

Jean-Charles Portais

List of Publications by Year in descending order

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92
papers

7,088
citations

117625

34
h-index

60623

81
g-index

99
all docs

99
docs citations

99
times ranked

8738
citing authors

#	ARTICLE	IF	CITATIONS
1	Strigolactone inhibition of shoot branching. <i>Nature</i> , 2008, 455, 189-194.	27.8	1,910
2	Strigolactones Stimulate Arbuscular Mycorrhizal Fungi by Activating Mitochondria. <i>PLoS Biology</i> , 2006, 4, e226.	5.6	693
3	Chemotherapy-Resistant Human Acute Myeloid Leukemia Cells Are Not Enriched for Leukemic Stem Cells but Require Oxidative Metabolism. <i>Cancer Discovery</i> , 2017, 7, 716-735.	9.4	582
4	Sampling for Metabolome Analysis of Microorganisms. <i>Analytical Chemistry</i> , 2007, 79, 3843-3849.	6.5	344
5	IsoCor: correcting MS data in isotope labeling experiments. <i>Bioinformatics</i> , 2012, 28, 1294-1296.	4.1	241
6	Demonstration of the ethylmalonyl-CoA pathway by using ¹³ C metabolomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4846-4851.	7.1	232
7	Engineering <i>Escherichia coli</i> for methanol conversion. <i>Metabolic Engineering</i> , 2015, 28, 190-201.	7.0	166
8	Acetate fluxes in <i>Escherichia coli</i> are determined by the thermodynamic control of the Pta-AckA pathway. <i>Scientific Reports</i> , 2017, 7, 42135.	3.3	129
9	Metabolic footprint of epiphytic bacteria on <i>Arabidopsis thaliana</i> leaves. <i>ISME Journal</i> , 2016, 10, 632-643.	9.8	113
10	Genome-scale reconstruction and system level investigation of the metabolic network of <i>Methylobacterium extorquens</i> AM1. <i>BMC Systems Biology</i> , 2011, 5, 189.	3.0	111
11	Metabolic flux determination in C6 glioma cells using carbon-13 distribution upon [1- ¹³ C]glucose incubation. <i>FEBS Journal</i> , 1993, 217, 457-468.	0.2	101
12	Production of carbon-13-labeled cadaverine by engineered <i>Corynebacterium glutamicum</i> using carbon-13-labeled methanol as co-substrate. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 10163-10176.	3.6	96
13	Chromatin-Bound MDM2 Regulates Serine Metabolism and Redox Homeostasis Independently of p53. <i>Molecular Cell</i> , 2016, 62, 890-902.	9.7	96
14	Quantitative metabolome analysis using liquid chromatography–high-resolution mass spectrometry. <i>Analytical Biochemistry</i> , 2008, 382, 94-100.	2.4	91
15	Determination of carbon labeling distribution of intracellular metabolites from single fragment ions by ion chromatography tandem mass spectrometry. <i>Analytical Biochemistry</i> , 2007, 360, 182-188.	2.4	88
16	The Ethylmalonyl-CoA Pathway Is Used in Place of the Glyoxylate Cycle by <i>Methylobacterium extorquens</i> AM1 during Growth on Acetate. <i>Journal of Biological Chemistry</i> , 2012, 287, 757-766.	3.4	77
17	Control of ATP homeostasis during the respiro–fermentative transition in yeast. <i>Molecular Systems Biology</i> , 2010, 6, 344.	7.2	69
18	NMR-based fluxomics: Quantitative 2D NMR methods for isotopomers analysis. <i>Phytochemistry</i> , 2007, 68, 2330-2340.	2.9	68

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19	Isocitrate dehydrogenase 1 mutations prime the all-trans retinoic acid myeloid differentiation pathway in acute myeloid leukemia. <i>Journal of Experimental Medicine</i> , 2016, 213, 483-497.	8.5	68
20	Response of the central metabolism of <i>Escherichia coli</i> to modified expression of the gene encoding the glucose-6-phosphate dehydrogenase. <i>FEBS Letters</i> , 2007, 581, 3771-3776.	2.8	65
21	influx_s: increasing numerical stability and precision for metabolic flux analysis in isotope labelling experiments. <i>Bioinformatics</i> , 2012, 28, 687-693.	4.1	65
22	Ultrafast Quantitative 2D NMR: An Efficient Tool for the Measurement of Specific Isotopic Enrichments in Complex Biological Mixtures. <i>Analytical Chemistry</i> , 2011, 83, 3112-3119.	6.5	63
23	Cytosolic NADPH Homeostasis in Glucose-starved Procyclic <i>Trypanosoma brucei</i> Relies on Malic Enzyme and the Pentose Phosphate Pathway Fed by Gluconeogenic Flux. <i>Journal of Biological Chemistry</i> , 2013, 288, 18494-18505.	3.4	61
24	Recent advances in high-throughput ¹³ C-fluxomics. <i>Current Opinion in Biotechnology</i> , 2017, 43, 104-109.	6.6	59
25	The Carbon Storage Regulator (Csr) System Exerts a Nutrient-Specific Control over Central Metabolism in <i>Escherichia coli</i> Strain Nissle 1917. <i>PLoS ONE</i> , 2013, 8, e66386.	2.5	57
26	Carbohydrate cycling in micro-organisms: what can ¹³ C-NMR tell us?. <i>FEMS Microbiology Reviews</i> , 2002, 26, 375-402.	8.6	56
27	Mitochondrial metabolism supports resistance to IDH mutant inhibitors in acute myeloid leukemia. <i>Journal of Experimental Medicine</i> , 2021, 218, .	8.5	56
28	Sampling of intracellular metabolites for stationary and non-stationary ¹³ C metabolic flux analysis in <i>Escherichia coli</i> . <i>Analytical Biochemistry</i> , 2014, 465, 38-49.	2.4	50
29	Improved riboflavin production with <i>Ashbya gossypii</i> from vegetable oil based on ¹³ C metabolic network analysis with combined labeling analysis by GC/MS, LC/MS, 1D, and 2D NMR. <i>Metabolic Engineering</i> , 2018, 47, 357-373.	7.0	50
30	Application of 2D-TOCSY NMR to the measurement of specific ¹³ C-enrichments in complex mixtures of ¹³ C-labeled metabolites. <i>Metabolic Engineering</i> , 2007, 9, 252-257.	7.0	48
31	Bio-based succinate from sucrose: High-resolution ¹³ C metabolic flux analysis and metabolic engineering of the rumen bacterium <i>Basfia succiniciproducens</i> . <i>Metabolic Engineering</i> , 2017, 44, 198-212.	7.0	46
32	Stable Isotope Labeling Highlights Enhanced Fatty Acid and Lipid Metabolism in Human Acute Myeloid Leukemia. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3325.	4.1	46
33	The post-transcriptional regulatory system CSR controls the balance of metabolic pools in upper glycolysis of <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2016, 100, 686-700.	2.5	42
34	Methodology for the Validation of Isotopic Analyses by Mass Spectrometry in Stable-Isotope Labeling Experiments. <i>Analytical Chemistry</i> , 2018, 90, 1852-1860.	6.5	40
35	ATP Synthesis-coupled and -uncoupled Acetate Production from Acetyl-CoA by Mitochondrial Acetate:Succinate CoA-transferase and Acetyl-CoA Thioesterase in <i>Trypanosoma</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 17186-17197.	3.4	39
36	Ablation of Succinate Production from Glucose Metabolism in the Procyclic <i>Trypanosomes</i> Induces Metabolic Switches to the Glycerol 3-Phosphate/Dihydroxyacetone Phosphate Shuttle and to Proline Metabolism. <i>Journal of Biological Chemistry</i> , 2010, 285, 32312-32324.	3.4	35

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37	IsoDesign: A software for optimizing the design of ¹³ C metabolic flux analysis experiments. <i>Biotechnology and Bioengineering</i> , 2014, 111, 202-208.	3.3	35
38	Physiological and Molecular Timing of the Glucose to Acetate Transition in <i>Escherichia coli</i> . <i>Metabolites</i> , 2013, 3, 820-837.	2.9	34
39	Gluconeogenesis is essential for trypanosome development in the tsetse fly vector. <i>PLoS Pathogens</i> , 2018, 14, e1007502.	4.7	34
40	Synthesis of dextrans with controlled amounts of α -1,2 linkages using the transglucosidase GBD α CD2. <i>Applied Microbiology and Biotechnology</i> , 2010, 86, 545-554.	3.6	33
41	A novel platform for automated high-throughput fluxome profiling of metabolic variants. <i>Metabolic Engineering</i> , 2014, 25, 8-19.	7.0	33
42	Multilevel interaction of the DnaK/DnaJ(HSP70/HSP40) stress-responsive chaperone machine with the central metabolism. <i>Scientific Reports</i> , 2017, 7, 41341.	3.3	33
43	Control and regulation of acetate overflow in <i>Escherichia coli</i> . <i>ELife</i> , 2021, 10, .	6.0	33
44	Glycerol supports growth of the <i>Trypanosoma brucei</i> bloodstream forms in the absence of glucose: Analysis of metabolic adaptations on glycerol-rich conditions. <i>PLoS Pathogens</i> , 2018, 14, e1007412.	4.7	32
45	UFJCOSEY: A Fast 3D NMR Method for Measuring Isotopic Enrichments in Complex Samples. <i>ChemPhysChem</i> , 2012, 13, 3098-3101.	2.1	31
46	Co-Consumption of Methanol and Succinate by <i>Methylobacterium extorquens</i> AM1. <i>PLoS ONE</i> , 2012, 7, e48271.	2.5	31
47	Fast Spatially Encoded 3D NMR Strategies for ¹³ C-Based Metabolic Flux Analysis. <i>Analytical Chemistry</i> , 2013, 85, 9751-9757.	6.5	29
48	Impact of kinetic isotope effects in isotopic studies of metabolic systems. <i>BMC Systems Biology</i> , 2015, 9, 64.	3.0	29
49	In vivo ¹³ C NMR determines metabolic fluxes and steady state in linseed embryos. <i>Phytochemistry</i> , 2007, 68, 2341-2350.	2.9	28
50	Isotopic Studies of Metabolic Systems by Mass Spectrometry: Using Pascal's Triangle To Produce Biological Standards with Fully Controlled Labeling Patterns. <i>Analytical Chemistry</i> , 2014, 86, 10288-10295.	6.5	27
51	Metabolic flux analysis in <i>Ashbya gossypii</i> using ¹³ C-labeled yeast extract: industrial riboflavin production under complex nutrient conditions. <i>Microbial Cell Factories</i> , 2018, 17, 162.	4.0	27
52	The emerging roles of lactate as a redox substrate and signaling molecule in adipose tissues. <i>Journal of Physiology and Biochemistry</i> , 2020, 76, 241-250.	3.0	26
53	Lactate Fluxes and Plasticity of Adipose Tissues: A Redox Perspective. <i>Frontiers in Physiology</i> , 2021, 12, 689747.	2.8	26
54	Targeting MDM2-dependent serine metabolism as a therapeutic strategy for liposarcoma. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	24

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55	Transketolase in <i>Trypanosoma brucei</i> . <i>Molecular and Biochemical Parasitology</i> , 2011, 179, 1-7.	1.1	23
56	¹⁵ N-NMR-Based Approach for Amino Acids-Based ¹³ C-Metabolic Flux Analysis of Metabolism. <i>Analytical Chemistry</i> , 2017, 89, 2101-2106.	6.5	23
57	Cyclic organization of the carbohydrate metabolism in <i>Sinorhizobium meliloti</i> . <i>FEBS Journal</i> , 1999, 265, 473-480.	0.2	22
58	Photobioreactor design for isotopic non-stationary ¹³ C-metabolic flux analysis (INST) Tj ETQq0 0 0 rgBT /Overlock 10 T 109, 3030-3040.	3.3	22
59	Quantitative metabolomics of the thermophilic methylotroph <i>Bacillus methanolicus</i> . <i>Microbial Cell Factories</i> , 2016, 15, 92.	4.0	22
60	Lactate fluxes mediated by the monocarboxylate transporter-1 are key determinants of the metabolic activity of beige adipocytes. <i>Journal of Biological Chemistry</i> , 2021, 296, 100137.	3.4	22
61	The Csr System Regulates <i>Escherichia coli</i> Fitness by Controlling Glycogen Accumulation and Energy Levels. <i>MBio</i> , 2017, 8, .	4.1	21
62	A deeper investigation on carbohydrate cycling in <i>Sinorhizobium meliloti</i> . <i>FEBS Letters</i> , 2001, 499, 45-49.	2.8	17
63	Isotopic profiling of ¹³ C-labeled biological samples by two-dimensional heteronuclear J-resolved nuclear magnetic resonance spectroscopy. <i>Analytical Biochemistry</i> , 2012, 427, 158-163.	2.4	17
64	Procytic trypanosomes recycle glucose catabolites and TCA cycle intermediates to stimulate growth in the presence of physiological amounts of proline. <i>PLoS Pathogens</i> , 2021, 17, e1009204.	4.7	16
65	Intuitive Visualization and Analysis of Multi-Omics Data and Application to <i>Escherichia coli</i> Carbon Metabolism. <i>PLoS ONE</i> , 2011, 6, e21318.	2.5	15
66	Comparative Analysis of ¹³ C-Enriched Metabolites Released in the Medium of Cerebellar and Cortical Astrocytes Incubated with [1- ¹³ C]Glucose. <i>FEBS Journal</i> , 1995, 231, 697-703.	0.2	13
67	Mechanism of gluconate synthesis in <i>Rhizobium meliloti</i> by using in vivo NMR. <i>FEBS Letters</i> , 1997, 412, 485-489.	2.8	12
68	Developmental stage-dependent metabolic regulation during meiotic differentiation in budding yeast. <i>BMC Biology</i> , 2014, 12, 60.	3.8	12
69	Plasmid-encoded biosynthetic genes alleviate metabolic disadvantages while increasing glucose conversion to shikimate in an engineered <i>Escherichia coli</i> strain. <i>Biotechnology and Bioengineering</i> , 2017, 114, 1319-1330.	3.3	12
70	Combined transcriptomics and metabolomics profiling of the heat shock response in the hyperthermophilic archaeon <i>Pyrococcus furiosus</i> . <i>Extremophiles</i> , 2019, 23, 101-118.	2.3	12
71	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. <i>PLoS Computational Biology</i> , 2020, 16, e1007799.	3.2	12
72	GC/MS-based ¹³ C metabolic flux analysis resolves the parallel and cyclic photomixotrophic metabolism of <i>Synechocystis</i> sp. PCC 6803 and selected deletion mutants including the Entner-Doudoroff and phosphoketolase pathways. <i>Microbial Cell Factories</i> , 2022, 21, 69.	4.0	11

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73	High-Throughput Workflow for Monitoring and Mining Bioprocess Data and Its Application to Inferring the Physiological Response of Escherichia coli to Perturbations. Applied and Environmental Microbiology, 2011, 77, 7040-7049.	3.1	10
74	Improved Isotopic Profiling by Pure Shift Heteronuclear 2D J-Resolved NMR Spectroscopy. Analytical Chemistry, 2018, 90, 4025-4031.	6.5	10
75	In vivo ¹³ C-NMR studies of polymer synthesis in Rhizobium meliloti M5N1 strain. , 1998, 58, 250-253.		9
76	Functional analysis of isoprenoid precursors biosynthesis by quantitative metabolomics and isotopologue profiling. Metabolomics, 2019, 15, 115.	3.0	8
77	Glycerol suppresses glucose consumption in trypanosomes through metabolic contest. PLoS Biology, 2021, 19, e3001359.	5.6	7
78	Theoretical Basis for Dynamic Label Propagation in Stationary Metabolic Networks under Step and Periodic Inputs. PLoS ONE, 2015, 10, e0144652.	2.5	6
79	Measurement of isotopic enrichments in ¹³ C-labelled molecules by 1D selective Zero-Quantum Filtered TOCSY NMR experiments. Comptes Rendus Chimie, 2008, 11, 480-485.	0.5	5
80	Exploring the Glucose Fluxotype of the E. coli y-ome Using High-Resolution Fluxomics. Metabolites, 2021, 11, 271.	2.9	5
81	IsoSolve: An Integrative Framework to Improve Isotopic Coverage and Consolidate Isotopic Measurements by Mass Spectrometry and/or Nuclear Magnetic Resonance. Analytical Chemistry, 2021, 93, 9428-9436.	6.5	5
82	Correction of MS Data for Naturally Occurring Isotopes in Isotope Labelling Experiments. Methods in Molecular Biology, 2014, 1191, 197-207.	0.9	5
83	Simultaneous Measurement of Metabolite Concentration and Isotope Incorporation by Mass Spectrometry. Analytical Chemistry, 2020, 92, 5890-5896.	6.5	4
84	The Trypanosome UDP-Glucose Pyrophosphorylase Is Imported by Piggybacking into Glycosomes, Where Unconventional Sugar Nucleotide Synthesis Takes Place. MBio, 2021, 12, e0037521.	4.1	4
85	An optimization method for untargeted MS-based isotopic tracing investigations of metabolism. Metabolomics, 2022, 18, .	3.0	1
86	IDH1 Mutation Enhances Catabolic Flexibility and Mitochondrial Dependencies to Favor Drug Resistance in Acute Myeloid Leukemia. SSRN Electronic Journal, 0, , .	0.4	0
87	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. , 2020, 16, e1007799.		0
88	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. , 2020, 16, e1007799.		0
89	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. , 2020, 16, e1007799.		0
90	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. , 2020, 16, e1007799.		0

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91	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. , 2020, 16, e1007799.		0
92	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. , 2020, 16, e1007799.		0