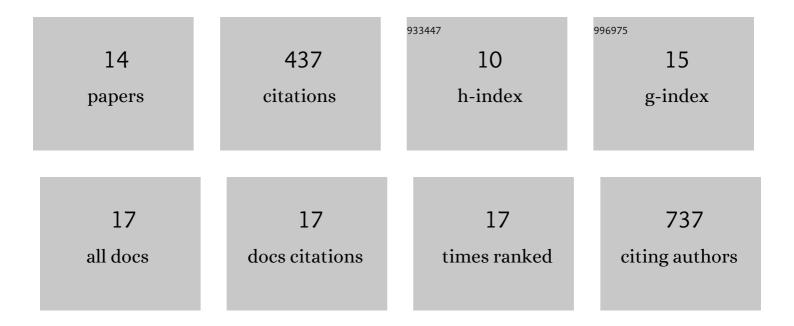
Matthew P Torres

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1099059/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Deciphering postâ€translational modification codes. FEBS Letters, 2013, 587, 1247-1257.	2.8	142
2	Genetic Analysis of Rare Human Variants of Regulators of G Protein Signaling Proteins and Their Role in Human Physiology and Disease. Pharmacological Reviews, 2018, 70, 446-474.	16.0	53
3	Structural Analysis of PTM Hotspots (SAPH-ire) – A Quantitative Informatics Method Enabling the Discovery of Novel Regulatory Elements in Protein Families. Molecular and Cellular Proteomics, 2015, 14, 2285-2297.	3.8	42
4	Sod1 integrates oxygen availability to redox regulate NADPH production and the thiol redoxome. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	32
5	Proteome-wide Structural Analysis of PTM Hotspots Reveals Regulatory Elements Predicted to Impact Biological Function and Disease. Molecular and Cellular Proteomics, 2016, 15, 3513-3528.	3.8	31
6	Predicted Functional Implications of Phosphorylation of Regulator of G Protein Signaling Protein in Plants. Frontiers in Plant Science, 2017, 8, 1456.	3.6	25
7	Tyrosine phosphorylation switching of a G protein. Journal of Biological Chemistry, 2018, 293, 4752-4766.	3.4	23
8	Genetic heterogeneity within collective invasion packs drives leader and follower cell phenotypes. Journal of Cell Science, 2019, 132, .	2.0	23
9	Negative Feedback Phosphorylation of GÎ ³ Subunit Ste18 and the Ste5 Scaffold Synergistically Regulates MAPK Activation in Yeast. Cell Reports, 2018, 23, 1504-1515.	6.4	21
10	Acylation of Superoxide Dismutase 1 (SOD1) at K122 Governs SOD1-Mediated Inhibition of Mitochondrial Respiration. Molecular and Cellular Biology, 2017, 37, .	2.3	16
11	Systematic analysis of non-structural protein features for the prediction of PTM function potential by artificial neural networks. PLoS ONE, 2017, 12, e0172572.	2.5	9
12	Systematic analysis of linker histone PTM hotspots reveals phosphorylation sites that modulate homologous recombination and DSB repair. DNA Repair, 2020, 86, 102763.	2.8	8
13	Combinatorial phosphorylation modulates the structure and function of the G protein $\hat{\rm I}^3$ subunit in yeast. Science Signaling, 2021, 14, .	3.6	4
14	SAPHâ€ire TFx: A Machine Learning Recommendation Model and Webtool for the Prediction of Functional Postâ€Translational Modifications. FASEB Journal, 2020, 34, 1-1.	0.5	4