

Keiji Kito

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

475
citations

933447

10
h-index

888059

17
g-index

19
all docs

19
docs citations

19
times ranked

790
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of an antibacterial polypeptide in mouse seminal vesicle secretions. <i>Journal of Reproductive Immunology</i> , 2021, 148, 103436.	1.9	1
2	Hydrophilic Shell Matrix Proteins of <i>Nautilus pompilius</i> and the Identification of a Core Set of Conchiferan Domains. <i>Genes</i> , 2021, 12, 1925.	2.4	7
3	Functional shell matrix proteins tentatively identified by asymmetric snail shell morphology. <i>Scientific Reports</i> , 2020, 10, 9768.	3.3	13
4	Genetic profiling of protein burden and nuclear export overload. <i>ELife</i> , 2020, 9, .	6.0	8
5	Identification of TGF β -induced proteins in non-endocrine mouse pituitary cell line TtT/GF by SILAC-assisted quantitative mass spectrometry. <i>Cell and Tissue Research</i> , 2019, 376, 281-293.	2.9	3
6	Insights into the Evolution of Shells and Love Darts of Land Snails Revealed from Their Matrix Proteins. <i>Genome Biology and Evolution</i> , 2019, 11, 380-397.	2.5	25
7	TGF β signaling reinforces pericyte properties of the non-endocrine mouse pituitary cell line TtT/GF. <i>Cell and Tissue Research</i> , 2018, 371, 339-350.	2.9	8
8	Estimating the protein burden limit of yeast cells by measuring the expression limits of glycolytic proteins. <i>ELife</i> , 2018, 7, .	6.0	46
9	Proteomics analysis for asymmetric inheritance of preexisting proteins between mother and daughter cells in budding yeast. <i>Genes To Cells</i> , 2017, 22, 591-601.	1.2	11
10	A strategy for absolute proteome quantification with mass spectrometry by hierarchical use of peptide α -concatenated standards. <i>Proteomics</i> , 2016, 16, 1457-1473.	2.2	13
11	Autophosphorylation of Specific Threonine and Tyrosine Residues in Arabidopsis CERK1 is Essential for the Activation of Chitin-Induced Immune Signaling. <i>Plant and Cell Physiology</i> , 2016, 57, 2312-2322.	3.1	35
12	Yeast Interspecies Comparative Proteomics Reveals Divergence in Expression Profiles and Provides Insights into Proteome Resource Allocation and Evolutionary Roles of Gene Duplication. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 218-235.	3.8	15
13	Proteome analysis of shell matrix proteins in the brachiopod <i>Laqueus rubellus</i> . <i>Proteome Science</i> , 2015, 13, 21.	1.7	24
14	Discrimination between stable and dynamic components of protein complexes by means of quantitative proteomics. <i>Proteomics</i> , 2008, 8, 2366-2370.	2.2	15
15	Absolute quantification of the budding yeast transcriptome by means of competitive PCR between genomic and complementary DNAs. <i>BMC Genomics</i> , 2008, 9, 574.	2.8	83
16	Mass Spectrometry-Based Approaches Toward Absolute Quantitative Proteomics. <i>Current Genomics</i> , 2008, 9, 263-274.	1.6	88
17	A Synthetic Protein Approach toward Accurate Mass Spectrometric Quantification of Component Stoichiometry of Multiprotein Complexes. <i>Journal of Proteome Research</i> , 2007, 6, 792-800.	3.7	80