Ludovic C Gillet

List of Publications by Year
in descending order

29 papers	6,594 citations	304743 22 h-index	454955 30 g-index
43 all docs	43 docs citations	43 times ranked	8062 citing authors

#	Article	IF	Citations
1	Combining CRISPRi and metabolomics for functional annotation of compound libraries. Nature Chemical Biology, 2022, 18, 482-491.	8.0	33
2	The impact of genomic variation on protein phosphorylation states and regulatory networks. Molecular Systems Biology, 2022, 18, e10712.	7.2	9
3	Dynamic 3D proteomes reveal protein functional alterations at high resolution in situ. Cell, 2021, 184, 545-559.e22.	28.9	82
4	System-Wide Profiling of Protein Complexes Via Size Exclusion Chromatographyâ€"Mass Spectrometry (SECâ€"MS). Methods in Molecular Biology, 2021, 2259, 269-294.	0.9	11
5	NÎ±-terminal acetylation of proteins by NatA and NatB serves distinct physiological roles in Saccharomyces cerevisiae. Cell Reports, 2021, 34, 108711.	6.4	26
6	Processing of the ribosomal ubiquitin-like fusion protein FUBI-eS30/FAU is required for 40S maturation and depends on USP36. ELife, 2021, 10, .	6.0	8
7	Puf6 primes 60S pre-ribosome nuclear export at low temperature. Nature Communications, 2021, 12, 4696.	12.8	8
8	Maturation Kinetics of a Multiprotein Complex Revealed by Metabolic Labeling. Cell, 2020, 183, 1785-1800.e26.	28.9	34
9	The GTPase Nog1 co-ordinates the assembly, maturation and quality control of distant ribosomal functional centers. ELife, 2020, 9, .	6.0	36
10	USP16 counteracts mono-ubiquitination of RPS27a and promotes maturation of the 40S ribosomal subunit. ELife, 2020, 9, .	6.0	37
11	Highâ€throughput proteomic analysis of <scp>FFPE</scp> tissue samples facilitates tumor stratification. Molecular Oncology, 2019, 13, 2305-2328.	4.6	100
12	Sensitive Quantitative Proteomics of Human Hematopoietic Stem and Progenitor Cells by Data-independent Acquisition Mass Spectrometry. Molecular and Cellular Proteomics, 2019, 18, 1454-1467.	3.8	43
13	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. IScience, 2019, 21, 664-680.	4.1	52
14	Dataâ€independent acquisitionâ€based <scp>SWATH</scp> â€•<scp>MS</scp> for quantitative proteomics: a tutorial. Molecular Systems Biology, 2018, 14, e8126.	7.2	701
15	A better scoring model for de novo peptide sequencing: the symmetric difference between explained and measured masses. Algorithms for Molecular Biology, 2017, 12, 12.	1.2	4
16	Mass Spectrometry Applied to Bottom-Up Proteomics: Entering the High-Throughput Era for Hypothesis Testing. Annual Review of Analytical Chemistry, 2016, 9, 449-472.	5.4	266
17	A multicenter study benchmarks software tools for label-free proteome quantification. Nature Biotechnology, 2016, 34, 1130-1136.	17.5	321
18	TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics. Nature Methods, 2016, 13, 777-783.	19.0	173

#	Article	IF	Citations
19	Building high-quality assay libraries for targeted analysis of SWATH MS data. Nature Protocols, 2015, 10, 426-441.	12.0	319
20	Reproducible and Consistent Quantification of the Saccharomyces cerevisiae Proteome by SWATH-mass spectrometry *. Molecular and Cellular Proteomics, 2015, 14, 739-749.	3.8	158
21	Rapid mass spectrometric conversion of tissue biopsy samples into permanent quantitative digital proteome maps. Nature Medicine, 2015, 21, 407-413.	30.7	358
22	Absolute Proteome Composition and Dynamics during Dormancy and Resuscitation of Mycobacterium tuberculosis. Cell Host and Microbe, 2015, 18, 96-108.	11.0	229
23	An open-source computational and data resource to analyze digital maps of immunopeptidomes. ELife, 2015, 4, .	6.0	107
24	Phosphoproteomic analyses reveal novel cross€modulation mechanisms between two signaling pathways in yeast. Molecular Systems Biology, 2014, 10, 767.	7.2	58
25	Conserved Peptide Fragmentation as a Benchmarking Tool for Mass Spectrometers and a Discriminating Feature for Targeted Proteomics. Molecular and Cellular Proteomics, 2014, 13, 2056-2071.	3.8	96
26	OpenSWATH enables automated, targeted analysis of data-independent acquisition MS data. Nature Biotechnology, 2014, 32, 219-223.	17.5	692
27	Quantifying protein interaction dynamics by SWATH mass spectrometry: application to the 14-3-3 system. Nature Methods, 2013, 10, 1246-1253.	19.0	302
28	Targeted Data Extraction of the MS/MS Spectra Generated by Data-independent Acquisition: A New Concept for Consistent and Accurate Proteome Analysis. Molecular and Cellular Proteomics, 2012, 11, O111.016717.	3.8	2,285
29	Homologous Recombination Rescues Mismatch-Repair-Dependent Cytotoxicity of SN1-Type Methylating Agents in S. cerevisiae. Current Biology, 2005, 15, 1395-1400.	3.9	33