

Trong Khoa Pham

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

1,423
citations

623734

14
h-index

713466

21
g-index

22
all docs

22
docs citations

22
times ranked

2197
citing authors

#	ARTICLE	IF	CITATIONS
1	Technical, Experimental, and Biological Variations in Isobaric Tags for Relative and Absolute Quantitation (iTRAQ). <i>Journal of Proteome Research</i> , 2007, 6, 821-827.	3.7	369
2	An insight into iTRAQ: where do we stand now?. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 1011-1027.	3.7	293
3	Isobaric Tags for Relative and Absolute Quantitation (iTRAQ) Reproducibility:Â Implication of Multiple Injections. <i>Journal of Proteome Research</i> , 2006, 5, 1232-1240.	3.7	191
4	A quantitative proteomic analysis of biofilm adaptation by the periodontal pathogen <i>Tannerella forsythia</i> . <i>Proteomics</i> , 2010, 10, 3130-3141.	2.2	83
5	Protein phosphorylation and its role in archaeal signal transduction. <i>FEMS Microbiology Reviews</i> , 2016, 40, 625-647.	8.6	72
6	Archaeal Signal Transduction: Impact of Protein Phosphatase Deletions on Cell Size, Motility, and Energy Metabolism in <i>Sulfolobus acidocaldarius</i> . <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3908-3923.	3.8	69
7	The Proteomic Response of <i>Saccharomyces cerevisiae</i> in Very High Glucose Conditions with Amino Acid Supplementation. <i>Journal of Proteome Research</i> , 2008, 7, 4766-4774.	3.7	49
8	Proteomic Analysis of <i>Saccharomyces cerevisiae</i> under High Gravity Fermentation Conditions. <i>Journal of Proteome Research</i> , 2006, 5, 3411-3419.	3.7	43
9	Methods in Quantitative Proteomics: Setting iTRAQ on the Right Track. <i>Current Proteomics</i> , 2011, 8, 17-30.	0.3	42
10	Macromolecular Fingerprinting of <i>Sulfolobus</i> Species in Biofilm: A Transcriptomic and Proteomic Approach Combined with Spectroscopic Analysis. <i>Journal of Proteome Research</i> , 2011, 10, 4105-4119.	3.7	41
11	Phosphopeptide enrichment for phosphoproteomic analysis - A tutorial and review of novel materials. <i>Analytica Chimica Acta</i> , 2020, 1129, 158-180.	5.4	41
12	Quantitative Proteomic Analysis of <i>Sulfolobus solfataricus</i> Membrane Proteins. <i>Journal of Proteome Research</i> , 2010, 9, 1165-1172.	3.7	23
13	Quantitative proteomic analysis of the exoelectrogenic bacterium <i>Arcobacter butzleri</i> ED-1 reveals increased abundance of a flagellin protein under anaerobic growth on an insoluble electrode. <i>Journal of Proteomics</i> , 2013, 78, 197-210.	2.4	23
14	Early Response of <i>Sulfolobus acidocaldarius</i> to Nutrient Limitation. <i>Frontiers in Microbiology</i> , 2018, 9, 3201.	3.5	21
15	Proteomic analysis of <i>Saccharomyces cerevisiae</i> . <i>Expert Review of Proteomics</i> , 2007, 4, 793-813.	3.0	15
16	Proteomic Analysis of Calcium Alginate-Immobilized <i>Saccharomyces cerevisiae</i> under High-Gravity Fermentation Conditions. <i>Journal of Proteome Research</i> , 2008, 7, 515-525.	3.7	15
17	Quantitative analysis of UV-A shock and short term stress using iTRAQ, pseudo selective reaction monitoring (pSRM) and GC-MS based metabolite analysis of the cyanobacterium <i>Nostoc punctiforme</i> ATCC 29133. <i>Journal of Proteomics</i> , 2014, 109, 332-355.	2.4	13
18	A cool tool for hot and sour Archaea: Proteomics of <i>Sulfolobus solfataricus</i> . <i>Proteomics</i> , 2013, 13, 2831-2850.	2.2	9

#	ARTICLE	IF	CITATIONS
19	Exposure to 1-Butanol Exemplifies the Response of the Thermoacidophilic Archaeon <i>Sulfolobus acidocaldarius</i> to Solvent Stress. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	8
20	Bioinformatic study of the relationship between protein regulation and sequence properties. <i>Genomics</i> , 2012, 100, 240-244.	2.9	2
21	An iTRAQ characterisation of the role of TolC during electron transfer from <i>Shewanella oneidensis</i> . <i>Proteomics</i> , 2016, 16, 2764-2775.	2.2	1
22	Natural Mutagenesis-Enabled Global Proteomic Study of Metabolic and Carbon Source Implications in Mutant Thermoacidophilic Archaeon <i>Sulfolobus solfataricus</i> PBL2025. <i>Journal of Proteome Research</i> , 2017, 16, 2370-2383.	3.7	0