

Anil K Madugundu

List of Publications by Year in descending order

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Version: 2024-02-01

158
papers

22,318
citations

44444

50
h-index

10679

143
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163
all docs

163
docs citations

163
times ranked

34612
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	1.8	9
2	TMT-Based Multiplexed Quantitation of <i>N</i> -Glycopeptides Reveals Glycoproteome Remodeling Induced by Oncogenic Mutations. <i>ACS Omega</i> , 2022, 7, 11023-11032.	1.6	7
3	Quantitative proteomic analysis of the frontal cortex in Alzheimer's disease. <i>Journal of Neurochemistry</i> , 2021, 156, 988-1002.	2.1	32
4	Expanding the clinical and metabolic phenotype of DPM2 deficient congenital disorders of glycosylation. <i>Molecular Genetics and Metabolism</i> , 2021, 132, 27-37.	0.5	10
5	Mutation-Specific and Common Phosphotyrosine Signatures of <i>KRAS</i> G12D and G13D Alleles. <i>Journal of Proteome Research</i> , 2021, 20, 670-683.	1.8	12
6	Quantitative Proteomics Reveals that the OGT Interactome Is Remodeled in Response to Oxidative Stress. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100069.	2.5	21
7	Proteomics-based approach for differentiation of age-related macular degeneration sub-types. <i>Indian Journal of Ophthalmology</i> , 2021, 69, 647.	0.5	7
8	Extensive heterogeneity of glycopeptides in plasma revealed by deep glycoproteomic analysis using size-exclusion chromatography. <i>Molecular Omics</i> , 2021, 17, 939-947.	1.4	15
9	Maternal serum lipidomics identifies lysophosphatidic acid as a predictor of small for gestational age neonates. <i>Molecular Omics</i> , 2021, 17, 956-966.	1.4	3
10	Integrated Proteomic and Phosphoproteomics Analysis of DKK3 Signaling Reveals Activated Kinase in the Most Aggressive Gallbladder Cancer. <i>Cells</i> , 2021, 10, 511.	1.8	9
11	Mapping the micro-proteome of the nuclear lamina and lamina-associated domains. <i>Life Science Alliance</i> , 2021, 4, e202000774.	1.3	26
12	Developmental partitioning of SYK and ZAP70 prevents autoimmunity and cancer. <i>Molecular Cell</i> , 2021, 81, 2094-2111.e9.	4.5	17
13	Mass Spectrometric Analysis of Urine from COVID-19 Patients for Detection of SARS-CoV-2 Viral Antigen and to Study Host Response. <i>Journal of Proteome Research</i> , 2021, 20, 3404-3413.	1.8	35
14	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.	1.0	8
15	Tyrosine Phosphoproteomics of Patient-Derived Xenografts Reveals Ephrin Type-B Receptor 4 Tyrosine Kinase as a Therapeutic Target in Pancreatic Cancer. <i>Cancers</i> , 2021, 13, 3404.	1.7	2
16	A mass spectrometry-based targeted assay for detection of SARS-CoV-2 antigen from clinical specimens. <i>EBioMedicine</i> , 2021, 69, 103465.	2.7	44
17	DIA-Based Proteome Profiling of Nasopharyngeal Swabs from COVID-19 Patients. <i>Journal of Proteome Research</i> , 2021, 20, 4165-4175.	1.8	21
18	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.	1.5	22

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19	Quantitative Tyrosine Phosphoproteome Profiling of AXL Receptor Tyrosine Kinase Signaling Network. <i>Cancers</i> , 2021, 13, 4234.	1.7	1
20	Proximity-Dependent Biotinylation to Elucidate the Interactome of TNK2 Nonreceptor Tyrosine Kinase. <i>Journal of Proteome Research</i> , 2021, 20, 4566-4577.	1.8	3
21	High-resolution mass spectrometric analysis of cardiolipin profiles in Barth syndrome. <i>Mitochondrion</i> , 2021, 60, 27-32.	1.6	2
22	Acute Kidney Injury in Severe COVID-19 Has Similarities to Sepsis-Associated Kidney Injury. <i>Mayo Clinic Proceedings</i> , 2021, 96, 2561-2575.	1.4	41
23	Proteomic Signature of Host Response to SARS-CoV-2 Infection in the Nasopharynx. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100134.	2.5	25
24	Very long-chain acyl-CoA synthetase 3 mediates onco-sphingolipid metabolism in malignant glioma. <i>Medical Research Archives</i> , 2021, 9, .	0.1	5
25	Cerebrospinal fluid lipidomics for biomarkers of Alzheimer's disease. <i>Molecular Omics</i> , 2021, 17, 454-463.	1.4	21
26	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.	1.7	9
27	A SISCAPA-based approach for detection of SARS-CoV-2 viral antigens from clinical samples. <i>Clinical Proteomics</i> , 2021, 18, 25.	1.1	10
28	Sorbitol Is a Severity Biomarker for <scp>PMM2â€CDG</scp> with Therapeutic Implications. <i>Annals of Neurology</i> , 2021, 90, 887-900.	2.8	22
29	Automated data-driven mass spectrometry for improved analysis of lipids with dual dissociation techniques. <i>Journal of Mass Spectrometry and Advances in the Clinical Lab</i> , 2021, 22, 43-49.	1.3	5
30	Proteomic Signatures of Diffuse and Intestinal Subtypes of Gastric Cancer. <i>Cancers</i> , 2021, 13, 5930.	1.7	9
31	Integrative phosphoproteome and interactome analysis of the role of Ubash3b in BCR-ABL signaling. <i>Leukemia</i> , 2020, 34, 301-305.	3.3	10
32	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.	1.8	10
33	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.	1.9	16
34	PASS-DIA: A Data-Independent Acquisition Approach for Discovery Studies. <i>Analytical Chemistry</i> , 2020, 92, 14466-14475.	3.2	19
35	High-quality nuclear genome for <i>Sarcoptes scabiei</i> â€”A critical resource for a neglected parasite. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008720.	1.3	25
36	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	13.5	273

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37	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.	1.0	22
38	Signature Fragment Ions of Biotinylated Peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 394-404.	1.2	8
39	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.	1.8	41
40	PIM1 kinase promotes gallbladder cancer cell proliferation via inhibition of proline-rich Akt substrate of 40 kDa (PRAS40). <i>Journal of Cell Communication and Signaling</i> , 2019, 13, 163-177.	1.8	12
41	Accurate Precursor Mass Assignment Improves Peptide Identification in Data-Independent Acquisition Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 8453-8460.	3.2	7
42	Family-Based Next-Generation Sequencing Study Identifies an <i>IL2RG</i> Variant in an Infant with Primary Immunodeficiency. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 285-290.	1.0	2
43	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019, 177, 1035-1049.e19.	13.5	498
44	Integrated Transcriptomic and Proteomic Analysis of Primary Human Umbilical Vein Endothelial Cells. <i>Proteomics</i> , 2019, 19, e1800315.	1.3	16
45	Integrated Transcriptomic and Proteomic Analysis of Human Eccrine Sweat Glands Identifies Missing and Novel Proteins. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1382-1395.	2.5	25
46	Quantitative Proteomic Profiling of Cerebrospinal Fluid to Identify Candidate Biomarkers for Alzheimer's Disease. <i>Proteomics - Clinical Applications</i> , 2019, 13, e1800105.	0.8	82
47	Hotspot SF3B1 mutations induce metabolic reprogramming and vulnerability to serine deprivation. <i>Journal of Clinical Investigation</i> , 2019, 129, 4708-4723.	3.9	41
48	Proteogenomic Analysis to Identify Missing Proteins from Haploid Cell Lines. <i>Proteomics</i> , 2018, 18, e1700386.	1.3	13
49	Proteomics of the Human Olfactory Tract. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 77-87.	1.0	6
50	BioSITE: A Method for Direct Detection and Quantitation of Site-Specific Biotinylation. <i>Journal of Proteome Research</i> , 2018, 17, 759-769.	1.8	70
51	Identification of long-lived synaptic proteins by proteomic analysis of synaptosome protein turnover. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3827-E3836.	3.3	122
52	Discovery of noncanonical translation initiation sites through mass spectrometric analysis of protein N termini. <i>Genome Research</i> , 2018, 28, 25-36.	2.4	75
53	Proteomic Analysis of the Human Anterior Pituitary Gland. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 759-769.	1.0	23
54	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.	3.8	263

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55	Phosphotyrosine profiling of human cerebrospinal fluid. <i>Clinical Proteomics</i> , 2018, 15, 29.	1.1	18
56	Phosphoproteomics of Retinoblastoma: A Pilot Study Identifies Aberrant Kinases. <i>Molecules</i> , 2018, 23, 1454.	1.7	12
57	Membrane Proteome of Invasive Retinoblastoma: Differential Proteins and Biomarkers. <i>Proteomics - Clinical Applications</i> , 2018, 12, e1700101.	0.8	15
58	A Next-Generation Sequencing-Based Molecular Approach to Characterize a Tick Vector in Lyme Disease. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 565-574.	1.0	2
59	Dissecting Candida Pathobiology: Post-Translational Modifications on the <i>Candida tropicalis</i> Proteome. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 544-552.	1.0	21
60	Homer1a drives homeostatic scaling-down of excitatory synapses during sleep. <i>Science</i> , 2017, 355, 511-515.	6.0	398
61	Data-Driven Discovery of Extravasation Pathway in Circulating Tumor Cells. <i>Scientific Reports</i> , 2017, 7, 43710.	1.6	32
62	Toward Postgenomics Ophthalmology: A Proteomic Map of the Human Choroid Retinal Pigment Epithelium Tissue. <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 114-122.	1.0	11
63	Next-Generation Sequencing Reveals Novel Mutations in X-linked Intellectual Disability. <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 295-303.	1.0	34
64	Proteomic composition and immunomodulatory properties of urinary bladder matrix scaffolds in homeostasis and injury. <i>Seminars in Immunology</i> , 2017, 29, 14-23.	2.7	73
65	Proteomic Analysis of the Human Olfactory Bulb. <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 440-453.	1.0	12
66	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.	1.0	23
67	PfCDPK1 mediated signaling in erythrocytic stages of <i>Plasmodium falciparum</i> . <i>Nature Communications</i> , 2017, 8, 63.	5.8	87
68	Integrating transcriptomic and proteomic data for accurate assembly and annotation of genomes. <i>Genome Research</i> , 2017, 27, 133-144.	2.4	60
69	The non-receptor tyrosine kinase TNK2/ACK1 is a novel therapeutic target in triple negative breast cancer. <i>Oncotarget</i> , 2017, 8, 2971-2983.	0.8	42
70	Common errors in mass spectrometry-based analysis of post-translational modifications. <i>Proteomics</i> , 2016, 16, 700-714.	1.3	106
71	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.	1.3	13
72	Unbiased identification of substrates of protein tyrosine phosphatase ptp β in <i>C. elegans</i> . <i>Molecular Oncology</i> , 2016, 10, 910-920.	2.1	16

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73	Proteogenomics of <i>Candida tropicalis</i> An Opportunistic Pathogen with Importance for Global Health. OMICS A Journal of Integrative Biology, 2016, 20, 239-247.	1.0	16
74	Characterization of human pineal gland proteome. Molecular BioSystems, 2016, 12, 3622-3632.	2.9	9
75	PyQuant: A Versatile Framework for Analysis of Quantitative Mass Spectrometry Data. Molecular and Cellular Proteomics, 2016, 15, 2829-2838.	2.5	24
76	Identification of GAPDH on the surface of <i>Plasmodium</i> sporozoites as a new candidate for targeting malaria liver invasion. Journal of Experimental Medicine, 2016, 213, 2099-2112.	4.2	45
77	A Comprehensive Proteomics Analysis of the Human Iris Tissue: Ready to Embrace Postgenomics Precision Medicine in Ophthalmology?. OMICS A Journal of Integrative Biology, 2016, 20, 510-519.	1.0	12
78	Proteomic profiling of retinoblastoma by high resolution mass spectrometry. Clinical Proteomics, 2016, 13, 29.	1.1	30
79	A dual specificity kinase, DYRK1A, as a potential therapeutic target for head and neck squamous cell carcinoma. Scientific Reports, 2016, 6, 36132.	1.6	36
80	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. Cell, 2016, 166, 755-765.	13.5	804
81	Long non-coding RNA expression in primary human monocytes. Genomics, 2016, 108, 37-45.	1.3	20
82	A pathway map of glutamate metabolism. Journal of Cell Communication and Signaling, 2016, 10, 69-75.	1.8	115
83	Using Quantitative Seroproteomics to Identify Antibody Biomarkers in Pancreatic Cancer. Cancer Immunology Research, 2016, 4, 225-233.	1.6	21
84	Proteogenomic Methods to Improve Genome Annotation. Methods in Molecular Biology, 2016, 1410, 77-89.	0.4	9
85	Dysregulation of splicing proteins in head and neck squamous cell carcinoma. Cancer Biology and Therapy, 2016, 17, 219-229.	1.5	25
86	A multi-omic analysis of human naïve CD4+ T cells. BMC Systems Biology, 2015, 9, 75.	3.0	43
87	Phosphoproteomic analysis reveals compensatory effects in the piriform cortex of VX nerve agent exposed rats. Proteomics, 2015, 15, 487-499.	1.3	19
88	Comprehensive Proteomics Analysis of Glycosomes from <i>Leishmania donovani</i> . OMICS A Journal of Integrative Biology, 2015, 19, 157-170.	1.0	27
89	Phosphotyrosine profiling identifies ephrin receptor A2 as a potential therapeutic target in esophageal squamous cell carcinoma. Proteomics, 2015, 15, 374-382.	1.3	38
90	Characterization of host response to <i>Cryptococcus neoformans</i> through quantitative proteomic analysis of cryptococcal meningitis co-infected with HIV. Molecular BioSystems, 2015, 11, 2529-2540.	2.9	10

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91	Proteomics of Human Aqueous Humor. OMICS A Journal of Integrative Biology, 2015, 19, 283-293.	1.0	46
92	PGTools: A Software Suite for Proteogenomic Data Analysis and Visualization. Journal of Proteome Research, 2015, 14, 2255-2266.	1.8	52
93	Widespread somatic L1 retrotransposition occurs early during gastrointestinal cancer evolution. Genome Research, 2015, 25, 1536-1545.	2.4	121
94	Tissue matrix arrays for high-throughput screening and systems analysis of cell function. Nature Methods, 2015, 12, 1197-1204.	9.0	140
95	Activating Mutations in <i>PIK3CA</i> Lead to Widespread Modulation of the Tyrosine Phosphoproteome. Journal of Proteome Research, 2015, 14, 3882-3891.	1.8	7
96	Phosphoproteomic Profiling Reveals Epstein-Barr Virus Protein Kinase Integration of DNA Damage Response and Mitotic Signaling. PLoS Pathogens, 2015, 11, e1005346.	2.1	53
97	Global phosphotyrosine survey in triple-negative breast cancer reveals activation of multiple tyrosine kinase signaling pathways. Oncotarget, 2015, 6, 29143-29160.	0.8	44
98	Proteogenomics. Proteomics, 2014, 14, 2631-2632.	1.3	9
99	Host response profile of human brain proteome in toxoplasma encephalitis co-infected with HIV. Clinical Proteomics, 2014, 11, 39.	1.1	18
100	Differential proteomic analysis of synovial fluid from rheumatoid arthritis and osteoarthritis patients. Clinical Proteomics, 2014, 11, 1.	1.1	113
101	Phosphoproteome of <i>Cryptococcus neoformans</i> . Journal of Proteomics, 2014, 97, 287-295.	1.2	41
102	Moving from unsequenced to sequenced genome: Reanalysis of the proteome of <i>Leishmania donovani</i> . Journal of Proteomics, 2014, 97, 48-61.	1.2	40
103	Proteogenomic analysis of pathogenic yeast <i>Cryptococcus neoformans</i> using high resolution mass spectrometry. Clinical Proteomics, 2014, 11, 5.	1.1	18
104	A draft map of the human proteome. Nature, 2014, 509, 575-581.	13.7	1,948
105	Proteomic analysis and genome annotation of <i>Pichia pastoris</i> , a recombinant protein expression host. Proteomics, 2014, 14, 2769-2779.	1.3	14
106	Annotation of the Zebrafish Genome through an Integrated Transcriptomic and Proteomic Analysis. Molecular and Cellular Proteomics, 2014, 13, 3184-3198.	2.5	52
107	Heterogeneity of Pancreatic Cancer Metastases in a Single Patient Revealed by Quantitative Proteomics. Molecular and Cellular Proteomics, 2014, 13, 2803-2811.	2.5	52
108	Activation of diverse signalling pathways by oncogenic <i>PIK3CA</i> mutations. Nature Communications, 2014, 5, 4961.	5.8	72

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109	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.	1.8	11
110	Proteomic analysis of human vitreous humor. <i>Clinical Proteomics</i> , 2014, 11, 29.	1.1	114
111	Neglected Tropical Diseases and Omics Science: Proteogenomics Analysis of the Promastigote Stage of <i>Leishmania major</i> Parasite. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 499-512.	1.0	35
112	Chromosome-centric Human Proteome Project: Deciphering Proteins Associated with Glioma and Neurodegenerative Disorders on Chromosome 12. <i>Journal of Proteome Research</i> , 2014, 13, 3178-3190.	1.8	23
113	Functional Annotation of Proteome Encoded by Human Chromosome 22. <i>Journal of Proteome Research</i> , 2014, 13, 2749-2760.	1.8	22
114	Proteomic analysis of human osteoarthritis synovial fluid. <i>Clinical Proteomics</i> , 2014, 11, 6.	1.1	122
115	Chromosome-centric Human Proteome Project (C-HPP): Chromosome 12. <i>Journal of Proteome Research</i> , 2014, 13, 3160-3165.	1.8	4
116	Proteomic analysis of purified protein derivative of <i>Mycobacterium tuberculosis</i> . <i>Clinical Proteomics</i> , 2013, 10, 8.	1.1	26
117	Quantitative proteomics for identifying biomarkers for Rabies. <i>Clinical Proteomics</i> , 2013, 10, 3.	1.1	27
118	Characterizing the normal proteome of human ciliary body. <i>Clinical Proteomics</i> , 2013, 10, 9.	1.1	37
119	A compendium of molecules involved in vector-pathogen interactions pertaining to malaria. <i>Malaria Journal</i> , 2013, 12, 216.	0.8	39
120	Access Guide to Human Proteinpedia. <i>Current Protocols in Bioinformatics</i> , 2013, 41, Unit 1.21.	25.8	19
121	A network map of BDNF/TRKB and BDNF/p75NTR signaling system. <i>Journal of Cell Communication and Signaling</i> , 2013, 7, 301-307.	1.8	72
122	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.	1.8	15
123	Proteomic profiling of serum samples from chikungunya-infected patients provides insights into host response. <i>Clinical Proteomics</i> , 2013, 10, 14.	1.1	25
124	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.	0.8	16
125	Human Protein Reference Database and Human Proteinpedia as resources for phosphoproteome analysis. <i>Molecular BioSystems</i> , 2012, 8, 453-463.	2.9	179
126	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.	2.5	76

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127	Quantitative proteomics for identifying biomarkers for tuberculous meningitis. <i>Clinical Proteomics</i> , 2012, 9, 12.	1.1	26
128	Proteogenomic Analysis of <i>Candida glabrata</i> using High Resolution Mass Spectrometry. <i>Journal of Proteome Research</i> , 2012, 11, 247-260.	1.8	42
129	A proteogenomic approach to map the proteome of an unsequenced pathogen “ <i>Leishmania donovani</i> ”. <i>Proteomics</i> , 2012, 12, 832-844.	1.3	42
130	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.	3.3	157
131	Proteogenomic Analysis of <i>Mycobacterium tuberculosis</i> By High Resolution Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.011445.	2.5	145
132	The dynamic stress-induced “O-GlcNAc” highlights functions for O-GlcNAc in regulating DNA damage/repair and other cellular pathways. <i>Amino Acids</i> , 2011, 40, 793-808.	1.2	103
133	Human Protein Reference Database and Human Proteinpedia as Discovery Resources for Molecular Biotechnology. <i>Molecular Biotechnology</i> , 2011, 48, 87-95.	1.3	87
134	Proteogenomics. <i>Proteomics</i> , 2011, 11, 620-630.	1.3	121
135	A proteogenomic analysis of <i>Anopheles gambiae</i> using high-resolution Fourier transform mass spectrometry. <i>Genome Research</i> , 2011, 21, 1872-1881.	2.4	58
136	Quantitative tissue proteomics of esophageal squamous cell carcinoma for novel biomarker discovery. <i>Cancer Biology and Therapy</i> , 2011, 12, 510-522.	1.5	102
137	Phosphoproteomics in cancer. <i>Molecular Oncology</i> , 2010, 4, 482-495.	2.1	159
138	NetPath: a public resource of curated signal transduction pathways. <i>Genome Biology</i> , 2010, 11, R3.	13.9	456
139	Human Protein Reference Database–2009 update. <i>Nucleic Acids Research</i> , 2009, 37, D767-D772.	6.5	2,882
140	Human Proteinpedia: a unified discovery resource for proteomics research. <i>Nucleic Acids Research</i> , 2009, 37, D773-D781.	6.5	75
141	Human Protein Reference Database and Human Proteinpedia as Discovery Tools for Systems Biology. <i>Methods in Molecular Biology</i> , 2009, 577, 67-79.	0.4	245
142	Application of mass spectrometry-based proteomics for biomarker discovery in neurological disorders. <i>Annals of Indian Academy of Neurology</i> , 2009, 12, 3-11.	0.2	9
143	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008, 26, 164-167.	9.4	155
144	Quantitative proteomics using stable isotope labeling with amino acids in cell culture. <i>Nature Protocols</i> , 2008, 3, 505-516.	5.5	190

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145	A Quantitative Proteomic Approach for Identification of Potential Biomarkers in Hepatocellular Carcinoma. <i>Journal of Proteome Research</i> , 2008, 7, 4289-4298.	1.8	121
146	Activated Epidermal Growth Factor Receptor as a Novel Target in Pancreatic Cancer Therapy. <i>Journal of Proteome Research</i> , 2008, 7, 4651-4658.	1.8	42
147	Comparisons of tyrosine phosphorylated proteins in cells expressing lung cancer-specific alleles of EGFR and KRAS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 14112-14117.	3.3	113
148	Plasma Proteome Database as a resource for proteomics research. <i>Proteomics</i> , 2005, 5, 3531-3536.	1.3	135
149	A functional annotation of subproteomes in human plasma. <i>Proteomics</i> , 2005, 5, 3506-3519.	1.3	82
150	A Proteomic Analysis of Human Hemodialysis Fluid. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 637-650.	2.5	60
151	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, p12-p12.	1.6	74
152	Analysis of protein phosphorylation using mass spectrometry: deciphering the phosphoproteome. <i>Trends in Biotechnology</i> , 2002, 20, 261-268.	4.9	877
153	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.	2.5	4,931
154	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.	3.2	306
155	A reassessment of the translation initiation codon in vertebrates. <i>Trends in Genetics</i> , 2001, 17, 685-687.	2.9	98
156	Proteomics to study genes and genomes. <i>Nature</i> , 2000, 405, 837-846.	13.7	2,173
157	Nucleotide sequence databases: a gold mine for biologists. <i>Trends in Biochemical Sciences</i> , 1999, 24, 276-280.	3.7	72
158	Proteomic alterations in extracellular vesicles induced by oncogenic <i>PIK3CA</i> mutations. <i>Proteomics</i> , 0, , 2200077.	1.3	2