

CURRICULUM VITAE

KUO-BIN LI

ADDRESS

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EDUCATION

- 10/1984–06/1988 B.S., Department of chemistry, National Taiwan University, Taipei, Taiwan
- 01/1992–10/1996 Ph.D., Department of chemistry, McGill University, Montréal, Québec, Canada.
Specialization: nuclear magnetic resonance(NMR) spectral analysis, protein structure determination, computational chemistry
Thesis: *Development of Computer-Assisted Resonance Assignment Methods for Protein Heteronuclear 3D NMR Spectra*
Supervisor: Prof. B. C. Sanctuary
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EMPLOYMENT

- 11/1996–01/1997 Postdoctoral research fellow, Department of chemistry, McGill University, Montréal, Québec, Canada.
Supervisor: Prof. B. C. Sanctuary
Specialization: NMR spectral analysis
- 02/1997–09/1999 Postdoctoral research fellow, Rowland Institute at Harvard, Harvard University, Cambridge 02142, Massachusetts, USA. (<http://www.rowland.harvard.edu>)
Supervisor: Dr. Jeff C. Hoch
Specialization: NMR spectral analysis, structural biology, distributed parallel programming
- 01/2000–11/2000 Research fellow, Bioinformatics division, Biomedical Engineering Center, Industrial Technology Research Institute, Taiwan
Specialization: pairwise sequence homology comparison, PC/workstation cluster computing
- 11/2000–09/2001 Senior bioinformatics consultant, DigiGenomics Inc., Taipei, Taiwan
Specialization: management of biological database, sequence annotation, DNA microarray

12/2001–07/2006	Research Scientist and Team Leader, Bioinformatics Institute, Agency for Science, Technology and Research (A*Star), Ministry of Trade, Singapore
07/2002–06/2006	Adjunct assistant professor, Department of biochemistry, National University of Singapore, Singapore
07/2003–06/2005	Master thesis supervisor, Singapore-Massachusetts Institute of Technology (MIT) Alliance, Program in high performance computation for engineered systems, National University of Singapore, Singapore
02/2008–present	Adjunct associate professor, Institute of Biomedical informatics, National Yang-Ming University, Taipei, Taiwan
08/2006–present	Associate Research Scientist, Center for Systems and Synthetic Biology, National Yang-Ming University, Taipei, Taiwan

RESEARCH INTERESTS

Non-coding RNA: microRNAs and their targets; phylogenetic footprinting and gene regulation by *cis*- and *trans*-acting RNA interactions; antisense transcripts as regulators of alternative splicing.

Protein functional analyses: protein family classification and functional prediction using amino acid properties (opposed to using homology comparison) and signal processing techniques.

Mutation analysis: determine a missense mutation in amino acid level is deleterious or not; connection between single nucleotide polymorphism and protein function.

Transcription factor binding sites: *ab initio* discovery of transcription factor binding sites using DNA-protein binding models and machine learning techniques.

Distributed Parallel Computing MPI programming and its application to bioinformatics applications

PUBLICATIONS

1. *Incorporating the use of amino acid properties to predict the significance of missense mutations*, Tze-Chuen Lee, Ann SG Lee and **Kuo-Bin Li**, *Amino Acids*, in press, 2008.
2. *Remote protein homology detection using recurrence quantification analysis and amino acid physicochemical properties*, Yuchen Yang, Erwin Tantoso and **Kuo-Bin Li**, *J. Theor. Biol.*, 2008, 252(1), 145-154.
3. *Profiling microRNA expression in hepatocellular carcinoma reveals microRNA-224 up-regulation and apoptosis inhibitor-5 as a microRNA-224-specific target*, Yu Wang, Alvin T. C. Lee, Joel Z. I. Ma, Jingbo Wang, Jianwei Ren, Yuchen Yang, Erwin Tantoso, **Kuo-Bin Li**, London L. P. J. Ooi, Patric Tan and Caroline G. L. Lee, *J. Biol. Chem.*, in press, 2008.
4. *AAIndexLoc: predicting subcellular localization of proteins based on a new representation of sequences using amino acid indices*, Erwin Tantoso and **Kuo-Bin Li**, *Amino Acids*, in press, 2008.
5. *Beyond string algorithms: protein sequence analysis using wavelet transforms*, Arun Krishnan and **Kuo-Bin Li**, in *Analysis of biological data: a soft computing approach*, Ed. S. Bandyopadhyay, U. Maulik and J. T. L. Wang, World Scientific, 2007.

6. *iHAP - integrated haplotype analysis pipeline for characterizing the haplotype structure of genes*, Chun Meng Song, Boon Huat Yeo, Erwin Tantoso, Yuchen Yang, Yun Ping Lim, **Kuo-Bin Li** and Gunaretnam Rajagopal, *BMC Bioinformatics*, 2006, 7, 525.
7. *Multiresolution analysis uncovers hidden conservation of properties in structurally and functionally similar proteins*, Gek Huey Chua, Arun, Krishnan, **Kuo-Bin Li** and Masaru Tomita, *Journal of Bioinformatics and Computational Biology*, 2006, 4(6), 1245-1267.
8. *In silico analysis of p53 using the p53 Knowledgebase: mutations, polymorphisms, microRNAs and pathways*, Yuchen Yang, Erwin Tantoso, Gek Huey Chua, Zhen Xuan Yeo, Felicia Soo Lee Ng, Sum Thai Wong, Cheuk Wang Chung and **Kuo-Bin Li**, *in silico Biology*, 2006, 7, 0005.
9. *How well do HapMap SNPs capture the untyped SNPs?* Erwin Tantoso, Yuchen Yang and **Kuo-Bin Li**, *BMC Genomics*, 2006, 7, 238.
10. *Protein subcellular localization prediction for Gram-negative bacteria using amino acid subalphabets and a combination of multiple support vector machines*, Jiren Wang, Wing-Kin Sung, Arun Krishnan and **Kuo-Bin Li**, *BMC Bioinformatics*, 2005, 6, 174.
11. *WebAllergen: a web server for predicting allergenic proteins*, Tariq Riaz, Hen Ley Hor, Arun Krishnan, Francis Tang and **Kuo-Bin Li**, *Bioinformatics*, 2005, 21(10), 2570-2571.
12. *A tabu search algorithm for post-processing multiple sequence alignment*, Tariq Riaz, Yi Wang and **Kuo-Bin Li**, *Journal of Bioinformatics and Computational Biology*, 2005, 3(1), 145-156.
13. *Immunohistochemical detection of Ki67 in breast cancer correlates with transcriptional regulation of genes related to apoptosis and cell death*, Puay Hoon Tan, Boon Huat Bay, George Yip, Sathiyamoorthy Selvarajan, Patrick Tan, Jeanne Wu, Chee How Lee and **Kuo-Bin Li**, *Modern Pathology*, 2005, 18(3), 374-381.
14. *Y-box binding protein, YB-1, as a marker of tumor aggressiveness and response to adjuvant chemotherapy in breast cancer*, Jingxiang Huang, Puay Hoon Tan, **Kuo-Bin Li**, Ken Matsumoto, Masafumi Tsujimoto and Boon Huat Bay, *International Journal of Oncology*, 2005, 26(3), 607-613.
15. *A Position-specific and consistency-based objective function for iterative multiple sequence Alignment*, Yi Wang, Tariq Riaz, Espen Enerly, Sheng Zeng and **Kuo-Bin Li**, in the *Proceedings of the 6th WSEAS International Conference on Mathematics and computers in biology and chemistry*, Buenos Ayres, Argentina, March 1-3, 2005.
16. *Multiple sequence alignment using an exhaustive and greedy algorithm*, Yi Wang and **Kuo-Bin Li**, *Journal of Bioinformatics and Computational Biology*, 2005, 3(2), 243-255.
17. *The quality of a multiple sequence alignment can be evaluated by a position-specific and consistency-based objective function*, Yi Wang, Tariq Riaz, Espen Enerly, Sheng Zeng and **Kuo-Bin Li**, *WSEAS Transactions on Mathematics and Computers in Biology and Biomedicine*, 2005, 2(2), 147-157.
18. *Natural antisense as potential regulator of alternative initiation, splicing and termination*, Espen Enerly, Zeng Sheng and **Kuo-Bin Li**, *in silico Biology*, 2005, 5, 0033.
19. *pSLIP: SVM based protein subcellular localization prediction using multiple physicochemical properties*, Deepak Sarda, Gek-Huey Chua, **Kuo-Bin Li**, and Arun Krishnan, *BMC Bioinformatics*, 2005, 6, 152.
20. *CMDWave: conserved motifs detection using wavelets*, Tariq Riaz, **Kuo-Bin Li**, Francis Tang and Arun Krishnan, *in silico Biology*, 2005, 5, 0038.

21. *Predicting allergenic proteins using wavelet transform*, Kuo-Bin Li, Praveen Issac and Arun Krishnan, *Bioinformatics*, **2004**, 20, 2572-2578.
22. *An adaptive iterative algorithm for refining multiple sequence alignment*, Yi Wang and Kuo-Bin Li, *Computational Biology and Chemistry*, **2004**, 28(2), 141-148.
23. *Multiple sequence alignment using tabu search*, Tariq Riaz, Yi Wang and Kuo-Bin Li, *Proceedings of the second Asia-Pacific Bioinformatics Conference*, Dunedin, New Zealand, **2004**.
24. *Rapid motif detection in protein sequences using wavelet transform*, Arun Krishnan, Kuo-Bin Li and Praveen Issac, *in silico Biology*, **2004**, 4, 0013.
25. *G-PRIMER, a greedy algorithm for selecting minimal primer set*, Jiren Wang, Kuo-Bin Li, and Wing-Kin Sung, *Bioinformatics*, **2004**, 20, 2473-2475.
26. *From genomes to drugs with bioinformatics*, Kuo-Bin Li, in *Novel compounds from Natural Products in the New Millennium, Potential and Challenges*, Ed. Benny K. H. Tan, B. H. Bay and Y. Z. Zhu, World Scientific, Singapore, **2004**.
27. *ClustalW-MPI: ClustalW Analysis Using Distributed and Parallel Computing*, Kuo-Bin Li, *Bioinformatics*, **2003**, 19(12), 1585-1586.
28. *Modern Spectrum Analysis in Multidimensional NMR Spectroscopy: Comparison of Linear-Prediction Extrapolation and Maximum-Entropy Reconstruction*, Alan S. Stern, Kuo-Bin Li, and Jeffrey C. Hoch, *J. Am. Chem. Soc.*, **2002**, 124(9), 1982-1993.
29. *Distributed Parallel Processing for Multidimensional Maximum Entropy Reconstruction*, Kuo-Bin Li, Alan S. Stern and Jeffrey C. Hoch, *J. Mag. Reson.*, **1998**, 134(1), 161-163.
30. *Automated assignment of proteins using heteronuclear 3D NMR. 1: Backbone spin systems extraction and creation of polypeptides*, Kuo-Bin Li and Bryan C. Sanctuary, *J. Chem. Inf. Comput. Sci.*, **1997**, 37(2), 359-366.
31. *Automated assignment of proteins using heteronuclear 3D NMR. 2: Side chain and sequence-specific assignment*, Kuo-Bin Li and Bryan C. Sanctuary, *J. Chem. Inf. Comput. Sci.*, **1997**, 37(3), 467-477.
32. *Automated extraction of amino acid spin systems in proteins using 3D HCCH-COSY/TOCSY spectroscopy and Constrained Partitioning Algorithm(CPA)*, Kuo-Bin Li and Bryan C. Sanctuary, *J. Chem. Inf. Comput. Sci.*, **1996**, 36(3), 585-593.