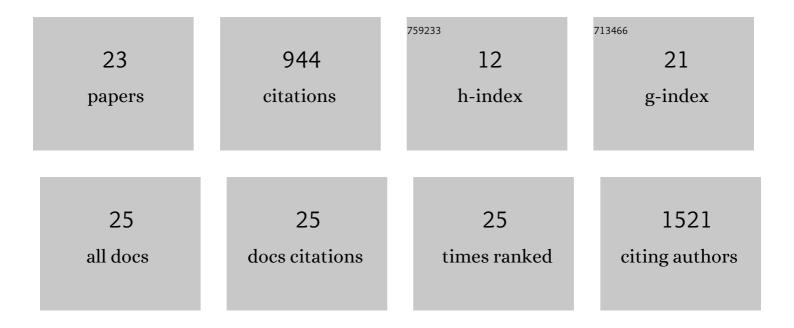
## Yifat Merbl

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4054767/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Histone degradation by the proteasome regulates chromatin and cellular plasticity. FEBS Journal, 2022, 289, 3304-3316.	4.7	11
2	SUMOylation of linker histone H1 drives chromatin condensation and restriction of embryonic cell fate identity. Molecular Cell, 2022, 82, 106-122.e9.	9.7	19
3	Maintaining Golgi Homeostasis: A Balancing Act of Two Proteolytic Pathways. Cells, 2022, 11, 780.	4.1	6
4	Tumor-reactive antibodies evolve from non-binding and autoreactive precursors. Cell, 2022, 185, 1208-1222.e21.	28.9	59
5	Gatekeepers of the Gut: The Roles of Proteasomes at the Gastrointestinal Barrier. Biomolecules, 2021, 11, 989.	4.0	5
6	Altered Protein Abundance and Localization Inferred from Sites of Alternative Modification by Ubiquitin and SUMO. Journal of Molecular Biology, 2021, 433, 167219.	4.2	4
7	Spatiotemporal Proteomic Analysis of Stress Granule Disassembly Using APEX Reveals Regulation by SUMOylation and Links to ALS Pathogenesis. Molecular Cell, 2020, 80, 876-891.e6.	9.7	154
8	Golgi organization is regulated by proteasomal degradation. Nature Communications, 2020, 11, 409.	12.8	73
9	Global views of proteasome-mediated degradation by mass spectrometry. Expert Review of Proteomics, 2019, 16, 711-716.	3.0	6
10	Global views of proteasome-mediated degradation by mass spectrometry. Expert Review of Proteomics, 2019, , .	3.0	1
11	Pro-inflammatory Cytokines Alter the Immunopeptidome Landscape by Modulation of HLA-B Expression. Frontiers in Immunology, 2019, 10, 141.	4.8	38
12	Phenotypic Screen Identifies JAK2 as a Major Regulator of FAT10 Expression. ACS Chemical Biology, 2019, 14, 2538-2545.	3.4	3
13	Personalized Ubiquitination Signatures for Predicting Response to Proteasome Inhibitor-Based Therapy of MM Patients. Blood, 2019, 134, 3371-3371.	1.4	0
14	Revealing the cellular degradome by mass spectrometry analysis of proteasome-cleaved peptides. Nature Biotechnology, 2018, 36, 1110-1116.	17.5	33
15	Neutralizing Gatad2a-Chd4-Mbd3/NuRD Complex Facilitates Deterministic Induction of Naive Pluripotency. Cell Stem Cell, 2018, 23, 412-425.e10.	11.1	59
16	Post-Translational Modification Profiling-Functional Proteomics for the Analysis of Immune Regulation. Methods in Molecular Biology, 2017, 1647, 139-152.	0.9	2
17	Post-translational modification profiling – A novel tool for mapping the protein modification landscape in cancer. Experimental Biology and Medicine, 2016, 241, 1475-1482.	2.4	21
18	Postâ€Translational Modification Profiling—a Highâ€Content Assay for Identifying Protein Modifications in Mammalian Cellular Systems. Current Protocols in Protein Science, 2014, 77, 27.8.1-27.8.13.	2.8	3

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#	Article	IF	CITATIONS
19	Profiling of Ubiquitin-like Modifications Reveals Features of Mitotic Control. Cell, 2013, 152, 1160-1172.	28.9	91
20	Protein microarrays for genome-wide posttranslational modification analysis. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2011, 3, 347-356.	6.6	23
21	A Systems Immunology Approach to the Host-Tumor Interaction: Large-Scale Patterns of Natural Autoantibodies Distinguish Healthy and Tumor-Bearing Mice. PLoS ONE, 2009, 4, e6053.	2.5	36
22	Large-scale detection of ubiquitination substrates using cell extracts and protein microarrays. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2543-2548.	7.1	87
23	Newborn humans manifest autoantibodies to defined self molecules detected by antigen microarray informatics. Journal of Clinical Investigation, 2007, 117, 712-718.	8.2	204