# Ludovic C Gillet

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2874489/publications.pdf

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|---|---|---|---|
| 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 | 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 |
| 2 | 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 |
| 3 | OpenSWATH enables automated, targeted analysis of data-independent acquisition MS data. Nature Biotechnology, 2014, 32, 219-223. | 17.5 | 692 |
| 4 | Rapid mass spectrometric conversion of tissue biopsy samples into permanent quantitative digital proteome maps. Nature Medicine, 2015, 21, 407-413. | 30.7 | 358 |
| 5 | A multicenter study benchmarks software tools for label-free proteome quantification. Nature Biotechnology, 2016, 34, 1130-1136. | 17.5 | 321 |
| 6 | Building high-quality assay libraries for targeted analysis of SWATH MS data. Nature Protocols, 2015, 10, 426-441. | 12.0 | 319 |
| 7 | Quantifying protein interaction dynamics by SWATH mass spectrometry: application to the 14-3-3 system. Nature Methods, 2013, 10, 1246-1253. | 19.0 | 302 |
| 8 | 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 |
| 9 | Absolute Proteome Composition and Dynamics during Dormancy and Resuscitation of Mycobacterium tuberculosis. Cell Host and Microbe, 2015, 18, 96-108. | 11.0 | 229 |
| 10 | TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics. Nature Methods, 2016, 13, 777-783. | 19.0 | 173 |
| 11 | Reproducible and Consistent Quantification of the Saccharomyces cerevisiae Proteome by SWATH-mass spectrometry *. Molecular and Cellular Proteomics, 2015, 14, 739-749. | 3.8 | 158 |
| 12 | An open-source computational and data resource to analyze digital maps of immunopeptidomes. ELife, 2015, 4, . | 6.0 | 107 |
| 13 | Highâ€throughput proteomic analysis of <scp>FFPE</scp> tissue samples facilitates tumor stratification. Molecular Oncology, 2019, 13, 2305-2328. | 4.6 | 100 |
| 14 | 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 |
| 15 | Dynamic 3D proteomes reveal protein functional alterations at high resolution in situ. Cell, 2021, 184, 545-559.e22. | 28.9 | 82 |
| 16 | Phosphoproteomic analyses reveal novel crossâ€modulation mechanisms between two signaling pathways in yeast. Molecular Systems Biology, 2014, 10, 767. | 7.2 | 58 |
| 17 | Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. IScience, 2019, 21, 664-680. | 4.1 | 52 |
| 18 | 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 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | USP16 counteracts mono-ubiquitination of RPS27a and promotes maturation of the 40S ribosomal subunit. ELife, 2020, 9, . | 6.0 | 37 |
| 20 | The GTPase Nog1 co-ordinates the assembly, maturation and quality control of distant ribosomal functional centers. ELife, 2020, 9, . | 6.0 | 36 |
| 21 | Maturation Kinetics of a Multiprotein Complex Revealed by Metabolic Labeling. Cell, 2020, 183, 1785-1800.e26. | 28.9 | 34 |
| 22 | Homologous Recombination Rescues Mismatch-Repair-Dependent Cytotoxicity of SN1-Type Methylating Agents in S. cerevisiae. Current Biology, 2005, 15, 1395-1400. | 3.9 | 33 |
| 23 | Combining CRISPRi and metabolomics for functional annotation of compound libraries. Nature Chemical Biology, 2022, 18, 482-491. | 8.0 | 33 |
| 24 | NÎ±-terminal acetylation of proteins by NatA and NatB serves distinct physiological roles in Saccharomyces cerevisiae. Cell Reports, 2021, 34, 108711. | 6.4 | 26 |
| 25 | 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 |
| 26 | The impact of genomic variation on protein phosphorylation states and regulatory networks. Molecular Systems Biology, 2022, 18, e10712. | 7.2 | 9 |
| 27 | 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 |
| 28 | Puf6 primes 60S pre-ribosome nuclear export at low temperature. Nature Communications, 2021, 12, 4696. | 12.8 | 8 |
| 29 | 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 |