 33, 1092-102	7.8	158
7	Analyzing the physiological signature of anabolic steroids in cattle urine using pyrolysis/metastable atom bombardment mass spectrometry and pattern recognition. <i>Analytical Chemistry</i> , 2002 , 74, 5393-4	0 48	41
6	Metabonomic assessment of physiological disruptions using 1H-13C HMBC-NMR spectroscopy combined with pattern recognition procedures performed on filtered variables. <i>Analytical Chemistry</i> , 2002 , 74, 2261-73	7.8	64
5	The Microbial Metabolite 4-Cresol Improves Glucose Homeostasis and Enhances Ecell Function		1
4	Microbiome Determinants and Physiological Effects of the Benzoate-Hippurate Microbial-Host Co-Metabolic Pathway		1
3	The microbial metabolite p-Cresol induces autistic-like behaviors in mice by remodeling the gut microbi	ota	3
2	Metabolic retroconversion of trimethylamine N-oxide and the gut microbiota		4
1	Microbiome Inhibition of IRAK-4 by Trimethylamine Mediates Metabolic and Immune Benefits in High-Fat-Diet-induced Insulin Resistance		2