

Anil K Madugundu

List of Publications by Year in descending order

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158
papers

22,318
citations

38742

50
h-index

9345

143
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163
all docs

163
docs citations

163
times ranked

30997
citing authors

#	ARTICLE	IF	CITATIONS
1	Stable Isotope Labeling by Amino Acids in Cell Culture, SILAC, as a Simple and Accurate Approach to Expression Proteomics. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 376-386.	3.8	4,931
2	Human Protein Reference Database--2009 update. <i>Nucleic Acids Research</i> , 2009, 37, D767-D772.	14.5	2,882
3	Proteomics to study genes and genomes. <i>Nature</i> , 2000, 405, 837-846.	27.8	2,173
4	A draft map of the human proteome. <i>Nature</i> , 2014, 509, 575-581.	27.8	1,948
5	Analysis of protein phosphorylation using mass spectrometry: deciphering the phosphoproteome. <i>Trends in Biotechnology</i> , 2002, 20, 261-268.	9.3	877
6	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	28.9	804
7	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019, 177, 1035-1049.e19.	28.9	498
8	NetPath: a public resource of curated signal transduction pathways. <i>Genome Biology</i> , 2010, 11, R3.	9.6	456
9	Homer1a drives homeostatic scaling-down of excitatory synapses during sleep. <i>Science</i> , 2017, 355, 511-515.	12.6	398
10	Detection of Tyrosine Phosphorylated Peptides by Precursor Ion Scanning Quadrupole TOF Mass Spectrometry in Positive Ion Mode. <i>Analytical Chemistry</i> , 2001, 73, 1440-1448.	6.5	306
11	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	28.9	273
12	CHES: a new human gene catalog curated from thousands of large-scale RNA sequencing experiments reveals extensive transcriptional noise. <i>Genome Biology</i> , 2018, 19, 208.	8.8	263
13	Human Protein Reference Database and Human Proteinpedia as Discovery Tools for Systems Biology. <i>Methods in Molecular Biology</i> , 2009, 577, 67-79.	0.9	245
14	Quantitative proteomics using stable isotope labeling with amino acids in cell culture. <i>Nature Protocols</i> , 2008, 3, 505-516.	12.0	190
15	Human Protein Reference Database and Human Proteinpedia as resources for phosphoproteome analysis. <i>Molecular BioSystems</i> , 2012, 8, 453-463.	2.9	179
16	Phosphoproteomics in cancer. <i>Molecular Oncology</i> , 2010, 4, 482-495.	4.6	159
17	Mutant proteins as cancer-specific biomarkers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 2444-2449.	7.1	157
18	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008, 26, 164-167.	17.5	155

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19	Proteogenomic Analysis of Mycobacterium tuberculosis By High Resolution Mass Spectrometry. Molecular and Cellular Proteomics, 2011, 10, M111.011445.	3.8	145
20	Tissue matrix arrays for high-throughput screening and systems analysis of cell function. Nature Methods, 2015, 12, 1197-1204.	19.0	140
21	Plasma Proteome Database as a resource for proteomics research. Proteomics, 2005, 5, 3531-3536.	2.2	135
22	Proteomic analysis of human osteoarthritis synovial fluid. Clinical Proteomics, 2014, 11, 6.	2.1	122
23	Identification of long-lived synaptic proteins by proteomic analysis of synaptosome protein turnover. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3827-E3836.	7.1	122
24	A Quantitative Proteomic Approach for Identification of Potential Biomarkers in Hepatocellular Carcinoma. Journal of Proteome Research, 2008, 7, 4289-4298.	3.7	121
25	Proteogenomics. Proteomics, 2011, 11, 620-630.	2.2	121
26	Widespread somatic L1 retrotransposition occurs early during gastrointestinal cancer evolution. Genome Research, 2015, 25, 1536-1545.	5.5	121
27	A pathway map of glutamate metabolism. Journal of Cell Communication and Signaling, 2016, 10, 69-75.	3.4	115
28	Proteomic analysis of human vitreous humor. Clinical Proteomics, 2014, 11, 29.	2.1	114
29	Comparisons of tyrosine phosphorylated proteins in cells expressing lung cancer-specific alleles of EGFR and KRAS. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 14112-14117.	7.1	113
30	Differential proteomic analysis of synovial fluid from rheumatoid arthritis and osteoarthritis patients. Clinical Proteomics, 2014, 11, 1.	2.1	113
31	Common errors in mass spectrometry-based analysis of post-translational modifications. Proteomics, 2016, 16, 700-714.	2.2	106
32	The dynamic stress-induced O-GlcNAc highlights functions for O-GlcNAc in regulating DNA damage/repair and other cellular pathways. Amino Acids, 2011, 40, 793-808.	2.7	103
33	Quantitative tissue proteomics of esophageal squamous cell carcinoma for novel biomarker discovery. Cancer Biology and Therapy, 2011, 12, 510-522.	3.4	102
34	A reassessment of the translation initiation codon in vertebrates. Trends in Genetics, 2001, 17, 685-687.	6.7	98
35	Human Protein Reference Database and Human Proteinpedia as Discovery Resources for Molecular Biotechnology. Molecular Biotechnology, 2011, 48, 87-95.	2.4	87
36	PfCDPK1 mediated signaling in erythrocytic stages of Plasmodium falciparum. Nature Communications, 2017, 8, 63.	12.8	87

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37	A functional annotation of subproteomes in human plasma. <i>Proteomics</i> , 2005, 5, 3506-3519.	2.2	82
38	Quantitative Proteomic Profiling of Cerebrospinal Fluid to Identify Candidate Biomarkers for Alzheimer's Disease. <i>Proteomics - Clinical Applications</i> , 2019, 13, e1800105.	1.6	82
39	LC-MS/MS Analysis of Differentially Expressed Glioblastoma Membrane Proteome Reveals Altered Calcium Signaling and Other Protein Groups of Regulatory Functions. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013565.	3.8	76
40	Human Proteinpedia: a unified discovery resource for proteomics research. <i>Nucleic Acids Research</i> , 2009, 37, D773-D781.	14.5	75
41	Discovery of noncanonical translation initiation sites through mass spectrometric analysis of protein N termini. <i>Genome Research</i> , 2018, 28, 25-36.	5.5	75
42	Stable Isotope Labeling with Amino Acids in Cell Culture (SILAC) for Studying Dynamics of Protein Abundance and Posttranslational Modifications. <i>Science Signaling</i> , 2005, 2005, pl2-pl2.	3.6	74
43	Proteomic composition and immunomodulatory properties of urinary bladder matrix scaffolds in homeostasis and injury. <i>Seminars in Immunology</i> , 2017, 29, 14-23.	5.6	73
44	Nucleotide sequence databases: a gold mine for biologists. <i>Trends in Biochemical Sciences</i> , 1999, 24, 276-280.	7.5	72
45	A network map of BDNF/TRKB and BDNF/p75NTR signaling system. <i>Journal of Cell Communication and Signaling</i> , 2013, 7, 301-307.	3.4	72
46	Activation of diverse signalling pathways by oncogenic PIK3CA mutations. <i>Nature Communications</i> , 2014, 5, 4961.	12.8	72
47	BioSITE: A Method for Direct Detection and Quantitation of Site-Specific Biotinylation. <i>Journal of Proteome Research</i> , 2018, 17, 759-769.	3.7	70
48	A Proteomic Analysis of Human Hemodialysis Fluid. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 637-650.	3.8	60
49	Integrating transcriptomic and proteomic data for accurate assembly and annotation of genomes. <i>Genome Research</i> , 2017, 27, 133-144.	5.5	60
50	A proteogenomic analysis of <i>Anopheles gambiae</i> using high-resolution Fourier transform mass spectrometry. <i>Genome Research</i> , 2011, 21, 1872-1881.	5.5	58
51	Phosphoproteomic Profiling Reveals Epstein-Barr Virus Protein Kinase Integration of DNA Damage Response and Mitotic Signaling. <i>PLoS Pathogens</i> , 2015, 11, e1005346.	4.7	53
52	Annotation of the Zebrafish Genome through an Integrated Transcriptomic and Proteomic Analysis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3184-3198.	3.8	52
53	Heterogeneity of Pancreatic Cancer Metastases in a Single Patient Revealed by Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2803-2811.	3.8	52
54	PGTools: A Software Suite for Proteogenomic Data Analysis and Visualization. <i>Journal of Proteome Research</i> , 2015, 14, 2255-2266.	3.7	52

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55	Proteomics of Human Aqueous Humor. <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 283-293.	2.0	46
56	Identification of GAPDH on the surface of <i>Plasmodium</i> sporozoites as a new candidate for targeting malaria liver invasion. <i>Journal of Experimental Medicine</i> , 2016, 213, 2099-2112.	8.5	45
57	A mass spectrometry-based targeted assay for detection of SARS-CoV-2 antigen from clinical specimens. <i>EBioMedicine</i> , 2021, 69, 103465.	6.1	44
58	Global phosphotyrosine survey in triple-negative breast cancer reveals activation of multiple tyrosine kinase signaling pathways. <i>Oncotarget</i> , 2015, 6, 29143-29160.	1.8	44
59	A multi-omic analysis of human naïve CD4+ T cells. <i>BMC Systems Biology</i> , 2015, 9, 75.	3.0	43
60	Activated Epidermal Growth Factor Receptor as a Novel Target in Pancreatic Cancer Therapy. <i>Journal of Proteome Research</i> , 2008, 7, 4651-4658.	3.7	42
61	Proteogenomic Analysis of <i>Candida glabrata</i> using High Resolution Mass Spectrometry. <i>Journal of Proteome Research</i> , 2012, 11, 247-260.	3.7	42
62	A proteogenomic approach to map the proteome of an unsequenced pathogen – <i>Leishmania donovani</i> . <i>Proteomics</i> , 2012, 12, 832-844.	2.2	42
63	The non-receptor tyrosine kinase TNK2/ACK1 is a novel therapeutic target in triple negative breast cancer. <i>Oncotarget</i> , 2017, 8, 2971-2983.	1.8	42
64	Phosphoproteome of <i>Cryptococcus neoformans</i> . <i>Journal of Proteomics</i> , 2014, 97, 287-295.	2.4	41
65	Surgery, Octreotide, Temozolomide, Bevacizumab, Radiotherapy, and Pegvisomant Treatment of an AIP Mutation-Positive Child. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2019, 104, 3539-3544.	3.6	41
66	Acute Kidney Injury in Severe COVID-19 Has Similarities to Sepsis-Associated Kidney Injury. <i>Mayo Clinic Proceedings</i> , 2021, 96, 2561-2575.	3.0	41
67	Hotspot SF3B1 mutations induce metabolic reprogramming and vulnerability to serine deprivation. <i>Journal of Clinical Investigation</i> , 2019, 129, 4708-4723.	8.2	41
68	Moving from unsequenced to sequenced genome: Reanalysis of the proteome of <i>Leishmania donovani</i> . <i>Journal of Proteomics</i> , 2014, 97, 48-61.	2.4	40
69	A compendium of molecules involved in vector-pathogen interactions pertaining to malaria. <i>Malaria Journal</i> , 2013, 12, 216.	2.3	39
70	Phosphotyrosine profiling identifies ephrin receptor A2 as a potential therapeutic target in esophageal squamous cell carcinoma. <i>Proteomics</i> , 2015, 15, 374-382.	2.2	38
71	Characterizing the normal proteome of human ciliary body. <i>Clinical Proteomics</i> , 2013, 10, 9.	2.1	37
72	A dual specificity kinase, DYRK1A, as a potential therapeutic target for head and neck squamous cell carcinoma. <i>Scientific Reports</i> , 2016, 6, 36132.	3.3	36

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73	Neglected Tropical Diseases and Omics Science: Proteogenomics Analysis of the Promastigote Stage of <i>Leishmania major</i> Parasite. OMICS A Journal of Integrative Biology, 2014, 18, 499-512.	2.0	35
74	Mass Spectrometric Analysis of Urine from COVID-19 Patients for Detection of SARS-CoV-2 Viral Antigen and to Study Host Response. Journal of Proteome Research, 2021, 20, 3404-3413.	3.7	35
75	Next-Generation Sequencing Reveals Novel Mutations in X-linked Intellectual Disability. OMICS A Journal of Integrative Biology, 2017, 21, 295-303.	2.0	34
76	Data-Driven Discovery of Extravasation Pathway in Circulating Tumor Cells. Scientific Reports, 2017, 7, 43710.	3.3	32
77	Quantitative proteomic analysis of the frontal cortex in Alzheimer's disease. Journal of Neurochemistry, 2021, 156, 988-1002.	3.9	32
78	Proteomic profiling of retinoblastoma by high resolution mass spectrometry. Clinical Proteomics, 2016, 13, 29.	2.1	30
79	Quantitative proteomics for identifying biomarkers for Rabies. Clinical Proteomics, 2013, 10, 3.	2.1	27
80	Comprehensive Proteomics Analysis of Glycosomes from <i>Leishmania donovani</i> . OMICS A Journal of Integrative Biology, 2015, 19, 157-170.	2.0	27
81	Quantitative proteomics for identifying biomarkers for tuberculous meningitis. Clinical Proteomics, 2012, 9, 12.	2.1	26
82	Proteomic analysis of purified protein derivative of Mycobacterium tuberculosis. Clinical Proteomics, 2013, 10, 8.	2.1	26
83	Mapping the micro-proteome of the nuclear lamina and lamina-associated domains. Life Science Alliance, 2021, 4, e202000774.	2.8	26
84	Proteomic profiling of serum samples from chikungunya-infected patients provides insights into host response. Clinical Proteomics, 2013, 10, 14.	2.1	25
85	Dysregulation of splicing proteins in head and neck squamous cell carcinoma. Cancer Biology and Therapy, 2016, 17, 219-229.	3.4	25
86	Integrated Transcriptomic and Proteomic Analysis of Human Eccrine Sweat Glands Identifies Missing and Novel Proteins. Molecular and Cellular Proteomics, 2019, 18, 1382-1395.	3.8	25
87	High-quality nuclear genome for <i>Sarcoptes scabiei</i> —A critical resource for a neglected parasite. PLoS Neglected Tropical Diseases, 2020, 14, e0008720.	3.0	25
88	Proteomic Signature of Host Response to SARS-CoV-2 Infection in the Nasopharynx. Molecular and Cellular Proteomics, 2021, 20, 100134.	3.8	25
89	PyQuant: A Versatile Framework for Analysis of Quantitative Mass Spectrometry Data. Molecular and Cellular Proteomics, 2016, 15, 2829-2838.	3.8	24
90	Chromosome-centric Human Proteome Project: Deciphering Proteins Associated with Glioma and Neurodegenerative Disorders on Chromosome 12. Journal of Proteome Research, 2014, 13, 3178-3190.	3.7	23

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91	Mosquito-Borne Diseases and Omics: Tissue-Restricted Expression and Alternative Splicing Revealed by Transcriptome Profiling of <i>Anopheles stephensi</i> . <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 488-497.	2.0	23
92	Proteomic Analysis of the Human Anterior Pituitary Gland. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 759-769.	2.0	23
93	Functional Annotation of Proteome Encoded by Human Chromosome 22. <i>Journal of Proteome Research</i> , 2014, 13, 2749-2760.	3.7	22
94	Multiplexed Phosphoproteomic Study of Brain in Patients with Alzheimer's Disease and Age-Matched Cognitively Healthy Controls. <i>OMICS A Journal of Integrative Biology</i> , 2020, 24, 216-227.	2.0	22
95	Analytical Sensitivity and Specificity of Four Point of Care Rapid Antigen Diagnostic Tests for SARS-CoV-2 Using Real-Time Quantitative PCR, Quantitative Droplet Digital PCR, and a Mass Spectrometric Antigen Assay as Comparator Methods. <i>Clinical Chemistry</i> , 2021, 67, 1545-1553.	3.2	22
96	Sorbitol Is a Severity Biomarker for <i>PMM2</i> with Therapeutic Implications. <i>Annals of Neurology</i> , 2021, 90, 887-900.	5.3	22
97	Using Quantitative Seroproteomics to Identify Antibody Biomarkers in Pancreatic Cancer. <i>Cancer Immunology Research</i> , 2016, 4, 225-233.	3.4	21
98	Dissecting <i>Candida</i> Pathobiology: Post-Translational Modifications on the <i>Candida tropicalis</i> Proteome. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 544-552.	2.0	21
99	Quantitative Proteomics Reveals that the OGT Interactome Is Remodeled in Response to Oxidative Stress. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100069.	3.8	21
100	DIA-Based Proteome Profiling of Nasopharyngeal Swabs from COVID-19 Patients. <i>Journal of Proteome Research</i> , 2021, 20, 4165-4175.	3.7	21
101	Cerebrospinal fluid lipidomics for biomarkers of Alzheimer's disease. <i>Molecular Omics</i> , 2021, 17, 454-463.	2.8	21
102	Long non-coding RNA expression in primary human monocytes. <i>Genomics</i> , 2016, 108, 37-45.	2.9	20
103	Access Guide to Human Proteinpedia. <i>Current Protocols in Bioinformatics</i> , 2013, 41, Unit 1.21.	25.8	19
104	Phosphoproteomic analysis reveals compensatory effects in the piriform cortex of VX nerve agent exposed rats. <i>Proteomics</i> , 2015, 15, 487-499.	2.2	19
105	PASS-DIA: A Data-Independent Acquisition Approach for Discovery Studies. <i>Analytical Chemistry</i> , 2020, 92, 14466-14475.	6.5	19
106	Host response profile of human brain proteome in toxoplasma encephalitis co-infected with HIV. <i>Clinical Proteomics</i> , 2014, 11, 39.	2.1	18
107	Proteogenomic analysis of pathogenic yeast <i>Cryptococcus neoformans</i> using high resolution mass spectrometry. <i>Clinical Proteomics</i> , 2014, 11, 5.	2.1	18
108	Phosphotyrosine profiling of human cerebrospinal fluid. <i>Clinical Proteomics</i> , 2018, 15, 29.	2.1	18

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109	Developmental partitioning of SYK and ZAP70 prevents autoimmunity and cancer. <i>Molecular Cell</i> , 2021, 81, 2094-2111.e9.	9.7	17
110	Multiple Mechanisms Contribute to Lateral Transfer of an Organophosphate Degradation (opd) Island in <i>Sphingobium fuliginis</i> ATCC 27551. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1541-1554.	1.8	16
111	Unbiased identification of substrates of protein tyrosine phosphatase ptp ϵ 3 in <i>C. elegans</i> . <i>Molecular Oncology</i> , 2016, 10, 910-920.	4.6	16
112	Proteogenomics of <i>Candida tropicalis</i> "An Opportunistic Pathogen with Importance for Global Health. <i>OMICS A Journal of Integrative Biology</i> , 2016, 20, 239-247.	2.0	16
113	Integrated Transcriptomic and Proteomic Analysis of Primary Human Umbilical Vein Endothelial Cells. <i>Proteomics</i> , 2019, 19, e1800315.	2.2	16
114	Transcriptomic Profiles of Confirmed Pediatric Tuberculosis Patients and Household Contacts Identifies Active Tuberculosis, Infection, and Treatment Response Among Indian Children. <i>Journal of Infectious Diseases</i> , 2020, 221, 1647-1658.	4.0	16
115	Heterogeneous Nuclear Ribonucleoproteins and Their Interactors Are a Major Class of Deregulated Proteins in Anaplastic Astrocytoma: A Grade III Malignant Glioma. <i>Journal of Proteome Research</i> , 2013, 12, 3128-3138.	3.7	15
116	Membrane Proteome of Invasive Retinoblastoma: Differential Proteins and Biomarkers. <i>Proteomics - Clinical Applications</i> , 2018, 12, e1700101.	1.6	15
117	Extensive heterogeneity of glycopeptides in plasma revealed by deep glycoproteomic analysis using size-exclusion chromatography. <i>Molecular Omics</i> , 2021, 17, 939-947.	2.8	15
118	Proteomic analysis and genome annotation of <i>Pichia pastoris</i> , a recombinant protein expression host. <i>Proteomics</i> , 2014, 14, 2769-2779.	2.2	14
119	A sequence upstream of canonical PDZ-binding motif within CFTR COOH-terminus enhances NHERF1 interaction. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2016, 311, L1170-L1182.	2.9	13
120	Proteogenomic Analysis to Identify Missing Proteins from Haploid Cell Lines. <i>Proteomics</i> , 2018, 18, e1700386.	2.2	13
121	A Comprehensive Proteomics Analysis of the Human Iris Tissue: Ready to Embrace Postgenomics Precision Medicine in Ophthalmology?. <i>OMICS A Journal of Integrative Biology</i> , 2016, 20, 510-519.	2.0	12
122	Proteomic Analysis of the Human Olfactory Bulb. <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 440-453.	2.0	12
123	Phosphoproteomics of Retinoblastoma: A Pilot Study Identifies Aberrant Kinases. <i>Molecules</i> , 2018, 23, 1454.	3.8	12
124	PIM1 kinase promotes gallbladder cancer cell proliferation via inhibition of proline-rich Akt substrate of 40kDa (PRAS40). <i>Journal of Cell Communication and Signaling</i> , 2019, 13, 163-177.	3.4	12
125	Mutation-Specific and Common Phosphotyrosine Signatures of <i>KRAS</i> G12D and G13D Alleles. <i>Journal of Proteome Research</i> , 2021, 20, 670-683.	3.7	12
126	Identification and Characterization of Proteins Encoded by Chromosome 12 as Part of Chromosome-centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2014, 13, 3166-3177.	3.7	11

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127	Toward Postgenomics Ophthalmology: A Proteomic Map of the Human Choroidâ€“Retinal Pigment Epithelium Tissue. <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 114-122.	2.0	11
128	Characterization of host response to <i>Cryptococcus neoformans</i> through quantitative proteomic analysis of cryptococcal meningitis co-infected with HIV. <i>Molecular BioSystems</i> , 2015, 11, 2529-2540.	2.9	10
129	Integrative phosphoproteome and interactome analysis of the role of Ubash3b in BCR-ABL signaling. <i>Leukemia</i> , 2020, 34, 301-305.	7.2	10
130	Center of Mass Calculation in Combination with MS/MS Allows Robust Identification of Single Amino Acid Polymorphisms in Clinical Measurements of Insulin-Like Growth Factor-1. <i>Journal of Proteome Research</i> , 2020, 19, 186-193.	3.7	10
131	Expanding the clinical and metabolic phenotype of DPM2 deficient congenital disorders of glycosylation. <i>Molecular Genetics and Metabolism</i> , 2021, 132, 27-37.	1.1	10
132	A SISCAPA-based approach for detection of SARS-CoV-2 viral antigens from clinical samples. <i>Clinical Proteomics</i> , 2021, 18, 25.	2.1	10
133	Proteogenomics. <i>Proteomics</i> , 2014, 14, 2631-2632.	2.2	9
134	Characterization of human pineal gland proteome. <i>Molecular BioSystems</i> , 2016, 12, 3622-3632.	2.9	9
135	Proteogenomic Methods to Improve Genome Annotation. <i>Methods in Molecular Biology</i> , 2016, 1410, 77-89.	0.9	9
136	Integrated Proteomic and Phosphoproteomics Analysis of DKK3 Signaling Reveals Activated Kinase in the Most Aggressive Gallbladder Cancer. <i>Cells</i> , 2021, 10, 511.	4.1	9
137	Reinspection of a Clinical Proteomics Tumor Analysis Consortium (CPTAC) Dataset with Cloud Computing Reveals Abundant Post-Translational Modifications and Protein Sequence Variants. <i>Cancers</i> , 2021, 13, 5034.	3.7	9
138	Application of mass spectrometry-based proteomics for biomarker discovery in neurological disorders. <i>Annals of Indian Academy of Neurology</i> , 2009, 12, 3-11.	0.5	9
139	Targeted Detection of SARS-CoV-2 Nucleocapsid Sequence Variants by Mass Spectrometric Analysis of Tryptic Peptides. <i>Journal of Proteome Research</i> , 2022, 21, 142-150.	3.7	9
140	Proteomic Signatures of Diffuse and Intestinal Subtypes of Gastric Cancer. <i>Cancers</i> , 2021, 13, 5930.	3.7	9
141	Signature Fragment Ions of Biotinylated Peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 394-404.	2.8	8
142	Digging deeper into the immunopeptidome: characterization of post-translationally modified peptides presented by MHC I. <i>Journal of Proteins and Proteomics</i> , 2021, 12, 151-160.	1.5	8
143	Activating Mutations in <i>PIK3CA</i> Lead to Widespread Modulation of the Tyrosine Phosphoproteome. <i>Journal of Proteome Research</i> , 2015, 14, 3882-3891.	3.7	7
144	Accurate Precursor Mass Assignment Improves Peptide Identification in Data-Independent Acquisition Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 8453-8460.	6.5	7

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145	Proteomics-based approach for differentiation of age-related macular degeneration sub-types. Indian Journal of Ophthalmology, 2021, 69, 647.	1.1	7
146	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
147	Proteomics of the Human Olfactory Tract. OMICS A Journal of Integrative Biology, 2018, 22, 77-87.	2.0	6
148	Very long-chain acyl-CoA synthetase 3 mediates onco-sphingolipid metabolism in malignant glioma. Medical Research Archives, 2021, 9, .	0.2	5
149	Automated data-driven mass spectrometry for improved analysis of lipids with dual dissociation techniques. Journal of Mass Spectrometry and Advances in the Clinical Lab, 2021, 22, 43-49.	2.4	5
150	Chromosome-centric Human Proteome Project (C-HPP): Chromosome 12. Journal of Proteome Research, 2014, 13, 3160-3165.	3.7	4
151	Maternal serum lipidomics identifies lysophosphatidic acid as a predictor of small for gestational age neonates. Molecular Omics, 2021, 17, 956-966.	2.8	3
152	Proximity-Dependent Biotinylation to Elucidate the Interactome of TNK2 Nonreceptor Tyrosine Kinase. Journal of Proteome Research, 2021, 20, 4566-4577.	3.7	3
153	A Next-Generation Sequencing-Based Molecular Approach to Characterize a Tick Vector in Lyme Disease. OMICS A Journal of Integrative Biology, 2018, 22, 565-574.	2.0	2
154	Family-Based Next-Generation Sequencing Study Identifies an <i>IL2RG</i> Variant in an Infant with Primary Immunodeficiency. OMICS A Journal of Integrative Biology, 2019, 23, 285-290.	2.0	2
155	Tyrosine Phosphoproteomics of Patient-Derived Xenografts Reveals Ephrin Type-B Receptor 4 Tyrosine Kinase as a Therapeutic Target in Pancreatic Cancer. Cancers, 2021, 13, 3404.	3.7	2
156	High-resolution mass spectrometric analysis of cardiolipin profiles in Barth syndrome. Mitochondrion, 2021, 60, 27-32.	3.4	2
157	Proteomic alterations in extracellular vesicles induced by oncogenic <i>PIK3CA</i> mutations. Proteomics, 0, , 2200077.	2.2	2
158	Quantitative Tyrosine Phosphoproteome Profiling of AXL Receptor Tyrosine Kinase Signaling Network. Cancers, 2021, 13, 4234.	3.7	1