

Mathieu Courcelles

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

1,752
citations

566801

15
h-index

752256

20
g-index

23
all docs

23
docs citations

23
times ranked

2960
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.	2.5	9
2	Head-to-tail cyclization of side chain-protected linear peptides to recapitulate genetically-encoded cyclized peptides. <i>Peptide Science</i> , 2022, 114, .	1.0	3
3	Immunopeptidomic Analyses of Colorectal Cancers With and Without Microsatellite Instability. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100228.	2.5	20
4	Most non-canonical proteins uniquely populate the proteome or immunopeptidome. <i>Cell Reports</i> , 2021, 34, 108815.	2.9	120
5	CAMAP: Artificial neural networks unveil the role of codon arrangement in modulating MHC-I peptides presentation. <i>PLoS Computational Biology</i> , 2021, 17, e1009482.	1.5	0
6	Extending the Comprehensiveness of Immunopeptidome Analyses Using Isobaric Peptide Labeling. <i>Analytical Chemistry</i> , 2020, 92, 9194-9204.	3.2	43
7	Proteogenomics Uncovers a Vast Repertoire of Shared Tumor-Specific Antigens in Ovarian Cancer. <i>Cancer Immunology Research</i> , 2020, 8, 544-555.	1.6	48
8	MAPDP: A Cloud-Based Computational Platform for Immunopeptidomics Analyses. <i>Journal of Proteome Research</i> , 2020, 19, 1873-1881.	1.8	11
9	The SysteMHC Atlas project. <i>Nucleic Acids Research</i> , 2018, 46, D1237-D1247.	6.5	119
10	Comparison of the MHC I Immunopeptidome Repertoire of B-Cell Lymphoblasts Using Two Isolation Methods. <i>Proteomics</i> , 2018, 18, e1700251.	1.3	59
11	Noncoding regions are the main source of targetable tumor-specific antigens. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	374
12	CLMSVault: A Software Suite for Protein Cross-Linking Mass-Spectrometry Data Analysis and Visualization. <i>Journal of Proteome Research</i> , 2017, 16, 2645-2652.	1.8	16
13	MHC class II-associated peptides derive from selective regions of the human genome. <i>Journal of Clinical Investigation</i> , 2016, 126, 4690-4701.	3.9	188
14	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, 7786-7791.	3.3	86
15	Phosphoproteome dynamics reveal novel ERK1/2 MAP kinase substrates with broad spectrum of functions. <i>Molecular Systems Biology</i> , 2013, 9, 669.	3.2	284
16	Occurrence and Detection of Phosphopeptide Isomers in Large-Scale Phosphoproteomics Experiments. <i>Journal of Proteome Research</i> , 2012, 11, 3753-3765.	1.8	25
17	Phosphorylation network rewiring by gene duplication. <i>Molecular Systems Biology</i> , 2011, 7, 504.	3.2	32
18	ProteoConnections: A bioinformatics platform to facilitate proteome and phosphoproteome analyses. <i>Proteomics</i> , 2011, 11, 2654-2671.	1.3	23

#	ARTICLE	IF	CITATIONS
19	Artifactual Sulfation of Silver-stained Proteins. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 506-518.	2.5	24
20	The Phagosomal Proteome in Interferon- γ -Activated Macrophages. <i>Immunity</i> , 2009, 30, 143-154.	6.6	206
21	Combined Enzymatic and Data Mining Approaches for Comprehensive Phosphoproteome Analyses. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 645-660.	2.5	58