Steven J Bark

List of Publications by Year in descending order

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STEVEN LRADK

#	Article	IF	CITATIONS
1	Functional and structural characterization of Hyp730, a highly conserved and dormancyâ€specific hypothetical membrane protein. MicrobiologyOpen, 2021, 10, e1154.	3.0	1
2	Human mesenchymal stem cell based intracellular dormancy model of Mycobacterium tuberculosis. Microbes and Infection, 2020, 22, 423-431.	1.9	9
3	A Universal Stress Protein That Controls Bacterial Stress Survival in Micrococcus luteus. Journal of Bacteriology, 2019, 201, .	2.2	12
4	Engineered ChymotrypsiN for Mass Spectrometry-Based Detection of Protein Glycosylation. ACS Chemical Biology, 2019, 14, 2616-2628.	3.4	10
5	Discovery of vascular Rho kinase (ROCK) inhibitory peptides. Experimental Biology and Medicine, 2019, 244, 940-951.	2.4	2
6	A color-based competition assay for studying bacterial stress responses in <i>Micrococcus luteus</i> . FEMS Microbiology Letters, 2019, 366, .	1.8	5
7	Twenty-Five Years of Investigating the Universal Stress Protein: Function, Structure, and Applications. Advances in Applied Microbiology, 2018, 102, 1-36.	2.4	54
8	Solid support resins and affinity purification mass spectrometry. Molecular BioSystems, 2017, 13, 456-462.	2.9	7
9	A Proteomic Signature of Dormancy in the Actinobacterium Micrococcus luteus. Journal of Bacteriology, 2017, 199, .	2.2	24
10	Extent of the Oxidative Side Reactions to Peptides and Proteins During the CuAAC Reaction. Bioconjugate Chemistry, 2016, 27, 2315-2322.	3.6	71
11	Observations on different resin strategies for affinity purification mass spectrometry of a tagged protein. Analytical Biochemistry, 2016, 515, 26-32.	2.4	7
12	Insights into the anti-angiogenic properties of phosphaplatins. Journal of Inorganic Biochemistry, 2016, 164, 5-16.	3.5	10
13	Formaldehyde scavengers function as novel antigen retrieval agents. Scientific Reports, 2015, 5, 17322.	3.3	6
14	Enhancing MALDI Time-Of-Flight Mass Spectrometer Performance through Spectrum Averaging. PLoS ONE, 2015, 10, e0120932.	2.5	8
15	Identification of Protein Complexes in mAKAP Signalosome by Mass Spectrometry. FASEB Journal, 2015, 29, 1025.2.	0.5	0
16	The Protein Architecture of Human Secretory Vesicles Reveals Differential Regulation of Signaling Molecule Secretion by Protein Kinases. PLoS ONE, 2012, 7, e41134.	2.5	11
17	NeuroPedia: neuropeptide database and spectral library. Bioinformatics, 2011, 27, 2772-2773.	4.1	63
18	Neuropeptidomic Components Generated by Proteomic Functions in Secretory Vesicles for Cell–Cell Communication. AAPS Journal, 2010, 12, 635-645.	4.4	23

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19	Proteomics of Dense Core Secretory Vesicles Reveal Distinct Protein Categories for Secretion of Neuroeffectors for Cellâ^'Cell Communication. Journal of Proteome Research, 2010, 9, 5002-5024.	3.7	48
20	Mass Spectrometry-Based Neuropeptidomics of Secretory Vesicles from Human Adrenal Medullary Pheochromocytoma Reveals Novel Peptide Products of Prohormone Processing. Journal of Proteome Research, 2010, 9, 5065-5075.	3.7	29
21	Linear and accurate quantitation of proenkephalin-derived peptides by isotopic labeling with internal standards and mass spectrometry. Analytical Biochemistry, 2009, 389, 18-26.	2.4	12
22	Detecting low-abundance vasoactive peptides in plasma: Progress toward absolute quantitation using nano liquid chromatography–mass spectrometry. Analytical Biochemistry, 2009, 394, 164-170.	2.4	27
23	Proteases for Processing Proneuropeptides into Peptide Neurotransmitters and Hormones. Annual Review of Pharmacology and Toxicology, 2008, 48, 393-423.	9.4	215
24	The future of proteomic analysis in biological systems and molecular medicine. Molecular BioSystems, 2007, 3, 14-17.	2.9	3
25	Differential Recovery of Peptides from Sample Tubes and the Reproducibility of Quantitative Proteomic Data. Journal of Proteome Research, 2007, 6, 4511-4516.	3.7	31
26	Secretory vesicle aminopeptidase B related to neuropeptide processing: molecular identification and subcellular localization to enkephalin- and NPY-containing chromaffin granules. Journal of Neurochemistry, 2007, 100, 1340-1350.	3.9	51
27	Proteomic Analysis of Human Immunodeficiency Virus Using Liquid Chromatography/Tandem Mass Spectrometry Effectively Distinguishes Specific Incorporated Host ProteinsJ. Proteome Res.2006,3, 530â^3538 Journal of Proteome Research, 2006, 5, 1279-1279.	3.7	1
28	Proteomic Analysis of Human Immunodeficiency Virus Using Liquid Chromatography/Tandem Mass Spectrometry Effectively Distinguishes Specific Incorporated Host Proteins. Journal of Proteome Research, 2006, 5, 530-538.	3.7	66
29	High-Temperature Protein Mass Mapping Using a Thermophilic Protease. Journal of the American Chemical Society, 2001, 123, 1774-1775.	13.7	36
30	A new scaffold for amide ligation. Bioorganic and Medicinal Chemistry, 2001, 9, 2323-2328.	3.0	67
31	Fluorescent Indicators of Peptide Cleavage in the Trafficking Compartments of Living Cells: Peptides Site-Specifically Labeled with Two Dyes. Methods, 2000, 20, 429-435.	3.8	14
32	A Highly Efficient Method for Site-Specific Modification of Unprotected Peptides after Chemical Synthesis. Journal of the American Chemical Society, 2000, 122, 3567-3573.	13.7	23
33	Engineering an unnatural Nα-anchored disulfide into BPTI by total chemical synthesis: structural and functional consequences. FEBS Letters, 1999, 460, 67-76.	2.8	16
34	All Four Homochiral Enantiomers of a Nuclear Localization Sequence Derived from c-Myc Serve as Functional Import Signals. Journal of Biological Chemistry, 1998, 273, 29764-29769.	3.4	22
35	Extending the Applicability of Native Chemical Ligation. Journal of the American Chemical Society, 1996, 118, 5891-5896.	13.7	264