

# 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	Linear Motif Atlas for Phosphorylation-Dependent Signaling. <i>Science Signaling</i> , 2008, 1, ra2.	3.6	418
2	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
3	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
4	Global Membrane Protein Interactome Analysis using In vivo Crosslinking and Mass Spectrometry-based Protein Correlation Profiling. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2476-2490.	3.8	61
5	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
6	Pharmacological Validation of <i>N</i> -Myristoyltransferase as a Drug Target in <i>Leishmania donovani</i> . <i>ACS Infectious Diseases</i> , 2019, 5, 111-122.	3.8	55
7	ANIA: ANnotation and Integrated Analysis of the 14-3-3 interactome. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bat085.	3.0	51
8	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
9	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
10	Proteomic Analysis of the Cell Cycle of Procyclic Form <i>Trypanosoma brucei</i> . <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1184-1195.	3.8	36
11	Proteome turnover in the bloodstream and procyclic forms of <i>Trypanosoma brucei</i> measured by quantitative proteomics. <i>Wellcome Open Research</i> , 2019, 4, 152.	1.8	27
12	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
13	Prediction of Protein Complexes in <i>Trypanosoma brucei</i> by Protein Correlation Profiling Mass Spectrometry and Machine Learning. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2254-2267.	3.8	24
14	Visualisation of proteome-wide ordered protein abundances in <i>Trypanosoma brucei</i> . <i>Wellcome Open Research</i> , 2022, 7, 34.	1.8	18
15	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
16	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
17	Single-subunit oligosaccharyltransferases of <i>Trypanosoma brucei</i> display different and predictable peptide acceptor specificities. <i>Journal of Biological Chemistry</i> , 2017, 292, 20328-20341.	3.4	14
18	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

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19	Nucleotide sugar biosynthesis occurs in the glycosomes of procyclic and bloodstream form <i>Trypanosoma brucei</i> . <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009132.	3.0	9
20	Both Intrinsic Substrate Preference and Network Context Contribute to Substrate Selection of Classical Tyrosine Phosphatases. <i>Journal of Biological Chemistry</i> , 2017, 292, 4942-4952.	3.4	8
21	Novel aspects of iron homeostasis in pathogenic bloodstream form <i>Trypanosoma brucei</i> . <i>PLoS Pathogens</i> , 2021, 17, e1009696.	4.7	7
22	Oligo targeting for profiling drug resistance mutations in the parasitic trypanosomatids. <i>Nucleic Acids Research</i> , 2022, 50, e79-e79.	14.5	5
23	Proteomic identification of the UDP-GlcNAc: PI 1-6 GlcNAc-transferase subunits of the glycosylphosphatidylinositol biosynthetic pathway of <i>Trypanosoma brucei</i> . <i>PLoS ONE</i> , 2021, 16, e0244699.	2.5	4
24	Control of Variant Surface Glycoprotein Expression by CFB2 in <i>Trypanosoma brucei</i> and Quantitative Proteomic Connections to Translation and Cytokinesis. <i>MSphere</i> , 2022, 7, e0006922.	2.9	4
25	The mRNA cap methyltransferase gene <i>TbCMT1</i> is not essential in vitro but is a virulence factor in vivo for bloodstream form <i>Trypanosoma brucei</i> . <i>PLoS ONE</i> , 2018, 13, e0201263.	2.5	2
26	Polysomal mRNA Association and Gene Expression in <i>Trypanosoma brucei</i> . <i>Wellcome Open Research</i> , 2021, 6, 36.	1.8	2
27	Development of Chemical Proteomics for the Folateome and Analysis of the Kinetoplastid Folateome. <i>ACS Infectious Diseases</i> , 2018, 4, 1475-1486.	3.8	1
28	Identifying the beta-site amyloid precursor protein cleaving enzyme 1 interactome through the proximity-dependent biotin identification assay. <i>Neuroscience Letters</i> , 2021, , 136302.	2.1	1
29	Visualisation of experimentally determined and predicted protein N-glycosylation and predicted glycosylphosphatidylinositol anchor addition in <i>Trypanosoma brucei</i> . <i>Wellcome Open Research</i> , 2022, 7, 33.	1.8	1