

Yanbao Yu

List of Publications by Year in descending order

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66
papers

23,854
citations

218677

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118850

62
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docs citations

74
times ranked

45402
citing authors

#	ARTICLE	IF	CITATIONS
1	Pandemic Influenza Infection Promotes Streptococcus pneumoniae Infiltration, Necrotic Damage, and Proteomic Remodeling in the Heart. MBio, 2022, 13, e0325721.	4.1	6
2	Application of nanomaterials in proteomics-driven precision medicine. Theranostics, 2022, 12, 2674-2686.	10.0	16
3	A genetic engineering strategy for editing near-infrared-II fluorophores. Nature Communications, 2022, 13, .	12.8	33
4	Oral Microbial Species and Virulence Factors Associated with Oral Squamous Cell Carcinoma. Microbial Ecology, 2021, 82, 1030-1046.	2.8	29
5	Protein signatures from blood plasma and urine suggest changes in vascular function and IL-12 signaling in elderly with a history of chronic diseases compared with an age-matched healthy cohort. GeroScience, 2021, 43, 593-606.	4.6	9
6	Lab-on-a-Filter Techniques for Economical, Effective, and Flexible Proteome Analysis. Methods in Molecular Biology, 2021, 2261, 25-34.	0.9	0
7	Influenza Causes MLKL-Driven Cardiac Proteome Remodeling During Convalescence. Circulation Research, 2021, 128, 570-584.	4.5	9
8	Protein and Microbial Biomarkers in Sputum Discern Acute and Latent Tuberculosis in Investigation of Pastoral Ethiopian Cohort. Frontiers in Cellular and Infection Microbiology, 2021, 11, 595554.	3.9	5
9	Urethral Catheter Biofilms Reveal Plasticity in Bacterial Composition and Metabolism and Withstand Host Immune Defenses in Hypoxic Environment. Frontiers in Medicine, 2021, 8, 667462.	2.6	4
10	Kinetic Multi-omic Analysis of Responses to SARS-CoV-2 Infection in a Model of Severe COVID-19. Journal of Virology, 2021, 95, e0101021.	3.4	21
11	The hepatocyte growth factor/c-met pathway is a key determinant of the fibrotic kidney local microenvironment. IScience, 2021, 24, 103112.	4.1	5
12	Serum integrative omics reveals the landscape of human diabetic kidney disease. Molecular Metabolism, 2021, 54, 101367.	6.5	20
13	Predictive Signatures of 19 Antibiotic-Induced <i>Escherichia coli</i> Proteomes. ACS Infectious Diseases, 2020, 6, 2120-2129.	3.8	8
14	Differences in plasma proteomes for active tuberculosis, latent tuberculosis and non-tuberculosis mycobacterial lung disease patients with and without ESAT-6/CFP10 stimulation. Proteome Science, 2020, 18, 10.	1.7	5
15	Global Proteome and Phosphoproteome Characterization of Sepsis-induced Kidney Injury. Molecular and Cellular Proteomics, 2020, 19, 2030-2047.	3.8	16
16	Salivary Bioscience and Periodontal Medicine. , 2020, , 419-447.		1
17	Detection of Neutrophil Extracellular Traps in Urine. Methods in Molecular Biology, 2019, 2021, 241-257.	0.9	6
18	Using Proteomics to Identify Inflammation During Urinary Tract Infection. Methods in Molecular Biology, 2019, 2021, 259-272.	0.9	13

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19	<i>Aerococcus urinae</i> and <i>Globicatella sanguinis</i> Persist in Polymicrobial Urethral Catheter Biofilms Examined in Longitudinal Profiles at the Proteomic Level. <i>Biochemistry Insights</i> , 2019, 12, 117862641987508.	3.3	6
20	Self-Assembled STrap for Global Proteomics and Salivary Biomarker Discovery. <i>Journal of Proteome Research</i> , 2019, 18, 1907-1915.	3.7	36
21	Impaired plasma membrane localization of ubiquitin ligase complex underlies 3-M syndrome development. <i>Journal of Clinical Investigation</i> , 2019, 129, 4393-4407.	8.2	14
22	Microbial metagenome of urinary tract infection. <i>Scientific Reports</i> , 2018, 8, 4333.	3.3	93
23	<i>Actinobaculum massiliense</i> Proteome Profiled in Polymicrobial Urethral Catheter Biofilms. <i>Proteomes</i> , 2018, 6, 52.	3.5	4
24	ProteoStorm: An Ultrafast Metaproteomics Database Search Framework. <i>Cell Systems</i> , 2018, 7, 463-467.e6.	6.2	27
25	S-Trap, an Ultrafast Sample-Preparation Approach for Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 2917-2924.	3.7	215
26	A Method to Generate and Analyze Modified Myristoylated Proteins. <i>ChemBioChem</i> , 2017, 18, 324-330.	2.6	6
27	Quick 96FASP for high throughput quantitative proteome analysis. <i>Journal of Proteomics</i> , 2017, 166, 1-7.	2.4	24
28	Type 1 Diabetes: Urinary Proteomics and Protein Network Analysis Support Perturbation of Lysosomal Function. <i>Theranostics</i> , 2017, 7, 2704-2717.	10.0	30
29	Characterization of Early-Phase Neutrophil Extracellular Traps in Urinary Tract Infections. <i>PLoS Pathogens</i> , 2017, 13, e1006151.	4.7	34
30	Comprehensive Metaproteomic Analyses of Urine in the Presence and Absence of Neutrophil-Associated Inflammation in the Urinary Tract. <i>Theranostics</i> , 2017, 7, 238-252.	10.0	34
31	The antiobesity factor <i>WDC1</i> suppresses adipogenesis via the <i>CRL4C^{WDC1}E3</i> ligase. <i>EMBO Reports</i> , 2016, 17, 638-647.	4.5	37
32	Hepatitis B Virus X Protein Promotes Degradation of SMC5/6 to Enhance HBV Replication. <i>Cell Reports</i> , 2016, 16, 2846-2854.	6.4	235
33	CRL4VprBP E3 Ligase Promotes Monoubiquitylation and Chromatin Binding of TET Dioxygenases. <i>Molecular Cell</i> , 2015, 57, 247-260.	9.7	90
34	Urine Sample Preparation in 96-well Filter Plates to Characterize Inflammatory and Infectious Diseases of the Urinary Tract. <i>Advances in Experimental Medicine and Biology</i> , 2015, 845, 77-87.	1.6	7
35	Diagnosing inflammation and infection in the urinary system via proteomics. <i>Journal of Translational Medicine</i> , 2015, 13, 111.	4.4	47
36	Similar Neutrophil-Driven Inflammatory and Antibacterial Responses in Elderly Patients with Symptomatic and Asymptomatic Bacteriuria. <i>Infection and Immunity</i> , 2015, 83, 4142-4153.	2.2	22

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37	Urinary Pellet Sample Preparation for Shotgun Proteomic Analysis of Microbial Infection and Host-Pathogen Interactions. <i>Methods in Molecular Biology</i> , 2015, 1295, 65-74.	0.9	21
38	Proteomes of pathogenic <i>Escherichia coli</i> / <i>Shigella</i> group surveyed in their host environments. <i>Expert Review of Proteomics</i> , 2014, 11, 593-609.	3.0	10
39	A chromatin activity-based chemoproteomic approach reveals a transcriptional repressor for gene-specific silencing. <i>Nature Communications</i> , 2014, 5, 5733.	12.8	34
40	The 3M Complex Maintains Microtubule and Genome Integrity. <i>Molecular Cell</i> , 2014, 54, 791-804.	9.7	61
41	Urine Sample Preparation in 96-Well Filter Plates for Quantitative Clinical Proteomics. <i>Analytical Chemistry</i> , 2014, 86, 5470-5477.	6.5	85
42	Whole human genome proteogenomic mapping for ENCODE cell line data: identifying protein-coding regions. <i>BMC Genomics</i> , 2013, 14, 141.	2.8	52
43	Protein Phosphatase 2A Catalytic Subunit $\hat{\pm}$ Plays a MyD88-Dependent, Central Role in the Gene-Specific Regulation of Endotoxin Tolerance. <i>Cell Reports</i> , 2013, 3, 678-688.	6.4	31
44	Cell Cycle-Regulated Protein Abundance Changes in Synchronously Proliferating HeLa Cells Include Regulation of Pre-mRNA Splicing Proteins. <i>PLoS ONE</i> , 2013, 8, e58456.	2.5	13
45	BCLAF1 is a radiation-induced H2AX-interacting partner involved in $\hat{3}$ H2AX-mediated regulation of apoptosis and DNA repair. <i>Cell Death and Disease</i> , 2012, 3, e359-e359.	6.3	73
46	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	27.8	15,516
47	Long noncoding RNAs are rarely translated in two human cell lines. <i>Genome Research</i> , 2012, 22, 1646-1657.	5.5	346
48	Incorporation of a fluorine diazirine group into phosphatidylinositol 4,5-bisphosphate to illustrate its interaction with ADP-ribosylation factor 1. <i>Organic and Biomolecular Chemistry</i> , 2012, 10, 5197.	2.8	6
49	The Mitochondrial Proteins NLRX1 and TUFM Form a Complex that Regulates Type I Interferon and Autophagy. <i>Immunity</i> , 2012, 36, 933-946.	14.3	241
50	Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108.	27.8	4,484
51	GOFAST: An Integrated Approach for Efficient and Comprehensive Membrane Proteome Analysis. <i>Analytical Chemistry</i> , 2012, 84, 9008-9014.	6.5	23
52	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). <i>PLoS Biology</i> , 2011, 9, e1001046.	5.6	1,257
53	Discovery of biomarker candidates for coronary artery disease from an APOE knock out mouse model using iTRAQ-based multiplex quantitative proteomics. <i>Proteomics</i> , 2011, 11, 2763-2776.	2.2	30
54	An optimized magnetite microparticle-based phosphopeptide enrichment strategy for identifying multiple phosphorylation sites in an immunoprecipitated protein. <i>Analytical Biochemistry</i> , 2011, 408, 19-31.	2.4	6

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55	Global analysis of the rat and human platelet proteome – the molecular blueprint for illustrating multi-functional platelets and cross-species function evolution. <i>Proteomics</i> , 2010, 10, 2444-2457.	2.2	33
56	Dissection of DEN-Induced Platelet Proteome Changes Reveals the Progressively Dys-Regulated Pathways Indicative of Hepatocarcinogenesis. <i>Journal of Proteome Research</i> , 2010, 9, 6207-6219.	3.7	7
57	Modulation of TLR Signaling by Multiple MyD88-Interacting Partners Including Leucine-Rich Repeat Fli-I-Interacting Proteins. <i>Journal of Immunology</i> , 2009, 182, 3450-3460.	0.8	75
58	Modifications of Superoxide Dismutase (SOD1) in Human Erythrocytes. <i>Journal of Biological Chemistry</i> , 2009, 284, 13940-13947.	3.4	106
59	Iterative Non-sharing Rule for Confident and Sensitive Protein Identification of Non-shotgun Proteomics. <i>Chinese Journal of Chemistry</i> , 2009, 27, 331-337.	4.9	0
60	Comprehensive profiling of metastasis-related proteins in paired hepatocellular carcinoma cells with different metastasis potentials. <i>Proteomics - Clinical Applications</i> , 2009, 3, 841-852.	1.6	11
61	Analysis of the protein complex associated with 14-3-3 epsilon by a deuterated-leucine labeling quantitative proteomics strategy. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2009, 877, 627-634.	2.3	26
62	In Vivo Profiling Endogenous Interactions with Knock-Out in Mammalian Cells. <i>Analytical Chemistry</i> , 2009, 81, 1411-1417.	6.5	7
63	Proteomic Dissection of Agonist-Specific TLR-Mediated Inflammatory Responses on Macrophages at Subcellular Resolution. <i>Journal of Proteome Research</i> , 2008, 7, 3180-3193.	3.7	15
64	Amino acid-coded tagging approaches in quantitative proteomics. <i>Expert Review of Proteomics</i> , 2007, 4, 25-37.	3.0	77
65	Preparation and stability of rhenium [188Re] sulfide suspension with different particle size distributions. <i>Journal of Radioanalytical and Nuclear Chemistry</i> , 2005, 265, 395-398.	1.5	1
66	A spinnable and automatable StageTip for high throughput peptide desalting and proteomics. <i>Protocol Exchange</i> , 0, , .	0.3	27