

# Erwin M Schoof

## List of Publications by Year in Descending Order

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**Version:** 2024-04-28

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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.

28  
papers

1,240  
citations

13  
h-index

30  
g-index

30  
ext. papers

1,637  
ext. citations

14.3  
avg, IF

4  
L-index

#	Paper	IF	Citations
28	Multiomic Profiling of Central Nervous System Leukemia Identifies mRNA Translation as a Therapeutic Target.. <i>Blood Cancer Discovery</i> , <b>2022</b> , 3, 16-31	7	0
27	Identification of the global miR-130a targetome reveals a role for TBL1XR1 in hematopoietic stem cell self-renewal and t(8;21) AML.. <i>Cell Reports</i> , <b>2022</b> , 38, 110481	10.6	0
26	Circadian regulation of protein cargo in extracellular vesicles.. <i>Science Advances</i> , <b>2022</b> , 8, eabc9061	14.3	5
25	PTBP1 promotes hematopoietic stem cell maintenance and red blood cell development by ensuring sufficient availability of ribosomal constituents.. <i>Cell Reports</i> , <b>2022</b> , 39, 110793	10.6	2
24	Quantitative single-cell proteomics as a tool to characterize cellular hierarchies. <i>Nature Communications</i> , <b>2021</b> , 12, 3341	17.4	53
23	Chitin Degradation Machinery and Secondary Metabolite Profiles in the Marine Bacterium S4059. <i>Marine Drugs</i> , <b>2021</b> , 19,	6	5
22	Organ-Specific, Fibroblast-Derived Matrix as a Tool for Studying Breast Cancer Metastasis. <i>Cancers</i> , <b>2021</b> , 13,	6.6	1
21	Proteomics identifies differences in fibrotic potential of extracellular vesicles from human tendon and muscle fibroblasts. <i>Cell Communication and Signaling</i> , <b>2020</b> , 18, 177	7.5	7
20	Characterization of glutathione proteome in CHO cells and its relationship with productivity and cholesterol synthesis. <i>Biotechnology and Bioengineering</i> , <b>2020</b> , 117, 3448-3458	4.9	4
19	Global view of the RAF-MEK-ERK module and its immediate downstream effectors. <i>Scientific Reports</i> , <b>2019</b> , 9, 10865	4.9	7
18	Mesenchymal stromal cell activation by breast cancer secretomes in bioengineered 3D microenvironments. <i>Life Science Alliance</i> , <b>2019</b> , 2,	5.8	20
17	Integrated Stress Response Activity Marks Stem Cells in Normal Hematopoiesis and Leukemia. <i>Cell Reports</i> , <b>2018</b> , 25, 1109-1117.e5	10.6	39
16	Ectopic miR-125a Expression Induces Long-Term Repopulating Stem Cell Capacity in Mouse and Human Hematopoietic Progenitors. <i>Cell Stem Cell</i> , <b>2016</b> , 19, 383-96	18	40
15	miR-126 Regulates Distinct Self-Renewal Outcomes in Normal and Malignant Hematopoietic Stem Cells. <i>Cancer Cell</i> , <b>2016</b> , 29, 214-28	24.3	118
14	Global proteomics dataset of miR-126 overexpression in acute myeloid leukemia. <i>Data in Brief</i> , <b>2016</b> , 9, 57-61	1.2	7
13	Integrative analysis of kinase networks in TRAIL-induced apoptosis provides a source of potential targets for combination therapy. <i>Science Signaling</i> , <b>2015</b> , 8, rs3	8.8	26
12	Kinome-wide decoding of network-attacking mutations rewiring cancer signaling. <i>Cell</i> , <b>2015</b> , 163, 202-1756.2	119	

11	The hypoxic cancer secretome induces pre-metastatic bone lesions through lysyl oxidase. <i>Nature</i> , <b>2015</b> , 522, 106-110	50.4	378
10	Dataset for the proteomic inventory and quantitative analysis of the breast cancer hypoxic secretome associated with osteotropism. <i>Data in Brief</i> , <b>2015</b> , 5, 621-5	1.2	5
9	Experimental and computational tools for analysis of signaling networks in primary cells. <i>Current Protocols in Immunology</i> , <b>2014</b> , 104, 11.11.1-11.11.23	4	2
8	CoreFlow: a computational platform for integration, analysis and modeling of complex biological data. <i>Journal of Proteomics</i> , <b>2014</b> , 100, 167-73	3.9	8
7	Modulation of the chromatin phosphoproteome by the Haspin protein kinase. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 1724-40	7.6	25
6	KinomeXplorer: an integrated platform for kinome biology studies. <i>Nature Methods</i> , <b>2014</b> , 11, 603-4	21.6	196
5	Navigating cancer network attractors for tumor-specific therapy. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 842-8	44.5	115
4	Mutational properties of amino acid residues: implications for evolvability of phosphorylatable residues. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2012</b> , 367, 2584-93	5.8	29
3	Response to Comment on "Positive Selection of Tyrosine Loss in Metazoan Evolution". <i>Science</i> , <b>2011</b> , 332, 917-917	33.3	15
2	Quantitative Single-Cell Proteomics as a Tool to Characterize Cellular Hierarchies		12
1	Real-Time Search Assisted Acquisition on a Tribrid Mass Spectrometer Improves Coverage in Multiplexed Single-Cell Proteomics		2