

**Li Liu, M.D.**

**Assistant Professor of Biomedical Informatics**  
 College of Health Solutions  
 Center for Personalized Diagnostics, Biodesign Institute  
 Arizona State University

**Adjunct Asst. Professor**  
 Department of Neurology  
 Mayo Clinic Arizona

**AREAS OF RESEARCH INTEREST**

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- Develop and apply computational methods to enable precision medicine
  - ❖ Biomarker discovery
  - ❖ Cancer subclonal development
  - ❖ Personalized immunotherapy
- Study the evolution of human genomes and the indications in diseases
  - ❖ Fine-map functional genomic elements
  - ❖ Gene-environment interaction in complex diseases
- Data analytics for biomedical applications
  - ❖ Statistical support to biomedical research
  - ❖ Software, databases and analytical pipelines to facilitate “omics” studies

**EDUCATION**

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M.D., Medicine, <i>Peking Union Medical College</i>	1999
M.S., Information System, <i>New Jersey Institute of Technology</i>	2001
B.S., Biochemistry, <i>Peking University</i>	1994

**POSITIONS & EMPLOYMENT**

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2015–present	Assistant Professor, Department of Biomedical Informatics Director, Bioinformatics Core Lab, Biodesign Institute Arizona State University
2017–present	Adjunct Assistant Professor, Department of Neurology, Mayo Clinic Medical School
2010–2015	Research Scientist, Arizona State University
2002–2010	Associate Scientist, Director, Bioinformatics Core Lab, University of Florida
2001–2002	Bioinformatics Consultant, TripodSoft, Inc.
1998 – 1999	Research Assistant, Immunology Peking Union Medical College
1997 – 1998	Medical Internship, Internal Medicine Peking Union Medical College Hospital

**HONORS & Awards**

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2017	Nomination of Searle Scholar (ASU Limited Submission)
2015	National Research Mentoring Network – Proposal Preparation Program
2014	1 <sup>st</sup> Place in the DREAM9 AML Challenge

**PROFESSIONAL MEMBERSHIPS**

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2014–Present	Member, International Society for Computational Biology
2018–Present	Member, Society for Molecular Biology and Evolution
2005–2010	Member, the Association of Biomolecular Resource Facilities
2004–2006	Member, Institute for Operations Research and the Management Sciences

**REVIEWER**

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Ad hoc manuscript reviewer for the following journals

- ❖ Molecular Biology and Evolution
- ❖ Bioinformatics
- ❖ BMC Bioinformatics
- ❖ BMC Medical Genomics
- ❖ Pacific Symposium on Biocomputing

Ad hoc grant reviewer for the following organizations

- ❖ Ireland Health Research Board
- ❖ ASU Limited Submission

**SERVICES**

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***University level***

2017–Present	Chair, BMI Recruitment Committee
2017–Present	Member, BMI Academic Program Committee
2018–Present	Member, CHS Affinity Network Committee
2016–Present	Advisor, Bioinformatics Workshop Series
2015–2018	Member, CHS Standards & Grievance Committee
2016–2017	Member, BMI Recruitment Committee
2016–2017	Grant reviewer, ASU Limited Submission
2016	Informatics Training Grant Planning Committee
2015	Member, CHS Student Engagement Committee

***State and National level***

2017	Instructor, a half-day workshop in Precision Medicine Leaders Summit
2017	Organizer, a discussion panel in Arizona SciTech Festival

***International level***

2018–Present	Guest Editor, Frontiers in Genetics
2016–Present	Grant reviewer, Health Research Board, Ireland

**TEACHING EXPERIENCE & RESPONSIBILITIES**

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2016–Present	Instructor, Modeling Biomedical Knowledge (BMI-311), ASU
2017–Present	Instructor, Topics in Translational Bioinformatics (BMI-330), ASU
2019–Present	Instructor, Modeling Biomedical Data (BMI-312), ASU
2016–2017	Instructor, BMI Symposium (BMI-570), ASU
2016	Instructor, Translational Bioinformatics (BMI-550), ASU

2017	Co-instructor, Introduction to Clinical Informatics (BMI-201), ASU
2015	Instructor, Introduction to Bioinformatics (BMI-101), ASU
2007-2008	Co-instructor, Functional Genomic Applications in Pharmacology and Toxicology, University of Florida (UF)
2006	Instructor, Pathway Analysis in Microarray Studies, UF
2004-2008	Instructor, Sequence Analysis: Theories and Applications, UF
2002-2005	Co-instructor, Molecular Cloning and Protein Chemistry, UF

## MENTORING AND ADVISING

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### Completed

<i>Abdulkadir Elmas, Ph.D.</i>	BMI, ASU	Mentor, 2016-2017
<i>Xin Guan, Ph.D.</i>	BMI, ASU	Co-chair, 2015-2017
<i>Brian Hanratty, M.S.</i>	BMI, ASU	Chair, 2015-2017
<i>Margaret Linan, M.S.</i>	BMI, ASU	Chair, 2015-2017
<i>Anna Freydenzon, M.S.</i>	BMI, ASU	Chair, 2015-2017
<i>Rabia Maqsood, M.S.</i>	BMI, ASU	Chair, 2015-2017
<i>Chaoxing Li, Ph.D.</i>	SOLS, ASU	Member, 2016-2017
<i>Caitlin Vose, Ph.D.</i>	SOLS, ASU	Member, 2016-2017
<i>Shobana Sekar, Ph.D.</i>	BMI, ASU	Member, 2017-2018

### Ongoing

<i>Navid Ahmadinejad (doctoral student)</i>	BMI, ASU	Chair, 2018-
<i>Pramod Chandrashekar (doctoral student)</i>	BMI, ASU	Chair, 2018-
<i>Michelle Winerip (doctoral student)</i>	BMI, ASU	Member, 2016-
<i>Laurel Bruce (doctoral student)</i>	Speech and Hearing Science, ASU	Member, 2018-
<i>Matteo Vaiente (doctoral student)</i>	BMI, ASU	Member, 2018-
<i>Richard Li (Honor's thesis)</i>	BME, ASU	Advisor, 2018-
<i>Shayna Troftgruben (capstone project)</i>	BMI, ASU	Advisor, 2018-
<i>Yara Hawwari (capstone project)</i>	BMI, ASU	Advisor, 2018-

## RESEARCH SUPPORT

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### Active research support

2016 – 2019	eQTL mega-analysis for functional assessment of multi-enhancer gene regulation (Role: PI);
2017 – 2019	Prioritize functional genetic variants in melanoma with network biology and evolution (Role: PI)
2017 – 2019	Genotype-Phenotype Associations in Reading Disorders (Role: Co-mentor)
2017 – 2019	Nanoplasmonic quantification of tumor-derived circulating extracellular vesicles (Role: Co-I)
2018 – 2023	Arizona Cancer and Evolution (ACE) Center (Role: Co-I)

### Completed research support

2013 – 2018	Rational design and targeted selection of DNA-scaffolded nicotine vaccines (Role: Co-I)
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2015 – 2018	Establish Bioinformatics infrastructure at Arizona State University (Role: PI)
2017 – 2018	Discovering the roles of cellular adaptability in late-onset Alzheimer's disease (Role: PI)
2016 – 2017	Subclonal diversity: prognostic role in acute myeloid leukemia patients with minimal residual disease (Role: PI)
2016 – 2017	Discovering immunosignatures of systemic lupus erythematosus (Role: PI)

## PATENTS

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2017	Inventor, Immunosignature microarray analysis and Immunosignatures in systemic lupus erythematosus (provisional, US Patent Number 62/547,748).
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## PUBLICATIONS

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### **Google scholar statistics (01/08/2019)**

	All	Since 2014
<u>Citations</u>	2516	1160
<u>h-index</u>	24	18
<u>i10-index</u>	34	30

### **Complete list of published work in NCBI MyBibliography:**

<https://www.ncbi.nlm.nih.gov/sites/myncbi/1jEAmB1g3JV5b/bibliography/40438753/public/?sort=date&direction=ascending>.

### **Journal articles:** (§ indicates co-first-author)

1. **Liu L**, Maxwell D, Patel R, Chandrashekar P, Gibson G, Kumar S. Biological relevance of predicted pathogenicity of noncoding variants. *Nature Communications* (accepted)
2. Jasbi P, Wang D, Cheng SL, Fei Q, Cui JY, **Liu L**, Wei Y, Raftery D, Gu H. (2019) Breast cancer detection using targeted plasma metabolomics. *Journal of Chromatography B* 1105:26-37
3. **Liu L**, Caselli R. (2018) Age stratification corrects bias in estimated hazards of APOE Genotype in Alzheimer's disease. *Alzheimer's & Dementia TRCI* 4:602–608
4. Li C, **Liu L**, Dinu V. (2018) Pathways of topological rank analysis (potra): a novel method to detect pathways involved in cancer. *PeerJ* 6:e4571
5. Arutla V, Leal J, Liu X, Sokalingam S, Raleigh M, Adaralegbe A, **Liu L**, Pentel P, Hecht S, Chang Y. (2017) Pre-screening of nicotine haptens in vitro to rank and select nicotine hapten-conjugate vaccines for in vivo functional tests. *ACS Combinatorial Science* 19(5):286-298
6. Xie G, Chastain-Gross R, Belanger M, Kumar D, Whitlock J, **Liu L**, Farmerie W, Zeng C, Daligault H, Han C., Brettin T, Progulske-Fox A. (2017) Genome sequence of *Porphyromonas gingivalis* Strain A7A1-28. *Genome Announcement* 5(10): e00021-17
7. **Liu L**, Chang Y, Yang T, Noren DP, Amina Q, Kornblau S, Ye J. (2016) Evolution-informed Modeling Improves Outcome Prediction for Cancers. *Evolutionary Applications* 10(1):68-76
8. **Liu L**, Tamura K, Sanderford M, Gray VE, Kumar S (2016) A Molecular Evolutionary Reference for the Human Variome. *Molecular Biology and Evolution* 33(1):245-54

9. Szedlak A, Smith N, **Liu L**, Paternostro G, Piermarocchi C. (2016) Evolutionary and topological properties of genes and community structures in human gene regulatory network. *PLoS Computational Biology* 12(6):e1005009
10. Noren DP, Long B, Norel R, Rhrissorakkrai K, Hess K, Hu W, Bisberg A, Schultz A, Engquist E, **Liu L**, Lin E, Chen, G, Xie H, Hunter G, Stepanov O, Norman T, Friend SH, Stolovitzky G, Kornboau S, Qutub AA. (2016) A Crowd Sourcing Approach to Developing and Assessing Prediction Algorithms for AML Prognosis. *PLoS Computational Biology* 12(6):e1004890
11. Gerek ZN, **Liu L**<sup>§</sup>, Gerold K, Biparva P, Thomas ED, Kumar S. (2015) Evolutionary Diagnosis of non-synonymous variants involved in differential drug response. *BMC Medical Genomics* 8;Suppl 1:S6
12. Chastain-Gross RP, Xie G, Belanger M, Kumar D, Whitlock JA, **Liu L**, Farmerie G, Daligault HE, Han CS, Brettin TS, Progulske-Fox A. (2015) Genome sequence of porphyromonas gingivalis strain A7436. *Genome Announcements* 3(5).e00927
13. Xie G, Chastain-Gross RP, Belanger M, Kumar D, Whitlock JA, **Liu L**, Farmerie G, Daligault HE, Han CS, Brettin TS, Progulske-Fox A. (2015) Genome sequence of porphyromonas gingivalis strain AJW4. *Genome Announcements* 3(6).e01304
14. Kumar S, **Liu L**. (2014) No positive selection for G-allele in a p53 response element in Europeans. *Cell* 157(7):1497-1499
15. Kumar S, Ye J, **Liu L** (2014) Reply to: "Proper reporting of predictor performance". *Nature Methods* 11(8):781-2
16. Gray VE, **Liu L**<sup>§</sup>, Nirankari R, Hornbeck P, Kumar S (2014) Signatures of natural selection on mutations of residues with multiple posttranslational modifications. *Molecular Biology and Evolution* 31(7):1641-5
17. Stecher G, **Liu L**, Sanderford M, Peterson D, Tamura K, Kumar S. (2014) MEGA-MD: molecular evolutionary genetics analysis software with mutational diagnosis of amino acid variation. *Bioinformatics* 30(9):1305-7
18. **Liu L**, Kumar S. (2013) Evolutionary balancing is critical for correctly forecasting disease associated amino acid variants. *Molecular Biology and Evolution* 30(6):1252-7
19. Wellensiek BP, Larsen AC, Stephens B, Kukurba K, Waern K, Briones N, **Liu L**, Snyder M, Jacobs BL, Kumar S, Chaput JC. (2013) Genome-wide profiling of human cap-independent translation-enhancing elements. *Nature Methods* 10(8):747-50
20. Yin L, Hou W, **Liu L**, Cai Y, Wallet MA, Gardner BP, Chang K, Lowe AC, Rodriguez CA, Sriaroon P, Farmerie WG, Sleasman JW, Goodenow MM (2013) IgM repertoire biodiversity is reduced in HIV-1 infection and systemic lupus erythematosus. *Frontiers in HIV and AIDS* doi:10.3389/fimmu.2013.00373
21. Kumar S, Sanderford M, Gray VE, Ye J, **Liu L** (2012) Evolutionary Diagnosis Method for Variants in Personal Exomes. *Nature Methods* 9(9):855-6
22. Dudley JT, Kim Y, **Liu L**, Markov GJ, Gerold K, Chen R, Butte AJ, Kumar S (2011) Human Genomic Disease Variants: A Neutral Evolutionary Explanation. *Genome Research* doi:10.1101/gr.133702.111
23. Kumar S, Dudley JT, Filipowski A, **Liu L** (2011) Phylomedicine: an evolutionary telescope to explore and diagnose the universe of disease mutations. *Trends in Genetics*. 27(9):377-86.
24. Yin L, **Liu L**, Sun Y, Hou W, Lowe AC, Gardner BP, Salemi M, Williams WB, Farmerie WG, Sleasman JW, Goodenow MM (2012) High-resolution deep sequencing reveals biodiversity, population structure, and persistence of HIV-1 quasispecies within host ecosystems. *Retrovirology* 9:108

25. Aggelen GV, Ankley GT, Baldwin WS, Bearden DW, Benson WH, Chipman JK, Collette TW, Craft JA, Denslow ND, Embry MR, Falciani F, George SG, Helbing CC, Hoekstra PF, Iguchi T, Kagami Y, Katsiadaki I, Kille P, **Liu L**, Lord PG, McIntyre T, O'Neill A, Osachoff H, Perkins DJ, Santos EM, Skirrow RC, Snape JR, Tyler CR, Versteeg D, Viant M, Volz DC, Williams TD, Yu L, (2010) Integrating Omic Technologies into Aquatic Ecological Risk Assessment and Environmental Monitoring: Hurdles, Achievements, and Future Outlook, *Environmental Health Perspectives*. 118(1):1-5
26. Spade DJ, Griffitt RJ, **Liu L**, Brown-Peterson NJ, Kroll KJ, Feswick a, Glazer RA, Barber DS, Denslow ND. (2010) Queen conch (*Strombus gigas*) testis regresses during the reproductive season at nearshore sites in the Florida Keys. *PloS one* 5(9):e12737
27. Paul A, **Liu L**, Laughner B, McClung S, Chen S, Ferl R. (2009) Comparative Interactomics: Analysis of Arabidopsis 14-3-3 complexes reveals highly conserved 14-3-3 interactions between humans and plants. *Journal of Proteome Research*. 8:1913-1924
28. Rosser CJ, **Liu L**, Sun Y, Villicana P, McCullers M, Porvasnik S, Young PR, Parker AS, Goodison S. (2009) Bladder cancer-associated gene expression signatures identified by profiling of exfoliated urothelia. *Cancer Epidemiology, Biomarkers and Prevention* 18(2):444-53.
29. Duan YP, Zhou LJ, Hall DG, Li WB, Doddapaneni H, Lin H, **Liu L**, Sun Y, Gabriel DW, Vahling CM, Williams K, Dickerman A, Gottwald T. (2009) Complete genome sequence of citrus huanglongbing bacterium, 'Candidatus Liberibacter asiaticus' obtained through metagenomics, *Molecular Plant-Microbe Interaction* 22(8):1011-20
30. Garcia-Reyero N, Kroll KJ, **Liu L**, Orlando EF, Watanabe KH, Sepúlveda MS, Villeneuve DL, Perkins EJ, Ankley GT, Denslow ND. (2009) Gene expression responses in male fathead minnows exposed to binary mixtures of an estrogen and antiestrogen. *BMC Genomics*. 13;10:308
31. Sun Y, Cai YP, **Liu L**, Yu F, Farrell M, McKendree W, Farmerie WG. (2009) ESPRIT: estimating species richness using large collections of 16S rRNA shotgun sequences. *Nucleic Acid Research* 37(10):e76
32. Yu F, Sun Y, **Liu L**, Farmerie WG. (2009) GSTaxClassifier: a genomic signature based taxonomic classifier for metagenomics data analysis. *Bioinformatics*. 4(1):46-49
33. Garcia-Reyero N, Adelman I, **Liu L**, Denslow N. (2008) Gene expression profiles of fathead minnows exposed to surface waters above and below a sewage treatment plant in Minnesota. *Marine Environmental Research* 66(1):134-6.
34. Garcia-Reyero N, Griffitt RJ, **Liu L**, Kroll KJ, Farmerie WG, Barber DS, Denslow ND. (2008) Construction of a robust microarray from a non-model species (largemouth bass) using pyrosequencing technology. *Journal of Fish Biology* 72(9):2354-2376
35. Sun Y, Goodison S, Li J, **Liu L**, Farmerie WG. (2007) Improved breast cancer prognosis through the combination of clinical and genetic markers. *Bioinformatics*. 23(1):30-37
36. Popp MP, **Liu L**, Timmers A, Esson DW, Shiroma L, Meyers C, Berceli S, Tao M, Wistow G, Schultz GS, Sherwood MB. (2007) Development of a Microarray Chip for Rabbit Ocular Research. *Molecular Vision*. 13:164-73
37. Luo X, Pan Q, **Liu L**, Chegini N. (2007) Genomic and proteomic profiling II: Comparative assessment of gene expression profiles in leiomyomas, keloids, and surgically-induced scars. *Reproductive Biology and Endocrinology* 5(1):35
38. Larkin P, Villeneuve DL, Knoebl I, Miracle AL, Carter BJ, **Liu L**, Denslow ND, Ankley GT. (2007) Development and validation of a 2,000-gene microarray for the fathead minnow (*Pimephales promelas*). *Environmental Toxicology and Chemistry*. 26(7):1497-506

39. Moroz LL, Edwards JR, Puthanveetil SV, Kohn A, Ha T, Heyland A, Knudsen B, Sahni A, Yu F, **Liu L**, Jezzini S, Sadreyev R, Lovell P, Iannuccilli W, Chen M, Nguyen T, Sheng H, Shaw R, Kalachikov S, Panchin Y, Farmerie WG, Russo JJ, Ju J, Kandel ER. (2006) The Neuronal Transcriptome of *Aplysia californica*: A Platform for the Neurogenomics of Defined Neurons, Neuronal Compartments and Neuronal Circuitry. *Cell*.127(7):1453-1467
40. Chao EM, **Liu L**, Farmerie WG, Keyhani NO (2006) EST analysis of cDNA libraries from the entomopathogenic fungus *Beauveria (Cordyceps) bassiana*. I. Evidence for stage-specific gene expression in aerial conidia, in vitro blastospores and submerged conidia. *Microbiology*. 152(Pt 9):2843-54.
41. Gabriel DW, Allen C, Schell M, Denny TP, Greenberg JT, Duan Y, Flores-Cruz Z, Huang Q, Clifford JM, Presting G, Gonzalez ET, Reddy J, Elphinstone J, Swanson J, Yao J, Mulholland V, **Liu L**, Farmerie WG, Patnaikuni M, Balogh B, Norman D, Alvarez A, Castillo JA, Jones J, Saddler G, Walunas T, Zhukov A, Mikhailova N (2006) Identification of open reading frames unique to a Select Agent: *Ralstonia solanacearum* race 3 biovar 2. *Molecular Plant-Microbe Interaction* 19(1):69-79
42. Farmerie WG, Hammer J, **Liu L**, Sahni A, Schneider M. (2005) Biological Workflow with BlastQuest. *Data and Knowledge Engineering*. 53(1):75-97
43. Kornberg LJ, Villaret D, Popp MP, **Liu L**, McLaren R, Brown H, and McFadden M. (2005) Gene Expression Profiling in Squamous Cell Carcinoma of the Oral Cavity Shows Abnormalities in Several Signaling Pathways. *Laryngoscope*. 115(4):690-8
44. Esson DW, Popp MP, **Liu L**, Schultz GS, Sherwood MB. (2004) Microarray analysis of the failure of filtering blebs in a rat model of glaucoma filtering surgery. *Investigative Ophthalmology and Visual Science*. 45(12):4450-62.
45. Cousins RJ, Blanchard RK, Popp MP, **Liu L**, Cao J, Moore JB and Green CL. (2003) A Global View of the Selectivity of Zinc Deprivation and Excess on Genes Expressed in Human THP-1 Mononuclear Cells. *Proceedings of the National Academy of Science* 100:6952-6957
46. Li YJ, **Liu L**, Zhang FC. (2003) The clinical significance of SSA antigen and its different positive expressions. *Zhonghua Nei Ke Za Zhi*. 42(3):165-8

#### **Conference presentations:**

- T1. Know-GRRF: domain-knowledge informed biomarker discovery with random forests. *6th International Work-conference on Bioinformatics and Biomedical Engineering*. Granada, Spain. 2018
- T2. Biological adaptability as a biomarker for risk assessment. Arizona Alzheimer's Consortium Annual Conference. Sedona, AZ, 2018
- T3. Fast fine mapping of causal eQTL variants. *International Symposium on Molecular Evolution and Medicine*, Philadelphia, PA, 2017
- T4. Evolution-informed Biomarker Discovery for Precision Oncology, *6th International Conference on Bioinformatics & Systems Biology*, Philadelphia, PA, 2016
- T5. Evolution-informed modeling. *RECOMB/ISCB Conference*, San Diego, CA, 2014
- T6. An evolutionary diagnosis method for variants in personal exomes. *Phylomedicine Symposium*, Tempe, AZ, 2012
- T7. Having A BLAST with BlastQuest: Where Do We Go From Here? *INFORMS Annual Meeting*, Denver, CO, 2004

#### **Conference proceedings:**

- C1. Guan X, **Liu L**. Know-GRRF: Domain-Knowledge Informed Biomarker Discovery with Random Forests. *6th International Work-conference on Bioinformatics and Biomedical Engineering*. Granada, Spain. 2018
- C2. Li Y, Wang J, Yang T, Chen J, **Liu L**, Zhan L, Hibar DP, Jahanshad N, Wang Y, Zhao S, Thompson PM, Ye J, (2016) Identification of Alzheimer's Disease Risk Factors by Tree-Structured Group Lasso Screening. *IEEE International Symposium on Biomedical Imaging*
- C3. Yang T, Wang J, Sun Q, Hibar DP, Jahanshad N, **Liu L**, Wang Y, Zhan L, Thompson PM, Ye J (2015) Detecting genetic risk factors for Alzheimer's disease in whole genome sequence data via lasso screening. *IEEE International Symposium on Biomedical Imaging*
- C4. Sun Y, **Liu L**, Popp M, Farmerie W. (2006) Estimation of Cross-hybridization Signals Using Support Vector Regression. *Proc. IEEE Symp. of Computations in Bioinformatics and Bioscience (SCBB'06)*
- C5. Goodison S, Popp M, Liu X, Farmerie WG, Casella G, **Liu L** (2006) A new meta-analysis method applied to prostate cancer profiles. *Proceedings of American Association of Cancer Research*, Volume 47

**Conference posters:**

- P1. Ahmadinejad N, **Liu L**. (2017) Decomposing cancer subclonal structures with model-based clustering. *International Symposium on Molecular Evolution and Medicine*, Philadelphia, PA,
- P2. Chandrasheka P, Elmas A, **Liu L**. (2017) Discover Immunosignature in Systemic Lupus Erythematosus. *Biodesign Scientific Retreat*, Scottsdale, AZ
- P3. Admadinejad N, **Liu L**. (2017) Model-base Hierarchical Clustering for Cancer Subclonal Detection. *Biodesign Scientific Retreat*, Scottsdale, AZ
- P4. **Liu L**, Zeng B, Kumar S, Gibson G. (2016) Discover eQTL with flexible LD structure and tree-guided group lasso, *Pacific Symposium on Biocomputing*, Waimea, HI
- P5. **Liu L**, Chang Y, Ye J, Kumar S. (2015) Distinct evolutionary and mutational patterns in oncogenes and tumor suppressor genes, *AACR Annual Meeting*, Philadelphia, PA