

BIOGRAPHICAL SKETCH

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NAME Link, Andrew J.		POSITION TITLE Associate Professor	
eRA COMMONS USER NAME (credential, e.g., agency login) linkaj			
EDUCATION/TRAINING <i>(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)</i>			
INSTITUTION AND LOCATION	DEGREE <i>(if applicable)</i>	YEAR(s)	FIELD OF STUDY
Washington University, St. Louis MO	B.S.	1987	Chemical Engineering
Washington University, St. Louis MO	B.A.	1987	Biology
Washington University, St. Louis MO	M.A.	1987	Biology
Harvard University, Cambridge, MA	Ph.D	1994	Genetics
University of Washington, Seattle, WA	Postdoctoral	1994-1998	Molecular Biotechnology

A. Positions and Honors

Positions and Employment

1987-1994	Graduate Research Associate, Genetics, Harvard Medical School, Boston, MA
1994-1998	Senior Research Fellow, Molecular Biotechnology, University of Washington, Seattle, WA
1998-1999	Scientist, Millennium Predictive Medicine, Inc., Cambridge, MA
1999-2005	Assistant Prof, Microbiology & Immunology, Vanderbilt University School of Medicine, Nashville, TN
2002-2005	Assistant Professor, Biochemistry, Vanderbilt University School of Medicine, Nashville, TN
2005-pres	Associate Prof, Microbiology & Immunology, Vanderbilt University School of Medicine, Nashville, TN

Other Experience and Professional Memberships

1997-	Molecular Biotechnology
1999-	Physiological Genomics
2000-	Proteomics (Senior Editor)
2004-	Molecular Systems Biology

Honors

1983-1984	Washington University Undergraduate Engineering Fellowship
1983	Member, Tau Beta Pi Engineering Honor Society
1995-1997	Postdoctoral Fellowship, Interdisciplinary Genomics Sciences
2000-2005	Ingram Assistant Professorship of Cancer Research
2001-2005	Kennedy Center Fellow

B. Selected peer- reviewed publications (in chronological order)

1. Link, A.J. and Olson, M.V. (1991). Physical map of the *Saccharomyces cerevisiae* genome at the 110-kilobase resolution. *Genetics* 127:681-698.
2. Link, A.J., Eng, J., and Yates III, J.R. (1996) Analyzing complex biological systems by using Micro-LC/ESI/MS/MS. *American Laboratory* 28: 27-30.
3. Link, A.J., Carmack, E., and Yate III, J.R. (1997) A strategy for the identification of proteins localized to subcellular spaces: Application to *E. coli* periplasmic proteins. *Inter. J. of Mass Spectrometry and Ion Processes* 160: 303-316.
4. Link, A.J., Robison, K., and Church, G.M. (1997) Comparing the predicted and observed properties of proteins encoded in the genome of *Escherichia coli*. *Electrophoresis* 18: 1259-1313.
5. Link, A.J., Hays, L.G., Carmack, E.B., and Yates III, J.R. (1997) Identifying the major proteome components of *Haemophilus influenzae* type-strain NCTC 8143. *Electrophoresis* 18: 1324-1334.
6. Link, A.J., Phillips, D.R. and Church, G.M. (1997) Methods for generating precise deletions and insertions in the genome of wild-type *Escherichia coli*: Application to open reading frame characterization. *J. Bacteriol.* 179:6228-6237.

7. Gatlin, C.L., Kleeman, G.R., Hays, L.G., Link, A.J., Yates III, J.R. (1998) Protein identification at the low femtomole level from silver stained gels using a new fritless electrospray interface for liquid chromatography-microspray and nanospray mass spectrometry. *Anal. Biochem.* 263: 93-101.
8. 2-D Gel Proteome Analysis Protocols. (1999) Link, A.J. (Ed.) *Methods in Molecular Biology*; vol: 112. Humana Press Inc, Totowa, NJ.
9. Link, A.J., Eng, J., Schieltz, D., Carmack, E., Mize, G., Morris, G., Garvik, B., Yates III, J. R. (1999) Direct analysis of protein complexes by mass spectrometry. *Nature Biotechnology* 17: 676-682.
10. Ohi, M.D., Link, A.J., Ren, L., Jennings, J.J., McDonald, W.H., Gould, K.L. (2002) Proteomics analysis reveals stable multi-protein complexes in both fission and budding yeasts containing Myb-related Cdc5p/Cef1p, novel pre-mRNA splicing factors, and snRNPs. *Mol. Cell. Bio.* 22: 2011-2024.
11. Sanders, S.L., Jennings, J.J., Canutescu, A., Link, A.J., Weil, P.A. (2002) Proteomics of the eukaryotic transcription machinery: identification of proteins associated with components of the general transcription factor TFIID. *MCB* 22:4723-4738.
12. Yoon, H.J., Feoktistova, A., Wolfe, B.A., Jennings, J.L., Link, A.J., Gould, K.L. (2002) Proteomics analysis identifies new components of the fission and budding yeast anaphase-promoting complexes. *Curr. Biol.* 12:2048-54.
13. Link, A.J. (2002) Multidimensional peptide separations in proteomics. *Trends in Biochemistry* 20:S8-S13.
14. Li, J., Jennings, J.J., Link, A.J., Patton, J.G. (2003) Regulation of alternative splicing by SRp86 and its interacting proteins. *MCB* 23: 7437-7447.
15. Yik, J.H., Chen, R., Nishimura, R., Jennings, J.L., Link, A.J., Zhou, Q. (2003) Inhibition of P-TEFb (CDC9/Cyclin T) kinase and RNA polymerase II transcription by the coordinated actions of HEXIM1 and 7SK snRNA. *Mol. Cell* 12: 971-982.
16. Link, A.J., Jennings, J.L., Washburn, M.P. (2003) Analysis of protein composition using multidimensional chromatography and mass spectrometry. *In* *Current Protocols in Protein Science* (J. E. Coligan, B. M. Dunn, D. W. Speicher, and P. T. Wingfield, eds.) John Wiley and Sons, New York. Chapter 23.1 pg. 1-25.
17. Kobor, M.S., Venkatasubrahmanyam, S., Meneghini, M.D., Gin, J.W., Jennings, J.L., Link, A.J., Madhani, H.D., Rine, J. (2004) A protein complex containing the conserved Swi2/Snf2-related ATPase Swr1p deposits histone variant H2A.Z into euchromatin. *PLoS Biology* 2: 587-599.
18. Sattlegger, E., Swanson, M.J., Ashcraft, E.A., Jennings, J.L., Fekete, R.A., Link, A.J., Hinnebusch, A.G. (2004) YIH1 is an actin-binding protein that inhibits protein kinase GCN2 and impairs general amino acid control when overexpressed. *JBC* 279:29952-29962.
19. Gould, K.L., Ren, L., Feoktistova, A.S., Jennings, J.L., Link, A.J. (2004) Tandem affinity purification and identification of protein complex components. *Methods* 33:239-244.
20. Powell, D.W., Weaver, C.M., Jennings, J.L., McAfee, K.J., He, Y., Weil, P.A., and Link, A.J. (2004) Cluster analysis of mass spectrometry data reveals a novel component of SAGA. *MCB* 24: 7249-7259.
21. Gerbasi, V.R., Weaver, C.M., Hill, S., Friedman, D.B., and Link, A.J. (2004) Yeast Asc1p and mammalian RACK1 are functionally orthologous core 40S ribosomal proteins that repress gene expression. *MCB* 24: 8276-8287.
22. Lewis, P.W., Beall, E.L., Fleischer, T.C., Georlette, D., Link, A.J., Botchan, M.R. (2004) Identification of a *Drosophila* Myb-E2F2/RBF complex that represses transcription. *Genes and Development.* 18:2929-2940.
23. An, H., Morrell, J.L., Jennings, J.L., Link, A.J., Gould, K.L. (2004) Requirements of Fission Yeast Septins for Complex Formation, Localization and Function. *Mol. Biol. Cell.* 15: 5551-5564.
24. Link, A.J., Fleischer, T.C., Weaver, C.M., Gerbasi, V.R., Jennings, J.L. (2005) Purifying protein complexes for mass spectrometry: applications to protein translation. *Methods.* 35: 274-290.
25. Sung, U., Jennings, J.L., Link, A.J., Blakely, R.D. (2005) Proteomic analysis of human norepinephrine transporter complexes reveals associations with protein phosphatase 2A anchoring subunit and 14-3-3 proteins. *Biochemical and Biophysical Research Communications.* 333:671-678.
26. Lominadze, G., Powell, D.W., Luerman, G.C., Link, A.J., Ward, R.A., McLeish, K.R. (2005) Proteomic Analysis of Human Neutrophil Granules. *Mol. Cell. Proteomics.* 4:1503-1521.
27. Duncan, D.T., Craig, R., Link, A.J. (2005) Parallel Tandem: a program for parallel processing of tandem mass spectra using PVM or MPI and X!Tandem. *J. of Proteome Research.* 4:1842-1847.
28. Dong, J., Lai, R., Jennings, J.L., Link, A.J., Hinnebusch, A.G. (2005) The novel ATP-binding cassette protein ARB1 is a shuttling factor that stimulates 40S and 60S ribosome biogenesis. *Mol. Cell. Biol.* 25: 9859-9873.
29. Powell, D.W., Merchant, L.M., Link, A. J. (2006) Discovery of regulatory molecular events and biomarkers using 2D capillary chromatography and mass spectrometry. *Expert Rev. Proteomics* 3:63-74.
30. Fleischer, T. C., Weaver, C. M., McAfee, K. J., Jennings, J. L., Link, A. J. (2006) Systematic identification and functional screens of uncharacterized proteins associated with eukaryotic translation complexes. *Genes and Dev.* 20:1294-1307.

31. McAfee, K. J., Duncan, D. T., Assink, M., Link, A.J. (2006) Analyzing proteomes and protein function using graphical comparative analysis of tandem mass spectrometry results. *Mol. Cell. Proteomics*. 5:1497-1513.
32. Peng, R., Hawkins, I., Link, A.J., Patton, J. G. (2006) The Splicing Factor PSF is part of a large complex that assembles in the absence of pre-mRNA and contains all 5 snRNPs. *RNA Biology*. 3: 69-76.
33. Yoon, H.-J., Feoktistova, A., Jennings, J.L., Link, A.J., Gould, K.L. (2006) Role of Hcn1 and its phosphorylation in fission yeast APC/C function. *J. Biol. Chem.* 281:32284-32293.
34. Venkov, C. D., Link, A. J., Jennings, J. L., Plieth, D., Inoue, Nagai, K., Xu, C., Dimitrova, Y. N., Rauscher III, F. J., Neilson, E. G. (2007) A new proximal activator of transcription in epithelial-mesenchymal transition. *J. Clin. Invest.* 117:482-491.
35. Hughes, A. L., Powell, D. W., Bard, M., Eckstein, J., Barbuch, R., Link, A. J., Espenshade, P. J. (2007) Dap1/PGRMC1 binds and regulates cytochrome P450 enzymes. *Cell Metabolism*. 5:143-149.
36. Gerbasi, V. R. and Link, A. J. (2007) The myotonic dystrophy type-2 gene ZNF9 promotes cap-independent translation. *Mol. Cell. Proteomics*. 6:1049-1058.
37. Bozulic, H.D., Malik, M.T., Powell, D.W., Nanez, A., Link, A. J., Ramos, K.S., Dean, W.L. (2007) Plasma membrane Ca(2+)-ATPase associates with CLP36 alpha-actinin and actin in human platelets. *Thromb. Haemost.* 97:587-597.
38. Yang, Z., Browning, C. F., Hallaq, H., Yermalitskaya, L., Esker, J., Hall, M. R., Link, A. J., Ham, A. L., McGrath, M. J., Mitchell, C. A., Murray, K. T. (2008) Four and a Half LIM Protein 1: A Partner for KCNA5 in Human Atrium. *Cardiovasc. Res.* 78:449-458.
39. Osipovich A. B., Jennings, J. L., Lin, Q, Link, A. J., Ruley, H. E. (2008) Dyggve-Melchior-Clausen Syndrome: Chondrodysplasia resulting from defects in intracellular vesicle traffic. *PNAS* 105:16171-16176.
40. Arnett, D. R., Jennings, J., Tabb D. L., Link A. J., Weil, P. A. (2008) A proteomic analysis of yeast Mot1p protein-protein associations: Insights into mechanism. *Mol. Cell. Proteomics*, 7:2090-2106.
41. *Proteomics: A Cold Spring Harbor Laboratory Course Manual*. Link, A. J. and Labaer, J. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, (in press).
42. Burg, J. S., Powell, D. W., Chai, R., Hughes, A. L., Link, A. J., Espenshade, P. J. Insig Regulates HMG-CoA Reductase by Controlling Enzyme Phosphorylation in Fission Yeast. *Cell Metabolism*. (in press).

C. Research Support

Ongoing Research Support

2 R01 GM064779-06A1 Link (PI) 7/1/07-5/31/11
NIH/NIGMS
Proteomic Analysis of Eukaryotic Protein Synthesis
The major goal is to determine the function of a subset of proteins linked to translations initiation.
Role: Principal Investigator

1 R21 AR055231-01 A1 Link (PI) 4/1/08-3/31/10
NIH/NIAMSD
Functional Analysis of ZNF9 in Myotonic Dystrophy Type 2
Myotonic dystrophy is the most common form of adult muscular dystrophy. The type 2 form of the disease is caused by expansion of CCTG repeats in the noncoding region of the gene ZNF9. This proposal investigates the functional role of ZNF9 in myotonic dystrophy type 2.
Role: Principal Investigator

N01 AI 40079 03 Joyce (PI) 9/30/04-9/29/09
NIH/NIAID
Large Scale Vaccinia Virus-Derived CTL Epitope Discovery
The major goal of this project is to characterise the immunodominant vaccinia-derived CTL epitope(s) presented by HLA class I molecules.
Role: Co-Investigator

2 R01 HL069452-05 A2 Hawiger (PI) 1/17/08-11/30/11
NIH/NHLBI

Superantigen-Induced Vascular Injury and DIC

The major goal of this project is to meet the urgent need for new anti-inflammatory drugs that attenuate acute lung vascular injury and DIC evoked by staphylococcal superantigens that often work in tandem with other viral and bacterial pathogens.

Role: Co-Investigator

1 R21 CA128695-01 Xu (PI) 8/7/07-7/31/09
NIH/NCI

Identification of Breast Tumor Secretome Changes Throughout Tumor Progression

In this project, in vivo microdialysis combined with quantitative proteomic techniques is proposed to systematically identify the temporal secretome changes during breast tumor initiation, progression and metastases in live mouse models.

Role: Co-Investigator

Completed Research Support

P01 HL68744 Ruley (PI); Hawiger (Prog. Dir) 12/1/01-11/30/06
NIH/NHLBI

Program Title: Functional Genomics of Inflammation

Project Title: Genetic and Proteomic Analysis of Inflammation

This project was focused on genome-wide and proteomic studies that are now possible as a result of efforts to sequence the human and mouse genomes. Both approaches were used to characterize genes and functional interactions among proteins that are important in inflammation.

Role: Co-Investigator

R01 ES011993 Weil (PI) 9/12/02-7/31/06
NIH/NIEHS

Proteomic Construction of Stress Regulated Networks

The major goal of this project was to use state of the art multidimensional tandem mass spectrometry methods to identify and molecularly characterize the protein-protein regulatory networks connecting the environment with key conserved transcription factors known to drive the gene-level protective changes in cellular RNA synthesis.

Role: Co-Principal Investigator

F32 GM073549 Link (PI) 6/1/04-5/30/06
NIH/NCI

Proteomic Analysis of Notch3 Complexes in Lung Cancer

This was a fellowship award for a postdoctoral fellow, Dr. David W. Powell, in Dr. Link's lab. The specific goal was to gain a better understanding of Notch3'S function in lung cancer biology by identifying and characterizing proteins that interact with its transcriptionally active intracellular domain (N3ICD) in Notch3-overexpressing lung tumor cell lines.

Role: Faculty Mentor