

Marcin Grynberg

List of Publications by Year in descending order

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46
papers

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331670

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223800

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49
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times ranked

4768
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	Disentangling the complexity of low complexity proteins. <i>Briefings in Bioinformatics</i> , 2020, 21, 458-472.	6.5	70
4	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
5	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
6	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
7	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
8	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
9	Global pentapeptide statistics are far away from expected distributions. <i>Scientific Reports</i> , 2018, 8, 15178.	3.3	7
10	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
11	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
12	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
13	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
14	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
15	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
16	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
17	<i>Bacillus anthracis</i> pXO1 plasmid encodes a putative membrane-bound bacteriocin. <i>PeerJ</i> , 2014, 2, e679.	2.0	1
18	Distinct Protein Classes in Human Red Cell Proteome Revealed by Similarity of Phylogenetic Profiles. <i>PLoS ONE</i> , 2013, 8, e54471.	2.5	3

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19	CLCAs - A Family of Metalloproteases of Intriguing Phylogenetic Distribution and with Cases of Substituted Catalytic Sites. PLoS ONE, 2013, 8, e62272.	2.5	19
20	Recurrent Horizontal Transfer of Bacterial Toxin Genes to Eukaryotes. Molecular Biology and Evolution, 2012, 29, 2223-2230.	8.9	91
21	A Novel Protein Kinase-Like Domain in a Selenoprotein, Widespread in the Tree of Life. PLoS ONE, 2012, 7, e32138.	2.5	61
22	Novel AlkB Dioxygenases—Alternative Models for In Silico and In Vivo Studies. PLoS ONE, 2012, 7, e30588.	2.5	65
23	The C2H2 zinc finger transcription factors are likely targets for Ni(ii) toxicity. Metallomics, 2011, 3, 1227.	2.4	18
24	LTR Retrotransposons in Fungi. PLoS ONE, 2011, 6, e29425.	2.5	94
25	Structural Insights into Inhibition of Bacillus anthracis Sporulation by a Novel Class of Non-heme Globin Sensor Domains. Journal of Biological Chemistry, 2011, 286, 8448-8458.	3.4	22
26	Comparative Genomic Analysis of Human Fungal Pathogens Causing Paracoccidioidomycosis. PLoS Genetics, 2011, 7, e1002345.	3.5	164
27	Independent Subtilases Expansions in Fungi Associated with Animals. Molecular Biology and Evolution, 2011, 28, 3395-3404.	8.9	51
28	Extending the Aerolysin Family: From Bacteria to Vertebrates. PLoS ONE, 2011, 6, e20349.	2.5	107
29	Adaptative Potential of the Lactococcus Lactis IL594 Strain Encoded in Its 7 Plasmids. PLoS ONE, 2011, 6, e22238.	2.5	56
30	Human hAtg2A protein expressed in yeast is recruited to preautophagosomal structure but does not complement autophagy defects of atg21 ^Δ strain.. Acta Biochimica Polonica, 2011, 58, .	0.5	8
31	Human hAtg2A protein expressed in yeast is recruited to preautophagosomal structure but does not complement autophagy defects of atg21 ^Δ strain. Acta Biochimica Polonica, 2011, 58, 365-74.	0.5	6
32	A widespread peroxiredoxin-like domain present in tumor suppression- and progression-implicated proteins. BMC Genomics, 2010, 11, 590.	2.8	26
33	Comparative genomic analyses of the human fungal pathogens <i>Coccidioides</i> and their relatives. Genome Research, 2009, 19, 1722-1731.	5.5	295
34	The Signal for Signaling, Found. PLoS Pathogens, 2009, 5, e1000398.	4.7	3
35	Mutational analysis of the AtNUDT7 Nudix hydrolase from Arabidopsis thaliana reveals residues required for protein quaternary structure formation and activity. Acta Biochimica Polonica, 2009, 56, 291-300.	0.5	2
36	The F658G substitution in Saccharomyces cerevisiae cohesin Irr1/Scs3 is semi-dominant in the diploid and disturbs mitosis, meiosis and the cell cycle. European Journal of Cell Biology, 2008, 87, 831-844.	3.6	4

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37	Putative type IV secretion genes in <i>Bacillus anthracis</i> . <i>Trends in Microbiology</i> , 2007, 15, 191-195.	7.7	14
38	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
39	The CHiPS Domain - Ancient Traces for the Hermansky-Pudlak Syndrome. <i>Traffic</i> , 2005, 6, 534-538.	2.7	15
40	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
41	Crystal Structure of the Actin Binding Domain of the Cyclase-Associated Protein. <i>Biochemistry</i> , 2004, 43, 10628-10641.	2.5	51
42	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
43	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
44	Domain analysis of the tubulin cofactor system: a model for tubulin folding and dimerization. <i>BMC Bioinformatics</i> , 2003, 4, 46.	2.6	41
45	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
46	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