Andrew J Link

List of Publications by Year
in descending order

64 papers	5,993 citations	218381 26 h-index	133063 59 g-index
64 all docs	64 docs citations	64 times ranked	7477 citing authors

#	Article	IF	Citations
1	Direct analysis of protein complexes using mass spectrometry. Nature Biotechnology, 1999, 17, 676-682.	9.4	2,201
2	A Protein Complex Containing the Conserved Swi2/Snf2-Related ATPase Swr1p Deposits Histone Variant H2A.Z into Euchromatin. PLoS Biology, 2004, 2, e131.	2.6	512
3	Proteomics of the Eukaryotic Transcription Machinery: Identification of Proteins Associated with Components of Yeast TFIID by Multidimensional Mass Spectrometry. Molecular and Cellular Biology, 2002, 22, 4723-4738.	1.1	285
4	Proteomic Analysis of Human Neutrophil Granules. Molecular and Cellular Proteomics, 2005, 4, 1503-1521.	2.5	281
5	The Paf1 complex physically and functionally associates with transcription elongation factors in vivo. EMBO Journal, 2002, 21, 1764-1774.	3.5	280
6	Systematic identification and functional screens of uncharacterized proteins associated with eukaryotic ribosomal complexes. Genes and Development, 2006, 20, 1294-1307.	2.7	248
7	Identification of a Drosophila Myb-E2F2/RBF transcriptional repressor complex. Genes and Development, 2004, 18, 2929-2940.	2.7	233
8	Proteomics Analysis Reveals Stable Multiprotein Complexes in Both Fission and Budding Yeasts Containing Myb-Related Cdc5p/Cef1p, Novel Pre-mRNA Splicing Factors, and snRNAs. Molecular and Cellular Biology, 2002, 22, 2011-2024.	1.1	193
9	Identifying the major proteome components ofHaemophilus influenzae type-strain NCTC 8143. Electrophoresis, 1997, 18, 1314-1334.	1.3	175
10	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
11	Cluster Analysis of Mass Spectrometry Data Reveals a Novel Component of SAGA. Molecular and Cellular Biology, 2004, 24, 7249-7259.	1.1	127
12	Identification and Characterization of Two Novel Proteins Affecting Fission Yeast Î³-tubulin Complex Function. Molecular Biology of the Cell, 2004, 15, 2287-2301.	0.9	108
13	Chapter 40 Identification and Quantification of Protein Posttranslational Modifications. Methods in Enzymology, 2009, 463, 725-763.	0.4	86
14	Multidimensional peptide separations in proteomics. Trends in Biotechnology, 2002, 20, s8-s13.	4.9	83
15	A Cell-Based Systems Biology Assessment of Human Blood to Monitor Immune Responses after Influenza Vaccination. PLoS ONE, 2015, 10, e0118528.	1.1	79
16	Automated Protein Identification Using Microcolumn Liquid Chromatography-Tandem Mass Spectrometry. , 1999, 112, 553-570.		71
17	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
18	Discovering naturally processed antigenic determinants that confer protective T cell immunity. Journal of Clinical Investigation, 2013, 123, 1976-1987.	3.9	58

#	Article	IF	Citations
19	YIH1 Is an Actin-binding Protein That Inhibits Protein Kinase GCN2 and Impairs General Amino Acid Control When Overexpressed. Journal of Biological Chemistry, 2004, 279, 29952-29962.	1.6	51
20	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
21	Cell-Based Systems Biology Analysis of Human AS03-Adjuvanted H5N1 Avian Influenza Vaccine Responses: A Phase I Randomized Controlled Trial. PLoS ONE, 2017, 12, e0167488.	1.1	48
22	Analyzing the Cryptome: Uncovering Secret Sequences. AAPS Journal, 2011, 13, 152-158.	2.2	40
23	Quantitative analysis of the secretome of TGFâ€Î² signalingâ€deficient mammary fibroblasts. Proteomics, 2010, 10, 2458-2470.	1.3	37
24	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
25	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
26	Purifying protein complexes for mass spectrometry: applications to protein translation. Methods, 2005, 35, 274-290.	1.9	30
27	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
28	Identification of Changing Ribosome Protein Compositions using Mass Spectrometry. Proteomics, 2018, 18, e1800217.	1.3	29
29	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
30	Proteomic contributions to our understanding of vaccine and immune responses. Proteomics - Clinical Applications, 2015, 9, 972-989.	0.8	26
31	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
32	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
33	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
34	In-Gel Trypsin Digest of Gel-Fractionated Proteins. Cold Spring Harbor Protocols, 2009, 2009, pdb.prot5110.	0.2	17
35	A Proteomics Analysis of Yeast Mot1p Protein-Protein Associations. Molecular and Cellular Proteomics, 2008, 7, 2090-2106.	2.5	16
36	Viral infection causes a shift in the self peptide repertoire presented by human MHC class I molecules. Proteomics - Clinical Applications, 2015, 9, 1035-1052.	0.8	16

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37	AS03-Adjuvanted H5N1 Avian Influenza Vaccine Modulates Early Innate Immune Signatures in Human Peripheral Blood Mononuclear Cells. Journal of Infectious Diseases, 2019, 219, 1786-1798.	1.9	16
38	Assessing the Components of the eIF3 Complex and their Phosphorylation Status. Journal of Proteome Research, 2011, 10, 1481-1494.	1.8	14
39	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
40	Microdialysis Combined with Proteomics for Protein Identification in Breast Tumor Microenvironment In Vivo. Cancer Microenvironment, 2011, 4, 61-71.	3.1	13
41	The Yeast Eukaryotic Translation Initiation Factor 2B Translation Initiation Complex Interacts with the Fatty Acid Synthesis Enzyme YBR159W and Endoplasmic Reticulum Membranes. Molecular and Cellular Biology, 2013, 33, 1041-1056.	1.1	13
42	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
43	A Novel Algorithm for Validating Peptide Identification from a Shotgun Proteomics Search Engine. Journal of Proteome Research, 2013, 12, 1108-1119.	1.8	11
44	Environmental Interactions and Epistasis Are Revealed in the Proteomic Responses to Complex Stimuli. PLoS ONE, 2015, 10, e0134099.	1.1	11
45	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
46	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
47	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
48	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
49	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
50	Analysis of Protein Composition Using Multidimensional Chromatography and Mass Spectrometry. Current Protocols in Protein Science, 2003, 34, Unit 23.1.	2.8	8
51	A Time‐Resolved Cryo‐EM Study of Saccharomyces cerevisiae 80S Ribosome Protein Composition in Response to a Change in Carbon Source. Proteomics, 2021, 21, 2000125.	1.3	7
52	Multiple Kernel Fuzzy SVM-Based Data Fusion for Improving Peptide Identification. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 804-809.	1.9	6
53	Proteomics show antigen presentation processes in human immune cells after AS03‐H5N1 vaccination. Proteomics, 2017, 17, 1600453.	1.3	6
54	Peptide identification based on fuzzy classification and clustering. Proteome Science, 2013, 11, S10.	0.7	5

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55	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
56	Growing and Harvesting TAP-Tagged Yeast Cells. Cold Spring Harbor Protocols, 2011, 2011, pdb.prot5604.	0.2	4
57	Critical Role for <i>Saccharomyces cerevisiae</i> Asc1p in Translational Initiation at Elevated Temperatures. Proteomics, 2018, 18, e1800208.	1.3	4
58	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
59	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
60	Targeted Identification of Protein Interactions in Eukaryotic mRNA Translation. Proteomics, 2020, 20, 1900177.	1.3	2
61	A cost-sensitive online learning method for peptide identification. BMC Genomics, 2020, 21, 324.	1.2	2
62	A fuzzy cluster-based algorithm for peptide identification. , 2012, , .		1
63	Improved classification model for peptide identification based on self-paced learning. , 2017, , .		1
64	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