

Curriculum Vitae
Zhaolei Zhang, Ph.D. Professor

CONTACT

Primary Office University of Toronto Donnelly Centre, 160 College Street, Room 608
Toronto], Ontario, Canada M5S 3E1
Telephone 416-946-0924
Email ZHAOLEI.ZHANG@UTORONTO.CA
Web <http://sites.utoronto.ca/zhangleb/>

EMPLOYMENT

07/2014 – Present Professor, Donnelly Centre for Cellular and Biomolecular Research (51%), Department of Molecular Genetics (49%), Faculty of Medicine, University of Toronto, Toronto, ON, CANADA; Cross-appointment at Department of Computer Science
07/2009 – 06/2014 Associate Professor (tenured), Banting Best Department of Medical Research (51%), Department of Molecular Genetics (49%), Faculty of Medicine, University of Toronto, Toronto, ON, CANADA; Cross-appointment at Department of Computer Science
11/2004 – 06/2009 Assistant Professor (tenure-stream), Banting Best Department of Medical Research (51%), Department of Molecular Genetics (49%), Faculty of Medicine, University of Toronto, Toronto, ON, CANADA

EDUCATION

Degrees

09/1995 – 12/2000 PhD, Biophysics (Structure Biology), University of California at Berkeley, Berkeley, CA, USA. Supervisor: Sung-Hou Kim
09/1989 – 06/1993 B.Sc., Biophysics, Department of Physics, NanKai University, Tianjin, China

Postgraduate, Research and Specialty Training

02/2001 – 10/2004 Post-doctoral Fellow, Bioinformatics, Department of Molecular Biophysics and Biochemistry (MBB), Yale University, New Haven, CT, USA.

HONOURS AND CAREER AWARDS

2008 One of 30 "Rising young investigators" named by Genome Technology magazine,
2008-2014 Canadian Institutes of Health Research (CIHR) New Investigator Salary Award
2006 Finalist - Maud Menten New Investigator Award, by Canadian Institutes of Health Research
2006-2011 Early Researcher Award by Ontario Ministry of Research and Innovation, Total Amount:
100,000 CAD

SERVICES

Administrative Activities

2021-Present Decanal Promotion Committee, Faculty of Medicine
2007-Present Departmental Examining Committee (Department of Molecular Genetics)
2011-Present Graduate Admission Committee (Department of Molecular Genetics)
2013-Present Promotion Committee (Donnelly Centre)

Editorial Services

2020 - present Associate Editor, PLOS Computational Biology

Grant Reviews

2021 European Science Foundation
2020 European Science Foundation
2019 National Institutes of Health GCAT Review Panel, European Science Foundation, CIHR Post-Doctoral Fellowship Review Committee member
2018 Hong Kong Health and Medical Research Fund (HMRF), UK Bloodwise Foundation, CIHR Post-Doctoral Fellowship Review Committee member, Dutch Cancer Society, The Netherlands Organisation for Health Research and Development, National Science Foundation China
2017 Swiss Institute of Bioinformatics, Hong Kong Health and Medical Research Fund (HMRF), Human Frontier Science Program, European Science Foundation, CIHR – Personalized Health Catalyst Grant, CIHR Post-Doctoral Fellowship Review Committee member
2016 Canadian Foundation of Innovation, CIHR Post-Doctoral Fellowship Review Committee member, Volkswagen Foundation, Hong Kong Health and Medical Research Fund (HMRF), The Dutch Technology Foundation (STW)
2015 Hong Kong Health and Medical Research Fund (HMRF), CIHR Post-Doctoral Fellowship Review Committee member
2014 UK Natural Environment Research Council of the UK, ad hoc reviewer, Canada Foundation for Innovation (CFI), ad hoc reviewer, CIHR Post-Doctoral Fellowship Review Committee member, Hong Kong Research Grant Council (RGC), Michael Smith Foundation for Health Research, external reviewer
2013 Hong Kong Research Grant Council (RGC), CIHR Post-Doctoral Fellowship Review Committee member
2012 CIHR Reviewer Panel member, Genomics (GMX), Human Frontier Science Program (HSFP) Career Development Award, Icelandic Research Fund, OGS (Ontario Graduate Scholarship) Fellowship Review Panel
2011 French National Research Agency (Agence Nationale de la Recherche), Oak Ridge Associated Universities - Pennsylvania Department of Health, Telethon Foundation (Italy)
2010 Alberta Heritage Foundation for Medical Research, NSF (US) ad hoc grant reviewer
2009 Telethon Foundation (Italy), Alberta Heritage Foundation for Medical Research, Netherlands Organisation for Scientific Research, European Science Foundation, NSERC Discovery Grants
2008 Telethon Foundation (Italy), UK Royal Society, Cancer Foundation UK, Quebec Fonds de recherche sur la nature et les technologies
2007 NSERC Discovery Grants
2006 Biomedical Research Council (BMRC) in Singapore
2005 Austrian Genome Research Programme (GEN-AU) Agency for Science

Manuscript Reviews (Incomplete)

BMC Bioinfo (1), BMC Evo Bio (3), BMC Genomics (4), Bioinformatics (16), Biology Direct (3), Biomolecules (1), Briefings in Functional Genomics and Proteomics (1), Canadian J of Microbiology (1), China Science (1), Comparative and Functional Genomics (1), Computational Biology and Chemistry (1), Computers in Biology and Medicine (1), Current Bioinformatics (1), Cytogenet Genome Res. (1), Database (1), Encyclopedia of Complexity and Systems Science (1), Evolutionary Genomics (1), FEBS (1), G3 (2), Genome Biology and Evolution (1), Gene (1), Genetics (1), Genome Biology (4), Genomic Medicine (1), Genome Research (6), Genomics (1), Genomics, Proteomics & Bioinformatics (1), Handbook of Research on Computational and Systems (1), Heredity (1), Human Mutation (1), ICIC (1), International Journal of Evolutionary Biology (1), J of Heredity (1), Journal of Bioinformatics and Computational Biology (2), Journal of Molecular Evolution (1), Mass Spec Reviews (1), Molecular Biology and Evolution (10), Molecular Cell Proteomics (1), Molecular BioSystems (1), Molecular Phylogenetics and Evolution (1), Nucleic Acids Research (11), Nature Communication (1), Nature Biotech (1), Nature Genetics (1), Nature Protocol (1), New Phytologist (1), PLOS Computational Biology (8), PLOS Genetics (3), PLOS One (7), PNAS (9), Proteins (5), Pacific Symposium in Biocomputing (2), RNA (2), Trends in Genetics (5)

PUBLICATIONS**Journal Articles**

- [1] Ying, S., Heung, T., **Zhang, Z.**, Yuen, R. and Bassett, A. (2022) Schizophrenia risk and microRNA targets overlapped by rare copy number variants in 22q11.2 deletion syndrome. *Under Review*.
- [2] Sun, S., Yang, J. and **Zhang, Z.** (2022) RNALigands: a database and web server for RNA - ligand interactions. *RNA*.
- [3] Song, J., Syed, N., Pu, S., Lee, H., Braunschweig, U., Ni, Z., Ahmed, N., Marcon, E., Zhong, G., Ray, D. *et al.* (2022) Regulation of alternative polyadenylation by the C2H2-zinc finger protein Sp1. *Under review*.
- [4] Ma, H., Wen, H., Xue, Z., Li, G. and **Zhang, Z.** (2022) RNANetMotif: identifying sequence-structure RNA network motifs in RNA-protein binding sites *Under Review*.
- [5] Liu, Y., Li, R., Luo, J. and Z, Z. (2022) Inferring RNA-binding protein target preferences using adversarial domain adaptation. *PLOS Computational Biology*, In Revision.
- [6] Kim, T., Lee, H., Capo-Chichi, J., Chang, M., Yoo, Y., Basi, G., Ketela, T., Smith, A., Tierens, A., Minden, M. *et al.* (2022) Single-cell proteogenomic sequencing allows early detection of relapse clone with CN-LOH at FLT3-ITD locus from initial diagnosis in AML. *In submission*.
- [7] Nabeel-Shah, S., Garg, J., Saettone, A., Ashraf, K., Lee, H., Wahab, S., Ahmed, N., Fine, J., Derynck, J., Pu, S. *et al.* (2021) Functional characterization of RebL1 highlights the evolutionary conservation of oncogenic activities of the RBBP4/7 orthologue in Tetrahymena thermophila. *Nucleic Acids Res*, **49**, 6196-6212.
- [8] Liu, S., Zhang, Y., Shang, X. and **Zhang, Z.** (2021) ProTICS reveals prognostic impact of tumor infiltrating immune cells in different molecular subtypes. *Brief Bioinform*.
- [9] Liao, S., Ragot, D., Nayyar, S., Suszko, A., **Zhang, Z.**, Wang, B. and Chauhan, V.S. (2021) Deep Learning Classification of Unipolar Electrograms in Human Atrial Fibrillation: Application in Focal Source Mapping. *Front Physiol*, **12**, 704122.
- [10] Liao, S., Kiros, J., Chen, J., **Zhang, Z.** and Chen, T. (2021) Improving domain adaptation in de-identification of electronic health records through self-training. *J Am Med Inform Assoc*, **28**, 2093-2100.
- [11] Dong, N., Bandura, J., **Zhang, Z.**, Wang, Y., Labadie, K., Noel, B., Davison, A., Koene, J.M., Sun, H.S., Coutellec, M.A. *et al.* (2021) Ion channel profiling of the Lymnaea stagnalis ganglia via transcriptome analysis. *BMC Genomics*, **22**, 18.
- [12] Daher-Reyes, G., Kim, T., Novitzky-Basso, I., Kim, K.H., Smith, A., Stockley, T., Capochichi, J.M., Al-Shaibani, Z., Pasic, I., Law, A. *et al.* (2021) Prognostic impact of the adverse molecular-genetic profile on long-term outcomes following allogeneic hematopoietic stem cell transplantation in acute myeloid leukemia. *Bone Marrow Transplant*.
- [13] Ahn, J.S., Kim, T., Jung, S.H., Ahn, S.Y., Jung, S.Y., Song, G.Y., Kim, M., Yang, D.H., Lee, J.J., Choi, S. *et al.* (2021) Allogeneic transplant can abrogate the risk of relapse in the patients of first remission acute myeloid leukemia with detectable measurable residual disease by next-generation sequencing. *Bone Marrow Transplant*, **56**, 1159-1170.
- [14] Liu, Y., Pan, C., Kong, D., Luo, J. and **Zhang, Z.** (2020) A Survey of Regulatory Interactions Among RNA Binding Proteins and MicroRNAs in Cancer. *Front Genet*, **11**, 515094.
- [15] Li, J., Ma, S., Chen, J., Hu, K., Li, Y., **Zhang, Z.**, Su, Z., Woodgett, J.R., Li, M. and Huang, Q. (2020) GSK-3beta Contributes to Parkinsonian Dopaminergic Neuron Death: Evidence From Conditional Knockout Mice and Tideglusib. *Front Mol Neurosci*, **13**, 81.
- [16] Kim, T., Moon, J.H., Ahn, J.S., Ahn, S.Y., Jung, S.H., Yang, D.H., Lee, J.J., Shin, M.G., Choi, S.H., Lee, J.Y. *et al.* (2020) RNA sequencing as an alternative tool for detecting measurable residual disease in core-binding factor acute myeloid leukemia. *Sci Rep*, **10**, 20119.
- [17] Hu, X., Liao, S., Bai, H., Gupta, S., Zhou, Y., Zhou, J., Jiao, L., Wu, L., Wang, M., Chen, X. *et al.* (2020) Long Noncoding RNA and Predictive Model To Improve Diagnosis of Clinically Diagnosed Pulmonary Tuberculosis. *J Clin Microbiol*, **58**.
- [18] Ahn, J.S., Kim, T., Jung, S.H., Ahn, S.Y., Jung, S.Y., Song, G.Y., Kim, M., Yang, D.H., Lee, J.J., Choi, S. *et al.* (2020) Allogeneic transplant can abrogate the risk of relapse in the patients of first remission acute myeloid leukemia with detectable measurable residual disease by next-generation sequencing. *Bone Marrow Transplant*.
- [19] Lee, H., **Zhang, Z.** and Krause, H.M. (2019) Long Noncoding RNAs and Repetitive Elements: Junk or Intimate Evolutionary Partners? *Trends Genet*, **35**, 892-902.

- [20] Hu, X., Liao, S., Bai, H., Wu, L., Wang, M., Wu, Q., Zhou, J., Jiao, L., Chen, X., Zhou, Y. *et al.* (2019) Integrating exosomal microRNAs and electronic health data improved tuberculosis diagnosis. *EBioMedicine*, **40**, 564-573.
- [21] Gallo, D., Kim, T., Szakal, B., Saayman, X., Narula, A., Park, Y., Branzei, D., **Zhang, Z.** and Brown, G.W. (2019) Rad5 Recruits Error-Prone DNA Polymerases for Mutagenic Repair of ssDNA Gaps on Undamaged Templates. *Mol Cell*, **73**, 900-914 e909.
- [22] Ahn, J.S., Kim, T., Kim, Y.K., Cho, Y.C., Cho, S., Jung, S.H., Ahn, S.Y., Jung, S.Y., Yang, D.H., Lee, J.J. *et al.* (2019) Remission clone in acute myeloid leukemia shows growth advantage after chemotherapy but is distinct from leukemic clone. *Exp Hematol*, **75**, 26-30.
- [23] Wang, Y., Li, Y., Yue, M., Wang, J., Kumar, S., Wechsler-Reya, R.J., **Zhang, Z.**, Ogawa, Y., Kellis, M., Duester, G. *et al.* (2018) N(6)-methyladenosine RNA modification regulates embryonic neural stem cell self-renewal through histone modifications. *Nat Neurosci*, **21**, 195-206.
- [24] Schneider, R., McKeever, P., Kim, T., Graff, C., van Swieten, J.C., Karydas, A., Boxer, A., Rosen, H., Miller, B.L., Laforce, R., Jr. *et al.* (2018) Downregulation of exosomal miR-204-5p and miR-632 as a biomarker for FTD: a GENFI study. *J Neurol Neurosurg Psychiatry*.
- [25] Kim, T., Moon, J.H., Ahn, J.S., Kim, Y.K., Lee, S.S., Ahn, S.Y., Jung, S.H., Yang, D.H., Lee, J.J., Choi, S.H. *et al.* (2018) Next-generation sequencing-based posttransplant monitoring of acute myeloid leukemia identifies patients at high risk of relapse. *Blood*, **132**, 1604-1613.
- [26] Ahn, J.S., Kim, H.J., Kim, Y.K., Lee, S.S., Ahn, S.Y., Jung, S.H., Yang, D.H., Lee, J.J., Park, H.J., Lee, J.Y. *et al.* (2018) Assessment of a new genomic classification system in acute myeloid leukemia with a normal karyotype. *Oncotarget*, **9**, 4961-4968.
- [27] McKeever, P.M., Kim, T., Hesketh, A.R., MacNair, L., Miletic, D., Favrin, G., Oliver, S.G., **Zhang, Z.**, St George-Hyslop, P. and Robertson, J. (2017) Cholinergic neuron gene expression differences captured by translational profiling in a mouse model of Alzheimer's disease. *Neurobiol Aging*, **57**, 104-119.
- [28] Leach, M.D., Kim, T., DiGregorio, S.E., Collins, C., **Zhang, Z.**, Duennwald, M.L. and Cowen, L.E. (2017) Candida albicans Is Resistant to Polyglutamine Aggregation and Toxicity. *G3 (Bethesda)*, **7**, 95-108.
- [29] Kim, T., Tyndel, M.S., **Zhang, Z.**, Ahn, J., Choi, S., Szardenings, M., Lipton, J.H., Kim, H.J. and Kim Dong Hwan, D. (2017) Exome sequencing reveals DNMT3A and ASXL1 variants associate with progression of chronic myeloid leukemia after tyrosine kinase inhibitor therapy. *Leuk Res*, **59**, 142-148.
- [30] Kim, T., Tyndel, M.S., Kim, H.J., Ahn, J.S., Choi, S.H., Park, H.J., Kim, Y.K., Yang, D.H., Lee, J.J., Jung, S.H. *et al.* (2017) The clonal origins of leukemic progression of myelodysplasia. *Leukemia*, **31**, 1928-1935.
- [31] Kim, T., Tyndel, M.S., Kim, H.J., Ahn, J.S., Choi, S.H., Park, H.J., Kim, Y.K., Kim, S.Y., Lipton, J.H., **Zhang, Z.** *et al.* (2017) Spectrum of somatic mutation dynamics in chronic myeloid leukemia following tyrosine kinase inhibitor therapy. *Blood*, **129**, 38-47.
- [32] Yimit, A., Kim, T., Anand, R., Meister, S., Ou, J., Haber, J.E., **Zhang, Z.** and Brown, G.W. (2016) MTE1 Functions with MPH1 in Double-Strand Break Repair. *Genetics*.
- [33] Styles, E.B., Founk, K.J., Zamparo, L.A., Sing, T.L., Altintas, D., Ribeyre, C., Ribaud, V., Rougemont, J., Mayhew, D., Costanzo, M. *et al.* (2016) Exploring Quantitative Yeast Phenomics with Single-Cell Analysis of DNA Damage Foci. *Cell Syst*, **3**, 264-277 e210.
- [34] Paul, J.M., Toosi, B., Vizeacoumar, F.S., Bhanumathy, K.K., Li, Y., Gerger, C., El Zawily, A., Freywald, T., Anderson, D.H., Mousseau, D. *et al.* (2016) Targeting synthetic lethality between the SRC kinase and the EPHB6 receptor may benefit cancer treatment. *Oncotarget*.
- [35] Olsen, J.B., Wong, L., Deimling, S., Miles, A., Guo, H., Li, Y., **Zhang, Z.**, Greenblatt, J.F., Emili, A. and Tropepe, V. (2016) G9a and ZNF644 Physically Associate to Suppress Progenitor Gene Expression during Neurogenesis. *Stem Cell Reports*, **7**, 454-470.
- [36] Kim, T., Yoshida, K., Kim, Y.K., Tyndel, M.S., Park, H.J., Choi, S.H., Ahn, J.S., Jung, S.H., Yang, D.H., Lee, J.J. *et al.* (2016) Clonal dynamics in a single AML case tracked for 9 years reveals the complexity of leukemia progression. *Leukemia*, **30**, 295-302.
- [37] Gu, Z., Jin, K., Crabbe, M.J., Zhang, Y., Liu, X., Huang, Y., Hua, M., Nan, P., **Zhang, Z.** and Zhong, Y. (2016) Enrichment analysis of Alu elements with different spatial chromatin proximity in the human genome. *Protein Cell*, **7**, 250-266.
- [38] Dibitto, D., Ferrari, M., Rawal, C.C., Balint, A., Kim, T., **Zhang, Z.**, Smolka, M.B., Brown, G.W., Marini, F. and Pelliccioli, A. (2016) Slx4 and Rtt107 control checkpoint signalling and DNA resection at double-strand breaks. *Nucleic Acids Res*, **44**, 669-682.
- [39] Yang, L., Wang, Y., **Zhang, Z.** and He, S. (2015) Comprehensive transcriptome analysis reveals accelerated genic evolution in a Tibet fish, *Gymnodiptychus pachycheilus*. *Genome Biol Evol*, **7**, 251-261.
- [40] Wong, K.C., Li, Y., Peng, C. and **Zhang, Z.** (2015) SignalSpider: probabilistic pattern discovery on multiple normalized ChIP-Seq signal profiles. *Bioinformatics*, **31**, 17-24.
- [41] Wong, K.C., Li, Y., Peng, C., Moses, A.M. and **Zhang, Z.** (2015) Computational learning on specificity-

- determining residue-nucleotide interactions. *Nucleic Acids Res*, **43**, 10180-10189.
- [42] Maly, R.H., Jessulat, M., Jin, K., Musso, G., Vlasblom, J., Phanse, S., **Zhang, Z.** and Babu, M. (2015) Mitochondrial targets for pharmacological intervention in human disease. *J Proteome Res*, **14**, 5-21.
- [43] Liang, C., Li, Y., Luo, J. and **Zhang, Z.** (2015) A novel motif-discovery algorithm to identify co-regulatory motifs in large transcription factor and microRNA co-regulatory networks in human. *Bioinformatics*, **31**, 2348-2355.
- [44] Li, Y. and **Zhang, Z.** (2015) Computational Biology in microRNA. *Wiley Interdiscip Rev RNA*, **6**, 435-452.
- [45] Li, Y., Wang, Y., **Zhang, Z.**, Zamudio, A.V. and Zhao, J.C. (2015) Genome-wide detection of high abundance N6-methyladenosine sites by microarray. *RNA*, **21**, 1511-1518.
- [46] Li, J., Ma, Z., Shi, M., Maly, R.H., Aoki, H., Minic, Z., Phanse, S., Jin, K., Wall, D.P., **Zhang, Z.** et al. (2015) Identification of Human Neuronal Protein Complexes Reveals Biochemical Activities and Convergent Mechanisms of Action in Autism Spectrum Disorders. *Cell Syst*, **1**, 361-374.
- [47] Jin, K., Musso, G., Vlasblom, J., Jessulat, M., Deineko, V., Negroni, J., Mosca, R., Maly, R., Nguyen-Tran, D.H., Aoki, H. et al. (2015) Yeast mitochondrial protein-protein interactions reveal diverse complexes and disease-relevant functional relationships. *J Proteome Res*, **14**, 1220-1237.
- [48] Jessulat, M., Maly, R.H., Nguyen-Tran, D.H., Deineko, V., Aoki, H., Vlasblom, J., Omid, K., Jin, K., Minic, Z., Hooshyar, M. et al. (2015) Spindle Checkpoint Factors Bub1 and Bub2 Promote DNA Double-Strand Break Repair by Nonhomologous End Joining. *Mol Cell Biol*, **35**, 2448-2463.
- [49] Jablonowski, C.M., Cussiol, J.R., Oberly, S., Yimit, A., Balint, A., Kim, T., **Zhang, Z.**, Brown, G.W. and Smolka, M.B. (2015) Termination of Replication Stress Signaling via Concerted Action of the Slx4 Scaffold and the PP4 Phosphatase. *Genetics*.
- [50] Balint, A., Kim, T., Gallo, D., Cussiol, J.R., Bastos de Oliveira, F.M., Yimit, A., Ou, J., Nakato, R., Gurevich, A., Shirahige, K. et al. (2015) Assembly of Slx4 signaling complexes behind DNA replication forks. *EMBO J*, **34**, 2182-2197.
- [51] Wong, K.C. and **Zhang, Z.** (2014) SNPdryad: predicting deleterious non-synonymous human SNPs using only orthologous protein sequences. *Bioinformatics*, **30**, 1112-1119.
- [52] Wang, Y., Li, Y., Toth, J.I., Petroski, M.D., **Zhang, Z.** and Zhao, J.C. (2014) N6-methyladenosine modification destabilizes developmental regulators in embryonic stem cells. *Nat Cell Biol*, **16**, 191-198.
- [53] Li, Y. and **Zhang, Z.** (2014) Potential microRNA-mediated oncogenic intercellular communication revealed by pan-cancer analysis. *Sci Rep*, **4**, 7097.
- [54] Li, Y., Liang, M. and **Zhang, Z.** (2014) Regression analysis of combined gene expression regulation in acute myeloid leukemia. *PLoS Comput Biol*, **10**, e1003908.
- [55] Li, Y., Liang, C., Wong, K.C., Luo, J. and **Zhang, Z.** (2014) Mirsynergy: detecting synergistic miRNA regulatory modules by overlapping neighbourhood expansion. *Bioinformatics*, **30**, 2627-2635.
- [56] Li, Y., Liang, C., Wong, K.C., Jin, K. and **Zhang, Z.** (2014) Inferring probabilistic miRNA-mRNA interaction signatures in cancers: a role-switch approach. *Nucleic Acids Res*, **42**, e76.
- [57] Li, Y., Liang, C., Easterbrook, S., Luo, J. and **Zhang, Z.** (2014) Investigating the functional implications of reinforcing feedback loops in transcriptional regulatory networks. *Mol Biosyst*, **10**, 3238-3248.
- [58] Li, Y., Goldenberg, A., Wong, K.C. and **Zhang, Z.** (2014) A probabilistic approach to explore human miRNA targetome by integrating miRNA-overexpression data and sequence information. *Bioinformatics*, **30**, 621-628.
- [59] Li, J., Kim, T., Nutiu, R., Ray, D., Hughes, T.R. and **Zhang, Z.** (2014) Identifying mRNA sequence elements for target recognition by human Argonaute proteins. *Genome Res*, **24**, 775-785.
- [60] Cromar, G., Wong, K.C., Loughran, N., On, T., Song, H., Xiong, X., **Zhang, Z.** and Parkinson, J. (2014) New tricks for "old" domains: how novel architectures and promiscuous hubs contributed to the organization and evolution of the ECM. *Genome Biol Evol*, **6**, 2897-2917.
- [61] Wong, K.C., Chan, T.M., Peng, C., Li, Y. and **Zhang, Z.** (2013) DNA motif elucidation using belief propagation. *Nucleic Acids Res*, **41**, e153.
- [62] Snider, J., Hanif, A., Lee, M.E., Jin, K., Yu, A.R., Graham, C., Chuk, M., Damjanovic, D., Wierzbicka, M., Tang, P. et al. (2013) Mapping the functional yeast ABC transporter interactome. *Nat Chem Biol*, **9**, 565-572.
- [63] Li, Y., Zhao, D.Y., Greenblatt, J.F. and **Zhang, Z.** (2013) RIPSeeker: a statistical package for identifying protein-associated transcripts from RIP-seq experiments. *Nucleic Acids Res*, **41**, e94.
- [64] Li, J. and **Zhang, Z.** (2013) miRNA regulatory variation in human evolution. *Trends Genet*, **29**, 116-124.
- [65] Choi, H., Jung, C., Sohn, S.K., Kim, S., Kim, H.J., Kim, Y.K., Kim, T., **Zhang, Z.**, Shin, E.S., Lee, J.E. et al. (2013) Genome-wide genotype-based risk model for survival in acute myeloid leukaemia patients with normal karyotype. *Br J Haematol*, **163**, 62-71.
- [66] Yang, Z., Dong, D., **Zhang, Z.**, Crabbe, M.J., Wang, L. and Zhong, Y. (2012) Preferential regulation of stably expressed genes in the human genome suggests a widespread expression buffering role of microRNAs. *BMC Genomics*, **13 Suppl 7**, S14.
- [67] Musso, G., Emili, A. and **Zhang, Z.** (2012) Characterization and evolutionary analysis of protein-protein

- interaction networks. *Methods Mol Biol*, **856**, 363-380.
- [68] Li, J., Liu, Y., Xin, X., Kim, T.S., Cabeza, E.A., Ren, J., Nielsen, R., Wrana, J.L. and **Zhang, Z.** (2012) Evidence for positive selection on a number of MicroRNA regulatory interactions during recent human evolution. *PLoS Genet*, **8**, e1002578.
- [69] Jin, K., Li, J., Vizeacoumar, F.S., Li, Z., Min, R., Zamparo, L., Vizeacoumar, F.J., Datti, A., Andrews, B., Boone, C. *et al.* (2012) PhenoM: a database of morphological phenotypes caused by mutation of essential genes in *Saccharomyces cerevisiae*. *Nucleic Acids Res*, **40**, D687-694.
- [70] Turinsky, A.L., Turner, B., Borja, R.C., Gleeson, J.A., Heath, M., Pu, S., Switzer, T., Dong, D., Gong, Y., On, T. *et al.* (2011) DAnCER: disease-annotated chromatin epigenetics resource. *Nucleic Acids Res*, **39**, D889-894.
- [71] Musso, G., Emili, A. and **Zhang, Z.** (2011) Filtering and interpreting large-scale experimental protein-protein interaction data. *Methods Mol Biol*, **781**, 295-309.
- [72] Li, Z., Vizeacoumar, F.J., Bahr, S., Li, J., Warringer, J., Vizeacoumar, F.S., Min, R., Vandersluis, B., Bellay, J., Devit, M. *et al.* (2011) Systematic exploration of essential yeast gene function with temperature-sensitive mutants. *Nat Biotechnol*, **29**, 361-367.
- [73] Gong, Y., **Zhang, Z.** and Houry, W.A. (2011) Bioinformatic approach to identify chaperone pathway relationship from large-scale interaction networks. *Methods Mol Biol*, **787**, 189-203.
- [74] Dong, D., Yuan, Z. and **Zhang, Z.** (2011) Evidences for increased expression variation of duplicate genes in budding yeast: from cis- to trans-regulation effects. *Nucleic Acids Res*, **39**, 837-847.
- [75] Dong, D., Shao, X. and **Zhang, Z.** (2011) Differential effects of chromatin regulators and transcription factors on gene regulation: a nucleosomal perspective. *Bioinformatics*, **27**, 147-152.
- [76] Dong, D., Shao, X., Deng, N. and **Zhang, Z.** (2011) Gene expression variations are predictive for stochastic noise. *Nucleic Acids Res*, **39**, 403-413.
- [77] Vizeacoumar, F.J., van Dyk, N., F, S.V., Cheung, V., Li, J., Sydorsky, Y., Case, N., Li, Z., Datti, A., Nislow, C. *et al.* (2010) Integrating high-throughput genetic interaction mapping and high-content screening to explore yeast spindle morphogenesis. *J Cell Biol*, **188**, 69-81.
- [78] Ren, J., Liu, Z., Gao, X., Jin, C., Ye, M., Zou, H., Wen, L., **Zhang, Z.**, Xue, Y. and Yao, X. (2010) MiCroKit 3.0: an integrated database of midbody, centrosome and kinetochore. *Nucleic Acids Res*, **38**, D155-160.
- [79] Ren, J., Jiang, C., Gao, X., Liu, Z., Yuan, Z., Jin, C., Wen, L., **Zhang, Z.**, Xue, Y. and Yao, X. (2010) PhosSNP for systematic analysis of genetic polymorphisms that influence protein phosphorylation. *Mol Cell Proteomics*, **9**, 623-634.
- [80] Pu, S., Turinsky, A.L., Vlasblom, J., On, T., Xiong, X., Emili, A., **Zhang, Z.**, Greenblatt, J., Parkinson, J. and Wodak, S.J. (2010) Expanding the landscape of chromatin modification (CM)-related functional domains and genes in human. *PLoS One*, **5**, e14122.
- [81] On, T., Xiong, X., Pu, S., Turinsky, A., Gong, Y., Emili, A., **Zhang, Z.**, Greenblatt, J., Wodak, S.J. and Parkinson, J. (2010) The evolutionary landscape of the chromatin modification machinery reveals lineage specific gains, expansions, and losses. *Proteins*, **78**, 2075-2089.
- [82] Min, R., van der Maaten, L., Yuan, Z., Bonner, A. and **Zhang, Z.** (2010), *27th International Conference on Machine Learning (ICML 2010)* Haifa, Israel.
- [83] Li, R., Fan, W., Tian, G., Zhu, H., He, L., Cai, J., Huang, Q., Cai, Q., Li, B., Bai, Y. *et al.* (2010) The sequence and de novo assembly of the giant panda genome. *Nature*, **463**, 311-317.
- [84] Li, J., Yuan, Z. and **Zhang, Z.** (2010) Revisiting the contribution of cis-elements to expression divergence between duplicated genes: the role of chromatin structure. *Mol Biol Evol*, **27**, 1461-1466.
- [85] Li, J., Yuan, Z. and **Zhang, Z.** (2010) The cellular robustness by genetic redundancy in budding yeast. *PLoS Genet*, **6**, e1001187.
- [86] Li, J., Min, R., Vizeacoumar, F.J., Jin, K., Xin, X. and **Zhang, Z.** (2010) Exploiting the determinants of stochastic gene expression in *Saccharomyces cerevisiae* for genome-wide prediction of expression noise. *Proc Natl Acad Sci U S A*, **107**, 10472-10477.
- [87] Li, J., Liu, Y., Kim, T., Min, R. and **Zhang, Z.** (2010) Gene expression variability within and between human populations and implications toward disease susceptibility. *PLoS Comput Biol*, **6**.
- [88] Li, J., Liu, Y., Dong, D. and **Zhang, Z.** (2010) Evolution of an X-linked primate-specific micro RNA cluster. *Mol Biol Evol*, **27**, 671-683.
- [89] Min, R., Stanley, D.A., Yuan, Z., Bonner, A. and **Zhang, Z.** (2009), *IEEE International Conference on Data Mining (ICDM 2009)* Miami, FL, USA.
- [90] Min, R., Kuang, R., Bonner, A. and **Zhang, Z.** (2009), *SIAM International Conference on Data Mining (SDM09)*, Sparks, Nevada, USA.
- [91] Min, R., Bonner, A., Li, J. and **Zhang, Z.** (2009) Learned random-walk kernels and empirical-map kernels for protein sequence classification. *J Comput Biol*, **16**, 457-474.
- [92] Li, J., Min, R., Bonner, A. and **Zhang, Z.** (2009) A probabilistic framework to improve microrna target prediction

- by incorporating proteomics data. *J Bioinform Comput Biol*, **7**, 955-972.
- [93] Kittanakom, S., Chuk, M., Wong, V., Snyder, J., Edmonds, D., Lydakis, A., **Zhang, Z.**, Auerbach, D. and Stagljar, I. (2009) Analysis of membrane protein complexes using the split-ubiquitin membrane yeast two-hybrid (MYTH) system. *Methods Mol Biol*, **548**, 247-271.
- [94] Guo, X., **Zhang, Z.**, Gerstein, M.B. and Zheng, D. (2009) Small RNAs originated from pseudogenes: cis- or trans-acting? *PLoS Comput Biol*, **5**, e1000449.
- [95] Gong, Y. and **Zhang, Z.** (2009) Global robustness and identifiability of random, scale-free, and small-world networks. *Ann N Y Acad Sci*, **1158**, 82-92.
- [96] Gong, Y., Kakihara, Y., Krogan, N., Greenblatt, J., Emili, A., **Zhang, Z.** and Houry, W.A. (2009) An atlas of chaperone-protein interactions in *Saccharomyces cerevisiae*: implications to protein folding pathways in the cell. *Mol Syst Biol*, **5**, 275.
- [97] Feng, Z.P., **Zhang, Z.**, van Kesteren, R.E., Straub, V.A., van Nierop, P., Jin, K., Nejatbakhsh, N., Goldberg, J.I., Spencer, G.E., Yeoman, M.S. *et al.* (2009) Transcriptome analysis of the central nervous system of the mollusc *Lymnaea stagnalis*. *BMC Genomics*, **10**, 451.
- [98] Dong, D., He, G., Zhang, S. and **Zhang, Z.** (2009) Evolution of olfactory receptor genes in primates dominated by birth-and-death process. *Genome Biol Evol*, **1**, 258-264.
- [99] Musso, G., Costanzo, M., Huangfu, M., Smith, A.M., Paw, J., San Luis, B.J., Boone, C., Giaever, G., Nislow, C., Emili, A. *et al.* (2008) The extensive and condition-dependent nature of epistasis among whole-genome duplicates in yeast. *Genome Res*, **18**, 1092-1099.
- [100] Li, J., Musso, G. and **Zhang, Z.** (2008) Preferential regulation of duplicated genes by microRNAs in mammals. *Genome Biol*, **9**, R132.
- [101] Gunewardena, S. and **Zhang, Z.** (2008) A hybrid model for robust detection of transcription factor binding sites. *Bioinformatics*, **24**, 484-491.
- [102] Davids, W. and **Zhang, Z.** (2008) The impact of horizontal gene transfer in shaping operons and protein interaction networks--direct evidence of preferential attachment. *BMC Evol Biol*, **8**, 23.
- [103] Borozan, I., Chen, L., Paeper, B., Heathcote, J.E., Edwards, A.M., Katze, M., **Zhang, Z.** and McGilvray, I.D. (2008) MAID : an effect size based model for microarray data integration across laboratories and platforms. *BMC Bioinformatics*, **9**, 305.
- [104] **Zhang, Z.**, Pang, A.W. and Gerstein, M. (2007) Comparative analysis of genome tiling array data reveals many novel primate-specific functional RNAs in human. *BMC Evol Biol*, **7 Suppl 1**, S14.
- [105] Musso, G.A., **Zhang, Z.** and Emili, A. (2007) Experimental and computational procedures for the assessment of protein complexes on a genome-wide scale. *Chem Rev*, **107**, 3585-3600.
- [106] Musso, G., **Zhang, Z.** and Emili, A. (2007) Retention of protein complex membership by ancient duplicated gene products in budding yeast. *Trends Genet*, **23**, 266-269.
- [107] Mockli, N., Deplazes, A., Hassa, P.O., **Zhang, Z.**, Peter, M., Hottiger, M.O., Stagljar, I. and Auerbach, D. (2007) Yeast split-ubiquitin-based cytosolic screening system to detect interactions between transcriptionally active proteins. *Biotechniques*, **42**, 725-730.
- [108] Karro, J.E., Yan, Y., Zheng, D., **Zhang, Z.**, Carriero, N., Cayting, P., Harrison, P. and Gerstein, M. (2007) Pseudogene.org: a comprehensive database and comparison platform for pseudogene annotation. *Nucleic Acids Res*, **35**, D55-60.
- [109] Gong, Y. and **Zhang, Z.** (2007) CellFrame: a data structure for abstraction of cell biology experiments and construction of perturbation networks. *Ann N Y Acad Sci*, **1115**, 249-266.
- [110] Gong, Y. and **Zhang, Z.** (2007) Alternative pathway approach for automating analysis and validation of cell perturbation networks and design of perturbation experiments. *Ann N Y Acad Sci*, **1115**, 267-285.
- [111] **Zhang, Z.**, Carriero, N., Zheng, D., Karro, J., Harrison, P.M. and Gerstein, M. (2006) PseudoPipe: an automated pseudogene identification pipeline. *Bioinformatics*, **22**, 1437-1439.
- [112] Gunewardena, S. and **Zhang, Z.** (2006) Accounting for structural properties and nucleotide co-variations in the quantitative prediction of binding affinities of protein-DNA interactions. *Pac Symp Biocomput*, 379-390.
- [113] Gunewardena, S., Jeavons, P. and **Zhang, Z.** (2006) Enhancing the prediction of transcription factor binding sites by incorporating structural properties and nucleotide covariations. *J Comput Biol*, **13**, 929-945.
- [114] Zheng, D., **Zhang, Z.**, Harrison, P.M., Karro, J., Carriero, N. and Gerstein, M. (2005) Integrated pseudogene annotation for human chromosome 22: evidence for transcription. *J Mol Biol*, **349**, 27-45.
- [115] Harrison, P.M., Zheng, D., **Zhang, Z.**, Carriero, N. and Gerstein, M. (2005) Transcribed processed pseudogenes in the human genome: an intermediate form of expressed retrosequence lacking protein-coding ability. *Nucleic Acids Res*, **33**, 2374-2383.
- [116] Gong, Y. and **Zhang, Z.** (2005) Alternative signaling pathways: when, where and why? *FEBS Lett*, **579**, 5265-5274.
- [117] **Zhang, Z.** and Gerstein, M. (2004) Large-scale analysis of pseudogenes in the human genome. *Curr Opin Genet*

- Dev*, **14**, 328-335.
- [118] **Zhang, Z.**, Carriero, N. and Gerstein, M. (2004) Comparative analysis of processed pseudogenes in the mouse and human genomes. *Trends Genet*, **20**, 62-67.
- [119] Lehnert, U., Xia, Y., Royce, T.E., Goh, C.S., Liu, Y., Senes, A., Yu, H., **Zhang, Z.L.**, Engelman, D.M. and Gerstein, M. (2004) Computational analysis of membrane proteins: genomic occurrence, structure prediction and helix interactions. *Q Rev Biophys*, **37**, 121-146.
- [120] **Zhang, Z.**, Harrison, P.M., Liu, Y. and Gerstein, M. (2003) Millions of years of evolution preserved: a comprehensive catalog of the processed pseudogenes in the human genome. *Genome Res*, **13**, 2541-2558.
- [121] **Zhang, Z.** and Gerstein, M. (2003) Reconstructing genetic networks in yeast. *Nat Biotechnol*, **21**, 1295-1297.
- [122] **Zhang, Z.** and Gerstein, M. (2003) Identification and characterization of over 100 mitochondrial ribosomal protein pseudogenes in the human genome. *Genomics*, **81**, 468-480.
- [123] **Zhang, Z.** and Gerstein, M. (2003) Of mice and men: phylogenetic footprinting aids the discovery of regulatory elements. *J Biol*, **2**, 11.
- [124] **Zhang, Z.** and Gerstein, M. (2003) The human genome has 49 cytochrome c pseudogenes, including a relic of a primordial gene that still functions in mouse. *Gene*, **312**, 61-72.
- [125] **Zhang, Z.** and Gerstein, M. (2003) Patterns of nucleotide substitution, insertion and deletion in the human genome inferred from pseudogenes. *Nucleic Acids Res*, **31**, 5338-5348.
- [126] Harrison, P.M., Milburn, D., **Zhang, Z.**, Bertone, P. and Gerstein, M. (2003) Identification of pseudogenes in the *Drosophila melanogaster* genome. *Nucleic Acids Res*, **31**, 1033-1037.
- [127] **Zhang, Z.L.**, Harrison, P.M. and Gerstein, M. (2002) Digging deep for ancient relics: a survey of protein motifs in the intergenic sequences of four eukaryotic genomes. *J Mol Biol*, **323**, 811-822.
- [128] **Zhang, Z.**, Harrison, P. and Gerstein, M. (2002) Identification and analysis of over 2000 ribosomal protein pseudogenes in the human genome. *Genome Res*, **12**, 1466-1482.
- [129] Luscombe, N.M., Qian, J., **Zhang, Z.**, Johnson, T. and Gerstein, M. (2002) The dominance of the population by a selected few: power-law behaviour applies to a wide variety of genomic properties. *Genome Biol*, **3**, RESEARCH0040.
- [130] Liu, Y., Luscombe, N.M., Alexandrov, V., Bertone, P., Harrison, P., **Zhang, Z.** and Gerstein, M. (2002) Structural genomics: a new era for pharmaceutical research. *Genome Biol*, **3**, REPORTS4004.
- [131] Echols, N., Harrison, P., Balasubramanian, S., Luscombe, N.M., Bertone, P., **Zhang, Z.** and Gerstein, M. (2002) Comprehensive analysis of amino acid and nucleotide composition in eukaryotic genomes, comparing genes and pseudogenes. *Nucleic Acids Res*, **30**, 2515-2523.
- [132] Balasubramanian, S., Harrison, P., Hegyi, H., Bertone, P., Luscombe, N., Echols, N., McGarvey, P., **Zhang, Z.** and Gerstein, M. (2002) SNPs on human chromosomes 21 and 22 -- analysis in terms of protein features and pseudogenes. *Pharmacogenomics*, **3**, 393-402.
- [133] **Zhang, Z.**, Berry, E.A., Huang, L.S. and Kim, S.H. (2000) Mitochondrial cytochrome bc1 complex. *Subcell Biochem*, **35**, 541-580.
- [134] Chi, Y.I., Huang, L.S., **Zhang, Z.**, Fernandez-Velasco, J.G. and Berry, E.A. (2000) X-ray structure of a truncated form of cytochrome f from *Chlamydomonas reinhardtii*. *Biochemistry*, **39**, 7689-7701.
- [135] Berry, E.A., **Zhang, Z.**, Bellamy, H.D. and Huang, L. (2000) Crystallographic location of two Zn(2+)-binding sites in the avian cytochrome bc(1) complex. *Biochim Biophys Acta*, **1459**, 440-448.
- [136] Crofts, A.R., Hong, S., **Zhang, Z.** and Berry, E.A. (1999) Physicochemical aspects of the movement of the Rieske iron sulfur protein during quinol oxidation by the bc(1) complex from mitochondria and photosynthetic bacteria. *Biochemistry*, **38**, 15827-15839.
- [137] Crofts, A.R., Guergova-Kuras, M., Huang, L., Kuras, R., **Zhang, Z.** and Berry, E.A. (1999) Mechanism of ubiquinol oxidation by the bc(1) complex: role of the iron sulfur protein and its mobility. *Biochemistry*, **38**, 15791-15806.
- [138] Berry, E.A., **Zhang, Z.**, Huang, L.S. and Kim, S.H. (1999) Structures of quinone-binding sites in bc complexes: functional implications. *Biochem Soc Trans*, **27**, 565-572.
- [139] Berry, E.A., Huang, L.S., **Zhang, Z.** and Kim, S.H. (1999) Structure of the avian mitochondrial cytochrome bc1 complex. *J Bioenerg Biomembr*, **31**, 177-190.
- [140] **Zhang, Z.**, Huang, L., Shulmeister, V.M., Chi, Y.I., Kim, K.K., Hung, L.W., Crofts, A.R., Berry, E.A. and Kim, S.H. (1998) Electron transfer by domain movement in cytochrome bc1. *Nature*, **392**, 677-684.
- [141] Saribas, A.S., Valkova-Valchanova, M., Tokito, M.K., **Zhang, Z.**, Berry, E.A. and Daldal, F. (1998) Interactions between the cytochrome b, cytochrome c1, and Fe-S protein subunits at the ubihydroquinone oxidation site of the bc1 complex of *Rhodobacter capsulatus*. *Biochemistry*, **37**, 8105-8114.

Book Chapters

- [1] Zhao DY, Li Y., Greenblatt J., **Zhang Z.** ncRNA-protein interactions in development and disease from the perspective of high-throughput studies, book Chapter in SYSTEMS ANALYSIS OF CHROMATIN-RELATED PROTEIN COMPLEXES IN CANCER, Springer Publishing ;
- [2] Musso G, Emili A, **Zhang Z.** Characterization and evolutionary analysis of protein-protein interaction networks. Book chapter in EVOLUTIONARY GENOMICS, Methods in Molecular Biology, 2012, Volume 856, Part 4, 363-380 ;
- [3] Gong Y, **Zhang Z.**, Houry WA. Bioinformatic approach to identify chaperone pathway relationship from large-scale interaction networks. Book chapter in Molecular Chaperones, Methods Mol Biol. 2011;787:189-203 ;
- [4] Musso G, Emili A, **Zhang Z.** Filtering and interpreting large-scale experimental protein-protein interaction data. Book chapter in Network Biology, Methods Mol Biol. 2011;781:295-309. PMID: 21877287.
- [5] Kittanakom S, Chuk M, Wong V, Snyder J, Edmonds D, Lydakis A, **Zhang Z.**, Auerbach D, Stagljar I. Analysis of membrane protein complexes using the split-ubiquitin membrane yeast two-hybrid (MYTH) system. Book chapter in YEAST FUNCTIONAL GENOMICS AND PROTEOMICS, Methods Mol Biol. 2009;548:247-71.
- [6] **Zhang Z.**, Berry EA, Huang LS, Kim SH. Mitochondrial cytochrome bc1 complex. Subcell Biochem. 2000;35:541-80. Review. PMID: 11192733.

Peer-reviewed conference publications

- [1] Min R., van der Maaten L., Yuan Z., Bonner A., **Zhang Z.** "Deep Supervised T-Distributed Embedding" 27th International Conference on Machine Learning (ICML 2010)
- [2] Min R., Stanley D.A., Yuan Z., Bonner A., and **Zhang Z.**, "A Deep Non-Linear Feature Mapping for Large-Margin kNN Classification" IEEE International Conference on Data Mining (ICDM 2009)
- [3] Min R., Kuang R., Bonner A., and **Zhang Z.** "Learning Random-Walk Kernels for Protein Remote Homology Identification and Motif Discovery" SIAM International Conference on Data Mining (SDM09) (2009)
- [4] Min R., Bonner A., and **Zhang Z.**, "Modifying Kernels Using Label Information Improves SVM Classification Performance" International Conference on Machine Learning and Applications (ICMLA 2007)
- [5] Gunewardena S, **Zhang Z.** Accounting for structural properties and nucleotide co-variations in the quantitative prediction of binding affinities of protein-DNA interactions. Pac Symp Biocomput. 2006:379-90.

SUPERVISION

Post-doctoral Fellows

- [1] Jianguo Chen, 2018/10 – Present
- [2] Razvan Nutiu, 2011/10 - 2012/11, Investigator, Novartis Cambridge, MA
- [3] Ke Steven Jin, 2010/11 – 2015/04, financial industry
- [4] Derek Dong, 2008/10 – 2011/04, faculty, East China Normal University, Shanghai
- [5] Yu Liu, 2007/07 – 2009/07, Research Associate, Case Western Reserve University
- [6] Ivan Borozan, 2006/05 – 2008/12, Research Associate, Ontario Institute of Cancer Research
- [7] Yunchen Gong, 2006/04 – 2008/06, Bioinformatician, U of T, Cell and Systems Biology
- [8] Wagied Davids, 2006/02 – 2009/03, Software developer
- [9] Sumedha Gunewardena, 2005/02 – 2008/10, Assistant Professor (Research), U of Kansas Med Center

Doctoral students

- [1] Hyunmin Lee, Computer Science, 2016/10 – Present
- [2] Shun Liao, Computer Science, 2015/09 – Present
- [3] Taehyung Simon Kim, Computer Science, 2013/01 – Present
- [4] Cadia Chan, Molecular Genetics, 2019/01 – Present, co-supervised with Mike Wilson
- [5] Ka-chun Wong, 2011/09 – 2014/12, Computer Science, Assis. Professor, City U Hong Kong
- [6] Yue Li, 2010/09 – 2014/12, Computer Science, Assis. Professor, McGill University
- [7] Lee Zamparo, 2008/09 – 2015/09, Computer Science, Researcher, Element AI
- [8] Jingjing Li, 2007/04 – 2011/06, Molecular Genetics, Assis. Professor, UC San Francisco
- [9] Emad Shenouda Andrews 2007/03 – 2013/12, Computer Science, co-supervised with Tony Bonner
- [10] Gabriel Musso, 2005/09 – 2009/12, Molecular Genetics, Chief Science Officer, BioSymetrics
- [11] Renqiang Martin Min, 2005/09 – 2010/09, Computer Science, Staff Researcher, NEC Labs, Princeton

Masters students

- [1] James Burns, 2020/04 – present, Molecular Genetics, co-supervision with Jack Greenblatt
- [2] Junjiang Lin, 2014/09 – 2016/03, Computer Science, Software engineer, Amazon
- [3] Akiko Sekikawa, 2010/09 – 2013/09, Molecular Genetics, pharmaceutical industry
- [4] Zineng Eric Yuan, 2008/09 – 2010/09, Molecular Genetics, software developer
- [5] Apostolos Lydakis, 2007/01 – 2009/02, Molecular Genetics, biotech industry
- [6] Sanna Mahmood, 2006/09 – 2009/11, Molecular Genetics, immigration attorney
- [7] Matthew Fagnani, 2005/09 – 2007/12, Molecular Genetics, co-supervised with Ben Blencowe

Visiting Scholars

- [1] Jae-sook Ahn, 2018/01 – 2020/02, Associate Professor, Chonnam National University Hwasun Hospital, Korea
- [2] Linda Qian Xing, 2011/09 – 2012/09, Associate Professor, Sun Yat-sen University, Guangzhou, China

Visiting graduate students

- [1] Saisai Sun, 10/2019 – present, Nankai University
- [2] Hongli Ma, 10/2019 – present, Shandong University
- [3] Ying Liu, 2018/10 – 2020/10, Hunan University
- [4] Shuhui Liu, 2018/10 – 2020/10, Northwest Polytech University
- [5] Xuejiao Hu, 2017/09 – 2019/08, Sichuan University
- [6] Chu Pan, 2017/03 – 2019/03, Hunan University
- [7] Liandong Yang, 2013/10 – 2014/10, Chinese Academy of Science, Institute of Hydrobiology
- [8] Cheng Liang, 2012/10 – 2014/09, Hunan University.