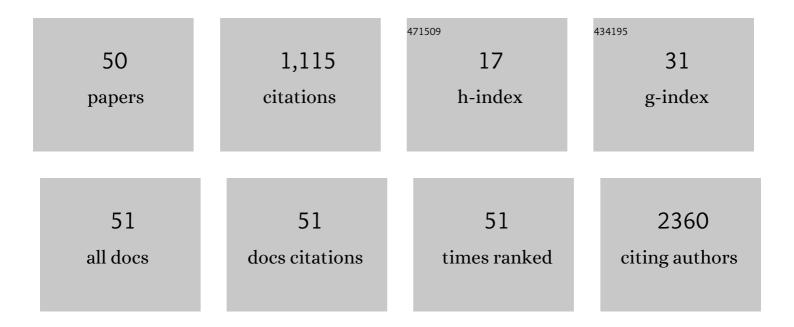
Mayank Saraswat

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4799757/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Plasma proteome of brain-dead organ donors predicts heart transplant outcome. Journal of Heart and Lung Transplantation, 2022, 41, 311-324.	0.6	7
2	Quantitative urine proteomics in pregnant women for the identification of predictive biomarkers for preeclampsia. Translational Medicine Communications, 2022, 7, .	1.4	2
3	TMT-Based Multiplexed Quantitation of <i>N</i> -Glycopeptides Reveals Glycoproteome Remodeling Induced by Oncogenic Mutations. ACS Omega, 2022, 7, 11023-11032.	3.5	7
4	Quantitative glycoproteomics of human milk and association with atopic disease. PLoS ONE, 2022, 17, e0267967.	2.5	5
5	Extensive heterogeneity of glycopeptides in plasma revealed by deep glycoproteomic analysis using size-exclusion chromatography. Molecular Omics, 2021, 17, 939-947.	2.8	15
6	DIA-Based Proteome Profiling of Nasopharyngeal Swabs from COVID-19 Patients. Journal of Proteome Research, 2021, 20, 4165-4175.	3.7	21
7	Proteomic Signature of Host Response to SARS-CoV-2 Infection in the Nasopharynx. Molecular and Cellular Proteomics, 2021, 20, 100134.	3.8	25
8	Sorbitol Is a Severity Biomarker for <scp>PMM2 DG</scp> with Therapeutic Implications. Annals of Neurology, 2021, 90, 887-900.	5.3	22
9	PASS-DIA: A Data-Independent Acquisition Approach for Discovery Studies. Analytical Chemistry, 2020, 92, 14466-14475.	6.5	19
10	Label-free proteomics reveals serum proteins whose levels differ between pancreatic ductal adenocarcinoma patients with short or long survival. Tumor Biology, 2020, 42, 101042832093641.	1.8	4
11	Extracellular vesicles from human plasma and serum are carriers of extravesicular cargo—Implications for biomarker discovery. PLoS ONE, 2020, 15, e0236439.	2.5	157
12	Label-free plasma proteomics identifies haptoglobin-related protein as candidate marker of idiopathic pulmonary fibrosis and dysregulation of complement and oxidative pathways. Scientific Reports, 2020, 10, 7787.	3.3	12
13	Plasma protein expression differs between colorectal cancer patients depending on primary tumor location. Cancer Medicine, 2020, 9, 5221-5234.	2.8	8
14	Comparing serum protein levels can aid in differentiating HPV-negative and -positive oropharyngeal squamous cell carcinoma patients. PLoS ONE, 2020, 15, e0233974.	2.5	11
15	Mass spectrometry–based lipidomics of oral squamous cell carcinoma tissue reveals aberrant cholesterol and glycerophospholipid metabolism — A Pilot study. Translational Oncology, 2020, 13, 100807.	3.7	23
16	Preoperative Radiotherapy Leads to Significant Differences in the Plasma Protein Profile of Rectal Cancer Patients. Oncology, 2020, 98, 493-500.	1.9	5
17	Extra-cellular vesicles carry proteome of cancer hallmarks. Frontiers in Bioscience - Landmark, 2020, 25, 398-436.	3.0	14

#	Article	IF	CITATIONS
19	Title is missing!. , 2020, 15, e0236439.		Ο
20	Title is missing!. , 2020, 15, e0236439.		0
21	Title is missing!. , 2020, 15, e0236439.		Ο
22	Differences and overlap in plasma protein expression during colorectal cancer progression. Translational Medicine Communications, 2019, 4, .	1.4	5
23	Plasma Proteomics Analysis Reveals Dysregulation of Complement Proteins and Inflammation in Acquired Obesity—A Study on Rare BMIâ€Discordant Monozygotic Twin Pairs. Proteomics - Clinical Applications, 2019, 13, 1800173.	1.6	11
24	Label-free serum proteomics and multivariate data analysis identifies biomarkers and expression trends that differentiate Intraductal papillary mucinous neoplasia from pancreatic adenocarcinoma and healthy controls. Translational Medicine Communications, 2019, 4, .	1.4	2
25	Identification of several plasma proteins whose levels in colorectal cancer patients differ depending on outcome. FASEB BioAdvances, 2019, 1, 723-730.	2.4	7
26	Label-free tissue proteomics can classify oral squamous cell carcinoma from healthy tissue in a stage-specific manner. Oral Oncology, 2018, 86, 206-215.	1.5	11
27	Patients with early-stage oropharyngeal cancer can be identified with label-free serum proteomics. British Journal of Cancer, 2018, 119, 200-212.	6.4	11
28	Colorectal cancer patients with different C-reactive protein levels and 5-year survival times can be differentiated with quantitative serum proteomics. PLoS ONE, 2018, 13, e0195354.	2.5	28
29	Tongue Cancer Patients Can be Distinguished from Healthy Controls by Specific <i>N</i> â€Glycopeptides Found in Serum. Proteomics - Clinical Applications, 2018, 12, e1800061.	1.6	18
30	Quantitative N-glycoproteomics reveals altered glycosylation levels of various plasma proteins in bloodstream infected patients. PLoS ONE, 2018, 13, e0195006.	2.5	19
31	Tongue cancer patients can be distinguished from healthy controls by specific N-glycopeptides found in serum Journal of Clinical Oncology, 2018, 36, e18047-e18047.	1.6	0
32	Human Spermatozoa Quantitative Proteomic Signature Classifies Normo- and Asthenozoospermia. Molecular and Cellular Proteomics, 2017, 16, 57-72.	3.8	69
33	Oral squamous cell carcinoma patients can be differentiated from healthy individuals with label-free serum proteomics. British Journal of Cancer, 2017, 117, 376-384.	6.4	16
34	Comparative proteomic profiling of the serum differentiates pancreatic cancer from chronic pancreatitis. Cancer Medicine, 2017, 6, 1738-1751.	2.8	39
35	Gene expression profiling, pathway analysis and subtype classification reveal molecular heterogeneity in hepatocellular carcinoma and suggest subtype specific therapeutic targets. Cancer Genetics, 2017, 216-217, 37-51.	0.4	35
36	Changes in plasma protein levels as an early indication of a bloodstream infection. PLoS ONE, 2017, 12, e0172987.	2.5	22

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37	N-Glycoproteomics of Human Seminal Plasma Glycoproteins. Journal of Proteome Research, 2016, 15, 991-1001.	3.7	23
38	N-linked (N-) Glycoproteomics of Urimary Exosomes*. Molecular and Cellular Proteomics, 2015, 14, 263-276.	3.8	60
39	Glycosylation patterns of kidney proteins differ in rat diabetic nephropathy. Kidney International, 2015, 87, 963-974.	5.2	23
40	Recovery of urinary nanovesicles from ultracentrifugation supernatants. Nephrology Dialysis Transplantation, 2013, 28, 1425-1433.	0.7	43
41	Preparative Purification of Recombinant Proteins: Current Status and Future Trends. BioMed Research International, 2013, 2013, 1-18.	1.9	122
42	Heparin and Heparin Binding Proteins: Potential Relevance to Reproductive Physiology. Current Protein and Peptide Science, 2013, 14, 61-69.	1.4	7
43	Human serum albumin as a new interacting partner of prolactin inducible protein in human seminal plasma. International Journal of Biological Macromolecules, 2012, 50, 317-322.	7.5	22
44	Development of a Rapid Sandwich Enzyme Linked Immunoassay Procedure for the Highly Sensitive Detection of Human Lipocalin-2/NGAL. Procedia Chemistry, 2012, 6, 141-148.	0.7	9
45	Comparative Study of the Developed Chemiluminescent, ELISA and SPR Immunoassay Formats for the Highly Sensitive Detection of Human Albumin. Procedia Chemistry, 2012, 6, 184-193.	0.7	14
46	Biochemical and Physical Characterisation of Urinary Nanovesicles following CHAPS Treatment. PLoS ONE, 2012, 7, e37279.	2.5	74
47	Human Epididymis Protein-4 (HE-4): A Novel Cross-Class Protease Inhibitor. PLoS ONE, 2012, 7, e47672.	2.5	45
48	Sample complexity reduction aids efficient detection of lowâ€abundant proteins from human amniotic fluid. Journal of Separation Science, 2010, 33, 1723-1729.	2.5	8
49	Differential proteomics of sperm: insights, challenges and future prospects. Biomarkers in Medicine, 2010, 4, 905-910.	1.4	13
50	Proteomic alterations in extracellular vesicles induced by oncogenic <i>PIK3CA</i> mutations. Proteomics, 0, , 2200077.	2.2	2