Jong Shin Yoo

List of Publications by Year
in descending order

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	Defect in cytosolic Neu2 sialidase abrogates lipid metabolism and impairs muscle function in vivo. Scientific Reports, 2022, 12, 3216.	3.3	5
2	Measuring fucosylated alphaâ€fetoprotein in hepatocellular carcinoma: A comparison of μTAS and parallel reaction monitoring. Proteomics - Clinical Applications, 2021, 15, 2000096.	1.6	2
3	Depletion of ST6GALNACIII retards A549 non-small cell lung cancer cell proliferation by downregulating transferrin receptor protein 1 expression. Biochemical and Biophysical Research Communications, 2021, 575, 78-84.	2.1	5
4	Community evaluation of glycoproteomics informatics solutions reveals high-performance search strategies for serum glycopeptide analysis. Nature Methods, 2021, 18, 1304-1316.	19.0	74
5	Flashlight into the Function of Unannotated C11orf52 using Affinity Purification Mass Spectrometry. Journal of Proteome Research, 2021, 20, 5340-5346.	3.7	2
6	Absolute Quantification of N-Glycosylation of Alpha-Fetoprotein Using Parallel Reaction Monitoring with Stable Isotope-Labeled N-Glycopeptide as an Internal Standard. Analytical Chemistry, 2020, 92, 12588-12595.	6.5	13
7	Bioinformatic Prediction of Gene Ontology Terms of Uncharacterized Proteins from Chromosome 11. Journal of Proteome Research, 2020, 19, 4907-4912.	3.7	3
8	Computational classification of core and outer fucosylation of Nâ€glycoproteins in human plasma using collisionâ€induced dissociation in mass spectrometry. Rapid Communications in Mass Spectrometry, 2020, 34, e8917.	1.5	5
9	Selective Identification of α-Galactosyl Epitopes in N-Glycoproteins Using Characteristic Fragment Ions from Higher-Energy Collisional Dissociation. Analytical Chemistry, 2020, 92, 13144-13154.	6.5	6
10	BMDMS-NP: A comprehensive ESI-MS/MS spectral library of natural compounds. Phytochemistry, 2020, 177, 112427.	2.9	11
11	Classification of Mucin-Type O-Glycopeptides Using Higher-Energy Collisional Dissociation in Mass Spectrometry. Analytical Chemistry, 2020, 92, 9772-9781.	6.5	16
12	Machine Learning Classifies Core and Outer Fucosylation of N-Glycoproteins Using Mass Spectrometry. Scientific Reports, 2020, 10, 318.	3.3	21
13	SAAVpedia: Identification, Functional Annotation, and Retrieval of Single Amino Acid Variants for Proteogenomic Interpretation. Journal of Proteome Research, 2019, 18, 4133-4142.	3.7	1
14	Mass spectrometry analysis of glycoprotein biomarkers in human blood of hepatocellular carcinoma. Expert Review of Proteomics, 2019, 16, 553-568.	3.0	5
15	Parallel reaction monitoring with multiplex immunoprecipitation of N-glycoproteins in human serum for detection of hepatocellular carcinoma. Analytical and Bioanalytical Chemistry, 2019, 411, 3009-3019.	3.7	28
16	Isomer separation of sialylated O- and N-linked glycopeptides using reversed-phase LCâ€"MS/MS at high temperature. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2019, 1110-1111, 101-107.	2.3	25
17	A Proteotranscriptomic-Based Computational Drug-Repositioning Method for Alzheimerâ€™s Disease. Frontiers in Pharmacology, 2019, 10, 1653.	3.5	18
18	Launching the C-HPP neXt-CP50 Pilot Project for Functional Characterization of Identified Proteins with No Known Function. Journal of Proteome Research, 2018, 17, 4042-4050.	3.7	41

#	ARTICLE	IF	CITATIONS
19	Identification of Missing Proteins in Human Olfactory Epithelial Tissue by Liquid Chromatographyâ€"Tandem Mass Spectrometry. Journal of Proteome Research, 2018, 17, 4320-4324.	3.7	14
20	Direct Monitoring of Fucosylated Glycopeptides of Alphaâ€"Fetoprotein in Human Serum for Early Hepatocellular Carcinoma by Liquid Chromatographyâ€"Tandem Mass Spectrometry with Immunoprecipitation. Proteomics - Clinical Applications, 2018, 12, e1800062.	1.6	20
21	Next Generation Proteomic Pipeline for Chromosome-Based Proteomic Research Using NeXtProt and GENCODE Databases. Journal of Proteome Research, 2017, 16, 4425-4434.	3.7	14
22	Direct analysis of site-specific N-glycopeptides of serological proteins in dried blood spot samples. Analytical and Bioanalytical Chemistry, 2017, 409, 4971-4981.	3.7	8
23	Integrated GlycoProteome Analyzer (I-GPA) for Automated Identification and Quantitation of Site-Specific N-Glycosylation. Scientific Reports, 2016, 6, 21175.	3.3	81
24	Analysis of fucosylation in liver-secreted N-glycoproteins from human hepatocellular carcinoma plasma using liquid chromatography with tandem mass spectrometry. Analytical and Bioanalytical Chemistry, 2016, 408, 7761-7774.	3.7	15
25	Characterization of Site-Specific *N*-Glycopeptide Isoforms of Î±-1-Acid Glycoprotein from an Interlaboratory Study Using LCâ€"MS/MS. Journal of Proteome Research, 2016, 15, 4146-4164.	3.7	35
26	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. Analytica Chimica Acta, 2015, 882, 38-48.	5.4	14
27	Quantitative mass spectrometric analysis of glycoproteins combined with enrichment methods. Mass Spectrometry Reviews, 2015, 34, 148-165.	5.4	69
28	In-depth analysis of site-specific N-glycosylation in vitronectin from human plasma by tandem mass spectrometry with immunoprecipitation. Analytical and Bioanalytical Chemistry, 2014, 406, 7999-8011.	3.7	31
29	MRM validation of targeted nonglycosylated peptides from N-glycoprotein biomarkers using direct trypsin digestion of undepleted human plasma. Journal of Proteomics, 2014, 98, 206-217.	2.4	15
30	Differential proteomic approach for identification and verification of aberrantly glycosylated proteins in adenocarcinoma lung cancer (ADLC) plasmas by lectin-capturing and targeted mass spectrometry. Journal of Proteomics, 2014, 106, 221-229.	2.4	11
31	Glyco-Analytical Multispecific Proteolysis (Glyco-AMP): A Simple Method for Detailed and Quantitative Glycoproteomic Characterization. Journal of Proteome Research, 2013, 12, 4414-4423.	3.7	42
32	Quantitative analysis of aberrant protein glycosylation in liver cancer plasma by AAL-enrichment and MRM mass spectrometry. Analyst, The, 2013, 138, 6454.	3.5	26
33	Quantitative proteomic analysis reveals that lipopolysaccharide induces mitogenâ€"activated protein kinaseâ€"dependent activation in human microglial cells. Electrophoresis, 2012, 33, 3756-3763.	2.4	10
34	A lectin-coupled, targeted proteomic mass spectrometry (MRM MS) platform for identification of multiple liver cancer biomarkers in human plasma. Journal of Proteomics, 2012, 75, 5507-5515.	2.4	56
35	Standard Guidelines for the Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2012, 11, 2005-2013.	3.7	135
36	A lectin-coupled, multiple reaction monitoring based quantitative analysis of human plasma glycoproteins by mass spectrometry. Analytical and Bioanalytical Chemistry, 2012, 402, 2101-2112.	3.7	25

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37	Improved ion transmission through the gate valve of a new hybrid ion guide for Fourier transform ion cyclotron resonance mass spectrometry. Rapid Communications in Mass Spectrometry, 2010, 24, 469-472.	1.5	2
38	Comparative Quantitation of Aberrant Glycoforms by Lectin-Based Glycoprotein Enrichment Coupled with Multiple-Reaction Monitoring Mass Spectrometry. Analytical Chemistry, 2010, 82, 4441-4447.	6.5	39
39	Alteration in the glycan pattern of pilin in a nonmotile mutant of Synechocystis sp. PCC 6803. Proteomics, 2009, 9, 1075-1086.	2.2	19
40	Quantitative Analysis of an Aberrant Glycoform of TIMP1 from Colon Cancer Serum by L-PHA-Enrichment and SISCAPA with MRM Mass Spectrometry. Journal of Proteome Research, 2009, 8, 4216-4224.	3.7	84
41	Island clustering analysis for the comparison of the membrane and the soluble protein fractions of human brain proteome. Proteomics, 2008, 8, 1149-1161.	2.2	5
42	The â€˜hybrid cellâ€™: a new compensated infinity cell for larger radius ion excitation in Fourier transform ion cyclotron resonance mass spectrometry. Rapid Communications in Mass Spectrometry, 2008, 22, 1423-1429.	1.5	9
43	Human microglial cells synthesize albumin in brain. Nature Precedings, 2008, , .	0.1	1
44	Arginine-mimic labeling with guanidinoethanethiol to increase mass sensitivity of lysine-terminated phosphopeptides by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. Rapid Communications in Mass Spectrometry, 2007, 21, 2204-2210.	1.5	14
45	Coupling of TiO₂â€“mediated enrichment and onâ€“bead guanidinoethanethiol labeling for effective phosphopeptide analysis by matrixâ€“assisted laser desorption/ionization mass spectrometry. Rapid Communications in Mass Spectrometry, 2007, 21, 3987-3994.	1.5	14
46	Human plasma proteome analysis by reversed sequence database search and molecular weight correlation based on a bacterial proteome analysis. Proteomics, 2006, 6, 1121-1132.	2.2	25
47	Profiling human brain proteome by multi-dimensional separations coupled with MS. Proteomics, 2006, 6, 4978-4986.	2.2	39
48	Utility of electrophoretically derived protein mass estimates as additional constraints in proteome analysis of human serum based on MS/MS analysis. Proteomics, 2005, 5, 3376-3385.	2.2	30
49	Dynamic identification of phosphopeptides using immobilized metal ion affinity chromatography enrichment, subsequent partialβ-elimination/chemical tagging and matrix-assisted laser desorption/ionization mass spectrometric analysis. Rapid Communications in Mass Spectrometry, 2004, 18, 2495-2501.	1.5	18
50	Efficiency improvement of peptide identification for an organism without complete genome sequence, using expressed sequence tag database and tandem mass spectral data. Proteomics, 2003, 3, 2305-2309.	2.2	19
51	Analysis of ceramides in cosmetics by reversed-phase liquid chromatography/electrospray ionization mass spectrometry with collision-induced dissociation. Rapid Communications in Mass Spectrometry, 2003, 17, 64-75.	1.5	49
52	Title is missing!. Journal of Inclusion Phenomena and Macrocyclic Chemistry, 2000, 36, 55-64.	1.6	40
53	Identification of acylated glycoglycerolipids from a cyanobacterium, Synechocystis sp., by tandem mass spectrometry. Lipids, 1999, 34, 847-853.	1.7	17