

Pierre Thibault

List of Publications by Year in descending order

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Version: 2024-02-01

90
papers

4,377
citations

109321

35
h-index

123424

61
g-index

94
all docs

94
docs citations

94
times ranked

6186
citing authors

#	ARTICLE	IF	CITATIONS
1	MhcVizPipe: A Quality Control Software for Rapid Assessment of Small- to Large-Scale Immunopeptidome Datasets. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100178.	3.8	9
2	Head-to-tail cyclization of side chain-protected linear peptides to recapitulate genetically encoded cyclized peptides. <i>Peptide Science</i> , 2022, 114, .	1.8	3
3	The microprotein Nrs1 rewires the G1/S transcriptional machinery during nitrogen limitation in budding yeast. <i>PLoS Biology</i> , 2022, 20, e3001548.	5.6	10
4	Immunopeptidomic Analyses of Colorectal Cancers With and Without Microsatellite Instability. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100228.	3.8	20
5	Immunopeptidomics: Reading the Immune Signal That Defines Self From Nonself. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100234.	3.8	3
6	Proteomics of Herpes Simplex Virus 1 Nuclear Capsids. <i>Journal of Virology</i> , 2021, 95, .	3.4	6
7	UM171 Preserves Epigenetic Marks that Are Reduced in Ex Vivo Culture of Human HSCs via Potentiation of the CLR3-KBTBD4 Complex. <i>Cell Stem Cell</i> , 2021, 28, 48-62.e6.	11.1	44
8	A bacterium-derived, cancer-associated immunopeptidome. <i>Oncolmmunology</i> , 2021, 10, 1918373.	4.6	2
9	A novel p53 regulator, C16ORF72/TAPR1, buffers against telomerase inhibition. <i>Aging Cell</i> , 2021, 20, e13331.	6.7	20
10	Most non-canonical proteins uniquely populate the proteome or immunopeptidome. <i>Cell Reports</i> , 2021, 34, 108815.	6.4	120
11	Crosstalk Between SUMO and Ubiquitin-Like Proteins: Implication for Antiviral Defense. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 671067.	3.7	15
12	Atypical acute myeloid leukemia-specific transcripts generate shared and immunogenic MHC class-I-associated epitopes. <i>Immunity</i> , 2021, 54, 737-752.e10.	14.3	58
13	Early defects in mucopolysaccharidosis type IIIC disrupt excitatory synaptic transmission. <i>JCI Insight</i> , 2021, 6, .	5.0	8
14	Proteomic strategies for characterizing ubiquitin-like modifications. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	21.2	6
15	Integration of Segmented Ion Fractionation and Differential Ion Mobility on a Q-Exactive Hybrid Quadrupole Orbitrap Mass Spectrometer. <i>Analytical Chemistry</i> , 2021, 93, 9817-9825.	6.5	11
16	CAMAP: Artificial neural networks unveil the role of codon arrangement in modulating MHC-I peptides presentation. <i>PLoS Computational Biology</i> , 2021, 17, e1009482.	3.2	0
17	A Roadmap Toward the Definition of Actionable Tumor-Specific Antigens. <i>Frontiers in Immunology</i> , 2020, 11, 583287.	4.8	22
18	H3.3 G34W Promotes Growth and Impedes Differentiation of Osteoblast-Like Mesenchymal Progenitors in Giant Cell Tumor of Bone. <i>Cancer Discovery</i> , 2020, 10, 1968-1987.	9.4	40

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19	The Origin and Immune Recognition of Tumor-Specific Antigens. <i>Cancers</i> , 2020, 12, 2607.	3.7	30
20	Extending the Comprehensiveness of Immunopectidome Analyses Using Isobaric Peptide Labeling. <i>Analytical Chemistry</i> , 2020, 92, 9194-9204.	6.5	43
21	Proteogenomics Uncovers a Vast Repertoire of Shared Tumor-Specific Antigens in Ovarian Cancer. <i>Cancer Immunology Research</i> , 2020, 8, 544-555.	3.4	48
22	Interferon, restriction factors and SUMO pathways. <i>Cytokine and Growth Factor Reviews</i> , 2020, 55, 37-47.	7.2	16
23	Imipridone Anticancer Compounds Ectopically Activate the ClpP Protease and Represent a New Scaffold for Antibiotic Development. <i>Genetics</i> , 2020, 214, 1103-1120.	2.9	36
24	MAPDP: A Cloud-Based Computational Platform for Immunopectidomics Analyses. <i>Journal of Proteome Research</i> , 2020, 19, 1873-1881.	3.7	11
25	Cross-talk between SUMOylation and ISGylation in response to interferon. <i>Cytokine</i> , 2020, 129, 155025.	3.2	17
26	Widespread and tissue-specific expression of endogenous retroelements in human somatic tissues. <i>Genome Medicine</i> , 2020, 12, 40.	8.2	30
27	Interplay of Ubiquitin-Like Modifiers Following Arsenic Trioxide Treatment. <i>Journal of Proteome Research</i> , 2020, 19, 1999-2010.	3.7	4
28	Quantitative SUMO proteomics identifies PIAS1 substrates involved in cell migration and motility. <i>Nature Communications</i> , 2020, 11, 834.	12.8	47
29	Cyclin B3 activates the Anaphase-Promoting Complex/Cyclosome in meiosis and mitosis. <i>PLoS Genetics</i> , 2020, 16, e1009184.	3.5	11
30	Mubritinib Targets the Electron Transport Chain Complex I and Reveals the Landscape of OXPHOS Dependency in Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2019, 36, 84-99.e8.	16.8	163
31	Accurate Quantitative Proteomic Analyses Using Metabolic Labeling and High Field Asymmetric Waveform Ion Mobility Spectrometry (FAIMS). <i>Journal of Proteome Research</i> , 2019, 18, 2129-2138.	3.7	28
32	Dynamic Phosphoproteomics Uncovers Signaling Pathways Modulated by Anti-oncogenic Sphingolipid Analogs. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 408-422.	3.8	12
33	Gas-Phase Enrichment of Multiply Charged Peptide Ions by Differential Ion Mobility Extend the Comprehensiveness of SUMO Proteome Analyses. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 1111-1124.	2.8	17
34	Promyelocytic Leukemia Protein (PML) Requirement for Interferon-induced Global Cellular SUMOylation. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1196-1208.	3.8	22
35	The SysteMHC Atlas project. <i>Nucleic Acids Research</i> , 2018, 46, D1237-D1247.	14.5	119
36	PTEN Deficiency and AMPK Activation Promote Nutrient Scavenging and Anabolism in Prostate Cancer Cells. <i>Cancer Discovery</i> , 2018, 8, 866-883.	9.4	141

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37	Comparison of the MHC I Immunopeptidome Repertoire of Bâ€Cell Lymphoblasts Using Two Isolation Methods. <i>Proteomics</i> , 2018, 18, e1700251.	2.2	59
38	Extended Synaptotagmin 1 Interacts with Herpes Simplex Virus 1 Glycoprotein M and Negatively Modulates Virus-Induced Membrane Fusion. <i>Journal of Virology</i> , 2018, 92, .	3.4	18
39	Noncoding regions are the main source of targetable tumor-specific antigens. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	374
40	Phospho-dependent recruitment of the yeast NuA4 acetyltransferase complex by MRX at DNA breaks regulates RPA dynamics during resection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10028-10033.	7.1	25
41	Monoubiquitination of ASXLs controls the deubiquitinase activity of the tumor suppressor BAP1. <i>Nature Communications</i> , 2018, 9, 4385.	12.8	35
42	A Novel Differential Ion Mobility Device Expands the Depth of Proteome Coverage and the Sensitivity of Multiplex Proteomic Measurements. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2051-2067.	3.8	106
43	Quantitative SUMO proteomics reveals the modulation of several PML nuclear body associated proteins and an anti-senescence function of UBC9. <i>Scientific Reports</i> , 2018, 8, 7754.	3.3	26
44	Combined Enrichment/Enzymatic Approach To Study Tightly Clustered Multisite Phosphorylation on Ser-Rich Domains. <i>Journal of Proteome Research</i> , 2018, 17, 3050-3060.	3.7	3
45	Mubritinib Targets the Electron Transport Chain Complex I and Reveals the Landscape of Mitochondrial Vulnerability in Acute Myeloid Leukemia. <i>Blood</i> , 2018, 132, 910-910.	1.4	1
46	Uncovering the SUMOylation and ubiquitylation crosstalk in human cells using sequential peptide immunopurification. <i>Nature Communications</i> , 2017, 8, 14109.	12.8	107
47	Time-resolved Phosphoproteome Analysis of Paradoxical RAF Activation Reveals Novel Targets of ERK. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 663-679.	3.8	26
48	CLMSVault: A Software Suite for Protein Cross-Linking Mass-Spectrometry Data Analysis and Visualization. <i>Journal of Proteome Research</i> , 2017, 16, 2645-2652.	3.7	16
49	Corrigendum to â€œIntroduction to the HUPO 2015 Special Issueâ€[J]. <i>Proteomics (2016) 1â€2</i> . <i>Journal of Proteomics</i> , 2017, 152, 355-356.	2.4	0
50	Immunogenic stress and death of cancer cells: Contribution of antigenicity vs adjuvanticity to immunosurveillance. <i>Immunological Reviews</i> , 2017, 280, 165-174.	6.0	82
51	Identification of cross talk between SUMOylation and ubiquitylation using a sequential peptide immunopurification approach. <i>Nature Protocols</i> , 2017, 12, 2354-2355.	12.0	26
52	Global and Site-Specific Changes in 5-Methylcytosine and 5-Hydroxymethylcytosine after Extended Post-mortem Interval. <i>Frontiers in Genetics</i> , 2016, 7, 120.	2.3	5
53	MHC class Iâ€associated peptides derive from selective regions of the human genome. <i>Journal of Clinical Investigation</i> , 2016, 126, 4690-4701.	8.2	188
54	ERAAP Shapes the Peptidome Associated with Classical and Nonclassical MHC Class I Molecules. <i>Journal of Immunology</i> , 2016, 197, 1035-1043.	0.8	41

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55	Gpr161 anchoring of PKA consolidates GPCR and cAMP signaling. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7786-7791.	7.1	86
56	Global proteogenomic analysis of human MHC class I-associated peptides derived from non-canonical reading frames. Nature Communications, 2016, 7, 10238.	12.8	210
57	Improvement of Quantitative Measurements in Multiplex Proteomics Using High-Field Asymmetric Waveform Spectrometry. Journal of Proteome Research, 2016, 15, 4653-4665.	3.7	55
58	Unraveling Site-Specific and Combinatorial Histone Modifications Using High-Resolution Mass Spectrometry in Histone Deacetylase Mutants of Fission Yeast. Journal of Proteome Research, 2016, 15, 2132-2142.	3.7	23
59	In vitro assay to determine SUMOylation sites on protein substrates. Nature Protocols, 2016, 11, 387-397.	12.0	7
60	Phosphoproteome dynamics of <i>Saccharomyces cerevisiae</i> under heat shock and cold stress. Molecular Systems Biology, 2015, 11, 813.	7.2	54
61	Enhancement of mass spectrometry performance for proteomic analyses using high-field asymmetric waveform ion mobility spectrometry (FAIMS). Journal of Mass Spectrometry, 2015, 50, 1181-1195.	1.6	34
62	Sample Collection Method Bias Effects in Quantitative Phosphoproteomics. Journal of Proteome Research, 2015, 14, 2998-3004.	3.7	13
63	Interplay Between Histone H3 Lysine 56 Deacetylation and Chromatin Modifiers in Response to DNA Damage. Genetics, 2015, 200, 185-205.	2.9	29
64	A Cell-Signaling Network Temporally Resolves Specific versus Promiscuous Phosphorylation. Cell Reports, 2015, 10, 1202-1214.	6.4	84
65	Proteome dynamics in health and disease. Journal of Proteomics, 2015, 118, 1.	2.4	0
66	Discovery of protein acetylation patterns by deconvolution of peptide isomer mass spectra. Nature Communications, 2015, 6, 8648.	12.8	16
67	The nature of self for T cells—a systems-level perspective. Current Opinion in Immunology, 2015, 34, 1-8.	5.5	61
68	Impact of genomic polymorphisms on the repertoire of human MHC class I-associated peptides. Nature Communications, 2014, 5, 3600.	12.8	111
69	Efficient sample processing for proteomics applications—Are we there yet?. Molecular Systems Biology, 2014, 10, 758.	7.2	5
70	Synergistic action of co-expressed xylanase/laccase mixtures against milled sugar cane bagasse. Process Biochemistry, 2014, 49, 1152-1161.	3.7	15
71	Rejection of Leukemic Cells Requires Antigen-Specific T Cells with High Functional Avidity. Biology of Blood and Marrow Transplantation, 2014, 20, 37-45.	2.0	10
72	Large-scale analysis of lysine SUMOylation by SUMO remnant immunoaffinity profiling. Nature Communications, 2014, 5, 5409.	12.8	115

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73	Phosphoproteomic analysis identifies the tumor suppressor PDCD4 as a RSK substrate negatively regulated by 14-3-3. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2918-27.	7.1	70
74	Biochemical properties of glycosylation and characterization of a histidine acid phosphatase (phytase) expressed in <i>Pichia pastoris</i> . Protein Expression and Purification, 2014, 99, 43-49.	1.3	26
75	UBAP2L is a novel BMI1-interacting protein essential for hematopoietic stem cell activity. Blood, 2014, 124, 2362-2369.	1.4	30
76	Engineering the Pattern of Protein Glycosylation Modulates the Thermostability of a GH11 Xylanase. Journal of Biological Chemistry, 2013, 288, 25522-25534.	3.4	59
77	Displacement of N/Q-rich Peptides on TiO ₂ Beads Enhances the Depth and Coverage of Yeast Phosphoproteome Analyses. Journal of Proteome Research, 2013, 12, 2905-2913.	3.7	27
78	Targeted Identification of SUMOylation Sites in Human Proteins Using Affinity Enrichment and Paralog-specific Reporter Ions. Molecular and Cellular Proteomics, 2013, 12, 2536-2550.	3.8	42
79	Ubp2l-Bmi-1-Rnf2 Define a Novel Polycomb Complex Essential For Self-Renewal Of Hematopoietic Stem Cells. Blood, 2013, 122, 736-736.	1.4	0
80	MHC I-associated peptides preferentially derive from transcripts bearing miRNA response elements. Blood, 2012, 119, e181-e191.	1.4	62
81	Sample preparation and analytical strategies for large-scale phosphoproteomics experiments. Seminars in Cell and Developmental Biology, 2012, 23, 843-853.	5.0	40
82	Improvement of Phosphoproteome Analyses Using FAIMS and Decision Tree Fragmentation. Application to the Insulin Signaling Pathway in <i>Drosophila melanogaster</i> S2 Cells. Journal of Proteome Research, 2012, 11, 927-940.	3.7	58
83	A Novel Proteomics Approach to Identify SUMOylated Proteins and Their Modification Sites in Human Cells. Molecular and Cellular Proteomics, 2011, 10, S1-S15.	3.8	125
84	The MHC I immunopeptidome conveys to the cell surface an integrative view of cellular regulation. Molecular Systems Biology, 2011, 7, 533.	7.2	113
85	Enhanced Sensitivity in Proteomics Experiments Using FAIMS Coupled with a Hybrid Linear Ion Trap/Orbitrap Mass Spectrometer. Journal of Proteome Research, 2009, 8, 3355-3366.	3.7	92
86	Combined Enzymatic and Data Mining Approaches for Comprehensive Phosphoproteome Analyses. Molecular and Cellular Proteomics, 2008, 7, 645-660.	3.8	58
87	The MHC class I peptide repertoire is molded by the transcriptome. Journal of Experimental Medicine, 2008, 205, 595-610.	8.5	174
88	Dedication to Robert Kinnear Boyd. Rapid Communications in Mass Spectrometry, 2006, 20, 1487-1491.	1.5	0
89	Improvement in Peptide Detection for Proteomics Analyses Using NanoLC-MS and High-Field Asymmetry Waveform Ion Mobility Mass Spectrometry. Analytical Chemistry, 2005, 77, 2176-2186.	6.5	108
90	Determination of the primary structure of peptides using fast atom bombardment mass spectrometry. Biological Mass Spectrometry, 1990, 19, 13-26.	0.5	31