

# 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 protein complexes in the yeast <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2006, 440, 637-643.	27.8	2,681
2	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
3	Interaction network containing conserved and essential protein complexes in <i>Escherichia coli</i> . <i>Nature</i> , 2005, 433, 531-537.	27.8	1,093
4	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
5	A Census of Human Soluble Protein Complexes. <i>Cell</i> , 2012, 150, 1068-1081.	28.9	781
6	Panorama of ancient metazoan macromolecular complexes. <i>Nature</i> , 2015, 525, 339-344.	27.8	478
7	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
8	Global Functional Atlas of <i>Escherichia coli</i> Encompassing Previously Uncharacterized Proteins. <i>PLoS Biology</i> , 2009, 7, e1000096.	5.6	331
9	eSGA: <i>E. coli</i> synthetic genetic array analysis. <i>Nature Methods</i> , 2008, 5, 789-795.	19.0	231
10	Interaction landscape of membrane-protein complexes in <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2012, 489, 585-589.	27.8	228
11	The binary protein-protein interaction landscape of <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2014, 32, 285-290.	17.5	218
12	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
13	Subcellular proteomics. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	21.2	159
14	PRISM, a Generic Large Scale Proteomic Investigation Strategy for Mammals*S. <i>Molecular and Cellular Proteomics</i> , 2003, 2, 96-106.	3.8	145
15	Protein-protein interaction networks: probing disease mechanisms using model systems. <i>Genome Medicine</i> , 2013, 5, 37.	8.2	124
16	A Global Analysis of the Receptor Tyrosine Kinase-Protein Phosphatase Interactome. <i>Molecular Cell</i> , 2017, 65, 347-360.	9.7	123
17	Global landscape of cell envelope protein complexes in <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2018, 36, 103-112.	17.5	110
18	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

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19	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
20	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
21	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
22	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
23	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
24	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
25	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
26	Human-Chromatin-Related Protein Interactions Identify a Demethylase Complex Required for Chromosome Segregation. <i>Cell Reports</i> , 2014, 8, 297-310.	6.4	72
27	DLG5 connects cell polarity and Hippo signaling protein networks by linking PAR-1 with MST1/2. <i>Genes and Development</i> , 2016, 30, 2696-2709.	5.9	67
28	EPIC: software toolkit for elution profile-based inference of protein complexes. <i>Nature Methods</i> , 2019, 16, 737-742.	19.0	67
29	PDX-derived organoids model in vivo drug response and secrete biomarkers. <i>JCI Insight</i> , 2020, 5, .	5.0	66
30	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
31	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
32	BrainMap Elucidates the Macromolecular Connectivity Landscape of Mammalian Brain. <i>Cell Systems</i> , 2020, 10, 333-350.e14.	6.2	48
33	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
34	Large-Scale Characterization and Analysis of the Murine Cardiac Proteome. <i>Journal of Proteome Research</i> , 2009, 8, 1887-1901.	3.7	45
35	Native KCC2 interactome reveals PACSIN1 as a critical regulator of synaptic inhibition. <i>ELife</i> , 2017, 6, .	6.0	44
36	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

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37	The phosphocarrier protein HPr of the bacterial phosphotransferase system globally regulates energy metabolism by directly interacting with multiple enzymes in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2017, 292, 14250-14257.	3.4	42
38	Single-platform multi-omic™ profiling: unified mass spectrometry and computational workflows for integrative proteomics and metabolomics analysis. <i>Molecular Omics</i> , 2018, 14, 307-319.	2.8	41
39	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
40	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
41	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
42	Determining composition of micron-scale protein deposits in neurodegenerative disease by spatially targeted optical microproteomics. <i>ELife</i> , 2015, 4, .	6.0	38
43	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
44	Conditional Epistatic Interaction Maps Reveal Global Functional Rewiring of Genome Integrity Pathways in <i>Escherichia coli</i> . <i>Cell Reports</i> , 2016, 14, 648-661.	6.4	34
45	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
46	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
47	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
48	FZD4 Marks Lateral Plate Mesoderm and Signals with NORRIN to Increase Cardiomyocyte Induction from Pluripotent Stem Cell-Derived Cardiac Progenitors. <i>Stem Cell Reports</i> , 2018, 10, 87-100.	4.8	32
49	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
50	Extracting high confidence protein interactions from affinity purification data: At the crossroads. <i>Journal of Proteomics</i> , 2015, 118, 63-80.	2.4	30
51	Integrative genomics positions <i>MRKN</i> 1 as a novel ribonucleoprotein within the embryonic stem cell gene regulatory network. <i>EMBO Reports</i> , 2015, 16, 1334-1357.	4.5	28
52	Imaging the future: the emerging era of single-cell spatial proteomics. <i>FEBS Journal</i> , 2021, 288, 6990-7001.	4.7	26
53	Monomeric 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
54	G9a and ZNF644 Physically Associate to Suppress Progenitor Gene Expression during Neurogenesis. <i>Stem Cell Reports</i> , 2016, 7, 454-470.	4.8	24

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55	Egr1 mediates the effect of insulin on leptin transcription in adipocytes. <i>Journal of Biological Chemistry</i> , 2019, 294, 5784-5789.	3.4	22
56	Scalable multiplex co-fractionation/mass spectrometry platform for accelerated protein interactome discovery. <i>Nature Communications</i> , 2022, 13, .	12.8	20
57	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> . <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	19
58	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
59	Triphenyl phosphate is a selective PPAR $\alpha$ modulator that does not induce brite adipogenesis in vitro and in vivo. <i>Archives of Toxicology</i> , 2020, 94, 3087-3103.	4.2	16
60	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
61	Exercise-responsive phosphoproteins in the heart. <i>Journal of Molecular and Cellular Cardiology</i> , 2017, 111, 61-68.	1.9	13
62	Protein Interaction Network Biology in Neuroscience. <i>Proteomics</i> , 2021, 21, e1900311.	2.2	13
63	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
64	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
65	MKRN2 Physically Interacts with GLE1 to Regulate mRNA Export and Zebrafish Retinal Development. <i>Cell Reports</i> , 2020, 31, 107693.	6.4	11
66	Recombinant Lloviu virus as a tool to study viral replication and host responses. <i>PLoS Pathogens</i> , 2022, 18, e1010268.	4.7	11
67	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
68	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
69	Neuralized-like protein 4 (NEURL4) mediates ADP-ribosylation of mitochondrial proteins. <i>Journal of Cell Biology</i> , 2022, 221, .	5.2	9
70	<i>Omics Notebook</i> : robust, reproducible and flexible automated multiomics exploratory analysis and reporting. <i>Bioinformatics Advances</i> , 2021, 1, .	2.4	8
71	DNAJB1-PRKACA in HEK293T cells induces LINC00473 overexpression that depends on PKA signaling. <i>PLoS ONE</i> , 2022, 17, e0263829.	2.5	6
72	Proteome-wide dataset supporting the study of ancient metazoan macromolecular complexes. <i>Data in Brief</i> , 2016, 6, 715-721.	1.0	5

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73	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
74	ZFC3H1 and U1-70K promote the nuclear retention of mRNAs with 5â€² splice site motifs within nuclear speckles. <i>Rna</i> , 2022, 28, 878-894.	3.5	5
75	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
76	Multiomic Metabolic Enrichment Network Analysis Reveals Metaboliteâ€“Protein Physical Interaction Subnetworks Altered in Cancer. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100189.	3.8	4
77	Applicability of Chromatographic Coâ€“Elution for Antibiotic Target Identification. <i>Proteomics</i> , 2021, 21, e2000038.	2.2	3
78	Enrichment of Phosphorylated Tau (Thr181) and Functionally Interacting Molecules in Chronic Traumatic Encephalopathy Brain-derived Extracellular Vesicles. , 2021, 12, 1376.		3
79	Mapping global protein contacts. <i>Science</i> , 2019, 365, 120-121.	12.6	3
80	Investigating Bacterial Protein Synthesis Using Systems Biology Approaches. <i>Advances in Experimental Medicine and Biology</i> , 2015, 883, 21-40.	1.6	2
81	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
82	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
83	Enhanced Proteomic Analysis by HPLC Prefractionation. , 0, , 1491-1501.		1
84	The cyclin dependent kinase inhibitor Roscovitine prevents diet-induced metabolic disruption in obese mice. <i>Scientific Reports</i> , 2021, 11, 20365.	3.3	1
85	Mapping global protein contacts. <i>Science</i> , 2019, 365, 120-121.	12.6	1
86	Proteinâ€“Protein Interaction Profiling in <i>Candida albicans</i> Revealed by Biochemical Purificationâ€“Mass Spectrometry (BP/MS). <i>Methods in Molecular Biology</i> , 2019, 2049, 203-211.	0.9	0
87	A reduced complexity cross between BALB/c substrains identifies <i>Zhx2</i> as a candidate gene underlying oxycodone metabolite brain concentration and stateâ€“dependent learning of opioid reward. <i>FASEB Journal</i> , 2022, 36, .	0.5	0
88	Pilot Study Showing Feasibility of Phosphoproteomic Profiling of Pathway-Level Molecular Alterations in Barrettâ€™s Esophagus. <i>Genes</i> , 2022, 13, 1215.	2.4	0