

Andrew Emili

List of Publications by Year in descending order

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Version: 2024-02-01

88
papers

12,271
citations

101543

36
h-index

56724

83
g-index

110
all docs

110
docs citations

110
times ranked

16269
citing authors

#	ARTICLE	IF	CITATIONS
1	Global Landscape of Native Protein Complexes in <i>Synechocystis</i> sp. PCC 6803. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 715-727.	6.9	13
2	Multioomic Metabolic Enrichment Network Analysis Reveals Metabolite-Protein Physical Interaction Subnetworks Altered in Cancer. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100189.	3.8	4
3	Recombinant Lloviu virus as a tool to study viral replication and host responses. <i>PLoS Pathogens</i> , 2022, 18, e1010268.	4.7	11
4	DNAJB1-PRKACA in HEK293T cells induces LINC00473 overexpression that depends on PKA signaling. <i>PLoS ONE</i> , 2022, 17, e0263829.	2.5	6
5	Neuralized-like protein 4 (NEURL4) mediates ADP-ribosylation of mitochondrial proteins. <i>Journal of Cell Biology</i> , 2022, 221, .	5.2	9
6	ZFC3H1 and U1-70K promote the nuclear retention of mRNAs with 5' splice site motifs within nuclear speckles. <i>Rna</i> , 2022, 28, 878-894.	3.5	5
7	Humanized mice reveal a macrophage-enriched gene signature defining human lung tissue protection during SARS-CoV-2 infection. <i>Cell Reports</i> , 2022, 39, 110714.	6.4	14
8	A reduced complexity cross between BALB/c substrains identifies <i>Zhx2</i> as a candidate gene underlying oxycodone metabolite brain concentration and state-dependent learning of opioid reward. <i>FASEB Journal</i> , 2022, 36, .	0.5	0
9	Scalable multiplex co-fractionation/mass spectrometry platform for accelerated protein interactome discovery. <i>Nature Communications</i> , 2022, 13, .	12.8	20
10	Pilot Study Showing Feasibility of Phosphoproteomic Profiling of Pathway-Level Molecular Alterations in Barrett's Esophagus. <i>Genes</i> , 2022, 13, 1215.	2.4	0
11	Protein Interaction Network Biology in Neuroscience. <i>Proteomics</i> , 2021, 21, e1900311.	2.2	13
12	Applicability of Chromatographic Co-elution for Antibiotic Target Identification. <i>Proteomics</i> , 2021, 21, e2000038.	2.2	3
13	Enrichment of Phosphorylated Tau (Thr181) and Functionally Interacting Molecules in Chronic Traumatic Encephalopathy Brain-derived Extracellular Vesicles. , 2021, 12, 1376.		3
14	Intracellular Density of <i>Wolbachia</i> Is Mediated by Host Autophagy and the Bacterial Cytoplasmic Incompatibility Gene <i>cifB</i> in a Cell Type-Dependent Manner in <i>Drosophila melanogaster</i> . <i>MBio</i> , 2021, 12, .	4.1	101
15	Imaging the future: the emerging era of single-cell spatial proteomics. <i>FEBS Journal</i> , 2021, 288, 6990-7001.	4.7	26
16	Subcellular proteomics. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	21.2	159
17	Patient-specific iPSCs carrying an SFTPC mutation reveal the intrinsic alveolar epithelial dysfunction at the inception of interstitial lung disease. <i>Cell Reports</i> , 2021, 36, 109636.	6.4	48
18	Interaction of tau with HNRNPA2B1 and N6-methyladenosine RNA mediates the progression of tauopathy. <i>Molecular Cell</i> , 2021, 81, 4209-4227.e12.	9.7	84

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19	<i>Omics Notebook</i> : robust, reproducible and flexible automated multiomics exploratory analysis and reporting. <i>Bioinformatics Advances</i> , 2021, 1, .	2.4	8
20	Usher syndrome type 1-associated gene, <i>pcdh15b</i> , is required for photoreceptor structural integrity in zebrafish. <i>DMM Disease Models and Mechanisms</i> , 2021, 14, .	2.4	12
21	Mass Spectrometry-Based Phosphoproteomics and Systems Biology: Approaches to Study T Lymphocyte Activation and Exhaustion. <i>Journal of Molecular Biology</i> , 2021, 433, 167318.	4.2	5
22	The cyclin dependent kinase inhibitor Roscovitine prevents diet-induced metabolic disruption in obese mice. <i>Scientific Reports</i> , 2021, 11, 20365.	3.3	1
23	Monomeric C-reactive protein via endothelial CD31 for neurovascular inflammation in an ApoE genotype-dependent pattern: A risk factor for Alzheimer's disease?. <i>Aging Cell</i> , 2021, 20, e13501.	6.7	25
24	Mass-Spectrometry-Based Functional Proteomic and Phosphoproteomic Technologies and Their Application for Analyzing Ex Vivo and In Vitro Models of Hypertrophic Cardiomyopathy. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13644.	4.1	2
25	A Mutation in <i>Hnrnp1</i> That Decreases Methamphetamine-Induced Reinforcement, Reward, and Dopamine Release and Increases Synaptosomal hnRNP H and Mitochondrial Proteins. <i>Journal of Neuroscience</i> , 2020, 40, 107-130.	3.6	39
26	Organoids Model Transcriptional Hallmarks of Oncogenic KRAS Activation in Lung Epithelial Progenitor Cells. <i>Cell Stem Cell</i> , 2020, 27, 663-678.e8.	11.1	86
27	TPR is required for the efficient nuclear export of mRNAs and lncRNAs from short and intron-poor genes. <i>Nucleic Acids Research</i> , 2020, 48, 11645-11663.	14.5	34
28	Triphenyl phosphate is a selective PPAR β modulator that does not induce brite adipogenesis in vitro and in vivo. <i>Archives of Toxicology</i> , 2020, 94, 3087-3103.	4.2	16
29	Mapping signalling perturbations in myocardial fibrosis via the integrative phosphoproteomic profiling of tissue from diverse sources. <i>Nature Biomedical Engineering</i> , 2020, 4, 889-900.	22.5	17
30	Actionable Cytopathogenic Host Responses of Human Alveolar Type 2 Cells to SARS-CoV-2. <i>Molecular Cell</i> , 2020, 80, 1104-1122.e9.	9.7	94
31	Dengue Virus Infection of <i>Aedes aegypti</i> Alters Extracellular Vesicle Protein Cargo to Enhance Virus Transmission. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6609.	4.1	10
32	BrainMap Elucidates the Macromolecular Connectivity Landscape of Mammalian Brain. <i>Cell Systems</i> , 2020, 10, 333-350.e14.	6.2	48
33	MKRN2 Physically Interacts with GLE1 to Regulate mRNA Export and Zebrafish Retinal Development. <i>Cell Reports</i> , 2020, 31, 107693.	6.4	11
34	Assessment of separation methods for extracellular vesicles from human and mouse brain tissues and human cerebrospinal fluids. <i>Methods</i> , 2020, 177, 35-49.	3.8	44
35	Modulation of lymphocyte-mediated tissue repair by rational design of heterocyclic aryl hydrocarbon receptor agonists. <i>Science Advances</i> , 2020, 6, eaay8230.	10.3	31
36	Loss of G-Protein Pathway Suppressor 2 Promotes Tumor Growth Through Activation of AKT Signaling. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 608044.	3.7	10

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37	PDX-derived organoids model in vivo drug response and secrete biomarkers. JCI Insight, 2020, 5, .	5.0	66
38	EPIC: software toolkit for elution profile-based inference of protein complexes. Nature Methods, 2019, 16, 737-742.	19.0	67
39	Egr1 mediates the effect of insulin on leptin transcription in adipocytes. Journal of Biological Chemistry, 2019, 294, 5784-5789.	3.4	22
40	Proteinâ€“Protein Interaction Profiling in <i>Candida albicans</i> Revealed by Biochemical Purificationâ€“Mass Spectrometry (BP/MS). Methods in Molecular Biology, 2019, 2049, 203-211.	0.9	0
41	Mapping global protein contacts. Science, 2019, 365, 120-121.	12.6	1
42	Mapping global protein contacts. Science, 2019, 365, 120-121.	12.6	3
43	FZD4 Marks Lateral Plate Mesoderm and Signals with NORRIN to Increase Cardiomyocyte Induction from Pluripotent Stem Cell-Derived Cardiac Progenitors. Stem Cell Reports, 2018, 10, 87-100.	4.8	32
44	The Nitrogen Regulatory PII Protein (GlnB) and <i>N</i> -Acetylglucosamine 6-Phosphate Epimerase (NanE) Allosterically Activate Glucosamine 6-Phosphate Deaminase (NagB) in <i>Escherichia coli</i> . Journal of Bacteriology, 2018, 200, .	2.2	19
45	Single-platform â€“multi-omicâ€™ profiling: unified mass spectrometry and computational workflows for integrative proteomicsâ€“metabolomics analysis. Molecular Omics, 2018, 14, 307-319.	2.8	41
46	Global landscape of cell envelope protein complexes in <i>Escherichia coli</i> . Nature Biotechnology, 2018, 36, 103-112.	17.5	110
47	The phosphocarrier protein HPr of the bacterial phosphotransferase system globally regulates energy metabolism by directly interacting with multiple enzymes in <i>Escherichia coli</i> . Journal of Biological Chemistry, 2017, 292, 14250-14257.	3.4	42
48	A Global Analysis of the Receptor Tyrosine Kinase-Protein Phosphatase Interactome. Molecular Cell, 2017, 65, 347-360.	9.7	123
49	Exercise-responsive phosphoproteins in the heart. Journal of Molecular and Cellular Cardiology, 2017, 111, 61-68.	1.9	13
50	Native KCC2 interactome reveals PACSIN1 as a critical regulator of synaptic inhibition. ELife, 2017, 6, .	6.0	44
51	C9a and ZNF644 Physically Associate to Suppress Progenitor Gene Expression during Neurogenesis. Stem Cell Reports, 2016, 7, 454-470.	4.8	24
52	DLG5 connects cell polarity and Hippo signaling protein networks by linking PAR-1 with MST1/2. Genes and Development, 2016, 30, 2696-2709.	5.9	67
53	Proteome-wide dataset supporting the study of ancient metazoan macromolecular complexes. Data in Brief, 2016, 6, 715-721.	1.0	5
54	Conditional Epistatic Interaction Maps Reveal Global Functional Rewiring of Genome Integrity Pathways in <i>Escherichia coli</i> . Cell Reports, 2016, 14, 648-661.	6.4	34

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55	Systematic Genetic Screens Reveal the Dynamic Global Functional Organization of the Bacterial Translation Machinery. <i>Cell Reports</i> , 2016, 17, 904-916.	6.4	34
56	Global phosphoproteomic profiling reveals perturbed signaling in a mouse model of dilated cardiomyopathy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12592-12597.	7.1	35
57	Simple and Effective Affinity Purification Procedures for Mass Spectrometry-Based Identification of Protein-Protein Interactions in Cell Signaling Pathways. <i>Methods in Molecular Biology</i> , 2016, 1394, 181-187.	0.9	2
58	Integrative genomics positions <i>MRN</i> as a novel ribonucleoprotein within the embryonic stem cell gene regulatory network. <i>EMBO Reports</i> , 2015, 16, 1334-1357.	4.5	28
59	Investigating Bacterial Protein Synthesis Using Systems Biology Approaches. <i>Advances in Experimental Medicine and Biology</i> , 2015, 883, 21-40.	1.6	2
60	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. <i>Nature Methods</i> , 2015, 12, 725-731.	19.0	109
61	Extracting high confidence protein interactions from affinity purification data: At the crossroads. <i>Journal of Proteomics</i> , 2015, 118, 63-80.	2.4	30
62	Novel function discovery with GeneMANIA: a new integrated resource for gene function prediction in <i>Escherichia coli</i> . <i>Bioinformatics</i> , 2015, 31, 306-310.	4.1	38
63	Panorama of ancient metazoan macromolecular complexes. <i>Nature</i> , 2015, 525, 339-344.	27.8	478
64	Determining composition of micron-scale protein deposits in neurodegenerative disease by spatially targeted optical microproteomics. <i>ELife</i> , 2015, 4, .	6.0	38
65	Quantitative Genome-Wide Genetic Interaction Screens Reveal Global Epistatic Relationships of Protein Complexes in <i>Escherichia coli</i> . <i>PLoS Genetics</i> , 2014, 10, e1004120.	3.5	96
66	The binary protein-protein interaction landscape of <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2014, 32, 285-290.	17.5	218
67	Human-Chromatin-Related Protein Interactions Identify a Demethylase Complex Required for Chromosome Segregation. <i>Cell Reports</i> , 2014, 8, 297-310.	6.4	72
68	Roles for Pbp1 and Caloric Restriction in Genome and Lifespan Maintenance via Suppression of RNA-DNA Hybrids. <i>Developmental Cell</i> , 2014, 30, 177-191.	7.0	57
69	The MoxR ATPase RavA and Its Cofactor ViaA Interact with the NADH:Ubiquinone Oxidoreductase I in <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2014, 9, e85529.	2.5	34
70	Protein-protein interaction networks: probing disease mechanisms using model systems. <i>Genome Medicine</i> , 2013, 5, 37.	8.2	124
71	A Census of Human Soluble Protein Complexes. <i>Cell</i> , 2012, 150, 1068-1081.	28.9	781
72	Interaction landscape of membrane-protein complexes in <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2012, 489, 585-589.	27.8	228

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73	Genetic Interaction Maps in <i>Escherichia coli</i> Reveal Functional Crosstalk among Cell Envelope Biogenesis Pathways. <i>PLoS Genetics</i> , 2011, 7, e1002377.	3.5	95
74	A Lentiviral Functional Proteomics Approach Identifies Chromatin Remodeling Complexes Important for the Induction of Pluripotency. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 811-823.	3.8	83
75	Quantifying <i>E. coli</i> Proteome and Transcriptome with Single-Molecule Sensitivity in Single Cells. <i>Science</i> , 2010, 329, 533-538.	12.6	1,860
76	Global Functional Atlas of <i>Escherichia coli</i> Encompassing Previously Uncharacterized Proteins. <i>PLoS Biology</i> , 2009, 7, e1000096.	5.6	331
77	Computational and experimental approaches to chart the <i>Escherichia coli</i> cell-envelope-associated proteome and interactome. <i>FEMS Microbiology Reviews</i> , 2009, 33, 66-97.	8.6	53
78	Large-Scale Characterization and Analysis of the Murine Cardiac Proteome. <i>Journal of Proteome Research</i> , 2009, 8, 1887-1901.	3.7	45
79	Sequential Peptide Affinity Purification System for the Systematic Isolation and Identification of Protein Complexes from <i>Escherichia coli</i> . <i>Methods in Molecular Biology</i> , 2009, 564, 373-400.	0.9	41
80	eSGA: <i>E. coli</i> synthetic genetic array analysis. <i>Nature Methods</i> , 2008, 5, 789-795.	19.0	231
81	Functional dissection of protein complexes involved in yeast chromosome biology using a genetic interaction map. <i>Nature</i> , 2007, 446, 806-810.	27.8	806
82	Global Survey of Organ and Organelle Protein Expression in Mouse: Combined Proteomic and Transcriptomic Profiling. <i>Cell</i> , 2006, 125, 173-186.	28.9	429
83	Global landscape of protein complexes in the yeast <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2006, 440, 637-643.	27.8	2,681
84	Interaction network containing conserved and essential protein complexes in <i>Escherichia coli</i> . <i>Nature</i> , 2005, 433, 531-537.	27.8	1,093
85	Conceptual Design for an Automated High-Throughput Magnetic Protein Complex Purification Workcell. <i>Journal of the Association for Laboratory Automation</i> , 2003, 8, 101-106.	2.8	4
86	PRISM, a Generic Large Scale Proteomic Investigation Strategy for Mammals. <i>Molecular and Cellular Proteomics</i> , 2003, 2, 96-106.	3.8	145
87	Splicing and transcription-associated proteins PSF and p54nrb/NonO bind to the RNA polymerase II CTD. <i>Rna</i> , 2002, 8, 1102-1111.	3.5	159
88	Enhanced Proteomic Analysis by HPLC Prefractionation. , 0, , 1491-1501.		1