

# Marco Y Hein

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

37  
papers

11,140  
citations

26  
h-index

42  
g-index

42  
ext. papers

15,573  
ext. citations

23.4  
avg, IF

6.24  
L-index

#	Paper	IF	Citations
37	OpenCell: Endogenous tagging for the cartography of human cellular organization.. <i>Science</i> , <b>2022</b> , 375, eabi6983	32.2	2
36	Mapping transcriptomic vector fields of single cells.. <i>Cell</i> , <b>2022</b> ,	54.5	6
35	The Hippo pathway controls myofibril assembly and muscle fiber growth by regulating sarcomeric gene expression. <i>ELife</i> , <b>2021</b> , 10,	8.6	7
34	Functional single-cell genomics of human cytomegalovirus infection. <i>Nature Biotechnology</i> , <b>2021</b> ,	43.2	7
33	MULTI-seq: sample multiplexing for single-cell RNA sequencing using lipid-tagged indices. <i>Nature Methods</i> , <b>2019</b> , 16, 619-626	21	158
32	Compromised function of the ESCRT pathway promotes endolysosomal escape of tau seeds and propagation of tau aggregation. <i>Journal of Biological Chemistry</i> , <b>2019</b> , 294, 18952-18966	5	45
31	msVolcano: A flexible web application for visualizing quantitative proteomics data. <i>Proteomics</i> , <b>2016</b> , 16, 2491-4	4.1	10
30	The Perseus computational platform for comprehensive analysis of (prote)omics data. <i>Nature Methods</i> , <b>2016</b> , 13, 731-40	21	3089
29	A genome-wide resource for the analysis of protein localisation in Drosophila. <i>ELife</i> , <b>2016</b> , 5, e12068	8.6	188
28	A Multiplexed Single-Cell CRISPR Screening Platform Enables Systematic Dissection of the Unfolded Protein Response. <i>Cell</i> , <b>2016</b> , 167, 1867-1882.e21	54.5	504
27	p53 down-regulates SARS coronavirus replication and is targeted by the SARS-unique domain and PLpro via E3 ubiquitin ligase RCHY1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, E5192-201	11.1	101
26	Polar Positioning of Phase-Separated Liquid Compartments in Cells Regulated by an mRNA Competition Mechanism. <i>Cell</i> , <b>2016</b> , 166, 1572-1584.e16	54.5	191
25	DNA repair. Proteomics reveals dynamic assembly of repair complexes during bypass of DNA cross-links. <i>Science</i> , <b>2015</b> , 348, 1253671	32.2	114
24	mRNA export through an additional cap-binding complex consisting of NCBP1 and NCBP3. <i>Nature Communications</i> , <b>2015</b> , 6, 8192	16.9	46
23	A human interactome in three quantitative dimensions organized by stoichiometries and abundances. <i>Cell</i> , <b>2015</b> , 163, 712-23	54.5	777
22	A Liquid-to-Solid Phase Transition of the ALS Protein FUS Accelerated by Disease Mutation. <i>Cell</i> , <b>2015</b> , 162, 1066-77	54.5	1321
21	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> , <b>2015</b> , 14, 120-35	7.3	157

20	COMMD1 is linked to the WASH complex and regulates endosomal trafficking of the copper transporter ATP7A. <i>Molecular Biology of the Cell</i> , <b>2015</b> , 26, 91-103	3-4	127
19	Accurate proteome-wide label-free quantification by delayed normalization and maximal peptide ratio extraction, termed MaxLFQ. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 2513-26	7-3	2506
18	Continuous T cell receptor signals maintain a functional regulatory T cell pool. <i>Immunity</i> , <b>2014</b> , 41, 722-36	9-14	198
17	A "proteomic ruler" for protein copy number and concentration estimation without spike-in standards. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 3497-506	7-3	319
16	Fractionation profiling: a fast and versatile approach for mapping vesicle proteomes and protein-protein interactions. <i>Molecular Biology of the Cell</i> , <b>2014</b> , 25, 3178-94	3-4	35
15	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> , <b>2014</b> , 25, 2984-92	3-4	25
14	A role of OCRL in clathrin-coated pit dynamics and uncoating revealed by studies of Lowe syndrome cells. <i>ELife</i> , <b>2014</b> , 3, e02975	8.6	76
13	SILAC-based proteomics of human primary endothelial cell morphogenesis unveils tumor angiogenic markers. <i>Molecular and Cellular Proteomics</i> , <b>2013</b> , 12, 3599-611	7-3	48
12	A systematic mammalian genetic interaction map reveals pathways underlying ricin susceptibility. <i>Cell</i> , <b>2013</b> , 152, 909-22	54-5	266
11	Proteomic Analysis of Cellular Systems <b>2013</b> , 3-25		12
10	NKT cell-TCR expression activates conventional T cells in vivo, but is largely dispensable for mature NKT cell biology. <i>PLoS Biology</i> , <b>2013</b> , 11, e1001589	9-4	29
9	Interaction between AP-5 and the hereditary spastic paraplegia proteins SPG11 and SPG15. <i>Molecular Biology of the Cell</i> , <b>2013</b> , 24, 2558-69	3-4	77
8	CCDC22 deficiency in humans blunts activation of proinflammatory NF- $\kappa$ B signaling. <i>Journal of Clinical Investigation</i> , <b>2013</b> , 123, 2244-56	15-3	62
7	Functional repurposing revealed by comparing <i>S. pombe</i> and <i>S. cerevisiae</i> genetic interactions. <i>Cell</i> , <b>2012</b> , 149, 1339-52	54-5	122
6	Decoding human cytomegalovirus. <i>Science</i> , <b>2012</b> , 338, 1088-93	32-2	431
5	OpenCell: proteome-scale endogenous tagging enables the cartography of human cellular organization		3
4	msVolcano: a flexible web application for visualizing quantitative proteomics data		2
3	MULTI-seq: Scalable sample multiplexing for single-cell RNA sequencing using lipid-tagged indices		12

2	Compromised function of the ESCRT pathway promotes endolysosomal escape of tau seeds and propagation of tau aggregation	1
1	Functional single-cell genomics of human cytomegalovirus infection	5