Crysten E Blaby-Haas

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3153397/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Plant GATA Factors: Their Biology, Phylogeny, and Phylogenomics. Annual Review of Plant Biology, 2022, 73, 123-148.	8.6	28
2	Zng1 is a GTP-dependent zinc transferase needed for activation of methionine aminopeptidase. Cell Reports, 2022, 39, 110834.	2.9	20
3	Colocality to Cofunctionality: Eukaryotic Gene Neighborhoods as a Resource for Function Discovery. Molecular Biology and Evolution, 2021, 38, 650-662.	3.5	14
4	Cyanobacteria provide a new paradigm in the regulation of cofactor dependence. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	1
5	Widespread polycistronic gene expression in green algae. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	30
6	Plant single-cell solutions for energy and the environment. Communications Biology, 2021, 4, 962.	2.0	23
7	Maturation of Rhodobacter capsulatus Multicopper Oxidase CutO Depends on the CopA Copper Efflux Pathway and Requires the cutF Product. Frontiers in Microbiology, 2021, 12, 720644.	1.5	8
8	From economy to luxury: Copper homeostasis in Chlamydomonas and other algae. Biochimica Et Biophysica Acta - Molecular Cell Research, 2020, 1867, 118822.	1.9	35
9	Leveraging computational genomics to understand the molecular basis of metal homeostasis. New Phytologist, 2020, 228, 1472-1489.	3.5	4
10	Comparative differential cuproproteomes of <i>Rhodobacter capsulatus</i> reveal novel copper homeostasis related proteins. Metallomics, 2020, 12, 572-591.	1.0	12
11	Human COQ10A and COQ10B are distinct lipid-binding START domain proteins required for coenzyme Q function. Journal of Lipid Research, 2019, 60, 1293-1310.	2.0	38
12	Comparative and Functional Algal Genomics. Annual Review of Plant Biology, 2019, 70, 605-638.	8.6	76
13	Cu Transport by the Extended Family of CcoA-like Transporters (CalT) in Proteobacteria. Scientific Reports, 2019, 9, 1208.	1.6	10
14	Regulation of Oxygenic Photosynthesis during Trophic Transitions in the Green Alga <i>Chromochloris zofingiensis</i> . Plant Cell, 2019, 31, 579-601.	3.1	61
15	The <i>cbb</i> ₃ -type cytochrome oxidase assembly factor CcoG is a widely distributed cupric reductase. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 21166-21175.	3.3	17
16	Using YFP as a Reporter of Gene Expression in the Green Alga Chlamydomonas reinhardtii. Methods in Molecular Biology, 2018, 1755, 135-148.	0.4	0
17	Gene Expression Analysis by Arylsulfatase Assays in the Green Alga Chlamydomonas reinhardtii. Methods in Molecular Biology, 2018, 1755, 149-161.	0.4	3
18	Proteases Shape the Chlamydomonas Secretome: Comparison to Classical Neuropeptide Processing Machinery. Proteomes, 2018, 6, 36.	1.7	28

#	Article	IF	CITATIONS
19	Widespread Distribution and Functional Specificity of the Copper Importer CcoA: Distinct Cu Uptake Routes for Bacterial Cytochrome <i>c</i> Oxidases. MBio, 2018, 9, .	1.8	25
20	Chlamydomonas reinhardtii LFO1 Is an IsdG Family Heme Oxygenase. MSphere, 2017, 2, .	1.3	15
21	Insights into the red algae and eukaryotic evolution from the genome of <i>Porphyra umbilicalis</i> (Bangiophyceae, Rhodophyta). Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6361-E6370.	3.3	233
22	Regulating cellular trace metal economy in algae. Current Opinion in Plant Biology, 2017, 39, 88-96.	3.5	52
23	Genomics and Functional Genomics in Chlamydomonas reinhardtii. Microbiology Monographs, 2017, , 1-26.	0.3	4
24	Characterization of Saccharomyces cerevisiae Coenzyme Q Biosynthetic Protein Coq11. FASEB Journal, 2017, 31, 781.9.	0.2	0
25	Ni induces the CRR1-dependent regulon revealing overlap and distinction between hypoxia and Cu deficiency responses in Chlamydomonas reinhardtii. Metallomics, 2016, 8, 679-691.	1.0	27
26	Early eukaryotic origins for cilia-associated bioactive peptide amidating activity. Journal of Cell Science, 2016, 129, 943-56.	1.2	24
27	Genomeâ€wide analysis on <i>Chlamydomonas reinhardtii</i> reveals the impact of hydrogen peroxide on protein stress responses and overlap with other stress transcriptomes. Plant Journal, 2015, 84, 974-988.	2.8	55
28	ldentification of Coq11, a New Coenzyme Q Biosynthetic Protein in the CoQ-Synthome in Saccharomyces cerevisiae. Journal of Biological Chemistry, 2015, 290, 7517-7534.	1.6	65
29	PHOTOSYSTEM II PROTEIN33, a Protein Conserved in the Plastid Lineage, Is Associated with the Chloroplast Thylakoid Membrane and Provides Stability to Photosystem II Supercomplexes in Arabidopsis. Plant Physiology, 2015, 167, 481-492.	2.3	46
30	Activation of Autophagy by Metals in Chlamydomonas reinhardtii. Eukaryotic Cell, 2015, 14, 964-973.	3.4	29
31	Evolution of a plant-specific copper chaperone family for chloroplast copper homeostasis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5480-7.	3.3	57
32	Lysosome-related Organelles as Mediators of Metal Homeostasis. Journal of Biological Chemistry, 2014, 289, 28129-28136.	1.6	114
33	The Chlamydomonas genome project: a decade on. Trends in Plant Science, 2014, 19, 672-680.	4.3	145
34	lron sparing and recycling in a compartmentalized cell. Current Opinion in Microbiology, 2013, 16, 677-685.	2.3	43
35	Genome of the long-living sacred lotus (Nelumbo nucifera Gaertn.). Genome Biology, 2013, 14, R41.	13.9	329
36	Iron economy in Chlamydomonas reinhardtii. Frontiers in Plant Science, 2013, 4, 337.	1.7	65

CRYSTEN E BLABY-HAAS

#	Article	IF	CITATIONS
37	Systems and <i>Trans</i> -System Level Analysis Identifies Conserved Iron Deficiency Responses in the Plant Lineage. Plant Cell, 2012, 24, 3921-3948.	3.1	142
38	The ins and outs of algal metal transport. Biochimica Et Biophysica Acta - Molecular Cell Research, 2012, 1823, 1531-1552.	1.9	173
39	YeiR: a metal-binding GTPase from Escherichia coli involved in metal homeostasis. Metallomics, 2012, 4, 488.	1.0	49
40	Synergistic use of plant-prokaryote comparative genomics for functional annotations. BMC Genomics, 2011, 12, S2.	1.2	43
41	Erratum to "Towards a Systems Approach in the Genetic Analysis of Archaea: Accelerating Mutant Construction and Phenotypic Analysis in <i>Haloferax volcanii</i> ― Archaea, 2011, 2011, 1-1.	2.3	26
42	Role of a Zn-independent DksA in Zn homeostasis and stringent response. Molecular Microbiology, 2011, 79, 700-715.	1.2	68
43	Mining high-throughput experimental data to link gene and function. Trends in Biotechnology, 2011, 29, 174-182.	4.9	45
44	Towards a Systems Approach in the Genetic Analysis of Archaea: Accelerating Mutant Construction and Phenotypic Analysis in <i>Haloferax volcanii</i> . Archaea, 2010, 2010, 1-11.	2.3	32
45	Polar algae flaunt their zinc assets. Nature Ecology and Evolution, 0, , .	3.4	0