

Yifat Merbl

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

944
citations

759233

12
h-index

713466

21
g-index

25
all docs

25
docs citations

25
times ranked

1521
citing authors

#	ARTICLE	IF	CITATIONS
1	Newborn humans manifest autoantibodies to defined self molecules detected by antigen microarray informatics. <i>Journal of Clinical Investigation</i> , 2007, 117, 712-718.	8.2	204
2	Spatiotemporal Proteomic Analysis of Stress Granule Disassembly Using APEX Reveals Regulation by SUMOylation and Links to ALS Pathogenesis. <i>Molecular Cell</i> , 2020, 80, 876-891.e6.	9.7	154
3	Profiling of Ubiquitin-like Modifications Reveals Features of Mitotic Control. <i>Cell</i> , 2013, 152, 1160-1172.	28.9	91
4	Large-scale detection of ubiquitination substrates using cell extracts and protein microarrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2543-2548.	7.1	87
5	Golgi organization is regulated by proteasomal degradation. <i>Nature Communications</i> , 2020, 11, 409.	12.8	73
6	Neutralizing Gatad2a-Chd4-Mbd3/NuRD Complex Facilitates Deterministic Induction of Naive Pluripotency. <i>Cell Stem Cell</i> , 2018, 23, 412-425.e10.	11.1	59
7	Tumor-reactive antibodies evolve from non-binding and autoreactive precursors. <i>Cell</i> , 2022, 185, 1208-1222.e21.	28.9	59
8	Pro-inflammatory Cytokines Alter the Immuno-peptidome Landscape by Modulation of HLA-B Expression. <i>Frontiers in Immunology</i> , 2019, 10, 141.	4.8	38
9	A Systems Immunology Approach to the Host-Tumor Interaction: Large-Scale Patterns of Natural Autoantibodies Distinguish Healthy and Tumor-Bearing Mice. <i>PLoS ONE</i> , 2009, 4, e6053.	2.5	36
10	Revealing the cellular degradome by mass spectrometry analysis of proteasome-cleaved peptides. <i>Nature Biotechnology</i> , 2018, 36, 1110-1116.	17.5	33
11	Protein microarrays for genome-wide posttranslational modification analysis. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011, 3, 347-356.	6.6	23
12	Post-translational modification profiling – A novel tool for mapping the protein modification landscape in cancer. <i>Experimental Biology and Medicine</i> , 2016, 241, 1475-1482.	2.4	21
13	SUMOylation of linker histone H1 drives chromatin condensation and restriction of embryonic cell fate identity. <i>Molecular Cell</i> , 2022, 82, 106-122.e9.	9.7	19
14	Histone degradation by the proteasome regulates chromatin and cellular plasticity. <i>FEBS Journal</i> , 2022, 289, 3304-3316.	4.7	11
15	Global views of proteasome-mediated degradation by mass spectrometry. <i>Expert Review of Proteomics</i> , 2019, 16, 711-716.	3.0	6
16	Maintaining Golgi Homeostasis: A Balancing Act of Two Proteolytic Pathways. <i>Cells</i> , 2022, 11, 780.	4.1	6
17	Gatekeepers of the Gut: The Roles of Proteasomes at the Gastrointestinal Barrier. <i>Biomolecules</i> , 2021, 11, 989.	4.0	5
18	Altered Protein Abundance and Localization Inferred from Sites of Alternative Modification by Ubiquitin and SUMO. <i>Journal of Molecular Biology</i> , 2021, 433, 167219.	4.2	4

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19	Post-Translational Modification Profiling—a High-Content Assay for Identifying Protein Modifications in Mammalian Cellular Systems. <i>Current Protocols in Protein Science</i> , 2014, 77, 27.8.1-27.8.13.	2.8	3
20	Phenotypic Screen Identifies JAK2 as a Major Regulator of FAT10 Expression. <i>ACS Chemical Biology</i> , 2019, 14, 2538-2545.	3.4	3
21	Post-Translational Modification Profiling-Functional Proteomics for the Analysis of Immune Regulation. <i>Methods in Molecular Biology</i> , 2017, 1647, 139-152.	0.9	2
22	Global views of proteasome-mediated degradation by mass spectrometry. <i>Expert Review of Proteomics</i> , 2019, , .	3.0	1
23	Personalized Ubiquitination Signatures for Predicting Response to Proteasome Inhibitor-Based Therapy of MM Patients. <i>Blood</i> , 2019, 134, 3371-3371.	1.4	0