

Siu Kwan Sze

List of Publications by Year in descending order

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255
papers

14,046
citations

23500

58
h-index

28224

105
g-index

274
all docs

274
docs citations

274
times ranked

22454
citing authors

#	ARTICLE	IF	CITATIONS
1	Exosome secreted by MSC reduces myocardial ischemia/reperfusion injury. <i>Stem Cell Research</i> , 2010, 4, 214-222.	0.3	1,831
2	Hypoxic Tumor Cell Modulates Its Microenvironment to Enhance Angiogenic and Metastatic Potential by Secretion of Proteins and Exosomes. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1085-1099.	2.5	459
3	Proteolytic Potential of the MSC Exosome Proteome: Implications for an Exosome-Mediated Delivery of Therapeutic Proteasome. <i>International Journal of Proteomics</i> , 2012, 2012, 1-14.	2.0	394
4	Human mesenchymal stem cell-conditioned medium improves cardiac function following myocardial infarction. <i>Stem Cell Research</i> , 2011, 6, 206-214.	0.3	379
5	Design and Synthesis of Minimalist Terminal Alkyne-Containing Diazirine Photo-Crosslinkers and Their Incorporation into Kinase Inhibitors for Cell- and Tissue-Based Proteome Profiling. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 8551-8556.	7.2	281
6	Sall4 Interacts with Nanog and Co-occupies Nanog Genomic Sites in Embryonic Stem Cells. <i>Journal of Biological Chemistry</i> , 2006, 281, 24090-24094.	1.6	253
7	Top-down mass spectrometry of a 29-kDa protein for characterization of any posttranslational modification to within one residue. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 1774-1779.	3.3	248
8	CDK5RAP2 stimulates microtubule nucleation by the β -tubulin ring complex. <i>Journal of Cell Biology</i> , 2010, 191, 1089-1095.	2.3	248
9	Elucidating the Secretion Proteome of Human Embryonic Stem Cell-derived Mesenchymal Stem Cells. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1680-1689.	2.5	240
10	HERC5 is an IFN-induced HECT-type E3 protein ligase that mediates type I IFN-induced ISGylation of protein targets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 10735-10740.	3.3	233
11	Secondary and tertiary structures of gaseous protein ions characterized by electron capture dissociation mass spectrometry and photofragment spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 15863-15868.	3.3	226
12	Hypoxia-induced tumor exosomes promote M2-like macrophage polarization of infiltrating myeloid cells and microRNA-mediated metabolic shift. <i>Oncogene</i> , 2019, 38, 5158-5173.	2.6	212
13	Raman spectroscopic characterization of carbonaceous aerosols. <i>Atmospheric Environment</i> , 2001, 35, 561-568.	1.9	198
14	MSC secretes at least 3 EV types each with a unique permutation of membrane lipid, protein and RNA. <i>Journal of Extracellular Vesicles</i> , 2016, 5, 29828.	5.5	187
15	Quantitative Time-course Profiling of Parasite and Host Cell Proteins in the Human Malaria Parasite <i>Plasmodium falciparum</i> . <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.006411.	2.5	145
16	The methyltransferase Ezh2 controls cell adhesion and migration through direct methylation of the extranuclear regulatory protein talin. <i>Nature Immunology</i> , 2015, 16, 505-516.	7.0	144
17	Selective labelling and eradication of antibiotic-tolerant bacterial populations in <i>Pseudomonas aeruginosa</i> biofilms. <i>Nature Communications</i> , 2016, 7, 10750.	5.8	137
18	Detection, Evaluation and Minimization of Nonenzymatic Deamidation in Proteomic Sample Preparation. <i>Molecular and Cellular Proteomics</i> , 2011, 10, O111.009381.	2.5	135

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19	Quantitative Secretomic Analysis of <i>Trichoderma reesei</i> Strains Reveals Enzymatic Composition for Lignocellulosic Biomass Degradation. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.012419-1-M111.012419-15.	2.5	126
20	Nanosecond Laser-Induced Photochemical Oxidation Method for Protein Surface Mapping with Mass Spectrometry. <i>Analytical Chemistry</i> , 2005, 77, 5814-5822.	3.2	124
21	PTEN-L is a novel protein phosphatase for ubiquitin dephosphorylation to inhibit PINK1-mediated mitophagy. <i>Cell Research</i> , 2018, 28, 787-802.	5.7	124
22	Quantitative profiling brain proteomes revealed mitochondrial dysfunction in Alzheimer's disease. <i>Molecular Brain</i> , 2019, 12, 8.	1.3	117
23	Cyclooxygenase-2 Inhibition Increases Mortality, Enhances Left Ventricular Remodeling, and Impairs Systolic Function After Myocardial Infarction in the Pig. <i>Circulation</i> , 2007, 115, 326-332.	1.6	113
24	Angiopoietin-like 4 Interacts with Matrix Proteins to Modulate Wound Healing*. <i>Journal of Biological Chemistry</i> , 2010, 285, 32999-33009.	1.6	113
25	Local Atherosclerotic Plaques Are a Source of Prognostic Biomarkers for Adverse Cardiovascular Events. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2010, 30, 612-619.	1.1	108
26	Quantitative iTRAQ Secretome Analysis of <i>Aspergillus niger</i> Reveals Novel Hydrolytic Enzymes. <i>Journal of Proteome Research</i> , 2010, 9, 3932-3940.	1.8	104
27	Dynamic expression of tRNA-derived small RNAs define cellular states. <i>EMBO Reports</i> , 2019, 20, e47789.	2.0	100
28	Extracellular vesicles are rapidly purified from human plasma by Protein Organic Solvent Precipitation (PROSPR). <i>Scientific Reports</i> , 2015, 5, 14664.	1.6	99
29	Brain site-specific proteome changes in aging-related dementia. <i>Experimental and Molecular Medicine</i> , 2013, 45, e39-e39.	3.2	98
30	Plasma-derived Extracellular Vesicles Contain Predictive Biomarkers and Potential Therapeutic Targets for Myocardial Ischemic (MI) Injury. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2628-2640.	2.5	97
31	Progerin reduces LAP2±-telomere association in Hutchinson-Gilford progeria. <i>ELife</i> , 2015, 4, .	2.8	96
32	SF3B1 Association with Chromatin Determines Splicing Outcomes. <i>Cell Reports</i> , 2015, 11, 618-629.	2.9	95
33	Simultaneous Characterization of Glyco- and Phosphoproteomes of Mouse Brain Membrane Proteome with Electrostatic Repulsion Hydrophilic Interaction Chromatography. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 635-647.	2.5	90
34	Adipocyte fatty acid binding protein in atherosclerotic plaques is associated with local vulnerability and is predictive for the occurrence of adverse cardiovascular events. <i>European Heart Journal</i> , 2011, 32, 1758-1768.	1.0	90
35	Identification of atrogen-1-targeted proteins during the myostatin-induced skeletal muscle wasting. <i>American Journal of Physiology - Cell Physiology</i> , 2012, 303, C512-C529.	2.1	90
36	Identification of Novel Functional Differences in Monocyte Subsets Using Proteomic and Transcriptomic Methods. <i>Journal of Proteome Research</i> , 2009, 8, 4028-4038.	1.8	89

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37	A Comparative Study of Electrostatic Repulsion-Hydrophilic Interaction Chromatography (ERLIC) versus SCX-IMAC-Based Methods for Phosphopeptide Isolation/Enrichment. <i>Journal of Proteome Research</i> , 2008, 7, 4869-4877.	1.8	88
38	Myostatin is a novel tumoral factor that induces cancer cachexia. <i>Biochemical Journal</i> , 2012, 446, 23-36.	1.7	85
39	Novel Application of Electrostatic Repulsion-Hydrophilic Interaction Chromatography (ERLIC) in Shotgun Proteomics: Comprehensive Profiling of Rat Kidney Proteome. <i>Journal of Proteome Research</i> , 2010, 9, 3520-3526.	1.8	84
40	Ribosome protection by antibiotic resistance ATP-binding cassette protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 5157-5162.	3.3	83
41	Structural determinants for peptide-bond formation by asparaginyl ligases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11737-11746.	3.3	81
42	Microvesicle protein levels are associated with increased risk for future vascular events and mortality in patients with clinically manifest vascular disease. <i>International Journal of Cardiology</i> , 2013, 168, 2358-2363.	0.8	79
43	Top down characterization of secreted proteins from <i>Mycobacterium tuberculosis</i> by electron capture dissociation mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2003, 14, 253-261.	1.2	76
44	Enrichment of extracellular vesicles from tissues of the central nervous system by PROSPR. <i>Molecular Neurodegeneration</i> , 2016, 11, 41.	4.4	76
45	Plasma Electron Capture Dissociation for the Characterization of Large Proteins by Top Down Mass Spectrometry. <i>Analytical Chemistry</i> , 2003, 75, 1599-1603.	3.2	74
46	Quantitative iTRAQ Secretome Analysis of Cellulolytic <i>Thermobifida fusca</i> . <i>Journal of Proteome Research</i> , 2010, 9, 3016-3024.	1.8	73
47	iTRAQ-based quantitative secretome analysis of <i>Phanerochaete chrysosporium</i> . <i>Journal of Proteomics</i> , 2011, 75, 642-654.	1.2	73
48	Quantitative proteomic analysis of lignocellulolytic enzymes by <i>Phanerochaete chrysosporium</i> on different lignocellulosic biomass. <i>Journal of Proteomics</i> , 2012, 75, 1493-1504.	1.2	73
49	Serum extracellular vesicle protein levels are associated with acute coronary syndrome. <i>European Heart Journal: Acute Cardiovascular Care</i> , 2013, 2, 53-60.	0.4	71
50	Hypoxia Modulates A431 Cellular Pathways Association to Tumor Radioresistance and Enhanced Migration Revealed by Comprehensive Proteomic and Functional Studies. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 485-498.	2.5	70
51	Proteome profiling reveals potential cellular targets of staurosporine using a clickable cell-permeable probe. <i>Chemical Communications</i> , 2011, 47, 11306.	2.2	68
52	Proteomic Analysis of pH and Strains Dependent Protein Secretion of <i>Trichoderma reesei</i> . <i>Journal of Proteome Research</i> , 2011, 10, 4579-4596.	1.8	68
53	Importance of TFEB acetylation in control of its transcriptional activity and lysosomal function in response to histone deacetylase inhibitors. <i>Autophagy</i> , 2018, 14, 1-17.	4.3	68
54	Hypoxia Activated EGFR Signaling Induces Epithelial to Mesenchymal Transition (EMT). <i>PLoS ONE</i> , 2012, 7, e49766.	1.1	65

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55	Hybridization of Pulsed-Q Dissociation and Collision-Activated Dissociation in Linear Ion Trap Mass Spectrometer for iTRAQ Quantitation. <i>Journal of Proteome Research</i> , 2008, 7, 4831-4840.	1.8	63
56	Phenotyping of an <i>In Vitro</i> Model of Ischemic Penumbra by iTRAQ-Based Shotgun Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 472-484.	1.8	63
57	Structural insights into the LCIB protein family reveals a new group of \hat{I}^2 -carbonic anhydrases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14716-14721.	3.3	61
58	Gender differences in white matter pathology and mitochondrial dysfunction in Alzheimer's disease with cerebrovascular disease. <i>Molecular Brain</i> , 2016, 9, 27.	1.3	58
59	Quantitative Neuroproteomics of an <i>In Vivo</i> Rodent Model of Focal Cerebral Ischemia/Reperfusion Injury Reveals a Temporal Regulation of Novel Pathophysiological Molecular Markers. <i>Journal of Proteome Research</i> , 2011, 10, 5199-5213.	1.8	57
60	Microwave-assisted specific chemical digestion for rapid protein identification. <i>Proteomics</i> , 2006, 6, 586-591.	1.3	56
61	Elucidating <i>In Vivo</i> Structural Dynamics in Integral Membrane Protein by Hydroxyl Radical Footprinting. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1999-2010.	2.5	56
62	Structure of a novel phosphotyrosine-binding domain in Hakai that targets E-cadherin. <i>EMBO Journal</i> , 2012, 31, 1308-1319.	3.5	56
63	Recent advances in mass spectrometric analysis of protein deamidation. <i>Mass Spectrometry Reviews</i> , 2017, 36, 677-692.	2.8	56
64	Heterochromatin Protein 1 \hat{I}^2 (HP1 \hat{I}^2) has distinct functions and distinct nuclear distribution in pluripotent versus differentiated cells. <i>Genome Biology</i> , 2015, 16, 213.	3.8	55
65	Thrombin and Plasmin Alter the Proteome of Neutrophil Extracellular Traps. <i>Frontiers in Immunology</i> , 2018, 9, 1554.	2.2	55
66	Simultaneous Analysis of Proteome, Phospho- and Glycoproteome of Rat Kidney Tissue with Electrostatic Repulsion Hydrophilic Interaction Chromatography. <i>PLoS ONE</i> , 2011, 6, e16884.	1.1	54
67	Quantitative proteomic study of <i>Aspergillus Fumigatus</i> secretome revealed deamidation of secretory enzymes. <i>Journal of Proteomics</i> , 2015, 119, 154-168.	1.2	53
68	Insight of brain degenerative protein modifications in the pathology of neurodegeneration and dementia by proteomic profiling. <i>Molecular Brain</i> , 2016, 9, 92.	1.3	53
69	Studies on the Proteome of Human Hair - Identification of Histones and Deamidated Keratins. <i>Scientific Reports</i> , 2018, 8, 1599.	1.6	52
70	Small Molecule Probe Suitable for <i>In Situ</i> Profiling and Inhibition of Protein Disulfide Isomerase. <i>ACS Chemical Biology</i> , 2013, 8, 2577-2585.	1.6	51
71	Materials Stiffness-Dependent Redox Metabolic Reprogramming of Mesenchymal Stem Cells for Secretome-Based Therapeutic Angiogenesis. <i>Advanced Healthcare Materials</i> , 2019, 8, e1900929.	3.9	49
72	A high-throughput peptidomic strategy to decipher the molecular diversity of cyclic cysteine-rich peptides. <i>Scientific Reports</i> , 2016, 6, 23005.	1.6	48

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73	Differential Association of Chromatin Proteins Identifies BAF60a/SMARCD1 as a Regulator of Embryonic Stem Cell Differentiation. <i>Cell Reports</i> , 2015, 10, 2019-2031.	2.9	47
74	Alzheimer's disease progression characterized by alterations in the molecular profiles and biogenesis of brain extracellular vesicles. <i>Alzheimer's Research and Therapy</i> , 2020, 12, 54.	3.0	47
75	Phosphoproteomics identified Endofin, DCBLD2, and KIAA0582 as novel tyrosine phosphorylation targets of EGF signaling and Iressa in human cancer cells. <i>Proteomics</i> , 2007, 7, 2384-2397.	1.3	46
76	Metabolic Adaptation to a Disruption in Oxygen Supply during Myocardial Ischemia and Reperfusion Is Underpinned by Temporal and Quantitative Changes in the Cardiac Proteome. <i>Journal of Proteome Research</i> , 2012, 11, 2331-2346.	1.8	46
77	The diagnostic and prognostic potential of plasma extracellular vesicles for cardiovascular disease. <i>Expert Review of Molecular Diagnostics</i> , 2015, 15, 1577-1588.	1.5	46
78	Evaluation of the Effect of Trypsin Digestion Buffers on Artificial Deamidation. <i>Journal of Proteome Research</i> , 2015, 14, 1308-1314.	1.8	46
79	Study of monocyte membrane proteome perturbation during lipopolysaccharide-induced tolerance using iTRAQ-based quantitative proteomic approach. <i>Proteomics</i> , 2010, 10, 2780-2789.	1.3	45
80	The CD14 ⁺ /lowCD16 ⁺ monocyte subset is more susceptible to spontaneous and oxidant-induced apoptosis than the CD14 ⁺ CD16 ⁺ subset. <i>Cell Death and Disease</i> , 2010, 1, e95-e95.	2.7	45
81	Brain-derived and circulating vesicle profiles indicate neurovascular unit dysfunction in early Alzheimer's disease. <i>Brain Pathology</i> , 2019, 29, 593-605.	2.1	44
82	Miniaturization of capillary isoelectric focusing. <i>Electrophoresis</i> , 2001, 22, 3968-3971.	1.3	43
83	Enhanced Separation and Characterization of Deamidated Peptides with RP-ERLIC-Based Multidimensional Chromatography Coupled with Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2012, 11, 1804-1811.	1.8	42
84	Capsinoids activate brown adipose tissue (BAT) with increased energy expenditure associated with subthreshold 18-fluorine fluorodeoxyglucose uptake in BAT-positive humans confirmed by positron emission tomography scan. <i>American Journal of Clinical Nutrition</i> , 2018, 107, 62-70.	2.2	42
85	Plasma biomarker discovery in preeclampsia using a novel differential isolation technology for circulating extracellular vesicles. <i>American Journal of Obstetrics and Gynecology</i> , 2014, 211, 380.e1-380.e13.	0.7	41
86	Quantitative mass spectrometry of human reticulocytes reveal proteome-wide modifications during maturation. <i>British Journal of Haematology</i> , 2018, 180, 118-133.	1.2	40
87	Brown Adipose Tissue: Multimodality Evaluation by PET, MRI, Infrared Thermography, and Whole-Body Calorimetry (TACTICAL-III). <i>Obesity</i> , 2019, 27, 1434-1442.	1.5	40
88	Comparative proteome analysis of 3T3-L1 adipocyte differentiation using iTRAQ-coupled 2D LC-MS/MS. <i>Journal of Cellular Biochemistry</i> , 2011, 112, 3002-3014.	1.2	38
89	Hypoxia-induced Changes to Integrin β 3 Glycosylation Facilitate Invasion in Epidermoid Carcinoma Cell Line A431. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3126-3137.	2.5	38
90	Quantitative Profiling of Chromatome Dynamics Reveals a Novel Role for HP1BP3 in Hypoxia-induced Oncogenesis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3236-3249.	2.5	38

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91	Discovery of Prognostic Biomarker Candidates of Lacunar Infarction by Quantitative Proteomics of Microvesicles Enriched Plasma. PLoS ONE, 2014, 9, e94663.	1.1	38
92	Capillary isoelectric focusing in pseudo-closed channel coupled to matrix assisted laser desorption/ionization mass spectrometry for protein analysis. Analyst, The, 2004, 129, 109.	1.7	36
93	Quantitative clinical proteomic study of autopsied human infarcted brain specimens to elucidate the deregulated pathways in ischemic stroke pathology. Journal of Proteomics, 2013, 91, 556-568.	1.2	36
94	Scalable and Effective Enrichment of Semiconducting Single-Walled Carbon Nanotubes by a Dual Selective Naphthalene-Based Azo Dispersant. Journal of the American Chemical Society, 2013, 135, 5569-5581.	6.6	36
95	Profiling of the Chromatin-associated Proteome Identifies HP1BP3 as a Novel Regulator of Cell Cycle Progression. Molecular and Cellular Proteomics, 2014, 13, 2183-2197.	2.5	36
96	<i>P. falciparum</i> RH5-Basigin interaction induces changes in the cytoskeleton of the host RBC. Cellular Microbiology, 2017, 19, e12747.	1.1	36
97	Brain ureido degenerative protein modifications are associated with neuroinflammation and proteinopathy in Alzheimer's disease with cerebrovascular disease. Journal of Neuroinflammation, 2017, 14, 175.	3.1	35
98	Oxidative stress promotes SIRT1 recruitment to the GADD34/PP1 complex to activate its deacetylase function. Cell Death and Differentiation, 2018, 25, 255-267.	5.0	35
99	Multiplex Imaging and Cellular Target Identification of Kinase Inhibitors via an Affinity-Based Proteome Profiling Approach. Scientific Reports, 2015, 5, 7724.	1.6	34
100	Elucidating the Structure of Cyclotides by Partial Acid Hydrolysis and LC-MS/MS Analysis. Analytical Chemistry, 2009, 81, 1079-1088.	3.2	33
101	Detection of four oxidation sites in viral prolyl-4-hydroxylase by top-down mass spectrometry. Protein Science, 2009, 12, 2320-2326.	3.1	32
102	Global molecular dysfunctions in gastric cancer revealed by an integrated analysis of the phosphoproteome and transcriptome. Cellular and Molecular Life Sciences, 2011, 68, 1983-2002.	2.4	32
103	Chronic oxidative stress promotes GADD34-mediated phosphorylation of the TAR DNA-binding protein TDP-43, a modification linked to neurodegeneration. Journal of Biological Chemistry, 2018, 293, 163-176.	1.6	32
104	Vimentin protects differentiating stem cells from stress. Scientific Reports, 2020, 10, 19525.	1.6	32
105	Oxidative Damage to the TCA Cycle Enzyme MDH1 Dysregulates Bioenergetic Enzymatic Activity in the Aged Murine Brain. Journal of Proteome Research, 2020, 19, 1706-1717.	1.8	32
106	Label free quantitative proteomic analysis of secretome by <i>Thermobifida fusca</i> on different lignocellulosic biomass. Journal of Proteomics, 2012, 75, 3694-3706.	1.2	31
107	Quantitative profiling of the rat heart myoblast secretome reveals differential responses to hypoxia and re-oxygenation stress. Journal of Proteomics, 2014, 98, 138-149.	1.2	31
108	iTRAQ Quantitative Clinical Proteomics Revealed Role of Na ⁺ K ⁺ -ATPase and Its Correlation with Deamidation in Vascular Dementia. Journal of Proteome Research, 2014, 13, 4635-4646.	1.8	31

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109	Characterization of Glutamine Deamidation by Long-Length Electrostatic Repulsion-Hydrophilic Interaction Chromatography-Tandem Mass Spectrometry (LERLIC-MS/MS) in Shotgun Proteomics. <i>Analytical Chemistry</i> , 2016, 88, 10573-10582.	3.2	31
110	Abundant neuroprotective chaperone Lipocalin-type prostaglandin D synthase (L-PGDS) disassembles the Amyloid- β fibrils. <i>Scientific Reports</i> , 2019, 9, 12579.	1.6	31
111	Mechanoregulation of Cancer-Associated Fibroblast Phenotype in Three-Dimensional Interpenetrating Hydrogel Networks. <i>Langmuir</i> , 2019, 35, 7487-7495.	1.6	31
112	Electrostatic Repulsion-Hydrophilic Interaction Chromatography (ERLIC) versus Strong Cation Exchange (SCX) for Fractionation of iTRAQ-Labeled Peptides. <i>Journal of Proteome Research</i> , 2011, 10, 5568-5574.	1.8	30
113	iTRAQ-based quantitative proteomic analysis of <i>Thermobifida fusca</i> reveals metabolic pathways of cellulose utilization. <i>Journal of Proteomics</i> , 2011, 74, 2112-2122.	1.2	30
114	Proteomic Analysis of Temperature Dependent Extracellular Proteins from <i>Aspergillus fumigatus</i> Grown under Solid-State Culture Condition. <i>Journal of Proteome Research</i> , 2013, 12, 2715-2731.	1.8	30
115	Novel pathophysiological markers are revealed by iTRAQ-based quantitative clinical proteomics approach in vascular dementia. <i>Journal of Proteomics</i> , 2014, 99, 54-67.	1.2	30
116	Dementia-linked amyloidosis is associated with brain protein deamidation as revealed by proteomic profiling of human brain tissues. <i>Molecular Brain</i> , 2016, 9, 20.	1.3	30
117	Plant-derived mitochondria-targeting cysteine-rich peptide modulates cellular bioenergetics. <i>Journal of Biological Chemistry</i> , 2019, 294, 4000-4011.	1.6	30
118	LEO1 Is Regulated by PRL-3 and Mediates Its Oncogenic Properties in Acute Myelogenous Leukemia. <i>Cancer Research</i> , 2014, 74, 3043-3053.	0.4	29
119	Ginkgotides: Proline-Rich Hevein-Like Peptides from Gymnosperm <i>Ginkgo biloba</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1639.	1.7	29
120	Dietary phytochemical PEITC restricts tumor development via modulation of epigenetic writers and erasers. <i>Scientific Reports</i> , 2017, 7, 40569.	1.6	29
121	Distinctive molecular signature and activated signaling pathways in aortic smooth muscle cells of patients with myocardial infarction. <i>Atherosclerosis</i> , 2018, 271, 237-244.	0.4	29
122	Proteomic Analysis of Aqueous Humor from Primary Open Angle Glaucoma Patients on Drug Treatment Revealed Altered Complement Activation Cascade. <i>Journal of Proteome Research</i> , 2018, 17, 2499-2510.	1.8	29
123	Turning an Asparaginyl Endopeptidase into a Peptide Ligase. <i>ACS Catalysis</i> , 2020, 10, 8825-8834.	5.5	29
124	ERO1 β promotes hypoxic tumor progression and is associated with poor prognosis in pancreatic cancer. <i>Oncotarget</i> , 2019, 10, 5970-5982.	0.8	29
125	Simultaneous Enrichment of Plasma Soluble and Extracellular Vesicular Glycoproteins Using Prolonged Ultracentrifugation-Electrostatic Repulsion-hydrophilic Interaction Chromatography (PUC-ERLIC) Approach*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1657-1671.	2.5	28
126	Uncovering Neurodegenerative Protein Modifications via Proteomic Profiling. <i>International Review of Neurobiology</i> , 2015, 121, 87-116.	0.9	28

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127	Cutting Edge: Synchronization of IRF1, JunB, and C/EBP β Activities during TLR3 \leftrightarrow TLR7 Cross-Talk Orchestrates Timely Cytokine Synergy in the Proinflammatory Response. <i>Journal of Immunology</i> , 2015, 195, 801-805.	0.4	28
128	Hypoxia-Induced Degenerative Protein Modifications Associated with Aging and Age-Associated Disorders. , 2020, 11, 341.		28
129	Protein abundance in multiplexed samples (PAMUS) for quantitation of <i>Trichoderma reesei</i> secretome. <i>Journal of Proteomics</i> , 2013, 83, 180-196.	1.2	27
130	Aqueous humor protein dysregulation in primary angle-closure glaucoma. <i>International Ophthalmology</i> , 2019, 39, 861-871.	0.6	27
131	Laser-induced fluorescence detection of non-covalently labeled protein in capillary isoelectric focusing. <i>Journal of Separation Science</i> , 2002, 25, 1119-1122.	1.3	26
132	High Myeloid-Related Protein. <i>Stroke</i> , 2010, 41, 2010-2015.	1.0	26
133	Temporal lobe proteins implicated in synaptic failure exhibit differential expression and deamidation in vascular dementia. <i>Neurochemistry International</i> , 2015, 80, 87-98.	1.9	26
134	Serum albumin cysteine trioxidation is a potential oxidative stress biomarker of type 2 diabetes mellitus. <i>Scientific Reports</i> , 2020, 10, 6475.	1.6	26
135	Synergism between Curdlan and GM-CSF Confers a Strong Inflammatory Signature to Dendritic Cells. <i>Journal of Immunology</i> , 2012, 188, 1789-1798.	0.4	25
136	Comparative evaluation of electrostatic repulsion \leftrightarrow hydrophilic interaction chromatography (ERLIC) and high-pH reversed phase (Hp-RP) chromatography in profiling of rat kidney proteome. <i>Journal of Proteomics</i> , 2013, 82, 254-262.	1.2	25
137	Proteomics of plaques and novel sources of potential biomarkers for atherosclerosis. <i>Proteomics - Clinical Applications</i> , 2013, 7, 490-503.	0.8	25
138	An iTRAQ-based proteomic analysis reveals dysregulation of neocortical synaptopodin in Lewy body dementias. <i>Molecular Brain</i> , 2017, 10, 36.	1.3	25
139	New insights into the brain protein metabolism of <i>Gastrodia elata</i> -treated rats by quantitative proteomics. <i>Journal of Proteomics</i> , 2012, 75, 2468-2479.	1.2	24
140	Genome-wide analysis in <i>Plasmodium falciparum</i> reveals early and late phases of RNA polymerase II occupancy during the infectious cycle. <i>BMC Genomics</i> , 2014, 15, 959.	1.2	24
141	Quantitative proteomic analysis of secretome of microbial consortium during saw dust utilization. <i>Journal of Proteomics</i> , 2012, 75, 5590-5603.	1.2	23
142	Tianma modulates proteins with various neuro-regenerative modalities in differentiated human neuronal SH-SY5Y cells. <i>Neurochemistry International</i> , 2012, 60, 827-836.	1.9	23
143	Deep proteomic profiling of human carotid atherosclerotic plaques using multidimensional LC \leftrightarrow MS/MS. <i>Proteomics - Clinical Applications</i> , 2014, 8, 631-635.	0.8	23
144	Global re \leftrightarrow wiring of p53 transcription regulation by the hepatitis B virus X protein. <i>Molecular Oncology</i> , 2016, 10, 1183-1195.	2.1	23

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