

# François Fenaille

## List of Publications by Year in descending order

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Version: 2024-02-01

88  
papers

2,372  
citations

218677

26  
h-index

243625

44  
g-index

90  
all docs

90  
docs citations

90  
times ranked

3965  
citing authors

#	ARTICLE	IF	CITATIONS
1	Hydrogen/deuterium exchange mass spectrometry in the world of small molecules. <i>Mass Spectrometry Reviews</i> , 2023, 42, 1300-1331.	5.4	8
2	Metabolomics for personalized medicine: the input of analytical chemistry from biomarker discovery to point-of-care tests. <i>Analytical and Bioanalytical Chemistry</i> , 2022, 414, 759-789.	3.7	43
3	Chronic Consumption of Cocoa Rich in Procyanidins Has a Marginal Impact on Gut Microbiota and on Serum and Fecal Metabolomes in Male Endurance Athletes. <i>Journal of Agricultural and Food Chemistry</i> , 2022, , .	5.2	4
4	Multiplex Detection of 24 Staphylococcal Enterotoxins in Culture Supernatant Using Liquid Chromatography Coupled to High-Resolution Mass Spectrometry. <i>Toxins</i> , 2022, 14, 249.	3.4	11
5	Mass Spectrometry for Neurobiomarker Discovery: The Relevance of Post-Translational Modifications. <i>Cells</i> , 2022, 11, 1279.	4.1	11
6	Top-Down Mass Spectrometry for Trace Level Quantification of Staphylococcal Enterotoxin A Variants. <i>Journal of Proteome Research</i> , 2022, 21, 547-556.	3.7	4
7	Cystine uptake inhibition potentiates front-line therapies in acute myeloid leukemia. <i>Leukemia</i> , 2022, 36, 1585-1595.	7.2	24
8	The Human Meconium Metabolome and Its Evolution during the First Days of Life. <i>Metabolites</i> , 2022, 12, 414.	2.9	3
9	PeakForest: a multi-platform digital infrastructure for interoperable metabolite spectral data and metadata management. <i>Metabolomics</i> , 2022, 18, .	3.0	4
10	Evaluation of erythropoietin biosimilars Epotin <sup>®</sup> , Hemax <sup>®</sup> and Jimaixin <sup>®</sup> by electrophoretic methods used for doping control analysis and specific N-glycan analysis revealed structural differences from original epoetin alfa drug Eprex <sup>®</sup> . <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2021, 194, 113750.	2.8	5
11	Quantitative Assessment of SARS-CoV-2 Virus in Nasopharyngeal Swabs Stored in Transport Medium by a Straightforward LC-MS/MS Assay Targeting Nucleocapsid, Membrane, and Spike Proteins. <i>Journal of Proteome Research</i> , 2021, 20, 1434-1443.	3.7	24
12	Metabotypes of <i>Pseudomonas aeruginosa</i> Correlate with Antibiotic Resistance, Virulence and Clinical Outcome in Cystic Fibrosis Chronic Infections. <i>Metabolites</i> , 2021, 11, 63.	2.9	20
13	Glutathione conjugates of the mercapturic acid pathway and guanine adduct as biomarkers of exposure to CEES, a sulfur mustard analog. <i>Analytical and Bioanalytical Chemistry</i> , 2021, 413, 1337-1351.	3.7	5
14	Piezo1-xerocytosis red cell metabolome shows impaired glycolysis and increased hemoglobin oxygen affinity. <i>Blood Advances</i> , 2021, 5, 84-88.	5.2	10
15	The effect of acute moderate-intensity exercise on the serum and fecal metabolomes and the gut microbiota of cross-country endurance athletes. <i>Scientific Reports</i> , 2021, 11, 3558.	3.3	44
16	Quantitative Determination of <i>Staphylococcus aureus</i> Enterotoxins Types A to I and Variants in Dairy Food Products by Multiplex Immuno-LC-MS/MS. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 2603-2610.	5.2	13
17	Mitochondrial metabolism supports resistance to IDH mutant inhibitors in acute myeloid leukemia. <i>Journal of Experimental Medicine</i> , 2021, 218, .	8.5	56
18	Small Mass but Strong Information: Diagnostic Ions Provide Crucial Clues to Correctly Identify Histone Lysine Modifications. <i>Proteomes</i> , 2021, 9, 18.	3.5	5

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19	First Direct Evidence of Interpartner Hydride/Deuteride Exchanges for Stored Sodiated Arginine/Fructose-6-phosphate Complex Anions within Salt-Solvated Structures. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1424-1440.	2.8	4
20	A mutation in SLC37A4 causes a dominantly inherited congenital disorder of glycosylation characterized by liver dysfunction. <i>American Journal of Human Genetics</i> , 2021, 108, 1040-1052.	6.2	7
21	Right Ventricle Remodeling Metabolic Signature in Experimental Pulmonary Hypertension Models of Chronic Hypoxia and Monocrotaline Exposure. <i>Cells</i> , 2021, 10, 1559.	4.1	10
22	H2B Type 1-K Accumulates in Senescent Fibroblasts with Persistent DNA Damage along with Methylated and Phosphorylated Forms of HMGA1. <i>Proteomes</i> , 2021, 9, 30.	3.5	3
23	Untargeted lipidomics uncovers lipid signatures that distinguish severe from moderate forms of acutely decompensated cirrhosis. <i>Journal of Hepatology</i> , 2021, 75, 1116-1127.	3.7	31
24	Normal transferrin patterns in congenital disorders of glycosylation with Golgi homeostasis disruption: apolipoprotein C-III at the rescue!. <i>Clinica Chimica Acta</i> , 2021, 519, 285-290.	1.1	2
25	Arginine-selective modulation of the lysosomal transporter PQLC2 through a gate-tuning mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	11
26	MAN1B1-CDG: Three new individuals and associated biochemical profiles. <i>Molecular Genetics and Metabolism Reports</i> , 2021, 28, 100775.	1.1	6
27	Combining Chemical Knowledge and Quantum Calculation for Interpreting Low-Energy Product Ion Spectra of Metabolite Adduct Ions: Sodiated Diterpene Diester Species as a Case Study. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 2499-2504.	2.8	4
28	SLC37A4-CDG: New biochemical insights for an emerging congenital disorder of glycosylation with major coagulopathy. <i>Clinica Chimica Acta</i> , 2021, 521, 104-106.	1.1	1
29	Trapped ion mobility spectrometry time-of-flight mass spectrometry for high throughput and high resolution characterization of human milk oligosaccharide isomers. <i>Analytica Chimica Acta</i> , 2021, 1180, 338878.	5.4	6
30	Evidence for the systemic diffusion of (2-chloroethyl)-ethyl-sulfide, a sulfur mustard analog, and its deleterious effects in brain. <i>Toxicology</i> , 2021, 462, 152950.	4.2	9
31	Ricin Antibodies™ Neutralizing Capacity against Different Ricin Isoforms and Cultivars. <i>Toxins</i> , 2021, 13, 100.	3.4	10
32	Development and Evaluation of an Immuno-MALDI-TOF Mass Spectrometry Approach for Quantification of the Abrin Toxin in Complex Food Matrices. <i>Toxins</i> , 2021, 13, 52.	3.4	3
33	ProMetIS, deep phenotyping of mouse models by combined proteomics and metabolomics analysis. <i>Scientific Data</i> , 2021, 8, 311.	5.3	6
34	Top-Down and Bottom-Up Proteomics of Circulating S100A8/S100A9 in Plasma of Septic Shock Patients. <i>Journal of Proteome Research</i> , 2020, 19, 914-925.	3.7	15
35	Blood metabolomics uncovers inflammation-associated mitochondrial dysfunction as a potential mechanism underlying ACLF. <i>Journal of Hepatology</i> , 2020, 72, 688-701.	3.7	223
36	CDG biochemical screening: Where do we stand?. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129652.	2.4	14

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37	Multi-omic analysis of gametogenesis reveals a novel signature at the promoters and distal enhancers of active genes. <i>Nucleic Acids Research</i> , 2020, 48, 4115-4138.	14.5	24
38	Development of a Mass Spectrometry Imaging Method for Detecting and Mapping Graphene Oxide Nanoparticles in Rodent Tissues. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1025-1036.	2.8	10
39	Three distinct glycosylation pathways are involved in the decoration of <i>Lactococcus lactis</i> cell wall glycopolymers. <i>Journal of Biological Chemistry</i> , 2020, 295, 5519-5532.	3.4	13
40	Comparative Evaluation of Data Dependent and Data Independent Acquisition Workflows Implemented on an Orbitrap Fusion for Untargeted Metabolomics. <i>Metabolites</i> , 2020, 10, 158.	2.9	42
41	A European proposal for quality control and quality assurance of tandem mass spectral libraries. <i>Environmental Sciences Europe</i> , 2020, 32, .	5.5	53
42	High plasma level of S100A8/S100A9 and S100A12 at admission indicates a higher risk of death in septic shock patients. <i>Scientific Reports</i> , 2019, 9, 15660.	3.3	52
43	A dual-chain assembly pathway generates the high structural diversity of cell-wall polysaccharides in <i>Lactococcus lactis</i> . <i>Journal of Biological Chemistry</i> , 2019, 294, 17612-17625.	3.4	25
44	Metabolomics using Fourier transform mass spectrometry. , 2019, , 325-356.		2
45	Proposal for a chemically consistent way to annotate ions arising from the analysis of reference compounds under ESI conditions: A prerequisite to proper mass spectral database constitution in metabolomics. <i>Journal of Mass Spectrometry</i> , 2019, 54, 567-582.	1.6	13
46	Comprehensive Preterm Breast Milk Metabotype Associated with Optimal Infant Early Growth Pattern. <i>Nutrients</i> , 2019, 11, 528.	4.1	26
47	Experimental evidence that electrospray-produced sodiated lysophosphatidyl ester structures exist essentially as protonated salts. <i>European Journal of Mass Spectrometry</i> , 2019, 25, 333-338.	1.0	3
48	Simultaneous quantification of tau and $\beta$ -synuclein in cerebrospinal fluid by high-resolution mass spectrometry for differentiation of Lewy Body Dementia from Alzheimer's Disease and controls. <i>Analyst</i> , The, 2019, 144, 6342-6351.	3.5	13
49	Metabolomic Investigation of <i>Staphylococcus aureus</i> Antibiotic Susceptibility by Liquid Chromatography Coupled to High-Resolution Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2019, 1871, 279-293.	0.9	12
50	Integrating mass spectrometry-based plasma (or serum) protein N-glycan profiling into the clinical practice?. <i>Annals of Translational Medicine</i> , 2019, 7, S225-S225.	1.7	3
51	Synthesis of plasmodione metabolites and <sup>13</sup> C-enriched plasmodione as chemical tools for drug metabolism investigation. <i>Organic and Biomolecular Chemistry</i> , 2018, 16, 2647-2665.	2.8	15
52	Evaluation of the High-Field Orbitrap Fusion for Compound Annotation in Metabolomics. <i>Analytical Chemistry</i> , 2018, 90, 3030-3035.	6.5	17
53	A capillary zone electrophoresis method for detection of Apolipoprotein C-III glycoforms and other related artifactually modified species. <i>Journal of Chromatography A</i> , 2018, 1532, 238-245.	3.7	13
54	New Antibody-Free Mass Spectrometry-Based Quantification Reveals That C9ORF72 Long Protein Isoform Is Reduced in the Frontal Cortex of Hexanucleotide-Repeat Expansion Carriers. <i>Frontiers in Neuroscience</i> , 2018, 12, 589.	2.8	23

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55	A novel subfamily of bacterial AAT-fold basic amino acid decarboxylases and functional characterization of its first representative: <i>Pseudomonas aeruginosa</i> LdcA. <i>Genome Biology and Evolution</i> , 2018, 10, 3058-3075.	2.5	11
56	CCDC115-CDG: A new rare and misleading inherited cause of liver disease. <i>Molecular Genetics and Metabolism</i> , 2018, 124, 228-235.	1.1	20
57	Complementarity of electrophoretic, mass spectrometric, and gene sequencing techniques for the diagnosis and characterization of congenital disorders of glycosylation. <i>Electrophoresis</i> , 2018, 39, 3123-3132.	2.4	29
58	Detection of <i>Yersinia pestis</i> in Complex Matrices by Intact Cell Immunocapture and Targeted Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2017, 1600, 69-83.	0.9	3
59	Histone variant H2A.J accumulates in senescent cells and promotes inflammatory gene expression. <i>Nature Communications</i> , 2017, 8, 14995.	12.8	131
60	Comparative analysis of native and permethylated human milk oligosaccharides by liquid chromatography coupled to high resolution mass spectrometry. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2017, 1071, 49-57.	2.3	30
61	Rapid Detection of Abrin Toxin and Its Isoforms in Complex Matrices by Immuno-Extraction and Quantitative High Resolution Targeted Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 11719-11727.	6.5	25
62	Data acquisition workflows in liquid chromatography coupled to high resolution mass spectrometry-based metabolomics: Where do we stand?. <i>Journal of Chromatography A</i> , 2017, 1526, 1-12.	3.7	101
63	Mechanisms governing the fragmentation of glycerophospholipids containing choline and ethanolamine polar head groups. <i>European Journal of Mass Spectrometry</i> , 2017, 23, 427-444.	1.0	13
64	Mechanistic study of competitive releases of H <sub>2</sub> O, NH <sub>3</sub> and CO <sub>2</sub> from deprotonated aspartic and glutamic acids: Role of conformation. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2017, 1047, 64-74.	2.3	3
65	N-Glycomics and N-Glycoproteomics of Human Cerebrospinal Fluid. <i>NeuroMethods</i> , 2017, , 161-177.	0.3	0
66	Mass spectrometry for the detection of bioterrorism agents: from environmental to clinical applications. <i>Journal of Mass Spectrometry</i> , 2016, 51, 183-199.	1.6	40
67	Tau Protein Quantification in Human Cerebrospinal Fluid by Targeted Mass Spectrometry at High Sequence Coverage Provides Insights into Its Primary Structure Heterogeneity. <i>Journal of Proteome Research</i> , 2016, 15, 667-676.	3.7	91
68	Evaluation of a combined glycomics and glycoproteomics approach for studying the major glycoproteins present in biofluids: Application to cerebrospinal fluid. <i>Rapid Communications in Mass Spectrometry</i> , 2015, 29, 461-473.	1.5	33
69	Multiplex Quantification of Protein Toxins in Human Biofluids and Food Matrices Using Immunoextraction and High-Resolution Targeted Mass Spectrometry. <i>Analytical Chemistry</i> , 2015, 87, 8473-8480.	6.5	62
70	Annotation of the <i>Staphylococcus aureus</i> Metabolome Using Liquid Chromatography Coupled to High-Resolution Mass Spectrometry and Application to the Study of Methicillin Resistance. <i>Journal of Proteome Research</i> , 2015, 14, 4863-4875.	3.7	24
71	High resolution mass spectrometry based techniques at the crossroads of metabolic pathways. <i>Mass Spectrometry Reviews</i> , 2014, 33, 471-500.	5.4	139
72	Bacterial Detection Using Unlabeled Phage Amplification and Mass Spectrometry through Structural and Nonstructural Phage Markers. <i>Journal of Proteome Research</i> , 2014, 13, 1450-1465.	3.7	13

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73	Identification and Validation of Specific Markers of Bacillus anthracis Spores by Proteomics and Genomics Approaches. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 716-732.	3.8	28
74	Detection of <i>Yersinia pestis</i> in Environmental and Food Samples by Intact Cell Immunocapture and Liquid Chromatography-Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2014, 86, 6144-6152.	6.5	28
75	Annotation of the human serum metabolome by coupling three liquid chromatography methods to high-resolution mass spectrometry. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2014, 966, 34-47.	2.3	100
76	Rapid Quantification of Clostridial Epsilon Toxin in Complex Food and Biological Matrixes by Immunopurification and Ultrapformance Liquid Chromatography-Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2012, 84, 5103-5109.	6.5	25
77	Deacetylation of H4-K16Ac and heterochromatin assembly in senescence. <i>Epigenetics and Chromatin</i> , 2012, 5, 15.	3.9	35
78	Comparison of approaches for purifying and desalting polymerase chain reaction products prior to electrospray ionization mass spectrometry. <i>Analytical Biochemistry</i> , 2010, 398, 272-274.	2.4	14
79	Evaluation of the LTQ-Orbitrap mass spectrometer for the analysis of polymerase chain reaction products. <i>Rapid Communications in Mass Spectrometry</i> , 2010, 24, 3501-3509.	1.5	3
80	Research Spotlight: Drug bioanalysis and biomarker discovery at the Commissariat à l'énergie atomique et aux énergies alternatives. <i>Bioanalysis</i> , 2010, 2, 713-717.	1.5	1
81	Ultra-High Performance Liquid Chromatography-Mass Spectrometry for the Fast Profiling of Histone Post-Translational Modifications. <i>Journal of Proteome Research</i> , 2010, 9, 5501-5509.	3.7	43
82	Mass Spectrometric Investigation of Molecular Variability of Grass Pollen Group 1 Allergens. <i>Journal of Proteome Research</i> , 2009, 8, 4014-4027.	3.7	32
83	Mass spectrometric characterization of N- and O-glycans of plasma-derived coagulation factor VII. <i>Glycoconjugate Journal</i> , 2008, 25, 827-842.	2.7	23
84	Detection of Ricin in Complex Samples by Immunocapture and Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry. <i>Journal of Proteome Research</i> , 2008, 7, 4154-4163.	3.7	65
85	Site-specific N-glycan characterization of human complement factor H. <i>Glycobiology</i> , 2007, 17, 932-944.	2.5	60
86	Combined use of 2,4,6-trihydroxyacetophenone as matrix and enzymatic deglycosylation in organic-aqueous solvent systems for the simultaneous characterization of complex glycoproteins and N-glycans by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2007, 21, 812-816.	1.5	12
87	Study of peptides containing modified lysine residues by tandem mass spectrometry: precursor ion scanning of hexanal-modified peptides. <i>Rapid Communications in Mass Spectrometry</i> , 2004, 18, 67-76.	1.5	38
88	Solid-state glycation of $\beta$ -lactoglobulin by lactose and galactose: localization of the modified amino acids using mass spectrometric techniques. <i>Journal of Mass Spectrometry</i> , 2004, 39, 16-28.	1.6	73