

# Moo-Jin Suh

## List of Publications by Year in descending order

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Version: 2024-02-01

26  
papers

1,039  
citations

516710

16  
h-index

580821

25  
g-index

28  
all docs

28  
docs citations

28  
times ranked

1872  
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteomic Analysis of Antibiotic Susceptibility in Enterobacteriaceae. <i>Methods in Molecular Biology</i> , 2021, 2296, 381-392.	0.9	1
2	Decreased Antibiotic Susceptibility Driven by Global Remodeling of the <i>Klebsiella pneumoniae</i> Proteome. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 657-668.	3.8	12
3	Antibiotic-dependent perturbations of extended spectrum beta-lactamase producing <i>Klebsiella pneumoniae</i> proteome. <i>Proteomics</i> , 2017, 17, 1700003.	2.2	12
4	Type 1 Diabetes: Urinary Proteomics and Protein Network Analysis Support Perturbation of Lysosomal Function. <i>Theranostics</i> , 2017, 7, 2704-2717.	10.0	30
5	Quantitative Differences in the Urinary Proteome of Siblings Discordant for Type 1 Diabetes Include Lysosomal Enzymes. <i>Journal of Proteome Research</i> , 2015, 14, 3123-3135.	3.7	26
6	Proteomics and Metaproteomics. , 2015, , 601-611.		0
7	Proteomes of pathogenic <i>Escherichia coli/Shigella</i> group surveyed in their host environments. <i>Expert Review of Proteomics</i> , 2014, 11, 593-609.	3.0	10
8	Urine Sample Preparation in 96-Well Filter Plates for Quantitative Clinical Proteomics. <i>Analytical Chemistry</i> , 2014, 86, 5470-5477.	6.5	85
9	Analysis of the Proteome of Intracellular <i>Shigella flexneri</i> Reveals Pathways Important for Intracellular Growth. <i>Infection and Immunity</i> , 2013, 81, 4635-4648.	2.2	45
10	Proteomic View of Interactions of Shiga Toxin-Producing <i>Escherichia coli</i> with the Intestinal Environment in Gnotobiotic Piglets. <i>PLoS ONE</i> , 2013, 8, e66462.	2.5	18
11	Development stage-specific proteomic profiling uncovers small, lineage specific proteins most abundant in the <i>Aspergillus Fumigatus</i> conidial proteome. <i>Proteome Science</i> , 2012, 10, 30.	1.7	56
12	Integrated next-generation sequencing of 16S rDNA and metaproteomics differentiate the healthy urine microbiome from asymptomatic bacteriuria in neuropathic bladder associated with spinal cord injury. <i>Journal of Translational Medicine</i> , 2012, 10, 174.	4.4	388
13	Characterizing the <i>Escherichia coli</i> O157:H7 Proteome Including Protein Associations with Higher Order Assemblies. <i>PLoS ONE</i> , 2011, 6, e26554.	2.5	20
14	Using chemical derivatization and mass spectrometric analysis to characterize the post-translationally modified <i>Staphylococcus aureus</i> surface protein G. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 1394-1404.	2.3	10
15	Retinol saturase promotes adipogenesis and is downregulated in obesity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1105-1110.	7.1	80
16	Limited proteolysis analysis of the ribosome is affected by subunit association. <i>Biopolymers</i> , 2009, 91, 410-422.	2.4	3
17	Integral and peripheral association of proteins and protein complexes with <i>Yersinia pestis</i> inner and outer membranes. <i>Proteome Science</i> , 2009, 7, 5.	1.7	26
18	Widespread Occurrence of Non-Enzymatic Deamidations of Asparagine Residues in <i>Yersinia pestis</i> Proteins Resulting from Alkaline pH Membrane Extraction Conditions. <i>The Open Proteomics Journal</i> , 2008, 1, 106-115.	0.4	5

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19	Cell proliferation inhibition and alterations in retinol esterification induced by phytanic acid and docosahexaenoic acid. <i>Journal of Lipid Research</i> , 2007, 48, 165-176.	4.2	16
20	Developing limited proteolysis and mass spectrometry for the characterization of ribosome topography. <i>Journal of the American Society for Mass Spectrometry</i> , 2007, 18, 1304-1317.	2.8	18
21	Structure Elucidation of Retinoids in Biological Samples Using Postsource Decay Laser Desorption/Ionization Mass Spectrometry after High-Performance Liquid Chromatography Separation. <i>Analytical Chemistry</i> , 2006, 78, 5719-5728.	6.5	7
22	Extending ribosomal protein identifications to unsequenced bacterial strains using matrix-assisted laser desorption/ionization mass spectrometry. <i>Proteomics</i> , 2005, 5, 4818-4831.	2.2	53
23	<i>Thermus thermophilus</i> L11 Methyltransferase, PrmA, Is Dispensable for Growth and Preferentially Modifies Free Ribosomal Protein L11 Prior to Ribosome Assembly. <i>Journal of Bacteriology</i> , 2004, 186, 5819-5825.	2.2	45
24	Investigation of Methods Suitable for the Matrix-Assisted Laser Desorption/Ionization Mass Spectrometric Analysis of Proteins from Ribonucleoprotein Complexes. <i>European Journal of Mass Spectrometry</i> , 2004, 10, 89-99.	1.0	26
25	Repair activities of 8-oxoguanine DNA glycosylase from <i>Archaeoglobus fulgidus</i> , a hyperthermophilic archaeon. <i>Mutation Research DNA Repair</i> , 2001, 486, 99-111.	3.7	25
26	Two Interaction Modes of the gp41-Derived Peptides with gp41 and Their Correlation with Antimembrane Fusion Activity. <i>Biochemical and Biophysical Research Communications</i> , 1999, 265, 625-629.	2.1	19