

CURRICULUM VITAE

Name: Leping Li

Education:

1987 - B.S. Medicinal Chemistry, Shanghai Medical University, P.R. China.
1994 - Ph.D. Medicinal Chemistry, The University of North Carolina at Chapel Hill (UNC-CH), Chapel Hill, NC.

Brief Chronology of Employment:

2003-current: Principal Investigator, NIEHS
2000 - 2003: Research Fellow, NIEHS.
1998 - 2000: Staff Scientist, National Institute for Occupational Safety and Health, Morgantown, WV, 26505 (duty station: NIEHS).
1995 - 1998: NIH IRTA Postdoctoral Fellow, NIEHS.
1994 - 1995: Postdoctoral Fellow, Department of Chemistry, UNC-CH.
1992 - 1994: Graduate Research Assistant, UNC-CH.
1987 - 1989: Graduate Research Assistant and Undergraduate Teaching Assistant, Shanghai Medical University, Shanghai, P.R. China.
1989 - 1991: Undergraduate Laboratory Teaching Assistant in Phar52L, School of Pharmacy, UNC-CH.

Awards and Honors:

NIH Award of Merit, 2003
NIH IRTA Postdoctoral Fellowship, 1995-1998, NIEHS.
Annual Academic Scholarship, Shanghai Medical University, Shanghai, P.R. China.
1982-1989.
Rong-Lin distinguished student award, Shanghai Medical University, Shanghai, P.R. China, 1987.
Distinguished student of the Higher Education Bureau of the City, Shanghai Higher Education Bureau, Shanghai, P.R. China, 1984.

Teaching and Mentoring:

2005 summer: Summer discovery program (Connie Chen, Brandeis University)
2002-2005: IRTA predoctoral student dissertation advisor (Weichun Huang, NCSU Bioinformatics Program)
2002-2004: IRTA postdoctoral student research advisor (DeLong Liu)
2001-2002: IRTA predoctoral student dissertation advisor (Jun Lu, NCSU)
1999-2000: Undergraduate thesis and research advisor (Kettering Univ., Michigan)
1989-1991: Teaching assistant in Phar52L, School of Pharmacy, UNC-CH
1986-1987: Undergraduate Biochemistry Lab, Shanghai Medical Univ.

Academic Appointment:

Adjunct assistant professor in genomics, the Bioinformatics Program, North Carolina State University (pending approval)

Professional Activity:

Serve as a frequent reviewer for Bioinformatics.

US Patent Application:

3'-Methoxy-6-pyrrolynyl-2-phenyl-4-quinolone and 6-pyrrolynyl-2-phenyl-4-quinolone, members of a group of compounds as potent anti-solid tumor agents, Kuo-Husing Lee, Hui-Kang Wang, and Leping Li (US005571822A).

Publications in Peer-Reviewed Journals:

1. Li, L., Wang, H.K., Fujioka, T., Chang, J.J., Kozuka, M., Konoshima, T., Estes, J., McPhail, A.T., McPhail, D.R., and Lee, K.H. Structure and stereochemistry of amorphispironone, a novel cytotoxic spironone type rotenoid from *Amorpha fruticosa*. *J. Chem. Soc. Chem. Commun.*, 1991, 22, 1652.
2. Li, L., Wang, H.K., Chang, J. J., McPhail, A.T., McPhail, D.R., Estes, J.R., and Lee, K.H. Antitumor agents 138. Rotenoids and isoflavones as cytotoxic constituents from *Amorpha fruticosa*. *J. Nat. Prod.*, 1993, 56, 690.
3. Terada, H., Kokumai, M., Konoshima, T., Kozuka, M., Haruna, M., Kazuo, I, Estes, J.R., Li, L, Wang, H.K., and Lee, K.H. Structural elucidation and chemical conversion of amorphispironone, a novel spironone from *Amorpha fruticosa*, to rotenoids. *Chem. Pharm. Bull.*, 1993, 41, 187.
4. Konoshima, T., Terada, H., Kokumai, M., Kozuka, M., Tokuda, H., Estes, J.R., Li, L., Wang, H.K., and Lee, K.H. Studies on inhibitors of skin tumor promotion, XII. Rotenoids from *Amorpha fruticosa*. *J. Nat. Prod.*, 1993, 56, 843.
5. Li, L, Wang, H.K., Kuo, S.C., Wu, T.S., Lednicer, D., Lin, C.M., Hamel, E., and Lee, K.H. Antitumor agents 150. 2',3',4',5',5,6,7-substituted 2-phenyl-4-quinolones and related compounds: their synthesis, cytotoxicity, and inhibition of tubulin polymerization. *J. Med. Chem.*, 1994, 37, 1126.
6. Li, L., Wang, H.K., Kuo, S.C., Wu, T.S., Lednicer, D., Lin, C.M., Hamel, E., and Lee, K.H. Antitumor agents 155. Synthesis and biological evaluation of 3', 6, 7-substituted 2-phenyl-4-quinolones as antimicrotubule agents. *J. Med. Chem.*, 1994, 37, 3400.
7. Shi, Q., Chen, K., Li, L., Chang, J.J., Autry, C., Kozuka, M., Konoshima, T., Estes, J.R., Lin, C.M., Hamel, E., and Lee, K.H. Antitumor agents. 154. Cytotoxic and antimitotic flavonols from *Polanisia dodecandra*. *J. Nat. Prod.*, 1995, 58, 475.
8. Li, L., Darden, T.A., Foley, C., Hiskey, R., and Pedersen, L.G. Homology modeling and molecular dynamics simulation of human prothrombin fragment 1. *Protein Sci.*, 1995, 4, 2341.

9. Li, L., Darden, T.A., Kominos, D., and Pedersen, L.G. Molecular dynamics simulations of the Kunitz domain of amyloid β -protein precursor. *Alzheimer's Res.*, 1995, 1, 185.
10. Li, L., Darden, T., Hiskey, R., and Pedersen, L. Homology modeling and molecular dynamic simulations of the Gla domains of factor IX and its G12A mutant. *J. Phys. Chem.*, 1996, 100, 2475.
11. Ibeanu, G.C., Ghanayem, B.I., Linko, P., Li, L., Pedersen, L.G., and Goldstein, J.A. Identification of residues 99, 220, 221, of human cytochrome P450 2C19 as key determinants of omeprazole hydroxylase activity. *J. Biol. Chem.*, 1996, 271, 12496.
12. Wolberg, A.S., Li, L., Cheung, W.-F., Hamaguchi, N., Pedersen, L.G., and Stafford, D.W. Characterization of gamma-carboxyglutamic acid residue 21 of human factor IX. *Biochemistry*, 1996, 35, 10321.
13. Li, L., Darden, T., Hiskey, R., and Pedersen, L. Homology modeling and molecular dynamics simulations of human prothrombin fragment 1 Protein. *Haemostasis*, 1996, 26 (suppl 1), 54.
14. Li, L., Darden, T., Furie, B., Furie, B., and Pedersen, L.G. Refinement of NMR-derived solution structure of the calcium bound Gla domain of human coagulation factor IX using a combination of a genetic algorithm and molecular dynamics simulation. *Biochemistry*, 1997, 36, 2132.
15. Bebenek, K., Beard, W.A., Darden, T.A., Li, L., Prasad, R., Luxon, B.A., Gorenstein, D.G., Wilson, S.H. and Kunkel, T.A. A minor groove binding track in reverse transcriptase. *Nature Struct. Biol.*, 1997, 3, 194.
16. Rigby, A.C., Baleja, J.D., Li, L., Pedersen, L.G., Furie, B.C. and Furie, B. Role of γ -carboxyglutamic acid in the calcium-induced structural transition of conantokin G, a conotoxin from the Marine snail *Conus geographus*. *Biochemistry*, 1997, 36, 15677.
17. Perera, L., Li, L., Darden, T., Monroe, D.M. and Pedersen L.G. Prediction of solution structure of the Ca^{2+} -bound γ -carboxyglutamic acid domains of protein S and homology growth arrest specific protein 6: use of the Particle mesh Ewald method. *Biophys. J.*, 1997, 73, 1847.
18. Warder, S.E., Prorok, M., Chen, Z., Li, L., Zhu, Y., Pedersen, L.G., Ni, F. and Castellio, F.J. The roles of individual γ -carboxyglutamate residues in the solution structure and cation-dependent properties of conantokin-T. *J. Biol. Chem.*, 1998, 273, 7512.
19. Chen, Z., Blandl, T., Prorok, M., Warders, S.E., Li, L., Zhu, Y., Pedersen, L.G., Ni, F., Castellino, F.J. Conformational changes in Conantokin-G induced upon bindings of calcium and magnesium as revealed by NMR structural analysis. *J. Biol. Chem.*, 1998, 273, 16248.

20. Beard, W.A., Bebenek, K., Darden, T.A., Li, L., Prasad, R., Kunkel, T. and Wilson, S. Vertical scanning mutagenesis of a critical tryptophan in the "minor groove binding track" of HIV-1 reverse transcriptase. *J. Biol. Chem.*, 1998, 273, 30435.
21. Klose, T.S., Ibeanu, G.C., Ghanayem, B.I., Pedersen, L.G., Li, L., Hall, S.D. and Goldstein, G.A. *Arch. Biochem. Biophys.*, 1998, 357, 240.
22. Darden, T.A., Perera, L., Li, L. and Pedersen, L.G. New tricks for modelers from the crystallography toolkit: the particle mesh Ewald algorithm and its use in nucleic acid simulations. *Structures*, 1999, 7, R55.
23. Li, L., Darden, T.A., Bartolotti, L., Kominos, D. and Pedersen, L.G. An atomic model for the pleated β -sheet structure of A β amyloid protofilaments. *Biophys. J.*, 1999, 76, 2871.
24. Bevan, D.R., Li, L., Pedersen, L.G. and Darden, T.A. Molecular dynamics simulations of d(CCAACGTTGG)₂ decamer. Influence of the crystal environment. *Biophys. J.*, 2000, 78, 668.
25. Li, L., Pedersen, L.G., Beard, W.A., Bebenek, K., Wilson, S.H., Kunkel, T.A. and Darden, T.A. A molecular dynamics model of HIV-1 reverse transcriptase complexed with DNA: comparison with experimental structures. *J. Mol. Modeling*, 2000, 6, 575.
26. Li, L., Darden, T.A., Weinberg, C.R., Levine, A.J. and Pedersen L.G. Gene assessment and sample classification for gene expression data using a genetic algorithm/k-nearest neighbor method. *Combinatorial Chemistry and High Throughput Screening*, 2001, 4, 727.
27. Li, L., Weinberg, C.R., Darden, T.A. and Pedersen L.G. Gene selection for sample classification based on gene expression data: study of sensitivity to choice of parameters of the GA/KNN method. *Bioinformatics*, 2001, 17, 1131.
28. King, L.M., Ma, J., Srettabunjong, S., Li, L., Graves, J., Bradbury, J.A., Spiecker, M., Liao, J.K., Mohrenweiser, H. and Zeldin, D.C. Cloning of the CYP2J2 gene and identification of functional polymorphisms. *Mol. Pharmacol.*, 2002, 61, 840.
29. Lobenhofer, E.K., Bennett, L., Li, L., Bushel, P. and Afshari, C. Regulation of DNA replication fork genes by 17 β -estradiol. *Mol. Endocrinol.*, 2002, 16, 1215.
30. Hamadeh, H.K., Bushel, P.R., Jayadev, J., Martin, K., DiSorbo, O., Sieber, S., Bennett, L., Li, L., Tennant, R., Stoll, R., Barrett, J.C., Blanchard, K., Paules, R.S., Afshari, C.A. Prediction of Compound Signature Using High Density Gene Expression Profiling. *Toxicol. Sci.*, 2002, 67, 232.

31. Hamadeh, H.K., Li, L., Stoltz, J., Bushel, P.R., Stoll, R., Blanchard, K., Jayadev, S., Afshari, C.A. "Elucidation of signal versus effect in toxicogenomic studies". *Applied Genomics and Proteomics*, 2002, 1, 37.
32. Peddada, S.D., Lobenhofer, E.K., Li, L., Afshari, C.A., Weinberg, C.R. and Umbach, D. Selecting and clustering genes using order restricted inference methodology with applications to time-course microarray data. *Bioinformatics*, 2003, 19, 834.
33. Hodges, L.C., Lobenhofer, E.K., Cook, J.D., Martin, K., Li, L., Bennett, L., Bushel, P. R., Afshari, C.A. and Walker, C.L. Molecular determinants of agonist and antagonist activity in breast cancer cells. *Mol. Cancer Res.*, 2003, 1, 300.
34. Katuta, Y., Li, L., Pedersen, L.C., Pedersen, L.G. and Negishi, M. Heparin sulfate N-sulfotransferase activity: reaction mechanism and substrate recognition. *Biochem. Soc. Trans.*, 2003, 31, 331.
35. Dowd, T.L., Rosen, J.L., Li, L. and Gundberg, C.M. The three dimensional structural of bovine calcium ion-bound osteocalcin using ^1H NMR spectroscopy. *Biochemistry*, 2003, 42, 7769.
36. Heinloth, A.N, Shackelford, R.E., Innes, C.L., Bennett, L., Li, L., Amin, R.P., Sieber, S.O., Flores, K.G., Bushel, P.R. and Paules, R.S. ATM-dependent and -independent gene expression changes in response to oxidative stress, gamma irradiation, and UV irradiation. *Radiation Res.*, 2003, 160, 273.
37. Heinloth, A.N, Shackelford, R.E., Innes, C.L., Bennett, L., Li, L., Amin, R.P., Sieber, S.O., Flores, K.G., Bushel, P.R. and Paules, R.S. Identification of Distinct and common gene expression changes after oxidative stress, γ - and UV-Radiation. *Mol. Carcinogen.*, 2003, 37, 65.
38. Cable, P.L., Wilson, C.A., Calzone, F.J., Rauscher, F.J.III, Scully, R., Livingston, D.M., Li, L., Futreal, P.A. and Afshari, C.A. Novel consensus DNA-binding sequence for BRCA1 protein complexes. *Mol. Carcinogen.*, 2003, 38, 85.
39. Li, L., Umbach, D.M., Terry, P. and Taylor, J.A. Application of the GA/KNN method to SELDI proteomics data. *Bioinformatics*, 2004, 20, 1638.
40. Liu, D., Umbach, D., Peddada, S., Li, L., and Crockett, P.W., and Weinberg, C.R. A random-periods model for expression of cell cycle genes. *Proc. Natl. Acad. Sci. USA*, 2004, 101, 7240.
41. Heinloth, A.N., Irwin, R.D., Boorman, G.A., Nettesheim, P., Fannin, R.D., Sieber, S.O., Snell, M.L., Tucker, C.J., Li, L., Travlos, G.S., Vansant, G., Blackshear, P.E., Tennant, R.W., Cunningham, M.L. and Paules, R.S. Gene Expression Profiling of Rat Livers Reveals Early Indicators of Potential Adverse Effects. *Toxicol. Sci.*, 2004, 80, 193.

42. Pedersen, L.G., Bartolotti, L. and Li, L. Deuterium and its Role in the Machinery of Evolution. *J. of Theoret. Biol.*, 2006, 238:914-8.
43. Liu, D., Peddada, S.D., Li, L. and Weinberg, C.R. Comparative analysis of activation times of circadian-related genes across tissues. *BMC Bioinformatics*, 2006, 7, 87.
44. Huang W, Umbach DM, Li L. Accurate anchoring alignment of divergent sequences. *Bioinformatics* 2006, 22, 29-34.
45. Huang, W., Umbach, D.M., Ohler, U., and Li, L. Optimized mixed Markov models for motif identification. *BMC Bioinformatics*, 2006, 7, 279.
46. Zhang, D. Stumpo, D.J., Graves, J.P., DeGraff, L.M., Grissom, S.F., Collins, J.B., Li, L., Zeldin, D.C. and Blackshear, P.J. Identification of potential target genes for transcription factor RFX4_v3 in the developing mouse brain, *J. Neurochem.*, 2006, 98, 860-875.
47. Lee, C.R., Bottone, F.G., Krahn, J.M., Li, L., Mohrenweiser, H.W., Molly E. Cook, M.E., Petrovich, R.M., Bell, D.A., Eling, T.E., and Zeldin, D.C. Identification and Functional Characterization of Polymorphisms in Human Cyclooxygenase-1 (PTGS1). *Pharmacogenetics and Genomics*, accepted.

Publications in Proceedings:

1. Li, L.; Pedersen, L.G.; Darden, T.A. and Weinberg, C.R. "Class Prediction and Discovery based on Gene Expression Data", 2000, Atlantic Symposium on Computational Biology, Genome Information Systems & Technology (<http://www.ee.duke.edu/CBGI/>), Duke University, NC.
2. Li, L.; Pedersen, L.G.; Darden, T.A. and Weinberg, C.R. "Computational Analysis of Leukemia Microarray Expression Data Using the GA/KNN Method". Critical Assessment of Techniques for Microarray Data Analysis (CAMDA'00 Conference) (<http://bioinformatics.duke.edu/CAMDA/>), 2000, Duke University, NC.

Invited Book Chapter:

1. Tropsha, A., Yan, Y., Schneider, S.E., Li, L., and Erickson, B.W. Relative free energies of folding and refolding of model secondary structure elements in aqueous solution. In: Peptides: Chemistry, Structure, Biology, Eds. R.S. Hodges and J.A. Smith, 1994, pp. 883.
2. Leping Li and Clarice R. Weinberg, "Gene selection and sample classification using a genetic algorithm/k-nearest neighbors method". In *Understanding and Using Microarray Analysis Techniques: A Practical Guide*. Edited by Werner Dubitzky *et al.*, Kluwer academic publishers.

Recently Invited Talks/lectures:

1. Li, L.; Darden, T.A.; Weinberg, C.R. and Pedersen, L.G. “Gene assessment and sample classification for gene expression data using a genetic algorithm/k-nearest neighbor method”, 2000, CIIT, RTP.
2. Li, L.; Pedersen, L.G.; Darden, T.A. and Weinberg, C.R. Critical Assessment of Techniques for Microarray Data Analysis (CAMDA'00 Conference) (<http://bioinformatics.duke.edu/CAMDA/>), 2000, Duke University, NC.
3. Li, L.; Pedersen, L.G.; Darden, T.A. and Weinberg, C.R. “Class Prediction and Discovery based on Gene Expression Data”, 2000, Atlantic Symposium on Computational Biology, Genome Information Systems & Technology (<http://www.ee.duke.edu/CBGI/>), Duke University, NC.
4. Li, L.; Weinberg, C.; Umbach, D. and Peddada, S. Testing for informative differences between categories based on small samples and very high-dimensional gene expression data. 2001, Research Triangle Institute, NC.
5. Panel Discussion on Bioinformatics/Genomics, North Carolina Central University, April, 2002.
6. Li, L. Pattern recognition. Bioinformatics class, North Carolina Central University, September, 2003.
7. Li, L. Gene function prediction based on motif patterns. NCSU Bioinformatics seminar series, North Carolina State Univ., April, 2004.