

Michele Tinti

List of Publications by Year in descending order

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29
papers

1,112
citations

623734

14
h-index

477307

29
g-index

34
all docs

34
docs citations

34
times ranked

2211
citing authors

#	ARTICLE	IF	CITATIONS
1	Visualisation of experimentally determined and predicted protein N-glycosylation and predicted glycosylphosphatidylinositol anchor addition in <i>Trypanosoma brucei</i> .. Wellcome Open Research, 2022, 7, 33.	1.8	1
2	Visualisation of proteome-wide ordered protein abundances in <i>Trypanosoma brucei</i> . Wellcome Open Research, 2022, 7, 34.	1.8	18
3	Control of Variant Surface Glycoprotein Expression by CFB2 in <i>Trypanosoma brucei</i> and Quantitative Proteomic Connections to Translation and Cytokinesis. MSphere, 2022, 7, e0006922.	2.9	4
4	Oligo targeting for profiling drug resistance mutations in the parasitic trypanosomatids. Nucleic Acids Research, 2022, 50, e79-e79.	14.5	5
5	Polysomal mRNA Association and Gene Expression in <i>Trypanosoma brucei</i> . Wellcome Open Research, 2021, 6, 36.	1.8	2
6	Nucleotide sugar biosynthesis occurs in the glycosomes of procyclic and bloodstream form <i>Trypanosoma brucei</i> . PLoS Neglected Tropical Diseases, 2021, 15, e0009132.	3.0	9
7	Proteomic identification of the UDP-GlcNAc: PI $\hat{1}\hat{1}\hat{6}$ GlcNAc-transferase subunits of the glycosylphosphatidylinositol biosynthetic pathway of <i>Trypanosoma brucei</i> . PLoS ONE, 2021, 16, e0244699.	2.5	4
8	Novel aspects of iron homeostasis in pathogenic bloodstream form <i>Trypanosoma brucei</i> . PLoS Pathogens, 2021, 17, e1009696.	4.7	7
9	Identifying the beta-site amyloid precursor protein cleaving enzyme 1 interactome through the proximity-dependent biotin identification assay. Neuroscience Letters, 2021, , 136302.	2.1	1
10	Pharmacological Validation of <i>N</i> -Myristoyltransferase as a Drug Target in <i>Leishmania donovani</i> . ACS Infectious Diseases, 2019, 5, 111-122.	3.8	55
11	Proteome turnover in the bloodstream and procyclic forms of <i>Trypanosoma brucei</i> measured by quantitative proteomics. Wellcome Open Research, 2019, 4, 152.	1.8	27
12	Proteomic Analysis of the Cell Cycle of Procyclic Form <i>Trypanosoma brucei</i> . Molecular and Cellular Proteomics, 2018, 17, 1184-1195.	3.8	36
13	The mRNA cap methyltransferase gene TbCMT1 is not essential in vitro but is a virulence factor in vivo for bloodstream form <i>Trypanosoma brucei</i> . PLoS ONE, 2018, 13, e0201263.	2.5	2
14	Development of Chemical Proteomics for the Folateome and Analysis of the Kinetoplastid Folateome. ACS Infectious Diseases, 2018, 4, 1475-1486.	3.8	1
15	Both Intrinsic Substrate Preference and Network Context Contribute to Substrate Selection of Classical Tyrosine Phosphatases. Journal of Biological Chemistry, 2017, 292, 4942-4952.	3.4	8
16	Single-subunit oligosaccharyltransferases of <i>Trypanosoma brucei</i> display different and predictable peptide acceptor specificities. Journal of Biological Chemistry, 2017, 292, 20328-20341.	3.4	14
17	Prediction of Protein Complexes in <i>Trypanosoma brucei</i> by Protein Correlation Profiling Mass Spectrometry and Machine Learning. Molecular and Cellular Proteomics, 2017, 16, 2254-2267.	3.8	24
18	Global Membrane Protein Interactome Analysis using In vivo Crosslinking and Mass Spectrometry-based Protein Correlation Profiling. Molecular and Cellular Proteomics, 2016, 15, 2476-2490.	3.8	61

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19	Identification of Caveolar Resident Proteins in Ventricular Myocytes Using a Quantitative Proteomic Approach: Dynamic Changes in Caveolar Composition Following Adrenoceptor Activation. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 596-608.	3.8	25
20	ANIA: ANnotation and Integrated Analysis of the 14-3-3 interactome. Database: the Journal of Biological Databases and Curation, 2014, 2014, bat085.	3.0	51
21	Identification of 2R-ohnologue gene families displaying the same mutation-load skew in multiple cancers. <i>Open Biology</i> , 2014, 4, 140029.	3.6	17
22	Evolution of signal multiplexing by 14-3-3-binding 2R-ohnologue protein families in the vertebrates. <i>Open Biology</i> , 2012, 2, 120103.	3.6	47
23	The capture of phosphoproteins by 14-3-3 proteins mediates actions of insulin. <i>Trends in Endocrinology and Metabolism</i> , 2011, 22, 429-436.	7.1	58
24	Identification of New Substrates of the Protein-tyrosine Phosphatase PTP1B by Bayesian Integration of Proteome Evidence. <i>Journal of Biological Chemistry</i> , 2011, 286, 4173-4185.	3.4	41
25	Tumor Suppressor Density-enhanced Phosphatase-1 (DEP-1) Inhibits the RAS Pathway by Direct Dephosphorylation of ERK1/2 Kinases. <i>Journal of Biological Chemistry</i> , 2009, 284, 22048-22058.	3.4	68
26	Linear Motif Atlas for Phosphorylation-Dependent Signaling. <i>Science Signaling</i> , 2008, 1, ra2.	3.6	418
27	Diverse driving forces underlie the invariant occurrence of the T42A, E139D, I282V and T468M SHP2 amino acid substitutions causing Noonan and LEOPARD syndromes. <i>Human Molecular Genetics</i> , 2008, 17, 2018-2029.	2.9	79
28	Analysis of the SAG5 locus reveals a distinct genomic organisation in virulent and avirulent strains of <i>Toxoplasma gondii</i> . <i>International Journal for Parasitology</i> , 2003, 33, 1605-1616.	3.1	12
29	The SAG5 locus of <i>Toxoplasma gondii</i> encodes three novel proteins belonging to the SAG1 family of surface antigens. <i>International Journal for Parasitology</i> , 2002, 32, 121-131.	3.1	14