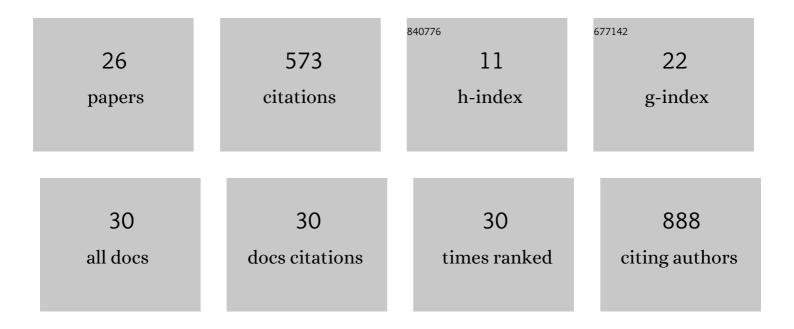


## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4314678/publications.pdf Version: 2024-02-01



VAN REN

#	Article	IF	CITATIONS
1	Profiling the Bisecting N-acetylglucosamine Modification in Amniotic Membrane via Mass Spectrometry. Genomics, Proteomics and Bioinformatics, 2022, 20, 648-656.	6.9	2
2	The tRNA discriminator base defines the mutual orthogonality of two distinct pyrrolysyl-tRNA synthetase/tRNAPyl pairs in the same organism. Nucleic Acids Research, 2022, 50, 4601-4615.	14.5	7
3	Systematic evaluation of IgG responses to SARS-CoV-2 spike protein-derived peptides for monitoring COVID-19 patients. Cellular and Molecular Immunology, 2021, 18, 621-631.	10.5	43
4	Accurate classification of COVIDâ€19 patients with different severity via machine learning. Clinical and Translational Medicine, 2021, 11, e323.	4.0	17
5	Systematic profiling of SARS-CoV-2-specific IgG epitopes at amino acid resolution. Cellular and Molecular Immunology, 2021, 18, 1067-1069.	10.5	14
6	Multi-platform omics analysis reveals molecular signature for COVID-19 pathogenesis, prognosis and drug target discovery. Signal Transduction and Targeted Therapy, 2021, 6, 155.	17.1	49
7	The trans-omics landscape of COVID-19. Nature Communications, 2021, 12, 4543.	12.8	75
8	A preliminary analysis of LncRNA biomarkers for schizophrenia. Epigenomics, 2021, 13, 1443-1458.	2.1	9
9	Discovery of Missing Proteins from an Aneuploidy Cell Line Using a Proteogenomic Approach. Journal of Proteome Research, 2021, 20, 5329-5339.	3.7	2
10	Pre- and Post-treatment Levels of Plasma Metabolites in Patients With Bipolar Depression. Frontiers in Psychiatry, 2021, 12, 747595.	2.6	6
11	Exploration of Missing Proteins by a Combination Approach to Enrich the Low-Abundance Hydrophobic Proteins from Four Cancer Cell Lines. Journal of Proteome Research, 2020, 19, 401-408.	3.7	9
12	D283 Med, a Cell Line Derived from Peritoneal Metastatic Medulloblastoma: A Good Choice for Missing Protein Discovery. Journal of Proteome Research, 2020, 19, 4857-4866.	3.7	5
13	Proteomic profiling and genome-wide mapping of O-GlcNAc chromatin-associated proteins reveal an O-GlcNAc-regulated genotoxic stress response. Nature Communications, 2020, 11, 5898.	12.8	19
14	Lipidomic Biomarkers of Extracellular Vesicles for the Prediction of Preterm Birth in the Early Second Trimester. Journal of Proteome Research, 2020, 19, 4104-4113.	3.7	14
15	Evaluation and minimization of nonspecific tryptic cleavages in proteomic sample preparation. Rapid Communications in Mass Spectrometry, 2020, 34, e8733.	1.5	10
16	Multiparameter Optimization of Two Common Proteomics Quantification Methods for Quantifying Low-Abundance Proteins. Journal of Proteome Research, 2019, 18, 461-468.	3.7	8
17	pClean: An Algorithm To Preprocess High-Resolution Tandem Mass Spectra for Database Searching. Journal of Proteome Research, 2019, 18, 3235-3244.	3.7	3
18	Alternative Strategy To Explore Missing Proteins with Low Molecular Weight. Journal of Proteome Research, 2019, 18, 4180-4188.	3.7	7

Yan Ren

#	Article	IF	CITATIONS
19	The defensive system of tree frog skin identified by peptidomics and RNA sequencing analysis. Amino Acids, 2019, 51, 345-353.	2.7	6
20	Reagents for Isobaric Labeling Peptides in Quantitative Proteomics. Analytical Chemistry, 2018, 90, 12366-12371.	6.5	33
21	Improvement of Peptide Separation for Exploring the Missing Proteins Localized on Membranes. Journal of Proteome Research, 2018, 17, 4152-4159.	3.7	12
22	Improved Peptide Retention Time Prediction in Liquid Chromatography through Deep Learning. Analytical Chemistry, 2018, 90, 10881-10888.	6.5	107
23	Digging More Missing Proteins Using an Enrichment Approach with ProteoMiner. Journal of Proteome Research, 2017, 16, 4330-4339.	3.7	26
24	Drug Resistance in Colorectal Cancer Cell Lines is Partially Associated with Aneuploidy Status in Light of Profiling Gene Expression. Journal of Proteome Research, 2016, 15, 4047-4059.	3.7	14
25	Evaluation of the Effect of Trypsin Digestion Buffers on Artificial Deamidation. Journal of Proteome Research, 2015, 14, 1308-1314.	3.7	46
26	Comparative evaluation of electrostatic repulsion–hydrophilic interaction chromatography (ERLIC) and high-pH reversed phase (Hp-RP) chromatography in profiling of rat kidney proteome. Journal of Proteomics, 2013, 82, 254-262.	2.4	25