

Kourosh Salehi-Ashtiani

List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

6,408
citations

126907

33
h-index

118850

62
g-index

68
all docs

68
docs citations

68
times ranked

12072
citing authors

#	ARTICLE	IF	CITATIONS
1	COT drives resistance to RAF inhibition through MAP kinase pathway reactivation. <i>Nature</i> , 2010, 468, 968-972.	27.8	1,325
2	Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. <i>Cell</i> , 2015, 161, 647-660.	28.9	482
3	Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing. <i>Cell</i> , 2016, 164, 805-817.	28.9	479
4	A public genome-scale lentiviral expression library of human ORFs. <i>Nature Methods</i> , 2011, 8, 659-661.	19.0	477
5	A Genomewide Search for Ribozymes Reveals an HDV-Like Sequence in the Human CPEB3 Gene. <i>Science</i> , 2006, 313, 1788-1792.	12.6	268
6	Metabolic network reconstruction of <i>Chlamydomonas</i> offers insight into light-driven algal metabolism. <i>Molecular Systems Biology</i> , 2011, 7, 518.	7.2	264
7	Next-generation sequencing to generate interactome datasets. <i>Nature Methods</i> , 2011, 8, 478-480.	19.0	258
8	The Landscape of <i>C. elegans</i> 3' UTRs. <i>Science</i> , 2010, 329, 432-435.	12.6	248
9	RNA Catalysis in Model Protocell Vesicles. <i>Journal of the American Chemical Society</i> , 2005, 127, 13213-13219.	13.7	242
10	In vitro evolution suggests multiple origins for the hammerhead ribozyme. <i>Nature</i> , 2001, 414, 82-84.	27.8	168
11	Analysis of the human E2 ubiquitin conjugating enzyme protein interaction network. <i>Genome Research</i> , 2009, 19, 1905-1911.	5.5	134
12	Protein interaction network of alternatively spliced isoforms from brain links genetic risk factors for autism. <i>Nature Communications</i> , 2014, 5, 3650.	12.8	131
13	The completion of the Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2009, 19, 2324-2333.	5.5	125
14	The ORFeome Collaboration: a genome-scale human ORF-clone resource. <i>Nature Methods</i> , 2016, 13, 191-192.	19.0	111
15	Mapping of HKT1;5 Gene in Barley Using GWAS Approach and Its Implication in Salt Tolerance Mechanism. <i>Frontiers in Plant Science</i> , 2018, 9, 156.	3.6	95
16	Whole-Genome Resequencing Reveals Extensive Natural Variation in the Model Green Alga <i>Chlamydomonas reinhardtii</i> . <i>Plant Cell</i> , 2015, 27, 2353-2369.	6.6	92
17	Metabolic network analysis integrated with transcript verification for sequenced genomes. <i>Nature Methods</i> , 2009, 6, 589-592.	19.0	83
18	Safranal induces DNA double-strand breakage and ER-stress-mediated cell death in hepatocellular carcinoma cells. <i>Scientific Reports</i> , 2018, 8, 16951.	3.3	82

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19	A Zebrafish Genetic Screen Identifies Neuromedin U as a Regulator of Sleep/Wake States. <i>Neuron</i> , 2016, 89, 842-856.	8.1	81
20	Advances in microalgal research and engineering development. <i>Current Opinion in Biotechnology</i> , 2019, 59, 157-164.	6.6	73
21	Saffron-Based Crocin Prevents Early Lesions of Liver Cancer: In vivo, In vitro and Network Analyses. <i>Recent Patents on Anti-Cancer Drug Discovery</i> , 2016, 11, 121-133.	1.6	70
22	Algal Cell Factories: Approaches, Applications, and Potentials. <i>Marine Drugs</i> , 2016, 14, 225.	4.6	65
23	Evidence for Transcript Networks Composed of Chimeric RNAs in Human Cells. <i>PLoS ONE</i> , 2012, 7, e28213.	2.5	61
24	SH3 interactome conserves general function over specific form. <i>Molecular Systems Biology</i> , 2013, 9, 652.	7.2	61
25	An integrative Raman microscopy-based workflow for rapid in situ analysis of microalgal lipid bodies. <i>Biotechnology for Biofuels</i> , 2015, 8, 164.	6.2	58
26	Manipulation of carbon flux into fatty acid biosynthesis pathway in <i>Dunaliella salina</i> using AccD and ME genes to enhance lipid content and to improve produced biodiesel quality. <i>Biofuel Research Journal</i> , 0, , 91-97.	13.3	56
27	Genome-wide expression analysis offers new insights into the origin and evolution of <i>Physcomitrella patens</i> stress response. <i>Scientific Reports</i> , 2015, 5, 17434.	3.3	54
28	DNA Methylation and Expression of the Genes Coding for Lactate Dehydrogenases A and C during Rodent Spermatogenesis1. <i>Biology of Reproduction</i> , 1991, 44, 527-535.	2.7	52
29	Yeast one-hybrid assays for gene-centered human gene regulatory network mapping. <i>Nature Methods</i> , 2011, 8, 1050-1052.	19.0	48
30	Large-scale genome sequencing reveals the driving forces of viruses in microalgal evolution. <i>Cell Host and Microbe</i> , 2021, 29, 250-266.e8.	11.0	48
31	Intracellular spectral repositioning of light enhances algal photosynthetic efficiency. <i>Science Advances</i> , 2017, 3, e1603096.	10.3	42
32	Efficient targeted transcript discovery via array-based normalization of RACE libraries. <i>Nature Methods</i> , 2008, 5, 629-635.	19.0	41
33	The in vitro selection world. <i>Methods</i> , 2016, 106, 3-13.	3.8	41
34	Expression of <i>neuroand</i> Neu differentiation factor in the olfactory mucosa of rat. <i>International Journal of Developmental Neuroscience</i> , 1996, 14, 801-811.	1.6	37
35	Chemical Mutagenesis and Fluorescence-Based High-Throughput Screening for Enhanced Accumulation of Carotenoids in a Model Marine Diatom <i>Phaeodactylum tricornutum</i> . <i>Marine Drugs</i> , 2018, 16, 272.	4.6	35
36	Sugar-stimulated CO ₂ sequestration by the green microalga <i>Chlorella vulgaris</i> . <i>Science of the Total Environment</i> , 2019, 654, 275-283.	8.0	31

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37	Molecular Mechanisms behind Safranal's Toxicity to HepG2 Cells from Dual Omics. <i>Antioxidants</i> , 2022, 11, 1125.	5.1	31
38	Isoform discovery by targeted cloning, 'deep-well' pooling and parallel sequencing. <i>Nature Methods</i> , 2008, 5, 597-600.	19.0	30
39	Microalgal Metabolic Network Model Refinement through High-Throughput Functional Metabolic Profiling. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 68.	4.1	29
40	Metabolic systems analysis to advance algal biotechnology. <i>Biotechnology Journal</i> , 2010, 5, 660-670.	3.5	28
41	Combined artificial high-silicate medium and LED illumination promote carotenoid accumulation in the marine diatom <i>Phaeodactylum tricornutum</i> . <i>Microbial Cell Factories</i> , 2019, 18, 209.	4.0	27
42	Differences in regulation of testis specific lactate dehydrogenase in rat and mouse occur at multiple levels. <i>Molecular Reproduction and Development</i> , 1993, 35, 1-7.	2.0	26
43	Hovlinc is a recently evolved class of ribozyme found in human lncRNA. <i>Nature Chemical Biology</i> , 2021, 17, 601-607.	8.0	26
44	Potential for Heightened Sulfur-Metabolic Capacity in Coastal Subtropical Microalgae. <i>IScience</i> , 2019, 11, 450-465.	4.1	23
45	Computational Approaches for Microalgal Biofuel Optimization: A Review. <i>BioMed Research International</i> , 2014, 2014, 1-12.	1.9	21
46	Genome-wide functional annotation and structural verification of metabolic ORFeome of <i>Chlamydomonas reinhardtii</i> . <i>BMC Genomics</i> , 2011, 12, S4.	2.8	17
47	A massively parallel barcoded sequencing pipeline enables generation of the first ORFeome and interactome map for rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11836-11842.	7.1	16
48	A high-quality genome assembly and annotation of the gray mangrove, <i>Avicennia marina</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	16
49	The genome and phenome of the green alga <i>Chloroidium</i> sp. UTEX 3007 reveal adaptive traits for desert acclimatization. <i>ELife</i> , 2017, 6, .	6.0	16
50	Large-scale RACE approach for proactive experimental definition of <i>C. elegans</i> ORFeome. <i>Genome Research</i> , 2009, 19, 2334-2342.	5.5	12
51	Systems level analysis of the <i>Chlamydomonas reinhardtii</i> metabolic network reveals variability in evolutionary co-conservation. <i>Molecular BioSystems</i> , 2016, 12, 2394-2407.	2.9	12
52	Integrated Analysis of Gene Network in Childhood Leukemia from Microarray and Pathway Databases. <i>BioMed Research International</i> , 2014, 2014, 1-7.	1.9	10
53	Characterizing algal blooms in a shallow & a deep channel. <i>Ocean and Coastal Management</i> , 2021, 213, 105840.	4.4	9
54	Alternative glycosylation controls endoplasmic reticulum dynamics and tubular extension in mammalian cells. <i>Science Advances</i> , 2021, 7, .	10.3	8

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55	GPCR Genes as Activators of Surface Colonization Pathways in a Model Marine Diatom. IScience, 2020, 23, 101424.	4.1	7
56	Toward Applications of Genomics and Metabolic Modeling to Improve Algal Biomass Productivity. Biofuel and Biorefinery Technologies, 2015, , 173-189.	0.3	5
57	Alternative Poly(A) Tails Meet miRNA Targeting in Caenorhabditis elegans. Genetics, 2017, 206, 755-756.	2.9	4
58	Expression profile of Ldh-a in the developing rat Rattus norvegicus testis suggests regulation at the translational level. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 1995, 110, 623-627.	1.6	3
59	Proteome expression moves in vitro: resources and tools for harnessing the human proteome. Nature Methods, 2008, 5, 1001-1002.	19.0	3
60	Single-Cell Characterization of Microalgal Lipid Contents with Confocal Raman Microscopy. Series in Bioengineering, 2016, , 363-382.	0.6	3
61	Ultrastructural Variability in the Locomotor Cortex of the Ciliated Protozoa, Mytilophilus pacificae. Journal of Eukaryotic Microbiology, 1997, 44, 471-479.	1.7	2
62	Molecular Genetic Techniques for Algal Bioengineering. Biofuel and Biorefinery Technologies, 2015, , 155-171.	0.3	2
63	Prospective Applications of Synthetic Biology for Algal Bioproduct Optimization. Biofuel and Biorefinery Technologies, 2015, , 137-154.	0.3	2
64	Testis-Specific Gene Transcription. , 1996, , 127-134.		1
65	Dataset on economic analysis of mass production of algae in LED-based photobioreactors. Data in Brief, 2019, 22, 137-139.	1.0	0
66	Protocol to generate and characterize biofouling transformants of a model marine diatom. STAR Protocols, 2021, 2, 100716.	1.2	0
67	High-Throughput Metabolic Profiling for Model Refinements of Microalgae. Journal of Visualized Experiments, 2021, , .	0.3	0