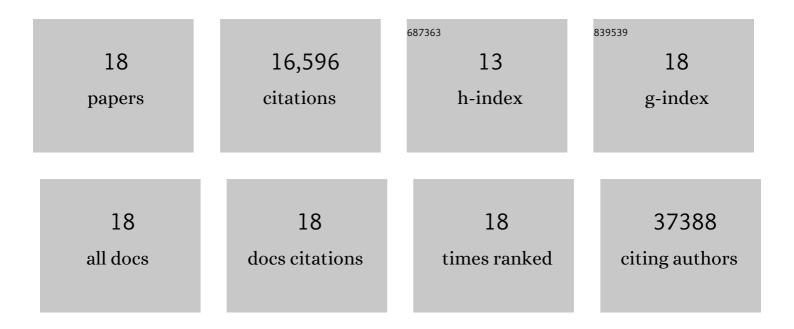
Asa Sivertsson

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1821204/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Tissue-based map of the human proteome. Science, 2015, 347, 1260419.	12.6	10,802
2	Analysis of the Human Tissue-specific Expression by Genome-wide Integration of Transcriptomics and Antibody-based Proteomics. Molecular and Cellular Proteomics, 2014, 13, 397-406.	3.8	2,819
3	A subcellular map of the human proteome. Science, 2017, 356, .	12.6	2,079
4	A genome-wide transcriptomic analysis of protein-coding genes in human blood cells. Science, 2019, 366, .	12.6	329
5	The human secretome. Science Signaling, 2019, 12, .	3.6	259
6	Enhanced validation of antibodies for research applications. Nature Communications, 2018, 9, 4130.	12.8	76
7	The Kidney Transcriptome and Proteome Defined by Transcriptomics and Antibody-Based Profiling. PLoS ONE, 2014, 9, e116125.	2.5	49
8	Contribution of Antibody-based Protein Profiling to the Human Chromosome-centric Proteome Project (C-HPP). Journal of Proteome Research, 2013, 12, 2439-2448.	3.7	48
9	Enhanced Validation of Antibodies Enables the Discovery of Missing Proteins. Journal of Proteome Research, 2020, 19, 4766-4781.	3.7	19
10	High throughput generation of a resource of the human secretome in mammalian cells. New Biotechnology, 2020, 58, 45-54.	4.4	16
11	Integration of Transcriptomics and Antibody-Based Proteomics for Exploration of Proteins Expressed in Specialized Tissues. Journal of Proteome Research, 2018, 17, 4127-4137.	3.7	15
12	Secretome-Based Screening in Target Discovery. SLAS Discovery, 2020, 25, 535-551.	2.7	15
13	Solid-phase cloning for high-throughput assembly of single and multiple DNA parts. Nucleic Acids Research, 2015, 43, e49-e49.	14.5	14
14	Genome-wide annotation of protein-coding genes in pig. BMC Biology, 2022, 20, 25.	3.8	14
15	Phenotypic Screen with the Human Secretome Identifies FGF16 as Inducing Proliferation of iPSC-Derived Cardiac Progenitor Cells. International Journal of Molecular Sciences, 2019, 20, 6037.	4.1	13
16	Pyrosequencing as an alternative to single-strand conformation polymorphism analysis for detection of N-ras mutations in human melanoma metastases. Clinical Chemistry, 2002, 48, 2164-70.	3.2	13
17	Discovery of Functional Alternatively Spliced PKM Transcripts in Human Cancers. Cancers, 2021, 13, 348.	3.7	8
18	TGFBR3L—An Uncharacterised Pituitary Specific Membrane Protein Detected in the Gonadotroph Cells in Non-Neoplastic and Tumour Tissue. Cancers, 2021, 13, 114.	3.7	8