

# Piero Giansanti

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/8549110/piero-giansanti-publications-by-citations.pdf>

**Version:** 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

26  
papers

1,480  
citations

16  
h-index

27  
g-index

27  
ext. papers

1,807  
ext. citations

11.3  
avg, IF

4.45  
L-index

#	Paper	IF	Citations
26	NF- $\kappa$ B-Independent Role of IKK $\alpha$ /IKK $\beta$ in Preventing RIPK1 Kinase-Dependent Apoptotic and Necroptotic Cell Death during TNF Signaling. <i>Molecular Cell</i> , <b>2015</b> , 60, 63-76	17.6	250
25	Six alternative proteases for mass spectrometry-based proteomics beyond trypsin. <i>Nature Protocols</i> , <b>2016</b> , 11, 993-1006	18.8	245
24	Recent developments in matrix solid-phase dispersion extraction. <i>Journal of Chromatography A</i> , <b>2010</b> , 1217, 2521-32	4.5	228
23	Quantitative and qualitative proteome characteristics extracted from in-depth integrated genomics and proteomics analysis. <i>Cell Reports</i> , <b>2013</b> , 5, 1469-78	10.6	96
22	Single-step enrichment by Ti <sup>4+</sup> -IMAC and label-free quantitation enables in-depth monitoring of phosphorylation dynamics with high reproducibility and temporal resolution. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 2426-34	7.6	80
21	An Augmented Multiple-Protease-Based Human Phosphopeptide Atlas. <i>Cell Reports</i> , <b>2015</b> , 11, 1834-43	10.6	78
20	Serine 25 phosphorylation inhibits RIPK1 kinase-dependent cell death in models of infection and inflammation. <i>Nature Communications</i> , <b>2019</b> , 10, 1729	17.4	69
19	ProteomicsDB: a multi-omics and multi-organism resource for life science research. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D1153-D1163	20.1	67
18	Daily rhythms in the cyanobacterium <i>synechococcus elongatus</i> probed by high-resolution mass spectrometry-based proteomics reveals a small defined set of cyclic proteins. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 2042-55	7.6	55
17	PhosphoPath: Visualization of Phosphosite-centric Dynamics in Temporal Molecular Networks. <i>Journal of Proteome Research</i> , <b>2015</b> , 14, 4332-41	5.6	48
16	In-house construction of a UHPLC system enabling the identification of over 4000 protein groups in a single analysis. <i>Analyst</i> , <b>2012</b> , 137, 3541-8	5	41
15	Liquid chromatography-negative ion atmospheric pressure photoionization tandem mass spectrometry for the determination of brominated flame retardants in environmental water and industrial effluents. <i>Journal of Chromatography A</i> , <b>2009</b> , 1216, 6400-9	4.5	41
14	Existence of hybrid structures in cationic liposome/DNA complexes revealed by their interaction with plasma proteins. <i>Colloids and Surfaces B: Biointerfaces</i> , <b>2011</b> , 82, 141-6	6	40
13	Interrogating cAMP-dependent kinase signaling in Jurkat T cells via a protein kinase A targeted immune-precipitation phosphoproteomics approach. <i>Molecular and Cellular Proteomics</i> , <b>2013</b> , 12, 3350-9	7.6	33
12	PZR coordinates Shp2 Noonan and LEOPARD syndrome signaling in zebrafish and mice. <i>Molecular and Cellular Biology</i> , <b>2014</b> , 34, 2874-89	4.8	25
11	Inhibition of the integrated stress response by viral proteins that block p-eIF2-eIF2B association. <i>Nature Microbiology</i> , <b>2020</b> , 5, 1361-1373	26.6	17
10	Opposite Electron-Transfer Dissociation and Higher-Energy Collisional Dissociation Fragmentation Characteristics of Proteolytic K/R(X) and (X)K/R Peptides Provide Benefits for Peptide Sequencing in Proteomics and Phosphoproteomics. <i>Journal of Proteome Research</i> , <b>2017</b> , 16, 852-861	5.6	15

9	Evaluating the promiscuous nature of tyrosine kinase inhibitors assessed in A431 epidermoid carcinoma cells by both chemical- and phosphoproteomics. <i>ACS Chemical Biology</i> , <b>2014</b> , 9, 1490-8	4.9	14
8	Effects of Acetylation and Phosphorylation on Subunit Interactions in Three Large Eukaryotic Complexes. <i>Molecular and Cellular Proteomics</i> , <b>2018</b> , 17, 2387-2401	7.6	10
7	Identification of 7 000-9 000 Proteins from Cell Lines and Tissues by Single-Shot Microflow LC-MS/MS. <i>Analytical Chemistry</i> , <b>2021</b> , 93, 8687-8692	7.8	9
6	Phosphoproteomics-mediated identification of Fer kinase as a target of mutant Shp2 in Noonan and LEOPARD syndrome. <i>PLoS ONE</i> , <b>2014</b> , 9, e106682	3.7	7
5	Dynamic remodelling of the human host cell proteome and phosphoproteome upon enterovirus infection. <i>Nature Communications</i> , <b>2020</b> , 11, 4332	17.4	7
4	PLK1-dependent phosphorylation restrains EBNA2 activity and lymphomagenesis in EBV-infected mice. <i>EMBO Reports</i> , <b>2021</b> , 22, e53007	6.5	1
3	Systems approach reveals distinct and shared signaling networks of the four PGE receptors in T cells. <i>Science Signaling</i> , <b>2021</b> , 14, eabc8579	8.8	1
2	Cytomegalovirus subverts macrophage identity. <i>Cell</i> , <b>2021</b> , 184, 3774-3793.e25	56.2	1
1	Prostaglandin E2 signaling networks in T cells revealed through a systems approach. <i>FASEB Journal</i> , <b>2019</b> , 33, lb258	0.9	