

Andrew J Link

List of Publications by Year in descending order

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64
papers

5,993
citations

218381

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docs citations

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times ranked

7477
citing authors

#	ARTICLE	IF	CITATIONS
1	A Time-Resolved Cryo-EM Study of <i>Saccharomyces cerevisiae</i> 80S Ribosome Protein Composition in Response to a Change in Carbon Source. <i>Proteomics</i> , 2021, 21, 2000125.	1.3	7
2	Targeted Identification of Protein Interactions in Eukaryotic mRNA Translation. <i>Proteomics</i> , 2020, 20, 1900177.	1.3	2
3	A cost-sensitive online learning method for peptide identification. <i>BMC Genomics</i> , 2020, 21, 324.	1.2	2
4	AS03-Adjuvanted H5N1 Avian Influenza Vaccine Modulates Early Innate Immune Signatures in Human Peripheral Blood Mononuclear Cells. <i>Journal of Infectious Diseases</i> , 2019, 219, 1786-1798.	1.9	16
5	Critical Role for <i>Saccharomyces cerevisiae</i> Asc1p in Translational Initiation at Elevated Temperatures. <i>Proteomics</i> , 2018, 18, e1800208.	1.3	4
6	Identification of Changing Ribosome Protein Compositions using Mass Spectrometry. <i>Proteomics</i> , 2018, 18, e1800217.	1.3	29
7	Proteomics show antigen presentation processes in human immune cells after AS03-H5N1 vaccination. <i>Proteomics</i> , 2017, 17, 1600453.	1.3	6
8	Improved classification model for peptide identification based on self-paced learning. , 2017, , .		1
9	Cell-Based Systems Biology Analysis of Human AS03-Adjuvanted H5N1 Avian Influenza Vaccine Responses: A Phase I Randomized Controlled Trial. <i>PLoS ONE</i> , 2017, 12, e0167488.	1.1	48
10	Multiple Kernel Fuzzy SVM-Based Data Fusion for Improving Peptide Identification. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 804-809.	1.9	6
11	Proteomic contributions to our understanding of vaccine and immune responses. <i>Proteomics - Clinical Applications</i> , 2015, 9, 972-989.	0.8	26
12	Viral infection causes a shift in the self peptide repertoire presented by human MHC class I molecules. <i>Proteomics - Clinical Applications</i> , 2015, 9, 1035-1052.	0.8	16
13	Environmental Interactions and Epistasis Are Revealed in the Proteomic Responses to Complex Stimuli. <i>PLoS ONE</i> , 2015, 10, e0134099.	1.1	11
14	A Cell-Based Systems Biology Assessment of Human Blood to Monitor Immune Responses after Influenza Vaccination. <i>PLoS ONE</i> , 2015, 10, e0118528.	1.1	79
15	A Novel Algorithm for Validating Peptide Identification from a Shotgun Proteomics Search Engine. <i>Journal of Proteome Research</i> , 2013, 12, 1108-1119.	1.8	11
16	Peptide identification based on fuzzy classification and clustering. <i>Proteome Science</i> , 2013, 11, S10.	0.7	5
17	The Yeast Eukaryotic Translation Initiation Factor 2B Translation Initiation Complex Interacts with the Fatty Acid Synthesis Enzyme YBR159W and Endoplasmic Reticulum Membranes. <i>Molecular and Cellular Biology</i> , 2013, 33, 1041-1056.	1.1	13
18	Discovering naturally processed antigenic determinants that confer protective T cell immunity. <i>Journal of Clinical Investigation</i> , 2013, 123, 1976-1987.	3.9	58

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19	A fuzzy cluster-based algorithm for peptide identification. , 2012, , .		1
20	Assessing the Components of the eIF3 Complex and their Phosphorylation Status. Journal of Proteome Research, 2011, 10, 1481-1494.	1.8	14
21	Saccharomyces cerevisiae Gis2 interacts with the translation machinery and is orthogonal to myotonic dystrophy type 2 protein ZNF9. Biochemical and Biophysical Research Communications, 2011, 406, 13-19.	1.0	34
22	Analyzing the Cryptome: Uncovering Secret Sequences. AAPS Journal, 2011, 13, 152-158.	2.2	40
23	Microdialysis Combined with Proteomics for Protein Identification in Breast Tumor Microenvironment In Vivo. Cancer Microenvironment, 2011, 4, 61-71.	3.1	13
24	Studies of the Mechanistic Details of the pH-dependent Association of Botulinum Neurotoxin with Membranes. Journal of Biological Chemistry, 2011, 286, 27011-27018.	1.6	22
25	Growing and Harvesting TAP-Tagged Yeast Cells. Cold Spring Harbor Protocols, 2011, 2011, pdb.prot5604.	0.2	4
26	Quantitative analysis of the secretome of TGF β 2 signaling-deficient mammary fibroblasts. Proteomics, 2010, 10, 2458-2470.	1.3	37
27	Identification of Residue-to-residue Contact between a Peptide Ligand and Its G Protein-coupled Receptor Using Periodate-mediated Dihydroxyphenylalanine Cross-linking and Mass Spectrometry. Journal of Biological Chemistry, 2010, 285, 39425-39436.	1.6	25
28	ZNF9 Activation of IRES-Mediated Translation of the Human ODC mRNA Is Decreased in Myotonic Dystrophy Type 2. PLoS ONE, 2010, 5, e9301.	1.1	27
29	In-Gel Trypsin Digest of Gel-Fractionated Proteins. Cold Spring Harbor Protocols, 2009, 2009, pdb.prot5110.	0.2	17
30	Chapter 40 Identification and Quantification of Protein Posttranslational Modifications. Methods in Enzymology, 2009, 463, 725-763.	0.4	86
31	Construction of Nucleic Acid Programmable Protein Arrays (NAPPA) 4: DNA Biotinylation, Precipitation, and Arraying of Samples. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5059.	0.2	9
32	Construction of Nucleic Acid Programmable Protein Arrays (NAPPA) 1: Coating Glass Slides with Amino Silane. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5056.	0.2	13
33	Construction of Nucleic Acid Programmable Protein Arrays (NAPPA) 2: Preparing Bacterial Cultures in a 96-Well Format: Figure 1.. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5057.	0.2	9
34	Construction of Nucleic Acid Programmable Protein Arrays (NAPPA) 3: Isolating DNA Plasmids in a 96-Well Plate Format. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5058-pdb.prot5058.	0.2	11
35	Construction of Nucleic Acid Programmable Protein Arrays (NAPPA) 5: Expressing Proteins on NAPPA Slides. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5060.	0.2	9
36	Construction of Nucleic Acid Programmable Protein Arrays (NAPPA) 6: Detecting Proteins on NAPPA Slides. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5061-pdb.prot5061.	0.2	9

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37	Construction of Nucleic Acid Programmable Protein Arrays (NAPPA) 7: Detecting DNA on NAPPA Slides. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5062-pdb.prot5062.	0.2	9
38	High-Throughput Cloning of Open Reading Frames (ORFs): Assembling Large Sets of Expression Constructs. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5050.	0.2	0
39	Using the Nucleic Acid Programmable Protein Array (NAPPA) for Identifying Protein-Protein Interactions: General Guidelines. Cold Spring Harbor Protocols, 2008, 2008, pdb.ip62.	0.2	4
40	Using the Nucleic Acid Programmable Protein Array (NAPPA) for Identifying Protein-Protein Interactions. Protocol 1: Coexpression of Query Protein on NAPPA Slides. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5108-pdb.prot5108.	0.2	2
41	A Proteomics Analysis of Yeast Mot1p Protein-Protein Associations. Molecular and Cellular Proteomics, 2008, 7, 2090-2106.	2.5	16
42	Dyggve-Melchior-Clausen syndrome: Chondrodysplasia resulting from defects in intracellular vesicle traffic. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16171-16176.	3.3	35
43	Using the Nucleic Acid Programmable Protein Array (NAPPA) for Identifying Protein-Protein Interactions. Protocol 2: Detection of Query Proteins on NAPPA Slides. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5109.	0.2	2
44	The Myotonic Dystrophy Type 2 Protein ZNF9 Is Part of an ITAF Complex That Promotes Cap-independent Translation. Molecular and Cellular Proteomics, 2007, 6, 1049-1058.	2.5	51
45	Systematic identification and functional screens of uncharacterized proteins associated with eukaryotic ribosomal complexes. Genes and Development, 2006, 20, 1294-1307.	2.7	248
46	Analyzing Proteomes and Protein Function Using Graphical Comparative Analysis of Tandem Mass Spectrometry Results. Molecular and Cellular Proteomics, 2006, 5, 1497-1513.	2.5	30
47	Discovery of regulatory molecular events and biomarkers using 2D capillary chromatography and mass spectrometry. Expert Review of Proteomics, 2006, 3, 63-74.	1.3	19
48	Proteomic Analysis of Human Neutrophil Granules. Molecular and Cellular Proteomics, 2005, 4, 1503-1521.	2.5	281
49	The Novel ATP-Binding Cassette Protein ARB1 Is a Shuttling Factor That Stimulates 40S and 60S Ribosome Biogenesis. Molecular and Cellular Biology, 2005, 25, 9859-9873.	1.1	60
50	Purifying protein complexes for mass spectrometry: applications to protein translation. Methods, 2005, 35, 274-290.	1.9	30
51	Yeast Asc1p and Mammalian RACK1 Are Functionally Orthologous Core 40S Ribosomal Proteins That Repress Gene Expression. Molecular and Cellular Biology, 2004, 24, 8276-8287.	1.1	159
52	Identification of a Drosophila Myb-E2F2/RBF transcriptional repressor complex. Genes and Development, 2004, 18, 2929-2940.	2.7	233
53	Cluster Analysis of Mass Spectrometry Data Reveals a Novel Component of SAGA. Molecular and Cellular Biology, 2004, 24, 7249-7259.	1.1	127
54	Identification and Characterization of Two Novel Proteins Affecting Fission Yeast $\hat{3}$ -tubulin Complex Function. Molecular Biology of the Cell, 2004, 15, 2287-2301.	0.9	108

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55	YIH1 Is an Actin-binding Protein That Inhibits Protein Kinase GCN2 and Impairs General Amino Acid Control When Overexpressed. <i>Journal of Biological Chemistry</i> , 2004, 279, 29952-29962.	1.6	51
56	A Protein Complex Containing the Conserved Swi2/Snf2-Related ATPase Swr1p Deposits Histone Variant H2A.Z into Euchromatin. <i>PLoS Biology</i> , 2004, 2, e131.	2.6	512
57	Analysis of Protein Composition Using Multidimensional Chromatography and Mass Spectrometry. <i>Current Protocols in Protein Science</i> , 2003, 34, Unit 23.1.	2.8	8
58	Proteomics Analysis Reveals Stable Multiprotein Complexes in Both Fission and Budding Yeasts Containing Myb-Related Cdc5p/Cef1p, Novel Pre-mRNA Splicing Factors, and snRNAs. <i>Molecular and Cellular Biology</i> , 2002, 22, 2011-2024.	1.1	193
59	Proteomics of the Eukaryotic Transcription Machinery: Identification of Proteins Associated with Components of Yeast TFIID by Multidimensional Mass Spectrometry. <i>Molecular and Cellular Biology</i> , 2002, 22, 4723-4738.	1.1	285
60	Multidimensional peptide separations in proteomics. <i>Trends in Biotechnology</i> , 2002, 20, s8-s13.	4.9	83
61	The Paf1 complex physically and functionally associates with transcription elongation factors in vivo. <i>EMBO Journal</i> , 2002, 21, 1764-1774.	3.5	280
62	Automated Protein Identification Using Microcolumn Liquid Chromatography-Tandem Mass Spectrometry. , 1999, 112, 553-570.		71
63	Direct analysis of protein complexes using mass spectrometry. <i>Nature Biotechnology</i> , 1999, 17, 676-682.	9.4	2,201
64	Identifying the major proteome components of Haemophilus influenzae type-strain NCTC 8143. <i>Electrophoresis</i> , 1997, 18, 1314-1334.	1.3	175