

Alberto ElÃ- as-Villalobos

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	The <i>O</i> -Mannosyltransferase PMT4 Is Essential for Normal Appressorium Formation and Penetration in <i>Ustilago maydis</i> . <i>Plant Cell</i> , 2009, 21, 3397-3412.	6.6	60
2	The General Transcriptional Repressor Tup1 Is Required for Dimorphism and Virulence in a Fungal Plant Pathogen. <i>PLoS Pathogens</i> , 2011, 7, e1002235.	4.7	52
3	Identification of <i>O</i> -mannosylated Virulence Factors in <i>Ustilago maydis</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002563.	4.7	48
4	The Hos2 Histone Deacetylase Controls <i>Ustilago maydis</i> Virulence through Direct Regulation of Mating-Type Genes. <i>PLoS Pathogens</i> , 2015, 11, e1005134.	4.7	37
5	Chaperone-mediated ordered assembly of the SAGA and NuA4 transcription co-activator complexes in yeast. <i>Nature Communications</i> , 2019, 10, 5237.	12.8	33
6	Endoplasmic Reticulum Glucosidases and Protein Quality Control Factors Cooperate to Establish Biotrophy in <i>Ustilago maydis</i> . <i>Plant Cell</i> , 2013, 25, 4676-4690.	6.6	27
7	New insights into the evolutionary conservation of the sole PIKK pseudokinase Tra1/TRRAP. <i>Biochemical Society Transactions</i> , 2019, 47, 1597-1608.	3.4	25
8	Protein glycosylation in the phytopathogen <i>Ustilago maydis</i> : From core oligosaccharide synthesis to the ER glycoprotein quality control system, a genomic analysis. <i>Fungal Genetics and Biology</i> , 2010, 47, 727-735.	2.1	14
9	Chromatin modification factors in plant pathogenic fungi: Insights from <i>Ustilago maydis</i> . <i>Fungal Genetics and Biology</i> , 2019, 129, 52-64.	2.1	13
10	The Hsp90 cochaperone TTT promotes cotranslational maturation of PIKKs prior to complex assembly. <i>Cell Reports</i> , 2021, 37, 109867.	6.4	9
11	Nuclear ingress of cytoplasmic bodies accompanies a boost in autophagy. <i>Life Science Alliance</i> , 2022, 5, e202101160.	2.8	8
12	The requirement for protein <i>O</i> -mannosylation for <i>Ustilago maydis</i> virulence seems to be linked to intrinsic aspects of the infection process rather than an altered plant response. <i>Plant Signaling and Behavior</i> , 2010, 5, 412-414.	2.4	7
13	Histone deacetylases: revealing the molecular base of dimorphism in pathogenic fungi. <i>Microbial Cell</i> , 2015, 2, 491-493.	3.2	7
14	Quantitative analysis of protein-RNA interactions in fission yeast. <i>STAR Protocols</i> , 2022, 3, 101373.	1.2	0