

Marcin Grynberg

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

2,355
citations

331670

21
h-index

223800

46
g-index

49
all docs

49
docs citations

49
times ranked

4768
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative genomic analyses of the human fungal pathogens <i>Coccidioides</i> and their relatives. <i>Genome Research</i> , 2009, 19, 1722-1731.	5.5	295
2	Tandem repeats lead to sequence assembly errors and impose multi-level challenges for genome and protein databases. <i>Nucleic Acids Research</i> , 2019, 47, 10994-11006.	14.5	236
3	A model species for agricultural pest genomics: the genome of the Colorado potato beetle, <i>Leptinotarsa decemlineata</i> (Coleoptera: Chrysomelidae). <i>Scientific Reports</i> , 2018, 8, 1931.	3.3	215
4	The retinitis pigmentosa GTPase regulator (RPGR)- interacting protein: Subverting RPGR function and participating in disk morphogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 3965-3970.	7.1	205
5	Comparative Genomic Analysis of Human Fungal Pathogens Causing Paracoccidioidomycosis. <i>PLoS Genetics</i> , 2011, 7, e1002345.	3.5	164
6	Extending the Aerolysin Family: From Bacteria to Vertebrates. <i>PLoS ONE</i> , 2011, 6, e20349.	2.5	107
7	LTR Retrotransposons in Fungi. <i>PLoS ONE</i> , 2011, 6, e29425.	2.5	94
8	Recurrent Horizontal Transfer of Bacterial Toxin Genes to Eukaryotes. <i>Molecular Biology and Evolution</i> , 2012, 29, 2223-2230.	8.9	91
9	PlaToLoCo: the first web meta-server for visualization and annotation of low complexity regions in proteins. <i>Nucleic Acids Research</i> , 2020, 48, W77-W84.	14.5	71
10	Disentangling the complexity of low complexity proteins. <i>Briefings in Bioinformatics</i> , 2020, 21, 458-472.	6.5	70
11	Novel AlkB Dioxygenases—Alternative Models for In Silico and In Vivo Studies. <i>PLoS ONE</i> , 2012, 7, e30588.	2.5	65
12	A Novel Protein Kinase-Like Domain in a Selenoprotein, Widespread in the Tree of Life. <i>PLoS ONE</i> , 2012, 7, e32138.	2.5	61
13	HEPN: a common domain in bacterial drug resistance and human neurodegenerative proteins. <i>Trends in Biochemical Sciences</i> , 2003, 28, 224-226.	7.5	59
14	Phosphorylation of spore coat proteins by a family of atypical protein kinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3482-91.	7.1	56
15	Adaptative Potential of the <i>Lactococcus Lactis</i> IL594 Strain Encoded in Its 7 Plasmids. <i>PLoS ONE</i> , 2011, 6, e22238.	2.5	56
16	Crystal Structure of the Actin Binding Domain of the Cyclase-Associated Protein. <i>Biochemistry</i> , 2004, 43, 10628-10641.	2.5	51
17	Independent Subtilases Expansions in Fungi Associated with Animals. <i>Molecular Biology and Evolution</i> , 2011, 28, 3395-3404.	8.9	51
18	Domain analysis of the tubulin cofactor system: a model for tubulin folding and dimerization. <i>BMC Bioinformatics</i> , 2003, 4, 46.	2.6	41

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19	Amino acid substitution equivalent to human chorea-acanthocytosis I2771R in yeast Vps13 protein affects its binding to phosphatidylinositol 3-phosphate. <i>Human Molecular Genetics</i> , 2017, 26, 1497-1510.	2.9	39
20	Sensor Domains Encoded in <i>Bacillus anthracis</i> Virulence Plasmids Prevent Sporulation by Hijacking a Sporulation Sensor Histidine Kinase. <i>Journal of Bacteriology</i> , 2006, 188, 6354-6360.	2.2	32
21	A widespread peroxiredoxin-like domain present in tumor suppression- and progression-implicated proteins. <i>BMC Genomics</i> , 2010, 11, 590.	2.8	26
22	Phosphatidylinositol-3-phosphate regulates response of cells to proteotoxic stress. <i>International Journal of Biochemistry and Cell Biology</i> , 2016, 79, 494-504.	2.8	23
23	Structural Insights into Inhibition of <i>Bacillus anthracis</i> Sporulation by a Novel Class of Non-heme Globin Sensor Domains. <i>Journal of Biological Chemistry</i> , 2011, 286, 8448-8458.	3.4	22
24	Genomic and Functional Characterization of the Unusual pLOCK 0919 Plasmid Harboring the <i>spaCBA</i> Pili Cluster in <i>Lactobacillus casei</i> LOCK 0919. <i>Genome Biology and Evolution</i> , 2016, 8, 202-217.	2.5	22
25	The <i>Aspergillus nidulans</i> <i>cysA</i> gene encodes a novel type of serine O-acetyltransferase which is homologous to homoserine O-acetyltransferases The GenBank accession number for the sequence reported in this paper is AF029885.. <i>Microbiology (United Kingdom)</i> , 2000, 146, 2695-2703.	1.8	19
26	CLCAs - A Family of Metalloproteases of Intriguing Phylogenetic Distribution and with Cases of Substituted Catalytic Sites. <i>PLoS ONE</i> , 2013, 8, e62272.	2.5	19
27	The C2H2 zinc finger transcription factors are likely targets for Ni(ii) toxicity. <i>Metallomics</i> , 2011, 3, 1227.	2.4	18
28	Comparative genomics and functional analysis of a highly adhesive dairy <i>Lactobacillus paracasei</i> subsp. <i>paracasei</i> IBB3423 strain. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 7617-7634.	3.6	17
29	Quantitative Conformational Analysis of Functionally Important Electrostatic Interactions in the Intrinsically Disordered Region of Delta Subunit of Bacterial RNA Polymerase. <i>Journal of the American Chemical Society</i> , 2019, 141, 16817-16828.	13.7	16
30	NERD: a DNA processing-related domain present in the anthrax virulence plasmid, pXO1. <i>Trends in Biochemical Sciences</i> , 2004, 29, 106-110.	7.5	15
31	The CHiPS Domain - Ancient Traces for the Hermansky-Pudlak Syndrome. <i>Traffic</i> , 2005, 6, 534-538.	2.7	15
32	Putative type IV secretion genes in <i>Bacillus anthracis</i> . <i>Trends in Microbiology</i> , 2007, 15, 191-195.	7.7	14
33	Functional and physical interactions of Faf1p, a <i>Saccharomyces cerevisiae</i> nucleolar protein. <i>Biochemical and Biophysical Research Communications</i> , 2004, 319, 349-357.	2.1	10
34	Human hAtg2A protein expressed in yeast is recruited to preautophagosomal structure but does not complement autophagy defects of <i>atg21^Δ</i> strain.. <i>Acta Biochimica Polonica</i> , 2011, 58, .	0.5	8
35	Global pentapeptide statistics are far away from expected distributions. <i>Scientific Reports</i> , 2018, 8, 15178.	3.3	7
36	Common low complexity regions for SARS-CoV-2 and human proteomes as potential multidirectional risk factor in vaccine development. <i>BMC Bioinformatics</i> , 2021, 22, 182.	2.6	7

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37	Human hAtg2A protein expressed in yeast is recruited to preautophagosomal structure but does not complement autophagy defects of atg21 ^Δ strain. <i>Acta Biochimica Polonica</i> , 2011, 58, 365-74.	0.5	6
38	Newly identified protein Imi1 affects mitochondrial integrity and glutathione homeostasis in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2015, 15, fov048.	2.3	5
39	The F658G substitution in <i>Saccharomyces cerevisiae</i> cohesin Irr1/Scs3 is semi-dominant in the diploid and disturbs mitosis, meiosis and the cell cycle. <i>European Journal of Cell Biology</i> , 2008, 87, 831-844.	3.6	4
40	An Engineered Distant Homolog of <i>Pseudomonas syringae</i> TTSS Effector From <i>Physcomitrella patens</i> Can Act as a Bacterial Virulence Factor. <i>Frontiers in Microbiology</i> , 2018, 9, 1060.	3.5	4
41	The Signal for Signaling, Found. <i>PLoS Pathogens</i> , 2009, 5, e1000398.	4.7	3
42	Distinct Protein Classes in Human Red Cell Proteome Revealed by Similarity of Phylogenetic Profiles. <i>PLoS ONE</i> , 2013, 8, e54471.	2.5	3
43	The proline-rich region of glyceraldehyde-3-phosphate dehydrogenase from human sperm may bind SH3 domains, as revealed by a bioinformatic study of low-complexity protein segments. <i>Molecular Reproduction and Development</i> , 2016, 83, 144-148.	2.0	3
44	Mutational analysis of the AtNUDT7 Nudix hydrolase from <i>Arabidopsis thaliana</i> reveals residues required for protein quaternary structure formation and activity. <i>Acta Biochimica Polonica</i> , 2009, 56, 291-300.	0.5	2
45	<i>Bacillus anthracis</i> pXO1 plasmid encodes a putative membrane-bound bacteriocin. <i>PeerJ</i> , 2014, 2, e679.	2.0	1
46	Ni ²⁺ -Assisted Hydrolysis May Affect the Human Proteome; Filaggrin Degradation Ex Vivo as an Example of Possible Consequences. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 828674.	3.5	1