

# Marco Y Hein

## List of Publications by Year in descending order

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Version: 2024-02-01

32  
papers

19,275  
citations

186265

28  
h-index

434195

31  
g-index

42  
all docs

42  
docs citations

42  
times ranked

33246  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Perseus computational platform for comprehensive analysis of (prote)omics data. <i>Nature Methods</i> , 2016, 13, 731-740.	19.0	6,181
2	Accurate Proteome-wide Label-free Quantification by Delayed Normalization and Maximal Peptide Ratio Extraction, Termed MaxLFQ. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2513-2526.	3.8	4,178
3	A Liquid-to-Solid Phase Transition of the ALS Protein FUS Accelerated by Disease Mutation. <i>Cell</i> , 2015, 162, 1066-1077.	28.9	2,182
4	A Human Interactome in Three Quantitative Dimensions Organized by Stoichiometries and Abundances. <i>Cell</i> , 2015, 163, 712-723.	28.9	1,132
5	A Multiplexed Single-Cell CRISPR Screening Platform Enables Systematic Dissection of the Unfolded Protein Response. <i>Cell</i> , 2016, 167, 1867-1882.e21.	28.9	819
6	Decoding Human Cytomegalovirus. <i>Science</i> , 2012, 338, 1088-1093.	12.6	546
7	A "Proteomic Ruler" for Protein Copy Number and Concentration Estimation without Spike-in Standards. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3497-3506.	3.8	530
8	MULTI-seq: sample multiplexing for single-cell RNA sequencing using lipid-tagged indices. <i>Nature Methods</i> , 2019, 16, 619-626.	19.0	421
9	A Systematic Mammalian Genetic Interaction Map Reveals Pathways Underlying Ricin Susceptibility. <i>Cell</i> , 2013, 152, 909-922.	28.9	332
10	A genome-wide resource for the analysis of protein localisation in <i>Drosophila</i> . <i>ELife</i> , 2016, 5, e12068.	6.0	315
11	Polar Positioning of Phase-Separated Liquid Compartments in Cells Regulated by an mRNA Competition Mechanism. <i>Cell</i> , 2016, 166, 1572-1584.e16.	28.9	283
12	Continuous T Cell Receptor Signals Maintain a Functional Regulatory T Cell Pool. <i>Immunity</i> , 2014, 41, 722-736.	14.3	262
13	Accurate Protein Complex Retrieval by Affinity Enrichment Mass Spectrometry (AE-MS) Rather than Affinity Purification Mass Spectrometry (AP-MS). <i>Molecular and Cellular Proteomics</i> , 2015, 14, 120-135.	3.8	231
14	COMMD1 is linked to the WASH complex and regulates endosomal trafficking of the copper transporter ATP7A. <i>Molecular Biology of the Cell</i> , 2015, 26, 91-103.	2.1	200
15	Proteomics reveals dynamic assembly of repair complexes during bypass of DNA cross-links. <i>Science</i> , 2015, 348, 1253671.	12.6	183
16	OpenCell: Endogenous tagging for the cartography of human cellular organization. <i>Science</i> , 2022, 375, eabi6983.	12.6	174
17	p53 down-regulates SARS coronavirus replication and is targeted by the SARS-unique domain and PL <sup>pro</sup> via E3 ubiquitin ligase RCHY1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5192-201.	7.1	172
18	Mapping transcriptomic vector fields of single cells. <i>Cell</i> , 2022, 185, 690-711.e45.	28.9	167

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19	Functional Repurposing Revealed by Comparing <i>S.Âpombe</i> and <i>S.Âcerevisiae</i> Genetic Interactions. <i>Cell</i> , 2012, 149, 1339-1352.	28.9	154
20	Compromised function of the ESCRT pathway promotes endolysosomal escape of tau seeds and propagation of tau aggregation. <i>Journal of Biological Chemistry</i> , 2019, 294, 18952-18966.	3.4	103
21	CCDC22 deficiency in humans blunts activation of proinflammatory NF-Î¸B signaling. <i>Journal of Clinical Investigation</i> , 2013, 123, 2244-2256.	8.2	101
22	A role of OCRL in clathrin-coated pit dynamics and uncoating revealed by studies of Lowe syndrome cells. <i>ELife</i> , 2014, 3, e02975.	6.0	97
23	Interaction between AP-5 and the hereditary spastic paraplegia proteins SPG11 and SPG15. <i>Molecular Biology of the Cell</i> , 2013, 24, 2558-2569.	2.1	95
24	mRNA export through an additional cap-binding complex consisting of NCBP1 and NCBP3. <i>Nature Communications</i> , 2015, 6, 8192.	12.8	89
25	Functional single-cell genomics of human cytomegalovirus infection. <i>Nature Biotechnology</i> , 2022, 40, 391-401.	17.5	60
26	SILAC-Based Proteomics of Human Primary Endothelial Cell Morphogenesis Unveils Tumor Angiogenic Markers. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3599-3611.	3.8	55
27	Fractionation profiling: a fast and versatile approach for mapping vesicle proteomes and proteinâprotein interactions. <i>Molecular Biology of the Cell</i> , 2014, 25, 3178-3194.	2.1	42
28	NKT Cell-TCR Expression Activates Conventional T Cells in Vivo, but Is Largely Dispensable for Mature NKT Cell Biology. <i>PLoS Biology</i> , 2013, 11, e1001589.	5.6	36
29	The <i>Caenorhabditis elegans</i> pericentriolar material components SPD-2 and SPD-5 are monomeric in the cytoplasm before incorporation into the PCM matrix. <i>Molecular Biology of the Cell</i> , 2014, 25, 2984-2992.	2.1	31
30	The Hippo pathway controls myofibril assembly and muscle fiber growth by regulating sarcomeric gene expression. <i>ELife</i> , 2021, 10, .	6.0	29
31	msVolcano: A flexible web application for visualizing quantitative proteomics data. <i>Proteomics</i> , 2016, 16, 2491-2494.	2.2	16
32	Proteomic Analysis of Cellular Systems. , 2013, , 3-25.		15