

# Anil K Madugundu

## List of Publications by Year in descending order

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Version: 2024-02-01

158  
papers

22,318  
citations

38742

50  
h-index

9345

143  
g-index

163  
all docs

163  
docs citations

163  
times ranked

30997  
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.	3.7	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.	3.5	7
3	Quantitative proteomic analysis of the frontal cortex in Alzheimer's disease. <i>Journal of Neurochemistry</i> , 2021, 156, 988-1002.	3.9	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.	1.1	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.	3.7	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.	3.8	21
7	Proteomics-based approach for differentiation of age-related macular degeneration sub-types. <i>Indian Journal of Ophthalmology</i> , 2021, 69, 647.	1.1	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.	2.8	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.	2.8	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.	4.1	9
11	Mapping the micro-proteome of the nuclear lamina and lamina-associated domains. <i>Life Science Alliance</i> , 2021, 4, e202000774.	2.8	26
12	Developmental partitioning of SYK and ZAP70 prevents autoimmunity and cancer. <i>Molecular Cell</i> , 2021, 81, 2094-2111.e9.	9.7	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.	3.7	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.	1.5	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.	3.7	2
16	A mass spectrometry-based targeted assay for detection of SARS-CoV-2 antigen from clinical specimens. <i>EBioMedicine</i> , 2021, 69, 103465.	6.1	44
17	DIA-Based Proteome Profiling of Nasopharyngeal Swabs from COVID-19 Patients. <i>Journal of Proteome Research</i> , 2021, 20, 4165-4175.	3.7	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.	3.2	22

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19	Quantitative Tyrosine Phosphoproteome Profiling of AXL Receptor Tyrosine Kinase Signaling Network. <i>Cancers</i> , 2021, 13, 4234.	3.7	1
20	Proximity-Dependent Biotinylation to Elucidate the Interactome of TNK2 Nonreceptor Tyrosine Kinase. <i>Journal of Proteome Research</i> , 2021, 20, 4566-4577.	3.7	3
21	High-resolution mass spectrometric analysis of cardiolipin profiles in Barth syndrome. <i>Mitochondrion</i> , 2021, 60, 27-32.	3.4	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.	3.0	41
23	Proteomic Signature of Host Response to SARS-CoV-2 Infection in the Nasopharynx. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100134.	3.8	25
24	Very long-chain acyl-CoA synthetase 3 mediates onco-sphingolipid metabolism in malignant glioma. <i>Medical Research Archives</i> , 2021, 9, .	0.2	5
25	Cerebrospinal fluid lipidomics for biomarkers of Alzheimer's disease. <i>Molecular Omics</i> , 2021, 17, 454-463.	2.8	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.	3.7	9
27	A SISCAPA-based approach for detection of SARS-CoV-2 viral antigens from clinical samples. <i>Clinical Proteomics</i> , 2021, 18, 25.	2.1	10
28	Sorbitol Is a Severity Biomarker for <scp>PMM2â€CDG</scp> with Therapeutic Implications. <i>Annals of Neurology</i> , 2021, 90, 887-900.	5.3	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.	2.4	5
30	Proteomic Signatures of Diffuse and Intestinal Subtypes of Gastric Cancer. <i>Cancers</i> , 2021, 13, 5930.	3.7	9
31	Integrative phosphoproteome and interactome analysis of the role of Ubash3b in BCR-ABL signaling. <i>Leukemia</i> , 2020, 34, 301-305.	7.2	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.	3.7	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.	4.0	16
34	PASS-DIA: A Data-Independent Acquisition Approach for Discovery Studies. <i>Analytical Chemistry</i> , 2020, 92, 14466-14475.	6.5	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.	3.0	25
36	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	28.9	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.	2.0	22
38	Signature Fragment Ions of Biotinylated Peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 394-404.	2.8	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.	3.6	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.	3.4	12
41	Accurate Precursor Mass Assignment Improves Peptide Identification in Data-Independent Acquisition Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 8453-8460.	6.5	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.	2.0	2
43	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019, 177, 1035-1049.e19.	28.9	498
44	Integrated Transcriptomic and Proteomic Analysis of Primary Human Umbilical Vein Endothelial Cells. <i>Proteomics</i> , 2019, 19, e1800315.	2.2	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.	3.8	25
46	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
47	Hotspot SF3B1 mutations induce metabolic reprogramming and vulnerability to serine deprivation. <i>Journal of Clinical Investigation</i> , 2019, 129, 4708-4723.	8.2	41
48	Proteogenomic Analysis to Identify Missing Proteins from Haploid Cell Lines. <i>Proteomics</i> , 2018, 18, e1700386.	2.2	13
49	Proteomics of the Human Olfactory Tract. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 77-87.	2.0	6
50	BioSITE: A Method for Direct Detection and Quantitation of Site-Specific Biotinylation. <i>Journal of Proteome Research</i> , 2018, 17, 759-769.	3.7	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.	7.1	122
52	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
53	Proteomic Analysis of the Human Anterior Pituitary Gland. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 759-769.	2.0	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.	8.8	263

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55	Phosphotyrosine profiling of human cerebrospinal fluid. <i>Clinical Proteomics</i> , 2018, 15, 29.	2.1	18
56	Phosphoproteomics of Retinoblastoma: A Pilot Study Identifies Aberrant Kinases. <i>Molecules</i> , 2018, 23, 1454.	3.8	12
57	Membrane Proteome of Invasive Retinoblastoma: Differential Proteins and Biomarkers. <i>Proteomics - Clinical Applications</i> , 2018, 12, e1700101.	1.6	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.	2.0	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.	2.0	21
60	Homer1a drives homeostatic scaling-down of excitatory synapses during sleep. <i>Science</i> , 2017, 355, 511-515.	12.6	398
61	Data-Driven Discovery of Extravasation Pathway in Circulating Tumor Cells. <i>Scientific Reports</i> , 2017, 7, 43710.	3.3	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.	2.0	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.	2.0	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.	5.6	73
65	Proteomic Analysis of the Human Olfactory Bulb. <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 440-453.	2.0	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.	2.0	23
67	PfCDPK1 mediated signaling in erythrocytic stages of <i>Plasmodium falciparum</i> . <i>Nature Communications</i> , 2017, 8, 63.	12.8	87
68	Integrating transcriptomic and proteomic data for accurate assembly and annotation of genomes. <i>Genome Research</i> , 2017, 27, 133-144.	5.5	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.	1.8	42
70	Common errors in mass spectrometry-based analysis of post-translational modifications. <i>Proteomics</i> , 2016, 16, 700-714.	2.2	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.	2.9	13
72	Unbiased identification of substrates of protein tyrosine phosphatase ptp $\beta$ in <i>C. elegans</i> . <i>Molecular Oncology</i> , 2016, 10, 910-920.	4.6	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.	2.0	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.	3.8	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.	8.5	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.	2.0	12
78	Proteomic profiling of retinoblastoma by high resolution mass spectrometry. Clinical Proteomics, 2016, 13, 29.	2.1	30
79	A dual specificity kinase, DYRK1A, as a potential therapeutic target for head and neck squamous cell carcinoma. Scientific Reports, 2016, 6, 36132.	3.3	36
80	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. Cell, 2016, 166, 755-765.	28.9	804
81	Long non-coding RNA expression in primary human monocytes. Genomics, 2016, 108, 37-45.	2.9	20
82	A pathway map of glutamate metabolism. Journal of Cell Communication and Signaling, 2016, 10, 69-75.	3.4	115
83	Using Quantitative Seroproteomics to Identify Antibody Biomarkers in Pancreatic Cancer. Cancer Immunology Research, 2016, 4, 225-233.	3.4	21
84	Proteogenomic Methods to Improve Genome Annotation. Methods in Molecular Biology, 2016, 1410, 77-89.	0.9	9
85	Dysregulation of splicing proteins in head and neck squamous cell carcinoma. Cancer Biology and Therapy, 2016, 17, 219-229.	3.4	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.	2.2	19
88	Comprehensive Proteomics Analysis of Glycosomes from <i>Leishmania donovani</i> . OMICS A Journal of Integrative Biology, 2015, 19, 157-170.	2.0	27
89	Phosphotyrosine profiling identifies ephrin receptor A2 as a potential therapeutic target in esophageal squamous cell carcinoma. Proteomics, 2015, 15, 374-382.	2.2	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. <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 283-293.	2.0	46
92	PGTools: A Software Suite for Proteogenomic Data Analysis and Visualization. <i>Journal of Proteome Research</i> , 2015, 14, 2255-2266.	3.7	52
93	Widespread somatic L1 retrotransposition occurs early during gastrointestinal cancer evolution. <i>Genome Research</i> , 2015, 25, 1536-1545.	5.5	121
94	Tissue matrix arrays for high-throughput screening and systems analysis of cell function. <i>Nature Methods</i> , 2015, 12, 1197-1204.	19.0	140
95	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
96	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
97	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
98	Proteogenomics. <i>Proteomics</i> , 2014, 14, 2631-2632.	2.2	9
99	Host response profile of human brain proteome in toxoplasma encephalitis co-infected with HIV. <i>Clinical Proteomics</i> , 2014, 11, 39.	2.1	18
100	Differential proteomic analysis of synovial fluid from rheumatoid arthritis and osteoarthritis patients. <i>Clinical Proteomics</i> , 2014, 11, 1.	2.1	113
101	Phosphoproteome of <i>Cryptococcus neoformans</i> . <i>Journal of Proteomics</i> , 2014, 97, 287-295.	2.4	41
102	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
103	Proteogenomic analysis of pathogenic yeast <i>Cryptococcus neoformans</i> using high resolution mass spectrometry. <i>Clinical Proteomics</i> , 2014, 11, 5.	2.1	18
104	A draft map of the human proteome. <i>Nature</i> , 2014, 509, 575-581.	27.8	1,948
105	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
106	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
107	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
108	Activation of diverse signalling pathways by oncogenic <i>PIK3CA</i> mutations. <i>Nature Communications</i> , 2014, 5, 4961.	12.8	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.	3.7	11
110	Proteomic analysis of human vitreous humor. <i>Clinical Proteomics</i> , 2014, 11, 29.	2.1	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.	2.0	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.	3.7	23
113	Functional Annotation of Proteome Encoded by Human Chromosome 22. <i>Journal of Proteome Research</i> , 2014, 13, 2749-2760.	3.7	22
114	Proteomic analysis of human osteoarthritis synovial fluid. <i>Clinical Proteomics</i> , 2014, 11, 6.	2.1	122
115	Chromosome-centric Human Proteome Project (C-HPP): Chromosome 12. <i>Journal of Proteome Research</i> , 2014, 13, 3160-3165.	3.7	4
116	Proteomic analysis of purified protein derivative of <i>Mycobacterium tuberculosis</i> . <i>Clinical Proteomics</i> , 2013, 10, 8.	2.1	26
117	Quantitative proteomics for identifying biomarkers for Rabies. <i>Clinical Proteomics</i> , 2013, 10, 3.	2.1	27
118	Characterizing the normal proteome of human ciliary body. <i>Clinical Proteomics</i> , 2013, 10, 9.	2.1	37
119	A compendium of molecules involved in vector-pathogen interactions pertaining to malaria. <i>Malaria Journal</i> , 2013, 12, 216.	2.3	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.	3.4	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.	3.7	15
123	Proteomic profiling of serum samples from chikungunya-infected patients provides insights into host response. <i>Clinical Proteomics</i> , 2013, 10, 14.	2.1	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.	1.8	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.	3.8	76



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127	Quantitative proteomics for identifying biomarkers for tuberculous meningitis. <i>Clinical Proteomics</i> , 2012, 9, 12.	2.1	26
128	Proteogenomic Analysis of <i>Candida glabrata</i> using High Resolution Mass Spectrometry. <i>Journal of Proteome Research</i> , 2012, 11, 247-260.	3.7	42
129	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
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.	7.1	157
131	Proteogenomic Analysis of <i>Mycobacterium tuberculosis</i> By High Resolution Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.011445.	3.8	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.	2.7	103
133	Human Protein Reference Database and Human Proteinpedia as Discovery Resources for Molecular Biotechnology. <i>Molecular Biotechnology</i> , 2011, 48, 87-95.	2.4	87
134	Proteogenomics. <i>Proteomics</i> , 2011, 11, 620-630.	2.2	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.	5.5	58
136	Quantitative tissue proteomics of esophageal squamous cell carcinoma for novel biomarker discovery. <i>Cancer Biology and Therapy</i> , 2011, 12, 510-522.	3.4	102
137	Phosphoproteomics in cancer. <i>Molecular Oncology</i> , 2010, 4, 482-495.	4.6	159
138	NetPath: a public resource of curated signal transduction pathways. <i>Genome Biology</i> , 2010, 11, R3.	9.6	456
139	Human Protein Reference Database–2009 update. <i>Nucleic Acids Research</i> , 2009, 37, D767-D772.	14.5	2,882
140	Human Proteinpedia: a unified discovery resource for proteomics research. <i>Nucleic Acids Research</i> , 2009, 37, D773-D781.	14.5	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.	0.9	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.	0.5	9
143	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008, 26, 164-167.	17.5	155
144	Quantitative proteomics using stable isotope labeling with amino acids in cell culture. <i>Nature Protocols</i> , 2008, 3, 505-516.	12.0	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.	3.7	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.	3.7	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.	7.1	113
148	Plasma Proteome Database as a resource for proteomics research. <i>Proteomics</i> , 2005, 5, 3531-3536.	2.2	135
149	A functional annotation of subproteomes in human plasma. <i>Proteomics</i> , 2005, 5, 3506-3519.	2.2	82
150	A Proteomic Analysis of Human Hemodialysis Fluid. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 637-650.	3.8	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.	3.6	74
152	Analysis of protein phosphorylation using mass spectrometry: deciphering the phosphoproteome. <i>Trends in Biotechnology</i> , 2002, 20, 261-268.	9.3	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.	3.8	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.	6.5	306
155	A reassessment of the translation initiation codon in vertebrates. <i>Trends in Genetics</i> , 2001, 17, 685-687.	6.7	98
156	Proteomics to study genes and genomes. <i>Nature</i> , 2000, 405, 837-846.	27.8	2,173
157	Nucleotide sequence databases: a gold mine for biologists. <i>Trends in Biochemical Sciences</i> , 1999, 24, 276-280.	7.5	72
158	Proteomic alterations in extracellular vesicles induced by oncogenic <i>PIK3CA</i> mutations. <i>Proteomics</i> , 0, , 2200077.	2.2	2