

Hyoung-Joo Lee

List of Publications by Year in descending order

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36
papers

1,414
citations

394286

19
h-index

360920

35
g-index

36
all docs

36
docs citations

36
times ranked

2250
citing authors

#	ARTICLE	IF	CITATIONS
1	Epsilon-Q: An Automated Analyzer Interface for Mass Spectral Library Search and Label-Free Protein Quantification. <i>Journal of Proteome Research</i> , 2017, 16, 4435-4445.	1.8	9
2	Next Generation Proteomic Pipeline for Chromosome-Based Proteomic Research Using NeXtProt and GENCODE Databases. <i>Journal of Proteome Research</i> , 2017, 16, 4425-4434.	1.8	14
3	gFinder: A Web-Based Bioinformatics Tool for the Analysis of <i>N</i> -Glycopeptides. <i>Journal of Proteome Research</i> , 2016, 15, 4116-4125.	1.8	12
4	Integrated Proteomic Pipeline Using Multiple Search Engines for a Proteogenomic Study with a Controlled Protein False Discovery Rate. <i>Journal of Proteome Research</i> , 2016, 15, 4082-4090.	1.8	34
5	Efficient Microscale Basic Reverse Phase Peptide Fractionation for Global and Targeted Proteomics. <i>Journal of Proteome Research</i> , 2016, 15, 2346-2354.	1.8	17
6	Quantitative Profiling Identifies Potential Regulatory Proteins Involved in Development from Dauer Stage to L4 Stage in <i>Caenorhabditis elegans</i> . <i>Journal of Proteome Research</i> , 2016, 15, 531-539.	1.8	2
7	Quantitative Profiling of Protein Tyrosine Kinases in Human Cancer Cell Lines by Multiplexed Parallel Reaction Monitoring Assays. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 682-691.	2.5	39
8	Chromosome-Based Proteomic Study for Identifying Novel Protein Variants from Human Hippocampal Tissue Using Customized neXtProt and GENCODE Databases. <i>Journal of Proteome Research</i> , 2015, 14, 5028-5037.	1.8	4
9	Integrated Proteomic and Genomic Analysis of Gastric Cancer Patient Tissues. <i>Journal of Proteome Research</i> , 2015, 14, 4995-5006.	1.8	7
10	Distinct Protein Expression Profiles of Solid-Pseudopapillary Neoplasms of the Pancreas. <i>Journal of Proteome Research</i> , 2015, 14, 3007-3014.	1.8	23
11	Combination of Multiple Spectral Libraries Improves the Current Search Methods Used to Identify Missing Proteins in the Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2015, 14, 4959-4966.	1.8	14
12	Proteogenomic Analysis of Human Chromosome 9-Encoded Genes from Human Samples and Lung Cancer Tissues. <i>Journal of Proteome Research</i> , 2014, 13, 137-146.	1.8	16
13	Abundance-Ratio-Based Semiquantitative Analysis of Site-Specific N-Linked Glycopeptides Present in the Plasma of Hepatocellular Carcinoma Patients. <i>Journal of Proteome Research</i> , 2014, 13, 2328-2338.	1.8	39
14	NSBP-1 mediates the effects of cholesterol on insulin/IGF-1 signaling in <i>Caenorhabditis elegans</i> . <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 1623-1636.	2.4	13
15	GenomewidePDB, a Proteomic Database Exploring the Comprehensive Protein Parts List and Transcriptome Landscape in Human Chromosomes. <i>Journal of Proteome Research</i> , 2013, 12, 106-111.	1.8	21
16	Comprehensive Genome-Wide Proteomic Analysis of Human Placental Tissue for the Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2013, 12, 2458-2466.	1.8	30
17	Chromosome 11-Centric Human Proteome Analysis of Human Brain Hippocampus Tissue. <i>Journal of Proteome Research</i> , 2013, 12, 97-105.	1.8	20
18	Standard Guidelines for the Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2012, 11, 2005-2013.	1.8	135

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19	The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. <i>Nature Biotechnology</i> , 2012, 30, 221-223.	9.4	281
20	Quantitative Proteomic Analysis of Human Embryonic Stem Cell Differentiation by 8-Plex iTRAQ Labelling. <i>PLoS ONE</i> , 2012, 7, e38532.	1.1	23
21	Enhanced peptide quantification using spectral count clustering and cluster abundance. <i>BMC Bioinformatics</i> , 2011, 12, 423.	1.2	10
22	A new versatile peptide-based size exclusion chromatography platform for global profiling and quantitation of candidate biomarkers in hepatocellular carcinoma specimens. <i>Proteomics</i> , 2011, 11, 1976-1984.	1.3	5
23	Contribution of sams-1 and pmt-1 to lipid homeostasis in adult <i>Caenorhabditis elegans</i> . <i>Journal of Biochemistry</i> , 2011, 149, 529-538.	0.9	49
24	Targeted Mass Spectrometric Approach for Biomarker Discovery and Validation with Nonglycosylated Tryptic Peptides from N-linked Glycoproteins in Human Plasma. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.009290.	2.5	38
25	Data management and functional annotation of the Korean reference plasma proteome. <i>Proteomics</i> , 2010, 10, 1250-1255.	1.3	8
26	FISH: Finding of identical spectra set for Homogenous peptide using two-stage clustering algorithm. , 2010, , .		0
27	Simple Method for Quantitative Analysis of N-Linked Glycoproteins in Hepatocellular Carcinoma Specimens. <i>Journal of Proteome Research</i> , 2010, 9, 308-318.	1.8	43
28	BiomarkerDigger: A versatile disease proteome database and analysis platform for the identification of plasma cancer biomarkers. <i>Proteomics</i> , 2009, 9, 3729-3740.	1.3	19
29	Quantitative analysis of phosphopeptides in search of the disease biomarker from the hepatocellular carcinoma specimen. <i>Proteomics</i> , 2009, 9, 3395-3408.	1.3	53
30	Human plasma carboxylesterase 1, a novel serologic biomarker candidate for hepatocellular carcinoma. <i>Proteomics</i> , 2009, 9, 3989-3999.	1.3	100
31	Establishment of a PF2D-MS/MS platform for rapid profiling and semiquantitative analysis of membrane protein biomarkers. <i>Proteomics</i> , 2008, 8, 2168-2177.	1.3	21
32	Application of a peptide-based PF2D platform for quantitative proteomics in disease biomarker discovery. <i>Proteomics</i> , 2008, 8, 3371-3381.	1.3	32
33	Protein Profiling of Human Plasma Samples by Two-Dimensional Electrophoresis. <i>Methods in Molecular Biology</i> , 2008, 428, 57-75.	0.4	18
34	Proteomic analysis of mammalian basic proteins by liquid-based two-dimensional column chromatography. <i>Proteomics</i> , 2006, 6, 1143-1150.	1.3	40
35	Biomarker discovery from the plasma proteome using multidimensional fractionation proteomics. <i>Current Opinion in Chemical Biology</i> , 2006, 10, 42-49.	2.8	104
36	Efficient prefractionation of low-abundance proteins in human plasma and construction of a two-dimensional map. <i>Proteomics</i> , 2005, 5, 3386-3396.	1.3	121