

# Matthew P Torres

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1099059/publications.pdf>

Version: 2024-02-01

14  
papers

437  
citations

933447

10  
h-index

996975

15  
g-index

17  
all docs

17  
docs citations

17  
times ranked

737  
citing authors

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