Pingbo Zhang

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2035215/publications.pdf

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42 papers	1,470 citations	361413 20 h-index	330143 37 g-index

42 all docs	42 docs citations	42 times ranked	2883 citing authors

#	Article	IF	Citations
1	Primary angle closure glaucoma is characterized by altered extracellular matrix homeostasis in the iris. Proteomics - Clinical Applications, 2021, 15, 2000094.	1.6	3
2	Novel Human Insulin Isoforms and CÎ±-Peptide Product in Islets of Langerhans and Choroid Plexus. Diabetes, 2021, 70, 2947-2956.	0.6	6
3	Elevated Plasma Growth and Differentiation Factor 15 Is Associated With Slower Gait Speed and Lower Physical Performance in Healthy Community-Dwelling Adults. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2020, 75, 175-180.	3.6	48
4	Targeted Metabolomics Shows Low Plasma Lysophosphatidylcholine 18:2 Predicts Greater Decline of Gait Speed in Older Adults: The Baltimore Longitudinal Study of Aging. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2019, 74, 62-67.	3.6	46
5	Low plasma lysophosphatidylcholines are associated with impaired mitochondrial oxidative capacity in adults in the Baltimore Longitudinal Study of Aging. Aging Cell, 2019, 18, e12915.	6.7	34
6	Tetra-linoleoyl cardiolipin depletion plays a major role in the pathogenesis of sarcopenia. Medical Hypotheses, 2019, 127, 142-149.	1.5	24
7	Relationship of Circulating Growth and Differentiation Factors 8 and 11 and Their Antagonists as Measured Using Liquid Chromatographyâ€“Tandem Mass Spectrometry With Age and Skeletal Muscle Strength in Healthy Adults. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2019, 74, 129-136.	3.6	12
8	The Human Eye Proteome Project: Updates on an Emerging Proteome. Proteomics, 2018, 18, e1700394.	2.2	57
9	Altered Plasma Amino Acids and Lipids Associated With Abnormal Glucose Metabolism and Insulin Resistance in Older Adults. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 3331-3339.	3.6	26
10	Plasma proteomic signature of age in healthy humans. Aging Cell, 2018, 17, e12799.	6.7	325
11	A targeted proteomic assay for the measurement of plasma proteoforms related to human aging phenotypes. Proteomics, 2017, 17, 1600232.	2.2	9
12	Anatomical differences of the protein profile in the rabbit sclera during growth. Experimental Eye Research, 2017, 154, 53-63.	2.6	6
13	Heart Failureâ€“Related Hyperphosphorylation in the Cardiac Troponin I C Terminus Has Divergent Effects on Cardiac Function In Vivo. Circulation: Heart Failure, 2017, 10, .	3.9	5
14	Heterogeneous Stromal Signaling within the Tumor Microenvironment Controls the Metastasis of Pancreatic Cancer. Cancer Research, 2017, 77, 41-52.	0.9	71
15	A robotic protocol for highâ€throughput processing of samples for selected reaction monitoring assays. Proteomics, 2017, 17, 1600339.	2.2	11
16	A novel, multiplexed targeted mass spectrometry assay for quantification of complement factor H (CFH) variants and CFHâ€related proteins 1â€“5 in human plasma. Proteomics, 2017, 17, 1600237.	2.2	18
17	A proteomic approach to understanding the pathogenesis of idiopathic macular hole formation. Clinical Proteomics, 2017, 14, 37.	2.1	11
18	Defining the proteome of human iris, ciliary body, retinal pigment epithelium, and choroid. Proteomics, 2016, 16, 1146-1153.	2.2	30

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19	The association of serum choline with linear growth failure in young children from rural Malawi. American Journal of Clinical Nutrition, 2016, 104, 191-197.	4.7	36
20	Plasma Biomarkers of Poor Muscle Quality in Older Men and Women from the Baltimore Longitudinal Study of Aging. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2016, 71, 1266-1272.	3.6	75
21	The proteome of normal human retrobulbar optic nerve and sclera. Proteomics, 2016, 16, 2592-2596.	2.2	17
22	Impaired ATP6V0A2 expression contributes to Golgi dispersion and glycosylation changes in senescent cells. Scientific Reports, 2015, 5, 17342.	3.3	22
23	Priorities and trends in the study of proteins in eye research, 1924â€“2014. Proteomics - Clinical Applications, 2015, 9, 1105-1122.	1.6	5
24	The proteome of human retina. Proteomics, 2015, 15, 836-840.	2.2	29
25	Cardiac troponin I Pro82Ser variant induces diastolic dysfunction, blunts Î²-adrenergic response, and impairs myofilament cooperativity. Journal of Applied Physiology, 2015, 118, 212-223.	2.5	10
26	A novel phosphorylation site, Serine 199, in the C-terminus of cardiac troponin I regulates calcium sensitivity and susceptibility to calpain-induced proteolysis. Journal of Molecular and Cellular Cardiology, 2015, 82, 93-103.	1.9	20
27	The C2 Domain and Altered ATP-Binding Loop Phosphorylation at Ser³⁵⁹ Mediate the Redox-Dependent Increase in Protein Kinase C-Î´ Activity. Molecular and Cellular Biology, 2015, 35, 1727-1740.	2.3	18
28	Targeted proteomics of myofilament phosphorylation and other protein posttranslational modifications. Proteomics - Clinical Applications, 2014, 8, 543-553.	1.6	13
29	Suppression of immunoglobulin production in human peripheral blood mononuclear cells by monocytes via secretion of heavy-chain ferritin. Immunobiology, 2014, 219, 149-157.	1.9	10
30	Mechanisms that regulate PKCÎ´â€dependent phosphorylation of cardiac troponin I: the role of the C2 domain and ATPâ€binding loop phosphorylation S357 (1081.2). FASEB Journal, 2014, 28, 1081.2.	0.5	0
31	Troponin I alterations detected by multiple-reaction monitoring: how might this impact the study of heart failure?. Expert Review of Proteomics, 2013, 10, 5-8.	3.0	6
32	PKCÎ±-Specific Phosphorylation of the Troponin Complex in Human Myocardium: A Functional and Proteomics Analysis. PLoS ONE, 2013, 8, e74847.	2.5	29
33	Multiple Reaction Monitoring to Identify Site-Specific Troponin I Phosphorylated Residues in the Failing Human Heart. Circulation, 2012, 126, 1828-1837.	1.6	126
34	Multiplex assays for biomarker research and clinical application: Translational science coming of age. Proteomics - Clinical Applications, 2010, 4, 271-284.	1.6	83
35	Proteomic identification of phosphatidylinositol (3,4,5) triphosphate-binding proteins in Dictyostelium discoideum. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 11829-11834.	7.1	33
36	Proteomic Profiling of the Silkworm Skeletal Muscle Proteins during Larvalâ^'Pupal Metamorphosis. Journal of Proteome Research, 2007, 6, 2295-2303.	3.7	25

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37	Proteome analysis of silk gland proteins from the silkworm,Bombyx mori. Proteomics, 2006, 6, 2586-2599.	2.2	77
38	Proteomic Studies of Isoforms of the P25 Component ofBombyx moriFibroin. Bioscience, Biotechnology and Biochemistry, 2005, 69, 2086-2093.	1.3	15
39	Superoxide Dismutase from the Silkworm,Bombyx mori: Sequence, Distribution, and Overexpression. Bioscience, Biotechnology and Biochemistry, 2005, 69, 507-514.	1.3	29
40	Molecular and biochemical characterization of manganese-containing superoxide dismutase from the silkworm, Bombyx mori. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2005, 142, 403-409.	1.6	19
41	Proteomic Studies of Lipopolysaccharide-induced Polypeptides in the Silkworm,Bombyx mori. Bioscience, Biotechnology and Biochemistry, 2004, 68, 1821-1823.	1.3	21
42	Utility of Dry Gel from Two-dimensional Electrophoresis for Peptide Mass Fingerprinting Analysis of Silkworm Proteins. Bioscience, Biotechnology and Biochemistry, 2004, 68, 2148-2154.	1.3	10