

Jean-Philippe Lambert

List of Publications by Year in descending order

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84
papers

7,301
citations

136740

32
h-index

74018

75
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93
all docs

93
docs citations

93
times ranked

13274
citing authors

#	ARTICLE	IF	CITATIONS
1	A Nutrient-Based Cellular Model to Characterize Acetylation-Dependent Protein-Protein Interactions. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 831758.	1.6	2
2	New insights into the DNA repair pathway choice with NuA4/TIP60. <i>DNA Repair</i> , 2022, 113, 103315.	1.3	5
3	Comprehensive Interactome Mapping of Nuclear Receptors Using Proximity Biotinylation. <i>Methods in Molecular Biology</i> , 2022, , 223-240.	0.4	2
4	MRG Proteins Are Shared by Multiple Protein Complexes With Distinct Functions. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100253.	2.5	8
5	Recurrent chromosomal translocations in sarcomas create a megacomplex that mislocalizes NuA4/TIP60 to Polycomb target loci. <i>Genes and Development</i> , 2022, 36, 664-683.	2.7	8
6	EPH receptor tyrosine kinases phosphorylate the PAR-3 scaffold protein to modulate downstream signaling networks. <i>Cell Reports</i> , 2022, 40, 111031.	2.9	8
7	Functional proteomics protocol for the identification of interaction partners in <i>Tetrahymena thermophila</i> . <i>STAR Protocols</i> , 2021, 2, 100362.	0.5	3
8	Protein context shapes the specificity of SH3 domain-mediated interactions in vivo. <i>Nature Communications</i> , 2021, 12, 1597.	5.8	35
9	DEPTOR Tyrosine Phosphorylation: A Novel Molecular Switch Involved in mTOR Activity. <i>FASEB Journal</i> , 2021, 35, .	0.2	0
10	Functional characterization of RebL1 highlights the evolutionary conservation of oncogenic activities of the RBBP4/7 orthologue in <i>Tetrahymena thermophila</i> . <i>Nucleic Acids Research</i> , 2021, 49, 6196-6212.	6.5	14
11	A proximity-dependent biotinylation map of a human cell. <i>Nature</i> , 2021, 595, 120-124.	13.7	263
12	Tyrosine phosphorylation of DEPTOR functions as a molecular switch to activate mTOR signaling. <i>Journal of Biological Chemistry</i> , 2021, 297, 101291.	1.6	8
13	Editorial: The Evolving Chromatin and Transcriptional Landscapes—Emerging Methods, Tools and Techniques. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 782776.	1.8	0
14	TBX2 controls a proliferative gene expression program in melanoma. <i>Genes and Development</i> , 2021, 35, 1657-1677.	2.7	7
15	Emerging tools to investigate bromodomain functions. <i>Methods</i> , 2020, 184, 40-52.	1.9	7
16	IRX3/5 regulate mitotic chromatid segregation and limb bud shape. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	4
17	Tuning Transcription Factor Availability through Acetylation-Mediated Genomic Redistribution. <i>Molecular Cell</i> , 2020, 79, 472-487.e10.	4.5	38
18	Machine learning analysis identifies genes differentiating triple negative breast cancers. <i>Scientific Reports</i> , 2020, 10, 10464.	1.6	25

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19	JMJD6 participates in the maintenance of ribosomal DNA integrity in response to DNA damage. <i>PLoS Genetics</i> , 2020, 16, e1008511.	1.5	13
20	Design and synthesis of dansyl-labeled inhibitors of steroid sulfatase for optical imaging. <i>Bioorganic and Medicinal Chemistry</i> , 2020, 28, 115368.	1.4	9
21	Nucleus-specific linker histones Hho1 and Mlh1 form distinct protein interactions during growth, starvation and development in <i>Tetrahymena thermophila</i> . <i>Scientific Reports</i> , 2020, 10, 168.	1.6	10
22	JMJD6 participates in the maintenance of ribosomal DNA integrity in response to DNA damage. , 2020, 16, e1008511.		0
23	JMJD6 participates in the maintenance of ribosomal DNA integrity in response to DNA damage. , 2020, 16, e1008511.		0
24	JMJD6 participates in the maintenance of ribosomal DNA integrity in response to DNA damage. , 2020, 16, e1008511.		0
25	JMJD6 participates in the maintenance of ribosomal DNA integrity in response to DNA damage. , 2020, 16, e1008511.		0
26	JMJD6 participates in the maintenance of ribosomal DNA integrity in response to DNA damage. , 2020, 16, e1008511.		0
27	JMJD6 participates in the maintenance of ribosomal DNA integrity in response to DNA damage. , 2020, 16, e1008511.		0
28	The Med31 Conserved Component of the Divergent Mediator Complex in <i>Tetrahymena thermophila</i> Participates in Developmental Regulation. <i>Current Biology</i> , 2019, 29, 2371-2379.e6.	1.8	13
29	Proteomics contribution to the elucidation of the steroid hormone receptors functions. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2019, 192, 105387.	1.2	3
30	Functional Proteomics of Nuclear Proteins in <i>Tetrahymena thermophila</i> : A Review. <i>Genes</i> , 2019, 10, 333.	1.0	11
31	Measurement and Analysis of Lysine Acetylation by KAT Complexes In Vitro and In Vivo. <i>Methods in Molecular Biology</i> , 2019, 1983, 57-77.	0.4	2
32	Proteomic Analysis of Histones H2A/H2B and Variant Hv1 in <i>Tetrahymena thermophila</i> Reveals an Ancient Network of Chaperones. <i>Molecular Biology and Evolution</i> , 2019, 36, 1037-1055.	3.5	12
33	BRN2 suppresses apoptosis, reprograms DNA damage repair, and is associated with a high somatic mutation burden in melanoma. <i>Genes and Development</i> , 2019, 33, 310-332.	2.7	35
34	Interactome Rewiring Following Pharmacological Targeting of BET Bromodomains. <i>Molecular Cell</i> , 2019, 73, 621-638.e17.	4.5	135
35	Targeted proteomics analyses of phosphorylation-dependent signalling networks. <i>Journal of Proteomics</i> , 2018, 189, 39-47.	1.2	9
36	The bromodomain-containing protein Ibd1 links multiple chromatin-related protein complexes to highly expressed genes in <i>Tetrahymena thermophila</i> . <i>Epigenetics and Chromatin</i> , 2018, 11, 10.	1.8	16

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37	Acetylation of PCNA Sliding Surface by Eco1 Promotes Genome Stability through Homologous Recombination. <i>Molecular Cell</i> , 2017, 65, 78-90.	4.5	38
38	Selective Targeting of Bromodomains of the Bromodomain-PHD Fingers Family Impairs Osteoclast Differentiation. <i>ACS Chemical Biology</i> , 2017, 12, 2619-2630.	1.6	41
39	Proteomic analysis of the human KEOPS complex identifies C14ORF142 as a core subunit homologous to yeast Gon7. <i>Nucleic Acids Research</i> , 2017, 45, 805-817.	6.5	49
40	Ydj1 governs fungal morphogenesis and stress response, and facilitates mitochondrial protein import via Mas1 and Mas2. <i>Microbial Cell</i> , 2017, 4, 342-361.	1.4	33
41	AIRE is a critical spindle-associated protein in embryonic stem cells. <i>ELife</i> , 2017, 6, .	2.8	19
42	SAINTq: Scoring protein-protein interactions in affinity purification mass spectrometry experiments with fragment or peptide intensity data. <i>Proteomics</i> , 2016, 16, 2238-2245.	1.3	45
43	Multivalent Histone and DNA Engagement by a PHD/BRD/PWWP Triple Reader Cassette Recruits ZMYND8 to K14ac-Rich Chromatin. <i>Cell Reports</i> , 2016, 17, 2724-2737.	2.9	86
44	BRPF3 and HBO1 regulates replication origin activation and histone H3K14 acetylation. <i>EMBO Journal</i> , 2016, 35, 176-192.	3.5	97
45	Data Independent Acquisition analysis in ProHits 4.0. <i>Journal of Proteomics</i> , 2016, 149, 64-68.	1.2	66
46	The TIP60 Complex Regulates Bivalent Chromatin Recognition by 53BP1 through Direct H4K20me Binding and H2AK15 Acetylation. <i>Molecular Cell</i> , 2016, 62, 409-421.	4.5	198
47	Dual action antifungal small molecule modulates multidrug efflux and TOR signaling. <i>Nature Chemical Biology</i> , 2016, 12, 867-875.	3.9	79
48	Promiscuous targeting of bromodomains by bromosporine identifies BET proteins as master regulators of primary transcription response in leukemia. <i>Science Advances</i> , 2016, 2, e1600760.	4.7	90
49	MSPLIT-DIA: sensitive peptide identification for data-independent acquisition. <i>Nature Methods</i> , 2015, 12, 1106-1108.	9.0	113
50	Proximity biotinylation and affinity purification are complementary approaches for the interactome mapping of chromatin-associated protein complexes. <i>Journal of Proteomics</i> , 2015, 118, 81-94.	1.2	234
51	Abstract IA19: Regulation of signaling interactomes in cancer., 2015, .		0
52	(R)-PFI-2 is a potent and selective inhibitor of SETD7 methyltransferase activity in cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12853-12858.	3.3	158
53	Incorporating DNA shearing in standard affinity purification allows simultaneous identification of both soluble and chromatin-bound interaction partners. <i>Journal of Proteomics</i> , 2014, 100, 55-59.	1.2	28
54	Cell cycle-regulated oscillator coordinates core histone gene transcription through histone acetylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14124-14129.	3.3	32

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55	Assessing cellular efficacy of bromodomain inhibitors using fluorescence recovery after photobleaching. <i>Epigenetics and Chromatin</i> , 2014, 7, 14.	1.8	69
56	The CRAPome: a contaminant repository for affinity purification mass spectrometry data. <i>Nature Methods</i> , 2013, 10, 730-736.	9.0	1,353
57	Mapping differential interactomes by affinity purification coupled with data-independent mass spectrometry acquisition. <i>Nature Methods</i> , 2013, 10, 1239-1245.	9.0	277
58	Myosin Phosphatase Modulates the Cardiac Cell Fate by Regulating the Subcellular Localization of Nkx2.5 in a Wnt/Rho-Associated Protein Kinase-Dependent Pathway. <i>Circulation Research</i> , 2013, 112, 257-266.	2.0	13
59	Conserved Asf1-importin β^2 physical interaction in growth and sexual development in the ciliate <i>Tetrahymena thermophila</i> . <i>Journal of Proteomics</i> , 2013, 94, 311-326.	1.2	20
60	mChIP-KAT-MS, a method to map protein interactions and acetylation sites for lysine acetyltransferases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1641-50.	3.3	38
61	Lnk adaptor suppresses radiation resistance and radiation-induced B-cell malignancies by inhibiting IL-11 signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20599-20604.	3.3	15
62	Histone Recognition and Large-Scale Structural Analysis of the Human Bromodomain Family. <i>Cell</i> , 2012, 149, 214-231.	13.5	1,368
63	Exploring the Yeast Acetylome Using Functional Genomics. <i>Cell</i> , 2012, 149, 936-948.	13.5	63
64	Using ProHits to Store, Annotate, and Analyze Affinity Purification Mass Spectrometry (AP-MS) Data. <i>Current Protocols in Bioinformatics</i> , 2012, 39, Unit8.16.	25.8	19
65	Mapping physical interactions within chromatin by proteomic approaches. <i>Proteomics</i> , 2012, 12, 1609-1622.	1.3	16
66	Development of a Multiplexed Microfluidic Proteomic Reactor and Its Application for Studying Protein-Protein Interactions. <i>Analytical Chemistry</i> , 2011, 83, 4095-4102.	3.2	34
67	Regulation of Septin Dynamics by the <i>Saccharomyces cerevisiae</i> Lysine Acetyltransferase NuA4. <i>PLoS ONE</i> , 2011, 6, e25336.	1.1	33
68	Restriction of histone gene transcription to S phase by phosphorylation of a chromatin boundary protein. <i>Genes and Development</i> , 2011, 25, 2489-2501.	2.7	40
69	Srf1 Is a Novel Regulator of Phospholipase D Activity and Is Essential to Buffer the Toxic Effects of C16:0 Platelet Activating Factor. <i>PLoS Genetics</i> , 2011, 7, e1001299.	1.5	12
70	New ammunition for the proteomic reactor: strong anion exchange beads and multiple enzymes enhance protein identification and sequence coverage. <i>Analytical and Bioanalytical Chemistry</i> , 2010, 397, 3421-3430.	1.9	10
71	Defining the budding yeast chromatin-associated interactome. <i>Molecular Systems Biology</i> , 2010, 6, 448.	3.2	58
72	Analysis of low-abundance proteins using the proteomic reactor with pH fractionation. <i>Talanta</i> , 2010, 80, 1526-1531.	2.9	16

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73	Of proteins and DNA's proteomic role in the field of chromatin research. <i>Molecular BioSystems</i> , 2010, 6, 30-37.	2.9	4
74	A Novel Proteomics Approach for the Discovery of Chromatin-associated Protein Networks. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 870-882.	2.5	95
75	Two-Color Cell Array Screen Reveals Interdependent Roles for Histone Chaperones and a Chromatin Boundary Regulator in Histone Gene Repression. <i>Molecular Cell</i> , 2009, 35, 340-351.	4.5	88
76	Functional Dissection of the NuA4 Histone Acetyltransferase Reveals Its Role as a Genetic Hub and that Eaf1 Is Essential for Complex Integrity. <i>Molecular and Cellular Biology</i> , 2008, 28, 2244-2256.	1.1	101
77	The Tale of Two Domains. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 560-572.	2.5	168
78	Large-scale mapping of human protein-protein interactions by mass spectrometry. <i>Molecular Systems Biology</i> , 2007, 3, 89.	3.2	850
79	Proteomics in 2005/2006: Developments, Applications and Challenges. <i>Analytical Chemistry</i> , 2007, 79, 4325-4344.	3.2	57
80	Tryptic digestion of ubiquitin standards reveals an improved strategy for identifying ubiquitinated proteins by mass spectrometry. <i>Proteomics</i> , 2007, 7, 868-874.	1.3	76
81	Analysis of protein interaction networks using mass spectrometry compatible techniques. <i>Analytica Chimica Acta</i> , 2006, 564, 10-18.	2.6	17
82	Stir bar sorptive extraction based on restricted access material for the direct extraction of caffeine and metabolites in biological fluids. <i>Journal of Chromatography A</i> , 2005, 1075, 43-49.	1.8	119
83	Proteomics: from Gel Based to Gel Free. <i>Analytical Chemistry</i> , 2005, 77, 3771-3788.	3.2	104
84	EPH Receptor Tyrosine Kinases Regulate Epithelial Morphogenesis and Phosphorylate the PAR-3 Scaffold Protein to Modulate Downstream Signaling Networks. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0