

Simone Sidoli

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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.

132
papers

3,636
citations

35
h-index

55
g-index

163
ext. papers

4,967
ext. citations

9.8
avg, IF

5.64
L-index

#	Paper	IF	Citations
132	Two distinct modes for propagation of histone PTMs across the cell cycle. <i>Genes and Development</i> , 2015 , 29, 585-90	12.6	226
131	Transcription factor cooperativity in early adipogenic hotspots and super-enhancers. <i>Cell Reports</i> , 2014 , 7, 1443-1455	10.6	163
130	High-Resolution Mapping of RNA-Binding Regions in the Nuclear Proteome of Embryonic Stem Cells. <i>Molecular Cell</i> , 2016 , 64, 416-430	17.6	161
129	Proteomics in chromatin biology and epigenetics: Elucidation of post-translational modifications of histone proteins by mass spectrometry. <i>Journal of Proteomics</i> , 2012 , 75, 3419-33	3.9	105
128	Genomic and Proteomic Resolution of Heterochromatin and Its Restriction of Alternate Fate Genes. <i>Molecular Cell</i> , 2017 , 68, 1023-1037.e15	17.6	99
127	Characterization of histone acylations links chromatin modifications with metabolism. <i>Nature Communications</i> , 2017 , 8, 1141	17.4	95
126	Complete Workflow for Analysis of Histone Post-translational Modifications Using Bottom-up Mass Spectrometry: From Histone Extraction to Data Analysis. <i>Journal of Visualized Experiments</i> , 2016 ,	1.6	90
125	Acetyl-CoA Metabolism Supports Multistep Pancreatic Tumorigenesis. <i>Cancer Discovery</i> , 2019 , 9, 416-435	4.4	88
124	Alcohol metabolism contributes to brain histone acetylation. <i>Nature</i> , 2019 , 574, 717-721	50.4	86
123	Domain-focused CRISPR screen identifies HRI as a fetal hemoglobin regulator in human erythroid cells. <i>Science</i> , 2018 , 361, 285-290	33.3	82
122	H3K9me3-heterochromatin loss at protein-coding genes enables developmental lineage specification. <i>Science</i> , 2019 , 363, 294-297	33.3	82
121	Sequential Window Acquisition of all Theoretical Mass Spectra (SWATH) Analysis for Characterization and Quantification of Histone Post-translational Modifications. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2420-8	7.6	76
120	EpiProfile Quantifies Histone Peptides With Modifications by Extracting Retention Time and Intensity in High-resolution Mass Spectra. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 1696-707	7.6	69
119	Loss of HP1 causes depletion of H3K27me3 from facultative heterochromatin and gain of H3K27me2 at constitutive heterochromatin. <i>Genome Research</i> , 2016 , 26, 97-107	9.7	68
118	Middle-down hybrid chromatography/tandem mass spectrometry workflow for characterization of combinatorial post-translational modifications in histones. <i>Proteomics</i> , 2014 , 14, 2200-11	4.8	68
117	Quantitative proteomics analysis of platelet-derived microparticles reveals distinct protein signatures when stimulated by different physiological agonists. <i>Journal of Proteomics</i> , 2015 , 121, 56-66	3.9	60
116	Precision mapping of coexisting modifications in histone H3 tails from embryonic stem cells by ETD-MS/MS. <i>Analytical Chemistry</i> , 2013 , 85, 8232-9	7.8	60

115	The PZP Domain of AF10 Senses Unmodified H3K27 to Regulate DOT1L-Mediated Methylation of H3K79. <i>Molecular Cell</i> , 2015 , 60, 319-27	17.6	57
114	Large scale analysis of co-existing post-translational modifications in histone tails reveals global fine structure of cross-talk. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1855-65	7.6	56
113	Histone Acetyltransferase p300 Induces De Novo Super-Enhancers to Drive Cellular Senescence. <i>Molecular Cell</i> , 2019 , 73, 684-698.e8	17.6	55
112	Systems Level Analysis of Histone H3 Post-translational Modifications (PTMs) Reveals Features of PTM Crosstalk in Chromatin Regulation. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 2715-29	7.6	53
111	Middle-down proteomics: a still unexploited resource for chromatin biology. <i>Expert Review of Proteomics</i> , 2017 , 14, 617-626	4.2	53
110	An integrated multi-omics approach identifies epigenetic alterations associated with Alzheimer's disease. <i>Nature Genetics</i> , 2020 , 52, 1024-1035	36.3	53
109	EpiProfile 2.0: A Computational Platform for Processing Epi-Proteomics Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2018 , 17, 2533-2541	5.6	51
108	Time-resolved Global and Chromatin Proteomics during Herpes Simplex Virus Type 1 (HSV-1) Infection. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, S92-S107	7.6	50
107	The C. elegans H3K27 demethylase UTX-1 is essential for normal development, independent of its enzymatic activity. <i>PLoS Genetics</i> , 2012 , 8, e1002647	6	50
106	Defining heterochromatin in C. elegans through genome-wide analysis of the heterochromatin protein 1 homolog HPL-2. <i>Genome Research</i> , 2015 , 25, 76-88	9.7	48
105	Low Resolution Data-Independent Acquisition in an LTQ-Orbitrap Allows for Simplified and Fully Untargeted Analysis of Histone Modifications. <i>Analytical Chemistry</i> , 2015 , 87, 11448-54	7.8	43
104	Progress in epigenetic histone modification analysis by mass spectrometry for clinical investigations. <i>Expert Review of Proteomics</i> , 2015 , 12, 499-517	4.2	42
103	Bottom-up and middle-down proteomics have comparable accuracies in defining histone post-translational modification relative abundance and stoichiometry. <i>Analytical Chemistry</i> , 2015 , 87, 3129-33	7.8	41
102	Top-down and Middle-down Protein Analysis Reveals that Intact and Clipped Human Histones Differ in Post-translational Modification Patterns. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 3142-53	7.6	41
101	H1 histones control the epigenetic landscape by local chromatin compaction. <i>Nature</i> , 2021 , 589, 293-298	50.4	40
100	Roles of H3K27me2 and H3K27me3 Examined during Fate Specification of Embryonic Stem Cells. <i>Cell Reports</i> , 2016 , 17, 1369-1382	10.6	39
99	Analyses of Histone Proteoforms Using Front-end Electron Transfer Dissociation-enabled Orbitrap Instruments. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 975-88	7.6	37
98	Recent Achievements in Characterizing the Histone Code and Approaches to Integrating Epigenomics and Systems Biology. <i>Methods in Enzymology</i> , 2017 , 586, 359-378	1.7	36

97	Paternal cocaine taking elicits epigenetic remodeling and memory deficits in male progeny. <i>Molecular Psychiatry</i> , 2017 , 22, 1641-1650	15.1	35
96	Quantitative chromatin proteomics reveals a dynamic histone post-translational modification landscape that defines asexual and sexual <i>Plasmodium falciparum</i> parasites. <i>Scientific Reports</i> , 2017 , 7, 607	4.9	34
95	Histone H4 acetylation and the epigenetic reader Brd4 are critical regulators of pluripotency in embryonic stem cells. <i>BMC Genomics</i> , 2016 , 17, 95	4.5	34
94	Proteome-wide acetylation dynamics in human cells. <i>Scientific Reports</i> , 2017 , 7, 10296	4.9	34
93	An HDAC3-PROX1 corepressor module acts on HNF4 α to control hepatic triglycerides. <i>Nature Communications</i> , 2017 , 8, 549	17.4	32
92	Phosphoproteomics reveals that glycogen synthase kinase-3 phosphorylates multiple splicing factors and is associated with alternative splicing. <i>Journal of Biological Chemistry</i> , 2017 , 292, 18240-18254	5.4	32
91	Characterization of Individual Histone Posttranslational Modifications and Their Combinatorial Patterns by Mass Spectrometry-Based Proteomics Strategies. <i>Methods in Molecular Biology</i> , 2017 , 1528, 121-148	1.4	31
90	Drawbacks in the use of unconventional hydrophobic anhydrides for histone derivatization in bottom-up proteomics PTM analysis. <i>Proteomics</i> , 2015 , 15, 1459-69	4.8	30
89	The Tumor Suppressor CIC Directly Regulates MAPK Pathway Genes via Histone Deacetylation. <i>Cancer Research</i> , 2018 , 78, 4114-4125	10.1	30
88	A Rapid Size-Exclusion Solid-Phase Extraction Step for Enhanced Sensitivity in Multi-Allergen Determination in Dark Chocolate and Biscuits by Liquid Chromatography Tandem Mass Spectrometry. <i>Food Analytical Methods</i> , 2013 , 6, 1144-1152	3.4	29
87	H3K23me2 is a new heterochromatic mark in <i>Caenorhabditis elegans</i> . <i>Nucleic Acids Research</i> , 2015 , 43, 9694-710	20.1	28
86	Tumor suppressor ASXL1 is essential for the activation of INK4B expression in response to oncogene activity and anti-proliferative signals. <i>Cell Research</i> , 2015 , 25, 1205-18	24.7	28
85	Identification of Nidogen 1 as a lung metastasis protein through secretome analysis. <i>Genes and Development</i> , 2017 , 31, 1439-1455	12.6	28
84	Metabolic labeling in middle-down proteomics allows for investigation of the dynamics of the histone code. <i>Epigenetics and Chromatin</i> , 2017 , 10, 34	5.8	25
83	Histone modification profiling reveals differential signatures associated with human embryonic stem cell self-renewal and differentiation. <i>Proteomics</i> , 2016 , 16, 448-58	4.8	25
82	One minute analysis of 200 histone posttranslational modifications by direct injection mass spectrometry. <i>Genome Research</i> , 2019 , 29, 978-987	9.7	24
81	Identification and Quantification of Histone PTMs Using High-Resolution Mass Spectrometry. <i>Methods in Enzymology</i> , 2016 , 574, 3-29	1.7	24
80	Epigenomic Reordering Induced by Polycomb Loss Drives Oncogenesis but Leads to Therapeutic Vulnerabilities in Malignant Peripheral Nerve Sheath Tumors. <i>Cancer Research</i> , 2019 , 79, 3205-3219	10.1	23

79	Interrogating Histone Acetylation and BRD4 as Mitotic Bookmarks of Transcription. <i>Cell Reports</i> , 2019 , 27, 400-415.e5	10.6	22
78	A mass spectrometry-based assay using metabolic labeling to rapidly monitor chromatin accessibility of modified histone proteins. <i>Scientific Reports</i> , 2019 , 9, 13613	4.9	21
77	Multicellular Tumor Spheroids Combined with Mass Spectrometric Histone Analysis To Evaluate Epigenetic Drugs. <i>Analytical Chemistry</i> , 2017 , 89, 2773-2781	7.8	20
76	Why proteomics is not the new genomics and the future of mass spectrometry in cell biology. <i>Journal of Cell Biology</i> , 2017 , 216, 21-24	7.3	19
75	Single Cell Proteomics by Data-Independent Acquisition To Study Embryonic Asymmetry in. <i>Analytical Chemistry</i> , 2019 , 91, 8891-8899	7.8	19
74	Histone H3K23-specific acetylation by MORF is coupled to H3K14 acylation. <i>Nature Communications</i> , 2019 , 10, 4724	17.4	18
73	QSER1 protects DNA methylation valleys from de novo methylation. <i>Science</i> , 2021 , 372,	33.3	18
72	Multiplexed data independent acquisition (MSX-DIA) applied by high resolution mass spectrometry improves quantification quality for the analysis of histone peptides. <i>Proteomics</i> , 2016 , 16, 2095-105	4.8	18
71	Integrated Analysis of Acetyl-CoA and Histone Modification via Mass Spectrometry to Investigate Metabolically Driven Acetylation. <i>Methods in Molecular Biology</i> , 2019 , 1928, 125-147	1.4	17
70	Lysine 4 of histone H3.3 is required for embryonic stem cell differentiation, histone enrichment at regulatory regions and transcription accuracy. <i>Nature Genetics</i> , 2020 , 52, 273-282	36.3	16
69	Extensive Characterization of Heavily Modified Histone Tails by 193 nm Ultraviolet Photodissociation Mass Spectrometry via a Middle-Down Strategy. <i>Analytical Chemistry</i> , 2018 , 90, 10425-10433 ¹⁶	7.8	16
68	Distinct Roles of Two Histone Methyltransferases in Transmitting H3K36me3-Based Epigenetic Memory Across Generations in. <i>Genetics</i> , 2018 , 210, 969-982	4	16
67	Integrating Proteomics and Targeted Metabolomics to Understand Global Changes in Histone Modifications. <i>Proteomics</i> , 2018 , 18, e1700309	4.8	15
66	PR-DUB maintains the expression of critical genes through FOXK1/2- and ASXL1/2/3-dependent recruitment to chromatin and H2AK119ub1 deubiquitination. <i>Genome Research</i> , 2020 , 30, 1119-1130	9.7	15
65	Long-term behavioral and cell-type-specific molecular effects of early life stress are mediated by H3K79me2 dynamics in medium spiny neurons. <i>Nature Neuroscience</i> , 2021 , 24, 667-676	25.5	15
64	Abnormal levels of histone methylation in the retinas of diabetic rats are reversed by minocycline treatment. <i>Scientific Reports</i> , 2017 , 7, 45103	4.9	14
63	Comparative proteomic analysis of histone post-translational modifications upon ischemia/reperfusion-induced retinal injury. <i>Journal of Proteome Research</i> , 2014 , 13, 2175-86	5.6	14
62	nuclear RNAi factor SET-32 deposits the transgenerational histone modification, H3K23me3. <i>ELife</i> , 2020 , 9,	8.9	14

61	Impaired cocaine-induced behavioral plasticity in the male offspring of cocaine-experienced sires. <i>European Journal of Neuroscience</i> , 2019 , 49, 1115-1126	3.5	14
60	Coordination between TGF- β cellular signaling and epigenetic regulation during epithelial to mesenchymal transition. <i>Epigenetics and Chromatin</i> , 2019 , 12, 11	5.8	13
59	Dynamic changes of histone H3 marks during <i>Caenorhabditis elegans</i> lifecycle revealed by middle-down proteomics. <i>Proteomics</i> , 2016 , 16, 459-64	4.8	13
58	Graphical Interpretation and Analysis of Proteins and their Ontologies (GiaPronto): A One-Click Graph Visualization Software for Proteomics Data Sets. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 1426-1431 ¹³	7.6	13
57	Mutant FOXL2 Hijacks SMAD4 and SMAD2/3 to Drive Adult Granulosa Cell Tumors. <i>Cancer Research</i> , 2020 , 80, 3466-3479	10.1	12
56	Quantitation of Single and Combinatorial Histone Modifications by Integrated Chromatography of Bottom-up Peptides and Middle-down Polypeptide Tails. <i>Journal of the American Society for Mass Spectrometry</i> , 2019 , 30, 2449-2459	3.5	11
55	Properly reading the histone code by MS-based proteomics. <i>Proteomics</i> , 2015 , 15, 2901-2	4.8	11
54	Deep profiling and custom databases improve detection of proteoforms generated by alternative splicing. <i>Genome Research</i> , 2019 , 29, 2046-2055	9.7	11
53	Protein Kinase C Epsilon Is a Key Regulator of Mitochondrial Redox Homeostasis in Acute Myeloid Leukemia. <i>Clinical Cancer Research</i> , 2018 , 24, 608-618	12.9	10
52	Analysis of the Effect of Intestinal Ischemia and Reperfusion on the Rat Neutrophils Proteome. <i>Frontiers in Molecular Biosciences</i> , 2018 , 5, 89	5.6	9
51	Proteogenomics analysis reveals specific genomic orientations of distal regulatory regions composed by non-canonical histone variants. <i>Epigenetics and Chromatin</i> , 2015 , 8, 13	5.8	8
50	Disruption of ATRX-RNA interactions uncovers roles in ATRX localization and PRC2 function. <i>Nature Communications</i> , 2020 , 11, 2219	17.4	8
49	Guide for protein fold change and p-value calculation for non-experts in proteomics. <i>Molecular Omics</i> , 2020 , 16, 573-582	4.4	8
48	Protective neutralizing antibodies from human survivors of Crimean-Congo hemorrhagic fever. <i>Cell</i> , 2021 , 184, 3486-3501.e21	56.2	8
47	One-shot analysis of translated mammalian lncRNAs with AHARIBO. <i>ELife</i> , 2021 , 10,	8.9	8
46	Neutrophil proteomic analysis reveals the participation of antioxidant enzymes, motility and ribosomal proteins in the prevention of ischemic effects by preconditioning. <i>Journal of Proteomics</i> , 2017 , 151, 162-173	3.9	7
45	Bullet points to evaluate the performance of the middle-down proteomics workflow for histone modification analysis. <i>Methods</i> , 2020 , 184, 86-92	4.6	7
44	Differential quantification of isobaric phosphopeptides using data-independent acquisition mass spectrometry. <i>Molecular BioSystems</i> , 2016 , 12, 2385-8		7

43	Nuclear phosphoproteome analysis of 3T3-L1 preadipocyte differentiation reveals system-wide phosphorylation of transcriptional regulators. <i>Proteomics</i> , 2017 , 17, 1600248	4.8	7
42	Assessment of Quantification Precision of Histone Post-Translational Modifications by Using an Ion Trap and down To 50 000 Cells as Starting Material. <i>Journal of Proteome Research</i> , 2018 , 17, 234-242	5.6	7
41	High performance mass spectrometry based proteomics reveals enzyme and signaling pathway regulation in neutrophils during the early stage of surgical trauma. <i>Proteomics - Clinical Applications</i> , 2017 , 11, 1600001	3.1	6
40	Toxoplasma gondii PPM3C, a secreted protein phosphatase, affects parasitophorous vacuole effector export. <i>PLoS Pathogens</i> , 2020 , 16, e1008771	7.6	6
39	VAL genes regulate vegetative phase change via miR156-dependent and independent mechanisms. <i>PLoS Genetics</i> , 2021 , 17, e1009626	6	6
38	Regulation of proline-directed kinases and the trans-histone code H3K9me3/H4K20me3 during human myogenesis. <i>Journal of Biological Chemistry</i> , 2019 , 294, 8296-8308	5.4	5
37	Isotopic Labeling and Quantitative Proteomics of Acetylation on Histones and Beyond. <i>Methods in Molecular Biology</i> , 2019 , 1977, 43-70	1.4	5
36	Type I and II PRMTs inversely regulate post-transcriptional intron retention through Sm and CHTOP methylation.. <i>ELife</i> , 2022 , 11,	8.9	5
35	Quantitative subcellular acyl-CoA analysis reveals distinct nuclear metabolism and isoleucine-dependent histone propionylation. <i>Molecular Cell</i> , 2021 ,	17.6	4
34	High throughput and low bias DNA methylation and hydroxymethylation analysis by direct injection mass spectrometry. <i>Analytica Chimica Acta</i> , 2021 , 1180, 338880	6.6	4
33	Comprehensive Map of the Artemisia annua Proteome and Quantification of Differential Protein Expression in Chemotypes Producing High versus Low Content of Artemisinin. <i>Proteomics</i> , 2020 , 20, e1900310	4.8	3
32	Enzymatic transfer of acetate on histones from lysine reservoir sites to lysine activating sites.. <i>Science Advances</i> , 2022 , 8, eabj5688	14.3	3
31	Genotype-specific features reduce the susceptibility of South American yellow fever virus strains to vaccine-induced antibodies.. <i>Cell Host and Microbe</i> , 2022 ,	23.4	3
30	Mass Spectrometry to Study Chromatin Compaction. <i>Biology</i> , 2020 , 9,	4.9	2
29	KYSS: mass spectrometry data quality assessment for protein analysis and large-scale proteomics. <i>Biochemical and Biophysical Research Communications</i> , 2014 , 445, 702-7	3.4	2
28	A Workflow for Ultra-rapid Analysis of Histone Post-translational Modifications with Direct-injection Mass Spectrometry. <i>Bio-protocol</i> , 2020 , 10, e3756	0.9	2
27	Transcriptomic and proteomic regulation through abundant, dynamic, and independent arginine methylation by Type I and Type II PRMTs		2
26	PAX8 orchestrates an angiogenic program through interaction with SOX17		2

25	Phosphoproteomic Analysis of Rat Neutrophils Shows the Effect of Intestinal Ischemia/Reperfusion and Preconditioning on Kinases and Phosphatases. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	2
24	Combinatorial Histone H3 Modifications Are Dynamically Altered in Distinct Cell Cycle Phases. <i>Journal of the American Society for Mass Spectrometry</i> , 2021 , 32, 1300-1311	3.5	2
23	White adipose remodeling during browning in mice involves YBX1 to drive thermogenic commitment. <i>Molecular Metabolism</i> , 2021 , 44, 101137	8.8	2
22	A Key Silencing Histone Mark on Chromatin Is Lost When Colorectal Adenocarcinoma Cells Are Depleted of Methionine by Methionine Methyltransferase. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 735303	5.6	2
21	Sample Preparation for Mass Spectrometry-based Identification of RNA-binding Regions. <i>Journal of Visualized Experiments</i> , 2017 ,	1.6	1
20	Optimization of calmodulin-affinity chromatography for brain and organelles. <i>EuPA Open Proteomics</i> , 2015 , 8, 55-67	0.1	1
19	Middle-Down MS is Ready to Answer Complex Questions in Chromatin Biology. <i>Proteomics</i> , 2018 , 18, e1800131	4.8	1
18	Application of Mass Spectrometry in Translational Epigenetics 2015 , 55-78		1
17	A dynamic and combinatorial histone code drives malaria parasite asexual and sexual development.. <i>Molecular and Cellular Proteomics</i> , 2022 , 100199	7.6	1
16	DNA methylation and hydroxymethylation analysis using a high throughput and low bias direct injection mass spectrometry platform.. <i>MethodsX</i> , 2021 , 8, 101585	1.9	1
15	Cytoplasmic Labile Iron Accumulates in Aging Stem Cells Perturbing a Key Rheostat for Identity Control. <i>Blood</i> , 2021 , 138, 3282-3282	2.2	1
14	Quantitative sub-cellular acyl-CoA analysis reveals distinct nuclear regulation		1
13	The Polycomb protein RING1B enables estrogen-mediated gene expression by promoting enhancer-promoter interaction and R-loop formation. <i>Nucleic Acids Research</i> , 2021 , 49, 9768-9782	20.1	1
12	Independent transcriptomic and proteomic regulation by type I and II protein arginine methyltransferases. <i>iScience</i> , 2021 , 24, 102971	6.1	1
11	The transcription factor PAX8 promotes angiogenesis in ovarian cancer through interaction with SOX17.. <i>Science Signaling</i> , 2022 , 15, eabm2496	8.8	0
10	Altered abundances of human immunoglobulin M and immunoglobulin G subclasses in Alzheimer's disease frontal cortex.. <i>Scientific Reports</i> , 2022 , 12, 6934	4.9	0
9	Methamphetamine Dysregulates Macrophage Functions and Autophagy to Mediate HIV Neuropathogenesis. <i>Biomedicines</i> , 2022 , 10, 1257	4.8	0
8	FLT3 Inhibition Downregulates EZH2 in AML and Promotes Myeloid Differentiation. <i>Blood</i> , 2021 , 138, 785-785	2.2	

- 7 FGF-2 induces a failure of cell cycle progression in cells harboring amplified K-Ras, revealing new insights into oncogene-induced senescence. *Molecular Omics*, **2021**, 17, 725-739 4-4
- 6 *Toxoplasma gondii* PPM3C, a secreted protein phosphatase, affects parasitophorous vacuole effector export **2020**, 16, e1008771
- 5 *Toxoplasma gondii* PPM3C, a secreted protein phosphatase, affects parasitophorous vacuole effector export **2020**, 16, e1008771
- 4 *Toxoplasma gondii* PPM3C, a secreted protein phosphatase, affects parasitophorous vacuole effector export **2020**, 16, e1008771
- 3 *Toxoplasma gondii* PPM3C, a secreted protein phosphatase, affects parasitophorous vacuole effector export **2020**, 16, e1008771
- 2 *Toxoplasma gondii* PPM3C, a secreted protein phosphatase, affects parasitophorous vacuole effector export **2020**, 16, e1008771
- 1 *Toxoplasma gondii* PPM3C, a secreted protein phosphatase, affects parasitophorous vacuole effector export **2020**, 16, e1008771