Jeffrey A Degrasse

List of Publications by Year in descending order

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| # | Article | IF | CITATIONS |
|----|---|----------------------|-------------|
| 1 | The influence of food matrices on aptamer selection by SELEX (systematic evolution of ligands by) Tj ETQq1 | 1 0.784314 rg 4.2 | BT10verlock |
| 2 | Purification and Characterization of Neurotoxin Complex from a Dual Toxin Gene Containing Clostridium Botulinum Strain PS-5. Protein Journal, 2013, 32, 288-296. | 0.7 | 2 |
| 3 | First report of the use of a saxitoxin–protein conjugate to develop a DNA aptamer to a small molecule toxin. Toxicon, 2013, 61, 30-37. | 0.8 | 88 |
| 4 | Novel Platform for the Detection of Staphylococcus aureus Enterotoxin B in Foods. Applied and Environmental Microbiology, 2013, 79, 1422-1427. | 1.4 | 16 |
| 5 | A Single-Stranded DNA Aptamer That Selectively Binds to Staphylococcus aureus Enterotoxin B. PLoS ONE, 2012, 7, e33410. | 1.1 | 93 |
| 6 | Solid core column technology applied to HPLC-FD of paralytic shellfish toxins. Toxicon, 2011, 57, 179-182. | 0.8 | 14 |
| 7 | Evaluation of protein expression in bovine bronchoalveolar fluid following challenge with <i>Mannheimia haemolytica</i> . Proteomics, 2011, 11, 3685-3697. | 1.3 | 17 |
| 8 | The proteomic advantage: Label-free quantification of proteins expressed in bovine milk during experimentally induced coliform mastitis. Veterinary Immunology and Immunopathology, 2010, 138, 252-266. | 0.5 | 52 |
| 9 | A Functional Proteomic Study of the Trypanosoma brucei Nuclear Pore Complex: An Informatic Strategy. Methods in Molecular Biology, 2010, 673, 231-238. | 0.4 | 11 |
| 10 | Evidence for a Shared Nuclear Pore Complex Architecture That Is Conserved from the Last Common Eukaryotic Ancestor. Molecular and Cellular Proteomics, 2009, 8, 2119-2130. | 2.5 | 200 |
| 11 | Acetylation of histone H4K4 is cell cycle regulated and mediated by HAT3 in <i>Trypanosoma brucei</i> . Molecular Microbiology, 2008, 67, 762-771. | 1.2 | 54 |
| 12 | High-Yield Isolation and Subcellular Proteomic Characterization of Nuclear and Subnuclear Structures from Trypanosomes. Methods in Molecular Biology, 2008, 463, 77-92. | 0.4 | 21 |
| 13 | Comprehensive analysis of diverse ribonucleoprotein complexes. Nature Methods, 2007, 4, 951-956. | 9.0 | 253 |
| 14 | I-DIRT, A General Method for Distinguishing between Specific and Nonspecific Protein Interactions. Journal of Proteome Research, 2005, 4, 1752-1756. | 1.8 | 134 |