

# Jong Shin Yoo

## List of Publications by Year in descending order

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53  
papers

1,335  
citations

361413

20  
h-index

361022

35  
g-index

57  
all docs

57  
docs citations

57  
times ranked

1781  
citing authors

#	ARTICLE	IF	CITATIONS
1	Standard Guidelines for the Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2012, 11, 2005-2013.	3.7	135
2	Quantitative Analysis of an Aberrant Glycoform of TIMP1 from Colon Cancer Serum by L-PHA-Enrichment and SISCAPA with MRM Mass Spectrometry. <i>Journal of Proteome Research</i> , 2009, 8, 4216-4224.	3.7	84
3	Integrated GlycoProteome Analyzer (I-GPA) for Automated Identification and Quantitation of Site-Specific N-Glycosylation. <i>Scientific Reports</i> , 2016, 6, 21175.	3.3	81
4	Community evaluation of glycoproteomics informatics solutions reveals high-performance search strategies for serum glycopeptide analysis. <i>Nature Methods</i> , 2021, 18, 1304-1316.	19.0	74
5	Quantitative mass spectrometric analysis of glycoproteins combined with enrichment methods. <i>Mass Spectrometry Reviews</i> , 2015, 34, 148-165.	5.4	69
6	A lectin-coupled, targeted proteomic mass spectrometry (MRM MS) platform for identification of multiple liver cancer biomarkers in human plasma. <i>Journal of Proteomics</i> , 2012, 75, 5507-5515.	2.4	56
7	Analysis of ceramides in cosmetics by reversed-phase liquid chromatography/electrospray ionization mass spectrometry with collision-induced dissociation. <i>Rapid Communications in Mass Spectrometry</i> , 2003, 17, 64-75.	1.5	49
8	Glyco-Analytical Multispecific Proteolysis (Glyco-AMP): A Simple Method for Detailed and Quantitative Glycoproteomic Characterization. <i>Journal of Proteome Research</i> , 2013, 12, 4414-4423.	3.7	42
9	Launching the C-HPP neXt-CP50 Pilot Project for Functional Characterization of Identified Proteins with No Known Function. <i>Journal of Proteome Research</i> , 2018, 17, 4042-4050.	3.7	41
10	Title is missing!. <i>Journal of Inclusion Phenomena and Macrocyclic Chemistry</i> , 2000, 36, 55-64.	1.6	40
11	Profiling human brain proteome by multi-dimensional separations coupled with MS. <i>Proteomics</i> , 2006, 6, 4978-4986.	2.2	39
12	Comparative Quantitation of Aberrant Glycoforms by Lectin-Based Glycoprotein Enrichment Coupled with Multiple-Reaction Monitoring Mass Spectrometry. <i>Analytical Chemistry</i> , 2010, 82, 4441-4447.	6.5	39
13	Characterization of Site-Specific N-Glycopeptide Isoforms of Î±-1-Acid Glycoprotein from an Interlaboratory Study Using LC-MS/MS. <i>Journal of Proteome Research</i> , 2016, 15, 4146-4164.	3.7	35
14	In-depth analysis of site-specific N-glycosylation in vitronectin from human plasma by tandem mass spectrometry with immunoprecipitation. <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 7999-8011.	3.7	31
15	Utility of electrophoretically derived protein mass estimates as additional constraints in proteome analysis of human serum based on MS/MS analysis. <i>Proteomics</i> , 2005, 5, 3376-3385.	2.2	30
16	Parallel reaction monitoring with multiplex immunoprecipitation of N-glycoproteins in human serum for detection of hepatocellular carcinoma. <i>Analytical and Bioanalytical Chemistry</i> , 2019, 411, 3009-3019.	3.7	28
17	Quantitative analysis of aberrant protein glycosylation in liver cancer plasma by AAL-enrichment and MRM mass spectrometry. <i>Analyst</i> , The, 2013, 138, 6454.	3.5	26
18	Human plasma proteome analysis by reversed sequence database search and molecular weight correlation based on a bacterial proteome analysis. <i>Proteomics</i> , 2006, 6, 1121-1132.	2.2	25

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19	A lectin-coupled, multiple reaction monitoring based quantitative analysis of human plasma glycoproteins by mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 402, 2101-2112.	3.7	25
20	Isomer separation of sialylated O- and N-linked glycopeptides using reversed-phase LC-MS/MS at high temperature. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2019, 1110-1111, 101-107.	2.3	25
21	Machine Learning Classifies Core and Outer Fucosylation of N-Glycoproteins Using Mass Spectrometry. <i>Scientific Reports</i> , 2020, 10, 318.	3.3	21
22	Direct Monitoring of Fucosylated Glycopeptides of Alpha-Fetoprotein in Human Serum for Early Hepatocellular Carcinoma by Liquid Chromatography-Tandem Mass Spectrometry with Immunoprecipitation. <i>Proteomics - Clinical Applications</i> , 2018, 12, e1800062.	1.6	20
23	Efficiency improvement of peptide identification for an organism without complete genome sequence, using expressed sequence tag database and tandem mass spectral data. <i>Proteomics</i> , 2003, 3, 2305-2309.	2.2	19
24	Alteration in the glycan pattern of pilin in a nonmotile mutant of <i>Synechocystis</i> sp. PCC 6803. <i>Proteomics</i> , 2009, 9, 1075-1086.	2.2	19
25	Dynamic identification of phosphopeptides using immobilized metal ion affinity chromatography enrichment, subsequent partial- $\alpha$ -elimination/chemical tagging and matrix-assisted laser desorption/ionization mass spectrometric analysis. <i>Rapid Communications in Mass Spectrometry</i> , 2004, 18, 2495-2501.	1.5	18
26	A Proteotranscriptomic-Based Computational Drug-Repositioning Method for Alzheimer's Disease. <i>Frontiers in Pharmacology</i> , 2019, 10, 1653.	3.5	18
27	Identification of acylated glycolipids from a cyanobacterium, <i>Synechocystis</i> sp., by tandem mass spectrometry. <i>Lipids</i> , 1999, 34, 847-853.	1.7	17
28	Classification of Mucin-Type <i>O</i> -Glycopeptides Using Higher-Energy Collisional Dissociation in Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 9772-9781.	6.5	16
29	MRM validation of targeted nonglycosylated peptides from N-glycoprotein biomarkers using direct trypsin digestion of undepleted human plasma. <i>Journal of Proteomics</i> , 2014, 98, 206-217.	2.4	15
30	Analysis of fucosylation in liver-secreted N-glycoproteins from human hepatocellular carcinoma plasma using liquid chromatography with tandem mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 7761-7774.	3.7	15
31	Arginine-mimic labeling with guanidinoethanethiol to increase mass sensitivity of lysine-terminated phosphopeptides by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2007, 21, 2204-2210.	1.5	14
32	Coupling of TiO <sub>2</sub> -mediated enrichment and on-bead guanidinoethanethiol labeling for effective phosphopeptide analysis by matrix-assisted laser desorption/ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2007, 21, 3987-3994.	1.5	14
33	Quantitative analysis of low-abundance serological proteins with peptide affinity-based enrichment and pseudo-multiple reaction monitoring by hybrid quadrupole time-of-flight mass spectrometry. <i>Analytica Chimica Acta</i> , 2015, 882, 38-48.	5.4	14
34	Next Generation Proteomic Pipeline for Chromosome-Based Proteomic Research Using NeXtProt and GENCODE Databases. <i>Journal of Proteome Research</i> , 2017, 16, 4425-4434.	3.7	14
35	Identification of Missing Proteins in Human Olfactory Epithelial Tissue by Liquid Chromatography-Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2018, 17, 4320-4324.	3.7	14
36	Absolute Quantification of <i>N</i> -Glycosylation of Alpha-Fetoprotein Using Parallel Reaction Monitoring with Stable Isotope-Labeled <i>N</i> -Glycopeptide as an Internal Standard. <i>Analytical Chemistry</i> , 2020, 92, 12588-12595.	6.5	13

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37	Differential proteomic approach for identification and verification of aberrantly glycosylated proteins in adenocarcinoma lung cancer (ADLC) plasmas by lectin-capturing and targeted mass spectrometry. <i>Journal of Proteomics</i> , 2014, 106, 221-229.	2.4	11
38	BMDMS-NP: A comprehensive ESI-MS/MS spectral library of natural compounds. <i>Phytochemistry</i> , 2020, 177, 112427.	2.9	11
39	Quantitative proteomic analysis reveals that lipopolysaccharide induces mitogen-activated protein kinase-dependent activation in human microglial cells. <i>Electrophoresis</i> , 2012, 33, 3756-3763.	2.4	10
40	The "hybrid cell"™: a new compensated infinity cell for larger radius ion excitation in Fourier transform ion cyclotron resonance mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2008, 22, 1423-1429.	1.5	9
41	Direct analysis of site-specific N-glycopeptides of serological proteins in dried blood spot samples. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 4971-4981.	3.7	8
42	Selective Identification of Î±-Galactosyl Epitopes in N-Glycoproteins Using Characteristic Fragment Ions from Higher-Energy Collisional Dissociation. <i>Analytical Chemistry</i> , 2020, 92, 13144-13154.	6.5	6
43	Island clustering analysis for the comparison of the membrane and the soluble protein fractions of human brain proteome. <i>Proteomics</i> , 2008, 8, 1149-1161.	2.2	5
44	Mass spectrometry analysis of glycoprotein biomarkers in human blood of hepatocellular carcinoma. <i>Expert Review of Proteomics</i> , 2019, 16, 553-568.	3.0	5
45	Computational classification of core and outer fucosylation of N-glycoproteins in human plasma using collision-induced dissociation in mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2020, 34, e8917.	1.5	5
46	Depletion of ST6GALNACIII retards A549 non-small cell lung cancer cell proliferation by downregulating transferrin receptor protein 1 expression. <i>Biochemical and Biophysical Research Communications</i> , 2021, 575, 78-84.	2.1	5
47	Defect in cytosolic Neu2 sialidase abrogates lipid metabolism and impairs muscle function in vivo. <i>Scientific Reports</i> , 2022, 12, 3216.	3.3	5
48	Bioinformatic Prediction of Gene Ontology Terms of Uncharacterized Proteins from Chromosome 11. <i>Journal of Proteome Research</i> , 2020, 19, 4907-4912.	3.7	3
49	Improved ion transmission through the gate valve of a new hybrid ion guide for Fourier transform ion cyclotron resonance mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2010, 24, 469-472.	1.5	2
50	Measuring fucosylated alpha-fetoprotein in hepatocellular carcinoma: A comparison of Î¼TAS and parallel reaction monitoring. <i>Proteomics - Clinical Applications</i> , 2021, 15, 2000096.	1.6	2
51	Flashlight into the Function of Unannotated C11orf52 using Affinity Purification Mass Spectrometry. <i>Journal of Proteome Research</i> , 2021, 20, 5340-5346.	3.7	2
52	Human microglial cells synthesize albumin in brain. <i>Nature Precedings</i> , 2008, , .	0.1	1
53	SAAVpedia: Identification, Functional Annotation, and Retrieval of Single Amino Acid Variants for Proteogenomic Interpretation. <i>Journal of Proteome Research</i> , 2019, 18, 4133-4142.	3.7	1