

Pierre Thibault

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.

85
papers

2,819
citations

29
h-index

51
g-index

94
ext. papers

3,772
ext. citations

9.1
avg. IF

5.2
L-index

#	Paper	IF	Citations
85	The microprotein Nrs1 rewires the G1/S transcriptional machinery during nitrogen limitation in budding yeast.. <i>PLoS Biology</i> , 2022 , 20, e3001548	9.7	0
84	Immunopeptidomic analyses of colorectal cancers with and without microsatellite instability.. <i>Molecular and Cellular Proteomics</i> , 2022 , 100228	7.6	1
83	CAMAP: Artificial neural networks unveil the role of codon arrangement in modulating MHC-I peptides presentation. <i>PLoS Computational Biology</i> , 2021 , 17, e1009482	5	
82	MhcVizPipe: A Quality Control Software for Rapid Assessment of Small- to Large-Scale Immunopeptidome Data Sets. <i>Molecular and Cellular Proteomics</i> , 2021 , 100178	7.6	0
81	A novel p53 regulator, C16ORF72/TAPR1, buffers against telomerase inhibition. <i>Aging Cell</i> , 2021 , 20, e13331	9.9	3
80	Most non-canonical proteins uniquely populate the proteome or immunopeptidome. <i>Cell Reports</i> , 2021 , 34, 108815	10.6	26
79	Crosstalk Between SUMO and Ubiquitin-Like Proteins: Implication for Antiviral Defense. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 671067	5.7	8
78	Atypical acute myeloid leukemia-specific transcripts generate shared and immunogenic MHC class-I-associated epitopes. <i>Immunity</i> , 2021 , 54, 737-752.e10	32.3	17
77	Proteomic strategies for characterizing ubiquitin-like modifications. <i>Nature Reviews Methods Primers</i> , 2021 , 1,		3
76	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	18	11
75	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	7.8	2
74	Extending the Comprehensiveness of Immunopeptidome Analyses Using Isobaric Peptide Labeling. <i>Analytical Chemistry</i> , 2020 , 92, 9194-9204	7.8	17
73	Proteogenomics Uncovers a Vast Repertoire of Shared Tumor-Specific Antigens in Ovarian Cancer. <i>Cancer Immunology Research</i> , 2020 , 8, 544-555	12.5	23
72	Interferon, restriction factors and SUMO pathways. <i>Cytokine and Growth Factor Reviews</i> , 2020 , 55, 37-47	17.9	8
71	Imipridone Anticancer Compounds Ectopically Activate the ClpP Protease and Represent a New Scaffold for Antibiotic Development. <i>Genetics</i> , 2020 , 214, 1103-1120	4	16
70	MAPDP: A Cloud-Based Computational Platform for Immunopeptidomics Analyses. <i>Journal of Proteome Research</i> , 2020 , 19, 1873-1881	5.6	7
69	Cross-talk between SUMOylation and ISGylation in response to interferon. <i>Cytokine</i> , 2020 , 129, 155025	4	8

68	Widespread and tissue-specific expression of endogenous retroelements in human somatic tissues. <i>Genome Medicine</i> , 2020 , 12, 40	14.4	14
67	Interplay of Ubiquitin-Like Modifiers Following Arsenic Trioxide Treatment. <i>Journal of Proteome Research</i> , 2020 , 19, 1999-2010	5.6	3
66	Cyclin B3 activates the Anaphase-Promoting Complex/Cyclosome in meiosis and mitosis. <i>PLoS Genetics</i> , 2020 , 16, e1009184	6	5
65	Quantitative SUMO proteomics identifies PIAS1 substrates involved in cell migration and motility. <i>Nature Communications</i> , 2020 , 11, 834	17.4	26
64	A Roadmap Toward the Definition of Actionable Tumor-Specific Antigens. <i>Frontiers in Immunology</i> , 2020 , 11, 583287	8.4	8
63	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	24.4	14
62	The Origin and Immune Recognition of Tumor-Specific Antigens. <i>Cancers</i> , 2020 , 12,	6.6	7
61	Proteomics of Herpes Simplex Virus Type 1 Nuclear Capsids. <i>Journal of Virology</i> , 2020 ,	6.6	3
60	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	5.6	15
59	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	24.3	75
58	Dynamic Phosphoproteomics Uncovers Signaling Pathways Modulated by Anti-oncogenic Sphingolipid Analogs. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 408-422	7.6	8
57	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	3.5	10
56	Promyelocytic Leukemia Protein (PML) Requirement for Interferon-induced Global Cellular SUMOylation. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 1196-1208	7.6	15
55	The SystemMHC Atlas project. <i>Nucleic Acids Research</i> , 2018 , 46, D1237-D1247	20.1	87
54	PTEN Deficiency and AMPK Activation Promote Nutrient Scavenging and Anabolism in Prostate Cancer Cells. <i>Cancer Discovery</i> , 2018 , 8, 866-883	24.4	96
53	Comparison of the MHC I Immunopeptidome Repertoire of B-Cell Lymphoblasts Using Two Isolation Methods. <i>Proteomics</i> , 2018 , 18, e1700251	4.8	37
52	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,	6.6	12
51	Combined Enrichment/Enzymatic Approach To Study Tightly Clustered Multisite Phosphorylation on Ser-Rich Domains. <i>Journal of Proteome Research</i> , 2018 , 17, 3050-3060	5.6	3

50	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	2.2	0
49	Noncoding regions are the main source of targetable tumor-specific antigens. <i>Science Translational Medicine</i> , 2018 , 10,	17.5	199
48	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	11.5	9
47	Monoubiquitination of ASXLs controls the deubiquitinase activity of the tumor suppressor BAP1. <i>Nature Communications</i> , 2018 , 9, 4385	17.4	24
46	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	7.6	65
45	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	4.9	20
44	Uncovering the SUMOylation and ubiquitylation crosstalk in human cells using sequential peptide immunopurification. <i>Nature Communications</i> , 2017 , 8, 14109	17.4	78
43	Time-resolved Phosphoproteome Analysis of Paradoxical RAF Activation Reveals Novel Targets of ERK. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 663-679	7.6	21
42	CLMSVault: A Software Suite for Protein Cross-Linking Mass-Spectrometry Data Analysis and Visualization. <i>Journal of Proteome Research</i> , 2017 , 16, 2645-2652	5.6	14
41	Corrigendum to "Introduction to the HUPO 2015 Special Issue" [J. Proteomics (2016) 1-2]. <i>Journal of Proteomics</i> , 2017 , 152, 355-356	3.9	
40	Immunogenic stress and death of cancer cells: Contribution of antigenicity vs adjuvanticity to immunosurveillance. <i>Immunological Reviews</i> , 2017 , 280, 165-174	11.3	52
39	Identification of cross talk between SUMOylation and ubiquitylation using a sequential peptide immunopurification approach. <i>Nature Protocols</i> , 2017 , 12, 2342-2358	18.8	17
38	Improvement of Quantitative Measurements in Multiplex Proteomics Using High-Field Asymmetric Waveform Spectrometry. <i>Journal of Proteome Research</i> , 2016 , 15, 4653-4665	5.6	44
37	Unraveling Site-Specific and Combinatorial Histone Modifications Using High-Resolution Mass Spectrometry in Histone Deacetylase Mutants of Fission Yeast. <i>Journal of Proteome Research</i> , 2016 , 15, 2132-42	5.6	5
36	In vitro assay to determine SUMOylation sites on protein substrates. <i>Nature Protocols</i> , 2016 , 11, 387-97	18.8	6
35	Global and Site-Specific Changes in 5-Methylcytosine and 5-Hydroxymethylcytosine after Extended Post-mortem Interval. <i>Frontiers in Genetics</i> , 2016 , 7, 120	4.5	4
34	MHC class I-associated peptides derive from selective regions of the human genome. <i>Journal of Clinical Investigation</i> , 2016 , 126, 4690-4701	15.9	123
33	ERAAP Shapes the Peptidome Associated with Classical and Nonclassical MHC Class I Molecules. <i>Journal of Immunology</i> , 2016 , 197, 1035-43	5.3	27

32	Gpr161 anchoring of PKA consolidates GPCR and cAMP signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 7786-91	11.5	59
31	Global proteogenomic analysis of human MHC class I-associated peptides derived from non-canonical reading frames. <i>Nature Communications</i> , 2016 , 7, 10238	17.4	127
30	A cell-signaling network temporally resolves specific versus promiscuous phosphorylation. <i>Cell Reports</i> , 2015 , 10, 1202-14	10.6	63
29	Discovery of protein acetylation patterns by deconvolution of peptide isomer mass spectra. <i>Nature Communications</i> , 2015 , 6, 8648	17.4	11
28	The nature of self for T cells-a systems-level perspective. <i>Current Opinion in Immunology</i> , 2015 , 34, 1-8	7.8	52
27	Phosphoproteome dynamics of <i>Saccharomyces cerevisiae</i> under heat shock and cold stress. <i>Molecular Systems Biology</i> , 2015 , 11, 813	12.2	41
26	Enhancement of mass spectrometry performance for proteomic analyses using high-field asymmetric waveform ion mobility spectrometry (FAIMS). <i>Journal of Mass Spectrometry</i> , 2015 , 50, 1181-95	9.2	23
25	Sample Collection Method Bias Effects in Quantitative Phosphoproteomics. <i>Journal of Proteome Research</i> , 2015 , 14, 2998-3004	5.6	9
24	Interplay between histone H3 lysine 56 deacetylation and chromatin modifiers in response to DNA damage. <i>Genetics</i> , 2015 , 200, 185-205	4	22
23	Large-scale analysis of lysine SUMOylation by SUMO remnant immunoaffinity profiling. <i>Nature Communications</i> , 2014 , 5, 5409	17.4	94
22	Phosphoproteomic analysis identifies the tumor suppressor PDCD4 as a RSK substrate negatively regulated by 14-3-3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E2918-27	11.5	54
21	Biochemical properties of glycosylation and characterization of a histidine acid phosphatase (phytase) expressed in <i>Pichia pastoris</i> . <i>Protein Expression and Purification</i> , 2014 , 99, 43-9	2	20
20	Autophagy's Contribution to Innate and Adaptive Immunity: An Overview 2014 , 267-278		
19	UBAP2L is a novel BMI1-interacting protein essential for hematopoietic stem cell activity. <i>Blood</i> , 2014 , 124, 2362-9	2.2	24
18	Impact of genomic polymorphisms on the repertoire of human MHC class I-associated peptides. <i>Nature Communications</i> , 2014 , 5, 3600	17.4	75
17	Synergistic action of co-expressed xylanase/laccase mixtures against milled sugar cane bagasse. <i>Process Biochemistry</i> , 2014 , 49, 1152-1161	4.8	13
16	Rejection of leukemic cells requires antigen-specific T cells with high functional avidity. <i>Biology of Blood and Marrow Transplantation</i> , 2014 , 20, 37-45	4.7	8
15	Engineering the pattern of protein glycosylation modulates the thermostability of a GH11 xylanase. <i>Journal of Biological Chemistry</i> , 2013 , 288, 25522-25534	5.4	49

14	Displacement of N/Q-rich peptides on TiO ₂ beads enhances the depth and coverage of yeast phosphoproteome analyses. <i>Journal of Proteome Research</i> , 2013 , 12, 2905-13	5.6	23
13	Targeted identification of SUMOylation sites in human proteins using affinity enrichment and paralog-specific reporter ions. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 2536-50	7.6	36
12	Ubp2l-Bmi-1-Rnf2 Define a Novel Polycomb Complex Essential For Self-Renewal Of Hematopoietic Stem Cells. <i>Blood</i> , 2013 , 122, 736-736	2.2	
11	MHC I-associated peptides preferentially derive from transcripts bearing miRNA response elements. <i>Blood</i> , 2012 , 119, e181-91	2.2	53
10	Sample preparation and analytical strategies for large-scale phosphoproteomics experiments. <i>Seminars in Cell and Developmental Biology</i> , 2012 , 23, 843-53	7.5	35
9	Improvement of phosphoproteome analyses using FAIMS and decision tree fragmentation. application to the insulin signaling pathway in <i>Drosophila melanogaster</i> S2 cells. <i>Journal of Proteome Research</i> , 2012 , 11, 927-40	5.6	54
8	A novel proteomics approach to identify SUMOylated proteins and their modification sites in human cells. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.004796	7.6	113
7	The MHC I immunopeptidome conveys to the cell surface an integrative view of cellular regulation. <i>Molecular Systems Biology</i> , 2011 , 7, 533	12.2	80
6	Enhanced sensitivity in proteomics experiments using FAIMS coupled with a hybrid linear ion trap/Orbitrap mass spectrometer. <i>Journal of Proteome Research</i> , 2009 , 8, 3355-66	5.6	75
5	Combined enzymatic and data mining approaches for comprehensive phosphoproteome analyses: application to cell signaling events of interferon-gamma-stimulated macrophages. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 645-60	7.6	50
4	The MHC class I peptide repertoire is molded by the transcriptome. <i>Journal of Experimental Medicine</i> , 2008 , 205, 595-610	16.6	127
3	Dedication to Robert Kinnear Boyd. <i>Rapid Communications in Mass Spectrometry</i> , 2006 , 20, 1487-91	2.2	
2	Improvement in peptide detection for proteomics analyses using NanoLC-MS and high-field asymmetry waveform ion mobility mass spectrometry. <i>Analytical Chemistry</i> , 2005 , 77, 2176-86	7.8	100
1	Determination of the primary structure of peptides using fast atom bombardment mass spectrometry. <i>Biological Mass Spectrometry</i> , 1990 , 19, 13-26		28