

Marc S Cortese

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

6,174
citations

257101

24
h-index

454577

30
g-index

34
all docs

34
docs citations

34
times ranked

5731
citing authors

#	ARTICLE	IF	CITATIONS
1	Rewiring of transcriptional networks as a major event leading to the diversity of asexual multicellularity in fungi. <i>Critical Reviews in Microbiology</i> , 2019, 45, 548-563.	2.7	29
2	Developmental regulators FlbE/D orchestrate the polarity site-to-nucleus dynamics of the fungal bZIP transcription factor FlbB. <i>Cellular and Molecular Life Sciences</i> , 2019, 76, 4369-4390.	2.4	14
3	The Early Asexual Development Regulator fluG Codes for a Putative Bifunctional Enzyme. <i>Frontiers in Microbiology</i> , 2019, 10, 778.	1.5	5
4	Tip-actin nucleus migration dynamics of the asexual development regulator <sc>FlbB</sc> in vegetative cells. <i>Molecular Microbiology</i> , 2015, 98, 607-624.	1.2	27
5	A second component of the SltA-dependent cation tolerance pathway in <i>Aspergillus nidulans</i> . <i>Fungal Genetics and Biology</i> , 2015, 82, 116-128.	0.9	16
6	High-throughput characterization of intrinsic disorder in proteins from the Protein Structure Initiative. <i>Journal of Structural Biology</i> , 2012, 180, 201-215.	1.3	34
7	GmcA Is a Putative Glucose-Methanol-Choline Oxidoreductase Required for the Induction of Asexual Development in <i>Aspergillus nidulans</i> . <i>PLoS ONE</i> , 2012, 7, e40292.	1.1	29
8	Elucidation of Functional Markers from <i>Aspergillus nidulans</i> Developmental Regulator FlbB and Their Phylogenetic Distribution. <i>PLoS ONE</i> , 2011, 6, e17505.	1.1	9
9	HPV-16 E5 down-regulates expression of surface HLA class I and reduces recognition by CD8 T cells. <i>Virology</i> , 2010, 407, 137-142.	1.1	118
10	All 4 dileucine motifs in the first hydrophobic domain of the E5 oncoprotein of human papillomavirus type 16 are essential for surface MHC class I downregulation activity and E5 endomembrane localization. <i>International Journal of Cancer</i> , 2010, 126, 1675-1682.	2.3	48
11	Effects of human papillomavirus type 16 E5 deletion mutants on epithelial morphology: functional characterization of each transmembrane domain. <i>Journal of General Virology</i> , 2010, 91, 521-530.	1.3	37
12	Adenovirus type 5 E4 Orf3 protein targets promyelocytic leukaemia (PML) protein nuclear domains for disruption via a sequence in PML isoform II that is predicted as a protein interaction site by bioinformatic analysis. <i>Journal of General Virology</i> , 2009, 90, 95-104.	1.3	37
13	Bovine papillomavirus type 1 oncoprotein E5 inhibits equine MHC class I and interacts with equine MHC I heavy chain. <i>Journal of General Virology</i> , 2009, 90, 2865-2870.	1.3	37
14	Intrinsic disorder in scaffold proteins: Getting more from less. <i>Progress in Biophysics and Molecular Biology</i> , 2008, 98, 85-106.	1.4	259
15	Structural Basis for Regulation of Protein Phosphatase 1 by Inhibitor-2. <i>Journal of Biological Chemistry</i> , 2007, 282, 28874-28883.	1.6	175
16	DisProt: the Database of Disordered Proteins. <i>Nucleic Acids Research</i> , 2007, 35, D786-D793.	6.5	711
17	Characterization of Molecular Recognition Features, MoRFs, and Their Binding Partners. <i>Journal of Proteome Research</i> , 2007, 6, 2351-2366.	1.8	433
18	Intrinsic Disorder in the Protein Data Bank. <i>Journal of Biomolecular Structure and Dynamics</i> , 2007, 24, 325-341.	2.0	140

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19	Analysis of Molecular Recognition Features (MoRFs). <i>Journal of Molecular Biology</i> , 2006, 362, 1043-1059.	2.0	672
20	Rational drug design via intrinsically disordered protein. <i>Trends in Biotechnology</i> , 2006, 24, 435-442.	4.9	225
21	Alternative splicing in concert with protein intrinsic disorder enables increased functional diversity in multicellular organisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8390-8395.	3.3	428
22	Flexible nets. The roles of intrinsic disorder in protein interaction networks. <i>FEBS Journal</i> , 2005, 272, 5129-5148.	2.2	1,052
23	DisProt: a database of protein disorder. <i>Bioinformatics</i> , 2005, 21, 137-140.	1.8	231
24	Comparing and Combining Predictors of Mostly Disordered Proteins. <i>Biochemistry</i> , 2005, 44, 1989-2000.	1.2	485
25	Uncovering the Unfoldome: Enriching Cell Extracts for Unstructured Proteins by Acid Treatment. <i>Journal of Proteome Research</i> , 2005, 4, 1610-1618.	1.8	71
26	Coupled Folding and Binding with α -Helix-Forming Molecular Recognition Elements. <i>Biochemistry</i> , 2005, 44, 12454-12470.	1.2	593
27	Structural, functional, and evolutionary analysis of moeZ, a gene encoding an enzyme required for the synthesis of the <i>Pseudomonas</i> metabolite, pyridine-2,6-bis(thiocarboxylic acid). <i>BMC Evolutionary Biology</i> , 2002, 2, 8.	3.2	17
28	Metal chelating properties of pyridine-2,6-bis(thiocarboxylic acid) produced by <i>Pseudomonas</i> spp. and the biological activities of the formed complexes. <i>BioMetals</i> , 2002, 15, 103-120.	1.8	59
29	Antimicrobial Properties of Pyridine-2,6-Dithiocarboxylic Acid, a Metal Chelator Produced by <i>Pseudomonas</i> spp. <i>Applied and Environmental Microbiology</i> , 2001, 67, 3934-3942.	1.4	43
30	A <i>Pseudomonas stutzeri</i> gene cluster encoding the biosynthesis of the CCl ₄ -dechlorination agent pyridine-2,6-bis(thiocarboxylic acid). <i>Environmental Microbiology</i> , 2000, 2, 407-416.	1.8	60