

# Andrew J Link

## List of Publications by Year in descending order

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64  
papers

5,993  
citations

218677

26  
h-index

133252

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. <i>Nature Biotechnology</i> , 1999, 17, 676-682.	17.5	2,201
2	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.	5.6	512
3	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.	2.3	285
4	Proteomic Analysis of Human Neutrophil Granules. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1503-1521.	3.8	281
5	The Paf1 complex physically and functionally associates with transcription elongation factors in vivo. <i>EMBO Journal</i> , 2002, 21, 1764-1774.	7.8	280
6	Systematic identification and functional screens of uncharacterized proteins associated with eukaryotic ribosomal complexes. <i>Genes and Development</i> , 2006, 20, 1294-1307.	5.9	248
7	Identification of a <i>Drosophila</i> Myb-E2F2/RBF transcriptional repressor complex. <i>Genes and Development</i> , 2004, 18, 2929-2940.	5.9	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. <i>Molecular and Cellular Biology</i> , 2002, 22, 2011-2024.	2.3	193
9	Identifying the major proteome components of <i>Haemophilus influenzae</i> type-strain NCTC 8143. <i>Electrophoresis</i> , 1997, 18, 1314-1334.	2.4	175
10	Yeast Asc1p and Mammalian RACK1 Are Functionally Orthologous Core 40S Ribosomal Proteins That Repress Gene Expression. <i>Molecular and Cellular Biology</i> , 2004, 24, 8276-8287.	2.3	159
11	Cluster Analysis of Mass Spectrometry Data Reveals a Novel Component of SAGA. <i>Molecular and Cellular Biology</i> , 2004, 24, 7249-7259.	2.3	127
12	Identification and Characterization of Two Novel Proteins Affecting Fission Yeast $\hat{1}^3$ -tubulin Complex Function. <i>Molecular Biology of the Cell</i> , 2004, 15, 2287-2301.	2.1	108
13	Chapter 40 Identification and Quantification of Protein Posttranslational Modifications. <i>Methods in Enzymology</i> , 2009, 463, 725-763.	1.0	86
14	Multidimensional peptide separations in proteomics. <i>Trends in Biotechnology</i> , 2002, 20, s8-s13.	9.3	83
15	A Cell-Based Systems Biology Assessment of Human Blood to Monitor Immune Responses after Influenza Vaccination. <i>PLoS ONE</i> , 2015, 10, e0118528.	2.5	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. <i>Molecular and Cellular Biology</i> , 2005, 25, 9859-9873.	2.3	60
18	Discovering naturally processed antigenic determinants that confer protective T cell immunity. <i>Journal of Clinical Investigation</i> , 2013, 123, 1976-1987.	8.2	58

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19	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.	3.4	51
20	The Myotonic Dystrophy Type 2 Protein ZNF9 Is Part of an ITAF Complex That Promotes Cap-independent Translation. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1049-1058.	3.8	51
21	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.	2.5	48
22	Analyzing the Cryptome: Uncovering Secret Sequences. <i>AAPS Journal</i> , 2011, 13, 152-158.	4.4	40
23	Quantitative analysis of the secretome of TGF $\beta$ 2 signaling-deficient mammary fibroblasts. <i>Proteomics</i> , 2010, 10, 2458-2470.	2.2	37
24	Dyggve-Melchior-Clausen syndrome: Chondrodysplasia resulting from defects in intracellular vesicle traffic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16171-16176.	7.1	35
25	<i>Saccharomyces cerevisiae</i> Gis2 interacts with the translation machinery and is orthogonal to myotonic dystrophy type 2 protein ZNF9. <i>Biochemical and Biophysical Research Communications</i> , 2011, 406, 13-19.	2.1	34
26	Purifying protein complexes for mass spectrometry: applications to protein translation. <i>Methods</i> , 2005, 35, 274-290.	3.8	30
27	Analyzing Proteomes and Protein Function Using Graphical Comparative Analysis of Tandem Mass Spectrometry Results. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1497-1513.	3.8	30
28	Identification of Changing Ribosome Protein Compositions using Mass Spectrometry. <i>Proteomics</i> , 2018, 18, e1800217.	2.2	29
29	ZNF9 Activation of IRES-Mediated Translation of the Human ODC mRNA Is Decreased in Myotonic Dystrophy Type 2. <i>PLoS ONE</i> , 2010, 5, e9301.	2.5	27
30	Proteomic contributions to our understanding of vaccine and immune responses. <i>Proteomics - Clinical Applications</i> , 2015, 9, 972-989.	1.6	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. <i>Journal of Biological Chemistry</i> , 2010, 285, 39425-39436.	3.4	25
32	Studies of the Mechanistic Details of the pH-dependent Association of Botulinum Neurotoxin with Membranes. <i>Journal of Biological Chemistry</i> , 2011, 286, 27011-27018.	3.4	22
33	Discovery of regulatory molecular events and biomarkers using 2D capillary chromatography and mass spectrometry. <i>Expert Review of Proteomics</i> , 2006, 3, 63-74.	3.0	19
34	In-Gel Trypsin Digest of Gel-Fractionated Proteins. <i>Cold Spring Harbor Protocols</i> , 2009, 2009, pdb.prot5110.	0.3	17
35	A Proteomics Analysis of Yeast Mot1p Protein-Protein Associations. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2090-2106.	3.8	16
36	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.	1.6	16

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37	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.	4.0	16
38	Assessing the Components of the eIF3 Complex and their Phosphorylation Status. <i>Journal of Proteome Research</i> , 2011, 10, 1481-1494.	3.7	14
39	Construction of Nucleic Acid Programmable Protein Arrays (NAPPA) 1: Coating Glass Slides with Amino Silane. <i>Cold Spring Harbor Protocols</i> , 2008, 2008, pdb.prot5056.	0.3	13
40	Microdialysis Combined with Proteomics for Protein Identification in Breast Tumor Microenvironment In Vivo. <i>Cancer Microenvironment</i> , 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. <i>Molecular and Cellular Biology</i> , 2013, 33, 1041-1056.	2.3	13
42	Construction of Nucleic Acid Programmable Protein Arrays (NAPPA) 3: Isolating DNA Plasmids in a 96-Well Plate Format. <i>Cold Spring Harbor Protocols</i> , 2008, 2008, pdb.prot5058-pdb.prot5058.	0.3	11
43	A Novel Algorithm for Validating Peptide Identification from a Shotgun Proteomics Search Engine. <i>Journal of Proteome Research</i> , 2013, 12, 1108-1119.	3.7	11
44	Environmental Interactions and Epistasis Are Revealed in the Proteomic Responses to Complex Stimuli. <i>PLoS ONE</i> , 2015, 10, e0134099.	2.5	11
45	Construction of Nucleic Acid Programmable Protein Arrays (NAPPA) 4: DNA Biotinylation, Precipitation, and Arraying of Samples. <i>Cold Spring Harbor Protocols</i> , 2008, 2008, pdb.prot5059.	0.3	9
46	Construction of Nucleic Acid Programmable Protein Arrays (NAPPA) 2: Preparing Bacterial Cultures in a 96-Well Format: Figure 1.. <i>Cold Spring Harbor Protocols</i> , 2008, 2008, pdb.prot5057.	0.3	9
47	Construction of Nucleic Acid Programmable Protein Arrays (NAPPA) 5: Expressing Proteins on NAPPA Slides. <i>Cold Spring Harbor Protocols</i> , 2008, 2008, pdb.prot5060.	0.3	9
48	Construction of Nucleic Acid Programmable Protein Arrays (NAPPA) 6: Detecting Proteins on NAPPA Slides. <i>Cold Spring Harbor Protocols</i> , 2008, 2008, pdb.prot5061-pdb.prot5061.	0.3	9
49	Construction of Nucleic Acid Programmable Protein Arrays (NAPPA) 7: Detecting DNA on NAPPA Slides. <i>Cold Spring Harbor Protocols</i> , 2008, 2008, pdb.prot5062-pdb.prot5062.	0.3	9
50	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
51	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.	2.2	7
52	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.	3.0	6
53	Proteomics show antigen presentation processes in human immune cells after AS03-H5N1 vaccination. <i>Proteomics</i> , 2017, 17, 1600453.	2.2	6
54	Peptide identification based on fuzzy classification and clustering. <i>Proteome Science</i> , 2013, 11, S10.	1.7	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.	0.3	4
56	Growing and Harvesting TAP-Tagged Yeast Cells. Cold Spring Harbor Protocols, 2011, 2011, pdb.prot5604.	0.3	4
57	Critical Role for <i>Saccharomyces cerevisiae</i> Asc1p in Translational Initiation at Elevated Temperatures. Proteomics, 2018, 18, e1800208.	2.2	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.	0.3	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.	0.3	2
60	Targeted Identification of Protein Interactions in Eukaryotic mRNA Translation. Proteomics, 2020, 20, 1900177.	2.2	2
61	A cost-sensitive online learning method for peptide identification. BMC Genomics, 2020, 21, 324.	2.8	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.	0.3	0