

Junjie Hou

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6915439/publications.pdf>

Version: 2024-02-01

17
papers

469
citations

687363

13
h-index

794594

19
g-index

20
all docs

20
docs citations

20
times ranked

1024
citing authors

#	ARTICLE	IF	CITATIONS
1	ASC deglutathionylation is a checkpoint for NLRP3 inflammasome activation. <i>Journal of Experimental Medicine</i> , 2021, 218, .	8.5	25
2	EI24 tethers endoplasmic reticulum and mitochondria to regulate autophagy flux. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 1591-1606.	5.4	20
3	Identification of Insulin-Responsive Transcription Factors That Regulate Glucose Production by Hepatocytes. <i>Diabetes</i> , 2019, 68, 1156-1167.	0.6	18
4	hTAC internalizes via both clathrin-dependent and clathrin-independent endocytosis in mammalian cells. <i>Protein and Cell</i> , 2018, 9, 896-901.	11.0	4
5	Proteomic analysis of insulin secretory granules in INS-1 β cells by protein correlation profiling. <i>Biophysics Reports</i> , 2018, 4, 329-338.	0.8	11
6	RNA-binding protein DDX1 is responsible for fatty acid-mediated repression of insulin translation. <i>Nucleic Acids Research</i> , 2018, 46, 12052-12066.	14.5	27
7	Temporal Proteomic Analysis of Pancreatic β -Cells in Response to Lipotoxicity and Glucolipotoxicity. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2119-2131.	3.8	25
8	Temporal Transcriptomic and Proteomic Landscapes of Deteriorating Pancreatic Islets in Type 2 Diabetic Rats. <i>Diabetes</i> , 2017, 66, 2188-2200.	0.6	54
9	Optimizing the fragment complementation of APEX2 for detection of specific protein-protein interactions in live cells. <i>Scientific Reports</i> , 2017, 7, 12039.	3.3	34
10	Integrated proteomic and N-glycoproteomic analyses of doxorubicin sensitive and resistant ovarian cancer cells reveal glycoprotein alteration in protein abundance and glycosylation. <i>Oncotarget</i> , 2017, 8, 13413-13427.	1.8	18
11	Long-term potentiation modulates synaptic phosphorylation networks and reshapes the structure of the postsynaptic interactome. <i>Science Signaling</i> , 2016, 9, rs8.	3.6	96
12	A new dimethyl labeling-based SID-MRM-MS method and its application to three proteases involved in insulin maturation. <i>Biophysics Reports</i> , 2015, 1, 71-80.	0.8	4
13	Chronic high glucose induced INS-1 β cell mitochondrial dysfunction: A comparative mitochondrial proteome with SILAC. <i>Proteomics</i> , 2013, 13, 3030-3039.	2.2	16
14	Testicular phosphoproteome in perfluorododecanoic acid-exposed rats. <i>Toxicology Letters</i> , 2013, 221, 91-101.	0.8	14
15	Enhanced MALDI-TOF MS Analysis of Phosphopeptides Using an Optimized DHAP/DAHC Matrix. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-12.	3.0	13
16	Phosphoproteome Analysis of Rat L6 Myotubes Using Reversed-Phase C18 Prefractionation and Titanium Dioxide Enrichment. <i>Journal of Proteome Research</i> , 2010, 9, 777-788.	3.7	38
17	Discovery and identification of potential biomarkers of pediatric Acute Lymphoblastic Leukemia. <i>Proteome Science</i> , 2009, 7, 7.	1.7	46