

Han Liang, Ph.D.

Barnhart Family Distinguished Professor in Targeted Therapies
Professor and Deputy Chair, Department of Bioinformatics and Computational Biology
Professor, Department of Systems Biology
The University of Texas MD Anderson Cancer Center

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EDUCATION

Ph.D. Quantitative and Computational Biology 9/2001–3/2006
Advisor: Laura F. Landweber
Department of Chemistry
Princeton University, Princeton, New Jersey, USA

B.S. Chemistry 9/1997–7/2001
Peking University, Beijing, China

POSITION

Academic Appointment

Barnhart Family Distinguished Professor in Targeted Therapies 10/2020–

Full Professor (tenured) 9/2018–
Department of Bioinformatics and Computational Biology
Department of Systems Biology (joint appointment)

Deputy Chair 1/2015–
Department of Bioinformatics and Computational Biology

Associate Professor (tenured) 12/2014–8/2018
Department of Bioinformatics and Computational Biology
Department of Systems Biology (joint appointment)

Assistant Professor 6/2009–11/2014
Department of Bioinformatics and Computational Biology
The University of Texas MD Anderson Cancer Center, Houston, TX, USA

Faculty Member 3/2011–
Graduate Program in Quantitative and Computational Biosciences (joint appointment)
Baylor College of Medicine, Houston, TX, USA

Regulator Member 9/2010–
Graduate Program in Biostatistics, Bioinformatics and Systems Biology (joint appointment)
The University of Texas Graduate School of Biomedical Sciences at Houston, TX, USA

Postdoctoral Research Scholar 5/2006–6/2009
Department of Ecology and Evolution
The University of Chicago, Chicago, IL, USA
Advisor: Wen-Hsiung Li

Other Appointments

Chair, Genomic Data Analysis Network m6A methylation AWG, **National Cancer Institute** 8/2023–
Member, **Damon Runyon Quantitative Biology Fellowship Award Committee** 8/2023–
Editorial Board Member, **Cancer Innovation** 6/2022–
Editorial Board Member, **Cancer Cell** 5/2020–
Editorial Board Member, **The Innovation Journal** 3/2020–
Editorial Board Member, **Genome Biology** 6/2019–
Inaugural contributing Faculty Member in Cancer Genetics Section, **F1000Prime** 3/2019–

Member, Executive Committee of Sherlock Lung project, National Cancer Institute , USA	9/2018-
Co-Chair, Genomic Data Commons QC Working Group, National Cancer Institute , USA	1/2017-5/2019
Senior Advisor, Biomarker Council, International Cancer Advocacy Network	9/2015-
Co-Leader, Pan-Cancer Whole Genome Project, International Cancer Genome Consortium	3/2014-2/2020
Chair, PanCanAtlas working groups, The Cancer Genome Atlas Research Network	4/2013-4/2018

HONORS, AWARDS AND FELLOWSHIPS

R. Lee Clark Prize, **MD Anderson Cancer Center** (2023)
Odyssey Fellowship Outstanding Research Publication Award, **MD Anderson Cancer Center** (2022)
Elected Fellow, **American Association for the Advancement of Science** (2020)
Barnhart Family Distinguished Professorship in Targeted Therapies, **MD Anderson Cancer Center** (2020)
Team Science Award, **American Association of Cancer Research** (2020)
Faculty Scholar Award, **MD Anderson Cancer Center** (2018)
“Wall of Science”, **MD Anderson Cancer Center** (2017, 2019, 2020, 2021, 2022, 2023)
Institutional nominee for the Blavatnik Award, **MD Anderson Cancer Center** (2016, 2020)
Signaling Breakthrough of the Year (RNA editing, Han et al. 2015), **Science Signaling** (2015)
STARS Award, **The University of Texas System** (2015)
Nomination for the Robert M. Chamberlain Distinguished Mentor Award, **MD Anderson** (2015-2019)
R. Lee Clark Fellow Award (junior faculty), **MD Anderson Cancer Center** (2014)
Uterine SPORE Career Development Award, **NIH/NCI** (2012, 2013)
Institutional nominee for Mary Kay Research Fund Competition, **MD Anderson Cancer Center** (2011)
SMBE Conference Travel Award, **Society of Molecular Biology and Evolution** (2008)
RNA Conference Travel Fellowship, **RNA Society** (2007)
Branco Weiss Fellowship Shortlist, **Society in Science**, Zürich (2006)
Association of Princeton Graduate Alumnae Travel Fellowship, **Princeton University** (2005)
Best Senior Thesis Award, **Peking University**, China (2001)
Outstanding Student Award, **Peking University**, China (2000)
Winner in China National Collegiate Scientific Entrepreneurial Project Competition (2000)
Dupont Fellowship, **Peking University**, China (1998)

GRANTS

Current

Core Director, 10%, Bioinformatics and Biostatistics Core, The University of Texas MD Anderson Cancer Center SPORE in Ovarian Cancer, NIH/NCI (funded)
PI: Anil Sood and Robert Bast (UTMDACC)

MPI, 10%, Systematic Characterization and Targeting of Neomorphic Drivers in Cancer, NIH/NCI, 9/1/2023-8/31/2028, \$1,944,000 (MDACC subaward amount, \$388,880/year)
Other PIs: Gordon Mills (contact PI, OHSU) and Ben Deneen (BCM)

Co-Investigator, **2%**, MD Anderson CLL Moonshot program, MDACC, 09/01/2023-8/31/2024
PI: Sabrina Bertilaccio (UTMDACC)

Co-Investigator, **5%**, Development of irreversible electroporation-based rational combinations to potentiate the activity of cancer immunotherapy against pancreatic ductal adenocarcinoma. NIH/NCI, 02/01/2022-3/31/2027, R01CA258540, \$2,984,165 (\$596,833/year)
PI: Chun Li (UTMDACC)

Co-Investigator, **5%**, Targeting the LIFR-LCN2 pathway to improve liver cancer therapy. NIH/NCI, 1/01/2023-12/31/2027, R01CA269140, \$2,400,655 (\$480,131/year)
PI: Li Ma (UTMDACC)

Co-Investigator, **2%**, A SIK2 Inhibitor, GRN-300 (ARN-3261), Enhances Response to Paclitaxel and PARP Inhibitors in Triple Negative Breast Cancer. American Cancer Society, 11/1/2022-10/31/2025, \$720,000 (\$240,000 per year)
PI: Robert Bast/Zhen Lu (UTMDACC)

Principal Investigator, The Cancer Proteome Atlas: an Integrated Bioinformatics Resource for Functional Cancer Proteomic Data, U24CA264128, NIH/NCI, 7/1/2022-6/30/2027, \$4,029,380 (\$818,276/year)

MPI, 10%, Mechanistic maps of adaptive responses to therapeutic stress to optimize combination therapies, U01CA253472, NIH/NCI, 4/1/2021-3/31/2026, \$979,495 (MDACC subaward amount, \$195,897/year)
Other PIs: Anil Korkut (MDACC) and Gordon Mills (contact PI, OHSU)

Principal Investigator, Characterization and modeling of m6A RNA methylation in cancer, R01CA251150, NIH/NCI, 9/1/2020-5/31/2025, \$2,765,653 (\$565,529/year)

Core Director, 10%, The University of Texas MD Anderson Cancer Center SPORE in Melanoma (Biostatistics and Bioinformatics Core), NIH/NCI, P50CA221703, 9/1/2019-5/31/2024 (\$262,794/year)
Overall PI: Michael Davis (UTMDACC)

Co-Investigator, **1%**, Cancer Center Support (CORE) Grant RPPA Functional Proteomics Core, NIH/NCI P30 CA011672, 7/1/2019-6/30/2024
PI: Yiling Lu (UTMADACC)

Training faculty, **0%**, Translational Genomics and Precision Medicine in Cancer Training Program, NIH/NCI, T32CA217789, 4/1/2018-3/31/2024
PI: Killary, Ann/Wistuba, Ignacio (UTMDACC)

Training faculty, **0%**, NLM Research Training Program in Biomedical Informatics and Data Science for Predoctoral and Postdoctoral Fellows, NIH/NCI, T15LM007093, 7/1/2022-6/30/2027
PI: Kaviraki, Lydia (Rice University)

Completed

Principal Investigator (subaward), NCE, **4%** Integrative bioinformatics and functional characterization of oncogenic driver aberrations in cancer. NIH/NCI, 9/6/2017-7/31/2023, U01CA217842, \$785,704 (\$157,141/year)
Overall PI: Gordon Mills (OHSU)

Training faculty, **0%**, Training in Precision Environmental Health Sciences (TPEHS), T32ES027801, 7/1/2018-6/30/2023
PI: Cheryl Walker (Baylor College of Medicine)

Principal Investigator (subaward), Computational Biology Training Program, CPRIT, RP170593, 12/7/2020-11/30/2022, \$67,688 (\$67,688/year), Trainee: Hu Chen
Overall PI: Montgomery Pettitt (UT Medical Branch)

Principal Investigator (contact), TCPA: an Integrated Bioinformatics Resource for Functional Cancer Proteomic Data, U24CA209851, NIH/NCI, 9/1/2016-8/31/2022, \$3,981,460 (\$796,328/year)

Principal Investigator, Retention fund, UTMDACC, 1/1/2015-12/31/2021, \$750,000 (\$150,000/year)

Principal Investigator, 2018 Faculty Scholar award, MDACC, 9/1/2018-8/31/2021, \$30,000 (\$10,000/year)

Co-Investigator, 4%, Integrated analysis of protein expression data from the Reverse Phase Protein Array (RPPA) platform, U24CA210950, NIH/NCI U24CA2019950, 9/13/2016-8/31/2021
PIs: Rehan Akbani, Gordon Mills, John Weinstein (UTMDACC)

Principal Investigator, Characterization and modeling of m6A RNA methylation in cancer, MDACC Bridge Fund, 8/1/2020-4/30/2021, \$75,000 (\$75,000/year)

Principal Investigator (subaward), Computational Biology Training Program, CPRIT, RP170593, 12/1/2019-11/30/2020, (\$67,890/year), Trainee: Mei-Ju Chen
Overall PI: Montgomery Pettitt (Medical Branch)

Co-Investigator, 5%, The Lorraine Dell Program in Bioinformatics for Personalization of Cancer Medicine, Michael and Susan Dell Foundation, 4/1/2012-10/4/2020 NCE
PI: John Weinstein (UTMDACC)

Principal Investigator, Systematic Functional Characterization of RNA Editing in Endometrial Cancer, R01CA175486, NIH/NCI, 4/22/2014-3/31/2020, \$1,660,000 (\$332,000/year)

Principal Investigator, TCPA: an Integrated Bioinformatics Resource for Functional Cancer Proteomic Data, (Integrative analysis of cancer single-cell transcriptomic and functional proteomic data 1 of 2), 3U24CA209851-02S, NIH/NCI, 9/1/2017-8/31/2019, \$160,000 (\$80,000/year)

Principal Investigator (subaward), Computational Biology Training Program, CPRIT, RP170593, 7/1/2018-6/30/2019, (\$63,191/year), Trainee: Yumeng Wang (2nd year renewed, declined)
Overall PI: Montgomery Pettitt (UT Medical Branch)

Principal Investigator (subaward), NLM Training Grant in Biomedical Informatics, T15LM007093 (Subaward No. R22031), NIH/NLM, 4/1/2018-3/31/2019, \$62,777 (\$62,777/year), Trainee: Parisa Imanirad
Overall PI: Lydia Karvraki (Rice University)

Co-Investigator, 7.5%, Bayesian Graphical Models for Integration of Omics Data, R01CA194391, NIH/NCI, 12/1/2015-8/31/2018
PI: Bani Mallick (Texas A&M University)

Principal Investigator, Science and Technology Acquisition and Retention (STARs) Award, The University of Texas System/UTMDACC, 6/1/2015-6/4/2018, \$500,000 (\$166,666/year)

Principal Investigator (subaward), NLM Training Grant in Biomedical Informatics, T15 LM007093 (Subaward No. R22621), NIH/NLM, 3/15/2016-2/28/2018, \$105,242 (\$52,621/year), Trainee: Han Chen
Overall PI: Lydia Karvraki (Rice University)

Principal Investigator, Systematic Functional Characterization of Expressed Pseudogenes in Cancer, RP140126, Cancer Prevention and Research Institute of Texas, 8/31/2014-2/28/2018, \$870,539 (\$290,180/year)

Training Faculty, 0% The Gulf Coast Consortia/Keck Center's NLM Biomedical Informatics and Computational Biology Training Grant, T15LM007093, NIH/NLM, 07/01/2012 - 06/30/2017
PI: Tony Gorry (Rice University)

MPI, Functional Consequences of RNA Editing in Human Cancer, MRP Bridge Funding For CPRIT Multiple Investigator Research Award, UTMDACC, 9/1/2015-8/31/2016, \$166,666 (\$166,666/year) (\$30,000 allocated to Liang lab)

Other PIs: Gordon Mills (UTMDACC), Patrick Hwu (UTMDACC), Kenneth Scott (Baylor College of Medicine)

Co-Investigator, 8%, Identification of non-coding RNAs to therapeutically target “undruggable” pathways in metastatic lung adenocarcinoma and squamous cell carcinoma, R35CA197452, NIH/NCI, 4/1/2016-8/31/2016
PI: Elsa Flores (UTMDACC)

Co-Investigator, 4%, Nuclear Architecture, ncRNAs and Epigenetics in Transcriptional Regulation by ER R00DK094981, NIH/NIDDK, 3/1/2014-5/31/2014 (8%), 9/1/2014-11/30/2014 (8%), 8/1/2015-8/31/2016 (4%)
PI: Chunru Lin (UTMDACC)

Co-Investigator, 5%, Integrative Pipeline for Analysis & Translational Application of TCGA Data (GDAC), U24CA143883, NIH/NCI, 3/1/2010-7/31/2016
PI: John Weinstein (UTMDACC)

Co-Investigator, Integrative Pipeline for Analysis & Translational Application of TCGA Data: The University of Texas MD Anderson TCGA Genome Data Analysis Center, U24CA143883S, NIH/NCI, 4/1/2016-7/31/2016
PI: John Weinstein (UTMDACC)

Principal Investigator, Systematic Functional Annotation of Somatic Mutations in Clinically Actionable Cancer Genes, R. Lee Clark Fellow Award, UTMDACC, 4/1/2014-3/31/2016, \$100,000 (\$50,000/year)

Principal Investigator, Start-up fund, UTMDACC, 9/1/2010-8/31/2015, \$390,000 (\$78,000/year)

Collaborator, 5%, MicroRNA regulation of metastasis, EMT and stem cells, R1004, Cancer Prevention and Research Institute of Texas, 8/1/2011-10/31/2011, 8/1/2014-1/31/2015, 8/1/2015-10/31/2015
PI: Li Ma (UTMDACC)

Principal Investigator, The Role of RNA Editing in Endometrial Turmorigenesis, Uterine SPORE Career Development Award, P50CA098258, NIH/NCI, 9/1/2012-8/31/2014, \$101,418 (\$50,709/year)

Principal Investigator, Multidimensional and Integrative Analysis of the Whole Transcriptome of Gastric Cancer, UTMDACC G.S. Hogan Gastrointestinal Cancer Research Fund, 9/1/2011-8/31/2013, \$99,804 (\$49,902/year)

Co-Investigator, 5% Advancing and Refining Ovarian Cancer Therapeutics: A proposal from the Ovarian Cancer Collaborative Group of the AMRF; Individual Project Title - Functional Genomics of Ovarian Cancer, Adelson Medical Research Foundation, 9/01/2012-8/31/2014
PI: Gordon Mills (UTMDACC)

Co-Investigator, 5%, MDACC Head&Neck SPORE, P50CA097007, NIH/NCI, 2/1/2013-7/31/2013
PI: Jeffery Myers (UTMDACC)

Statistician, 5%, Center Support Grant – Bioinformatics Shared Resource (PP-SR22), P30CA016672, NIH/NCI,
PI: Ronald DePinho (UTMDACC)

Co-Investigator, 84%, University of Maryland, Baltimore Biomarker Reference Laboratory, U24CA115091, NIH/NCI (Subcontract from University of Maryland-Baltimore), 6/1/2012-6/30/2012
PI: Sen Subrata (UTMDACC)

Co-Investigator, 15%, ARRA: Integrative Pipeline for Analysis & Translational Application of TCGA Data (GDAC) Supplement, U24CA14388302S1, NIH/NCI
PI: John Weinstein (UTMDACC)

Co-Investigator, 14%, MD Anderson Gynecologic Spore for Uterine Cancers (PP-4A), P50CA098258, NIH/NCI, 6/1/2011-8/31/2011
PI: Karen Lu (UTMDACC)

Co-Investigator, 10%, Molecular Predictors of the Mechanism of Chemotherapy Failure in Malignant Gliomas, JSMF #220020249 LAB-02486, James McDonnell Foundation, 9/1/2010-8/31/2011
PI: Daniel Cahill (UTMDACC)

PUBLICATIONS

H-index = 87, total citations >50,000 times

PI summary: 167 papers, 133 named author papers, 119 research articles, 51 corresponding-author papers:
1 Cell, 9 Cancer Cell, 1 Nature Biotechnology, 1 Nature Genetics, 1 Nature Methods, 1 Nature Metabolism, 1 Nature Aging, 1 Gastroenterology, 1 Gut, 2 Cell Systems, 6 Nature Communications, 2 Science Advances, 1 Journal of Clinical Investigation, 1 Advanced Science, 2 Genome Res, 1 Genome Biology, 3 Cancer Res, 1 Clinical Cancer Research, 1 Nucleic Acids Res, 1 JITC, 3 Cell Reports, 1 NPJ Precision Oncology, 1 PLoS Genetics, 1 JCO Cancer Clinical Informatics, 1 Oncogene, 1 Genomics, Proteomics and Bioinformatics, 1 Human Molecular Genetics, 1 Molecular & Cellular Proteomics, 1 Bioinformatics, 1 Biometrics, 1 BMC Genomics

*co-first author; #corresponding author

As a faculty member (key publications in blue)

1. Chen Z, **Liang H**, Wei P. (2023) Data-adaptive and pathway-based tests for association studies between somatic mutations and germline variations in human cancers. **Genetic Epidemiology** (in press)
2. Lin W, Luo Y, Wu J, Zhang H, Jin G, Guo C, Zhou H, **Liang H**[#], Xu X[#].(2023) Loss of ADAR1 in macrophages in combination with interferon gamma suppress tumor growth by remodeling the tumor microenvironment. **Journal for ImmunoTherapy of Cancer** (in press)
3. Luo Y, **Liang H**. (2023) Single-cell dissection of tumor microenvironmental response and resistance to cancer therapy. **Trends in Genetics** 39(10):758-772
4. Li X, Wang Y, Deng S, Zhu G, Wang C, Johnson NA, Zhang Z, Tirado CR, Xu Y, Metang LA, Gonzalez J, Mukherji A, Ye J, Yang Y, Peng W, Tang Y, Hofstad M, Xie Z, Yoon H, Chen L, Liu X, Chen S, Zhu H, Strand D, **Liang H**, Raj G, He HH, Mendell JT, Li B, Wang T, Mu P. (2023) Loss of SYNCRIP unleashes APOBEC-driven mutagenesis, tumor heterogeneity, and AR-targeted therapy resistance in prostate cancer. **Cancer Cell** 41(8): 1427-1449
5. Shen X^{*}, Gao X^{*}, Luo Y^{*}, Xu Q, Fan Y, Hong S, Huang Z, Liu X, Wang Q, Wang D, Lu L, Wu C[#], **Liang H**[#], Wang L[#]. (2023) Cxyc finger protein 1 maintains homeostasis and function of intestinal group 3 innate lymphoid cells with aging. **Nature Aging** 3(8):965-981
6. Li L^{*}, Gu Y^{*}, Zhang M^{*}, Shi X^{*}, Li Z^{*}, Xu X, Sun T, Dong Y, Xue C, Zhu X, Lv R, Jiao K, Ji X, Wang L, Zhang Y, Liang Z[#], Jin Y[#], Yin R[#], Wu M[#], **Liang H**[#]. (2023) HRD Effects on First-line Adjuvant Chemotherapy and PARPi Maintenance Therapy in Chinese Ovarian Cancer Patients. **NPJ Precision Oncology** 7(1): 51
7. Chen J^{*}, Liu K^{*}, Luo Y^{*}, Kang M, Wang J, Chen G, Qi J, Wu W, Wang B, Han Y, Shi L, Wang K, Han X, Ma X, Liu W, Ding Y, Wang L, **Liang H**[#], Wang L[#], Chen J[#]. (2023) Single-cell Profiling of Tumor Immune Microenvironment Reveals Immune Irresponsiveness in Gastric Signet-ring Cell Carcinoma. **Gastroenterology** 165(1): 88-103

8. Bao C, Chen O, Sheng H, Zhang J, Luo Y, Hayes B, **Liang H**, Liedtke W, Ji R, Abrahan SN. (2023) A Mast Cell-Thermoregulatory Neuron Circuit Axis Regulates Hypothermia in Anaphylaxis. **Science Immunity** 8(81): eadc9417
9. Luo Y, **Liang H**. (2023) Cancer Cells Employ the Most Prolific RNA Editors: A Closer Look at the Single Cell Level. (Invited Commentary) **Cancer Research** 83(3):351-353
10. Hahn AW, Menk AV, Rivadeneira DB, Augustin RC, Xu M, Li J, Wu X, Mishra AK, Gide TN, Quek C, Zang Y, Spencer CN, Menzies AM, Daniel CR, Hudgens CW, Nowicki T, Haydu LE, Khan MAW, Gopalakrishnan V, Burton EM, Malke J, Simon JM, Bernatchez C, Putluri N, Woodman SE, Vashisht Gopal YN, Guerrieri R, Fischer GM, Wang J, Wani KM, Thompson JF, Lee JE, Hwu P, Ajami N, Gershenwald JE, Long GV, Scolyer RA, Tetzlaff MT, Lazar AJ, Schadendorf D, Wargo JA, Kirkwood JM, DeBerardinis RJ, Liang H, Futreal A, Zhang J, Wilmott JS, Peng W, Davies MA, Delgoffe GM, Najjar YG, McQuade JL. (2023) Obesity Is Associated with Altered Tumor Metabolism in Metastatic Melanoma. **Clin Cancer Research** 29(1):154-164.
11. Peng X, Zhang S, Wang Y, Zhou Z, Yu Z, Zhong Z, Zhang L, Chen Z, Claret FX, Elkabets M, Wang F, Wang R[#], **Liang H**[#], Lin HW[#] Kong D[#]. (2023) Stelletin B sensitizes glioblastoma to DNA-damaging treatments by suppressing PI3K-mediated homologous recombination repair. **Advanced Science** 10(3):e2205529
12. Fujita M, Chen MM, Siwak DR, Sasagawa S, Oosawa-Tatsuguchi A, Arihiro K, Ono A, Miura R, Maejima K, Aikata H, Ueno M, Hayami S, Yamaue H, Chayama K, Lee JS, Lu Y, Mills GB, **Liang H**, Nishizuka SS, Nakagawa, H. (2022) Proteo-genomic Characterization of Virus-associated Liver Cancers Reveals Potential Subtypes and Therapeutic Targets. **Nature Communications** 13(1):6481
13. Zhou Z*, Chen MM*, Luo Y*, Mojumdar K, Peng X, Chen H, Kumar S, Akbani R, Lu Y, **Liang H**. (2022) Tumor-intrinsic SIRPA promotes sensitivity to checkpoint inhibition immunotherapy in melanoma. **Cancer Cell** 40(11): 1324-1340
14. Stur E, Bayraktar E, Molin GZ, Wu SY, Manga-la LS, Yao H, Wang Y, Ram PT, Corvigno S, Chen H, **Liang H**, Tworoger SS, Levine DA, Lutgendorf SK, Liu J, Moore K, Baggerly KA, Karlan BY, Sood AK. (2022) Molecular Analysis of Short- versus Long-Term Survivors of High-Grade Serous Ovarian Carcinoma. **Cancers** 14(17): 4198
15. Lu Z, Mao W, Yang H, Santiago-O'Farrill JM, Rask PJ, Mondal J, Chen H, Ivan C, Liu X, Liu C, Xi Y, Masuda K, Carrami EM, Chen M, Tang Y, Pang L, Lakomy DS, Calin GA, **Liang H**, Ahmed AA, Vankayalapati H, Bast RC Jr. (2022) SIK2 inhibition enhances PARP inhibitor activity synergistically in ovarian and triple-negative breast cancers. **The Journal of Clinical Investigation** 132(11): e146471
16. Peng X*, Luo Y*, Li H, Guo X, Chen H, Ji X, **Liang H**. (2022) RNA editing increases the nucleotide diversity of SARS-CoV-2 in human host cells. **PLoS Genetics** 18(3):e1010130
17. Li J, Lu H, Ng PK, Pantazi A, Ip CK, Jeong K, Amador B, Tran R, Tsang Y, Yang L, Song X, Dogruluk T, Ren X, Hadjipanayis A, Bristow CA, Lee S, Kucherlapati M, Parfenov M, Tang J, Seth S, Mahadeshwar HS, Mojumdar K, Zeng D, Zhang J, Protopopov A, Seidman JG, Creighton CJ, Lu Y, Sahni N, Shaw KR, Meric-Bernstam F, Futreal A, Chin L, Scott KL, Kucherlapati R[#], Mills GB[#], **Liang H**[#]. (2022). A functional genomic approach to actionable gene fusions for precision oncology. **Science Advances** 8(6): eabm2382
18. Luo Y, **Liang H**. (2022) Convergent usage of amino acids in human cancers as a reversed process of tissue development. **Genomics, Proteomics and Bioinformatics** 20(1): 147-162
19. Yao F, Deng Y, Zhao Y, Mei Y, Zhang Y, Liu X, Martinez C, Su X, Rosato R, Teng H, Hang Q, Yap S, Chen D, Wang Y, Chen MM, Zhang M, **Liang H**, Xie D, Chen X, Zhu H, Chang J, You JM, Sun Y, Gan B,

- Ma L. (2021) A targetable LIFR—NF-κB—LCN2 axis controls liver tumorigenesis and vulnerability to ferroptosis. **Nature Communications** 12(1):7333
20. Sun M, Wang Y, Zheng C, Wei Y, Hou J, Zhang P, He W, Lv X, Ding Y, **Liang H**, Hon CC, Chen X, Xu H, Chen Y. (2021) Systematic functional interrogation of human pseudogenes using CRISPi. **Genome Biology** 22(1):240
21. Mizuno S, Yamaguchi R, Hasegawa T, Hayashi S, Fujita M, Zhang F, Koh Y, Lee SY, Yoon SS, Shimizu E, Komura M, Fujimoto K, Nagai M, Kato M, **Liang H**, Miyano S, Zhang Z, Nakagawa H, Imoto S. (2021) Immunogenomic pan-cancer landscape reveals immune escape mechanisms and immunoediting Histories. **Scientific Reports** 111:1573
22. Lin J, Peng X, Dong K, Long J Guo X, Li H, Bai Y, , Yang X, Wang D, Lu X, Mao Y, Sang X, Ji X, Zhao H#, **Liang H**#. (2021) Genomic characterization of co-existing neoplasia and carcinoma lesions reveals distinct evolutionary paths of gallbladder cancer. **Nature Communications** 12:4753
23. Zong X, Zhang Y, Peng X, Cao D, Yu M, Wang J, Li H, Guo X, **Liang H**#, Yang J#. (2021) Analysis of the genomic landscape of yolk sac tumors reveals mechanisms of evolution and chemoresistance. **Nature Communications** 12:3579
24. **Liang H**. (2021). More reliable breast cancer risk assessment for every woman. **Cancer Cell** 39(4): 457-459 [Spotlight]
25. Mei Y, Chen MM, **Liang H**, Ma L. (2021) A four-gene signature predicts survival and anti-CTLA4 immunotherapeutic responses based on immune classification of melanoma. **Communications Biology** 4(1):383
26. Li J*, Chen H*, Wang Y*, Chen MM*, **Liang H**. (2021) Next-generation analytics for omics data. **Cancer Cell** 39(1), 3-6
27. Zhao W, Li J, Chen M, Luo Y, Ju Z, Nesser NK, Johnson-Camacho K, Boniface CT, Lawrence Y, Pande NY, Spellman PT, Davies MA, Herlyn M, Gray JW, von Euw E, Slamon DJ, Schultz A, Kumar SV, Korkut A, Akbani R, Brugge JS, Lu Y, Mills GB, **Liang H**. (2020) Large-scale characterization of drug responses of clinically relevant proteins in cancer cell lines. **Cancer Cell** 38(6):829-843
28. Chen H, **Liang H**. (2020) A high-resolution map of human enhancer RNA loci characterizes super-enhancer activities in cancer. **Cancer Cell** 38(5):701-715
29. Liang J, Wang L, Wang C, Shen J, Su B, Jeong K, Zhao W, Lu Y, Jain A, Zhou Z, **Liang H**, Sun S, Lu C, Xu Z, Yu Q, Shao S, Chen X, Gao M, Claret F, Ding Z, Chen J, Chen P, Barton M, Peng G, Mills GM, Amy Heimerberger. (2020) Verteporfin inhibits PD-L1 through autophagy and the STAT1-IRF1-TRIM28 signaling axis exerting in vivo anticancer therapeutic efficacy. **Cancer Immunology Research** 8(7): 952-965
30. Bhattacharyya R, Ha MJ, Liu Q, Akbani R, **Liang H**, Baladandayuthapani V. (2020) Personalized network modeling of the pan-cancer patient and cell line interactome. **JCO Clinical Cancer Informatics** 4:399-411
31. Chen M, Li J, Mills GB, **Liang H**. (2020) Predicting cancer cell line dependencies from the protein expression data of reverse-phase protein arrays. **JCO Clinical Cancer Informatics** 4:357-366
32. Tsang S, Wang Y, Kong K, Grzeskowiak C, Zagorodna O, Dogruluk T, Lu H, Villafane N, Bhavana VH, Moreno D, Elsea SH, **Liang H**, Mills GB, Scott KL. (2020) Differential expression of MAGE-A6 toggles autophagy to promote pancreatic cancer progression. **eLife** e48963

33. Li Z*, Gao X*, Peng X*, Chen M*, Li Z*, Wei B*, Wen X, Wei B, Dong Y, Bu Z, Wu A, Wu Q, Zhang L, Li Z, Liu Y, Jia S, Zhang L, Tang L, Shan F, Lv G, Shen L, Ji X, **Liang H**[#], Ji J[#]. (2020) Multi-omics characterization of molecular features of gastric cancer correlated with response to neoadjuvant chemotherapy. [Science Advances](#) 6(9): e4211
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- Recommended by Faculty of 1000
- As a PhD Graduate Student**
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- This review article (version 2.0) was updated in 2013
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- Highlighted in **Briefings in Bioinformatics** 7(2):198-199
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182. **Liang H**, Landweber LF, Fresco JR. (2005) Are stop codons recognized by base triplets in the large ribosomal RNA subunit? **RNA** 11(10): 1478-1484
183. **Liang H**, Landweber LF. (2005) Molecular mimicry: quantitative methods to study structural similarity between protein and RNA. **RNA** 11(8):1167-1172
184. **Liang H**, Cavalcanti AR, Landweber LF. (2005) Conservation of tandem stop codons in yeasts. **Genome Biology** 6(4): R31

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As an Undergraduate Student

186. **Liang H**, Li JJ, Li XD, Tang FL, Yuan G. (2002) Study on the Interaction between Distamycin Analogs and DNA from Herring Sperm by Fluorimetry. **Chinese Chemical letters** 13: 1001-1002

SOFTWARE DEVELOPMENT

1. **DrBioRight**, a natural language-oriented, AI-driven analytics for omic data
Website: <http://drbioright.org>
2. **TCeA**, a data portal for human enhancer RNAs in cancer
Website: <http://bioinformatics.mdanderson.org/public-software/tcea>
3. **TCMA**, A data portal for mitochondrial alterations in cancer
Website: <http://bioinformatics.mdanderson.org/public-software/tcma>
4. **FASMIC**, a data portal for experiment-based functional impacts of somatic alterations in cancer
Website: <http://bioinformatics.mdanderson.org/public-software/fasmic>
5. **TANRIC**, an integrative analytic platform for lncRNAs in cancer
Website: <http://bioinformatics.mdanderson.org/public-software/tanric>
6. **TCPA** (including MCLP and CPPA), a data portal for cancer RPPA-based functional proteomics data
Website: <http://tcpaportal.org>
7. **BM-Map**, a genomic loci mapping refiner for mapping multireads
Website: <http://bioinformatics.mdanderson.org/public-software/bm-map>
8. **SurvNet**, a web server for identifying network biomarkers that most correlate with patient survival data
Website: <http://bioinformatics.mdanderson.org/public-software/survnet>
9. **SWAKK**, a web server for detecting amino acid sites under positive selection using sliding window substitution rate analysis
Website: <http://bioinformatics.mdanderson.org/public-software/swakk>

CONFERENCE PRESENTATIONS

1. Empower The Cancer Proteome Atlas with An AI-driven Chatbot. [Oral Presentation]. 2023 ITCR Annual meeting, Chicago, IL, USA (9/12/2023)
2. Fill the gap between cancer omics data and precision cancer medicine. [invited talk] Gordon Research Conference on Cancer Genetics and Epigenetics, Lucca, Italy (5/24/2023)
3. Fill the gap between big cancer data and precision cancer medicine. [invited talk] Cell Symposium: Hallmarks of Cancer 2022. San Diego, CA, USA (11/2/2022)
4. Artificial intelligence, big data, and cancer systems. [invited talk] 18th Annual Dan L Duncan Comprehensive Cancer Center Symposium "Technology and Data Innovations for a Cure" Houston, TX, USA (9/23/2022)
5. An expanded protein expression atlas of human cancers. [Oral Presentation]. 2022 ITCR Annual meeting, Saint Louis, MO, USA (9/14/2022)

6. How Big omics data and AI help drug development? [invited talk] The 18th Society of Chinese Bioscientists in America (SCBA) International Symposium, Boston, MA, USA. (7/30/2022)
7. Big omics data and AI-driven data mining facilitate drug development. [invited talk], PhIRDA seminar series, China Pharmaceutical Innovation and Research Development Association. (5/19/2022)
8. How does AI help address the challenges of big omic data? [invited talk] Gulf Coast Consortium AI in Human Health Symposium. (5/17/2022)
9. Big genomics data and artificial intelligence: from bioinformatics tools to intellectual partners. [invited talk] Young Scholar Forum for Interdisciplinary Research of Mathematics, Computer Science, and Life Sciences. Zoom (5/14/2022)
10. Enhancer RNAs in Human Cancer [Invited Talk] Young Bioinformatics PI seminar series. Zoom (5/13/2022)
11. Fill the gap between big data and precision cancer medicine. T32 TGPM Community Forum, UT MD Anderson, Houston, TX, USA (2/9/2022)
12. Artificial intelligence, Big Data and Cancer Systems. [Invited Talk] The 10th International Workshop on Cancer Systems Biology (ISCB), Changchun, China (8/1/2021)
13. Characterization of hypoxia-associated molecular features to aid hypoxia-targeted therapy. [Invited Talk] AACR Annual Meeting 2021 (4/15/2021)
14. Cancer genomics data analysis, artificial intelligence and molecular diagnostics. [Invited Talk] Haishang Examiner Forum (10/19/2020)
15. Data mining of big cancer genomic data and artificial intelligence. [Invited Talk] Future Forum YOSIA Webinar (10/17/2020)
16. Big data mining of women's cancers. Chinese Association of Clinical Oncology Annual meeting 2020. (9/22/2020)
17. Data mining of big cancer genomic data and artificial intelligence. [Invited Talk] 2020 Young Scientist Cancer Research Symposium (9/19/2020)
18. Perspective on metabolic data analysis. [Invited Talk] BioNovoGene 2020 Metabolomics Symposium, Suzhou, China (7/23/2020)
19. DrOncoRight: A natural language-oriented, AI-driven analytics for cancer omic data. Invited Talk] AACR Annual Meeting 2020 (6/24/2020)
20. How AI helps address the challenge of big cancer genomic data? [Invited Talk], 2019 Symposia on Cancer Research (Leading Edge in Cancer Research), UT MD Anderson, Houston, TX, USA (11/22/2019)
21. Novel Insights into Immunotherapy by Deep Mining of Big Cancer Genomic Data. [Invited Talk] 2019 Future Science Prize, Precision Medicine Symposium, Beijing, China (11/15/2019)
22. How Big Cancer Omics Data can Help the Decision of Drug Development? [Invited Talk] China Trials 12, Shanghai, China (11/13/2019)
23. Big Data Mining for Precision Cancer Medicine. [Invited Talk] The West Lake Gastric Cancer Symposium, Hangzhou, China (10/25/2019)

24. At the Beginning of the End of Cancer Genomics. [Invited Talk] The International Bioinformatics Workshop (IBW) 2019, Beijing, China (8/3/2019)
25. Comprehensive Analysis of Molecular differences between Male and Female Patients. [Invited Talk] the 17th Society of Chinese Bioscientists in American (SCBA) International Symposium, Kunming, China (7/27/2019)
26. Novel Insights into Immunotherapy by Deep Mining of Big Cancer Genomic Data. [Invited Talk] The 9th International Workshop on Cancer Systems Biology, Changchun, China (6/30/2019)
27. Novel Insights into Immunotherapy by Deep Mining of Big Cancer Genomic Data. [Invited Talk] The 5th Precision Medicine and Gene Sequencing Conference, Beijing China (6/29/2019)
28. Systematic Identification of Cancer Therapeutic Liabilities through Adaptive Functional Proteomics. [Oral Presentation]. ITCR Annual meeting, Salt Lake City, UT, USA (5/30/2019)
29. The role of RNA editing in diversifying the cancer genome. [Invited Talk]. AACR Annual Meeting 2019, Atlanta, GA, USA (4/2/2019)
30. The role of RNA editing in diversifying the microRNA functions in cancer [Oral Presentation]. AACR Annual Meeting 2019, Atlanta, GA, USA (4/2/2019)
31. Novel Insights into Immunotherapy by Deep Mining of Big Cancer Genomic Data. [Post presentation] AACR Annual Meeting 2019, Atlanta, GA, USA (4/2/2019)
32. Novel Insights into Immunotherapy by Deep Mining of Big Cancer Genomic Data. [Invited Talk] BCM QCB Research Symposium, MD Anderson, Houston, TX, USA (3/28/2019)
33. The Cancer Proteome Atlas: A Comprehensive Bioinformatics Resource for Functional Cancer Proteomic Data. [Invited talk] the 8th Global RPPA Workshop, Tokyo, Japan (3/25/2019)
34. Mining of Big Cancer Genomic Data for Precision Medicine. [Invited Talk] the 3rd Summit Symposium for Precision Medicine. Jinan, Shandong, China (10/12/2018)
35. Novel Insights into Immunotherapy by Deep Mining of Big Cancer Genomic Data. [Invited Talk] Symposia on Cancer Research 2018, MD Anderson, Houston, TX, USA (10/4/2018)
36. Systematic Identification of cancer therapeutic liabilities through adaptive functional proteomics. [Contributed Talk] "Big Data and Cancer Precision Medicine", Nature Publish Group, Boston, MA, USA (10/1/2018)
37. The role of enhancers in cancer development: From evolutionary origin to immunotherapy. [poster presentation] TCGA Legacy: Multi-Omic Studies in Cancer", Cell Press, Washington, DC, USA (9/29/2018)
38. Maximize the Utility of Cancer Genomic Data. [Invited Talk] "Bioinformatics & Cancer" Symposium. Texas A&M University, College Station, TX, USA (9/21/2018)
39. The Cancer Proteome Atlas, TCPA: An Integrated Bioinformatics Resource for Functional Cancer Proteomic Data. [Contributed talk] ITCR 2018 Annual Meeting. Bethesda, MD, USA (5/24/2018)
40. Big Data Mining in Precision Cancer Medicine. [Invited Talk] 6th China-European Gynecological Endoscopy Peak Summit Symposium. Guangzhou, China (5/19/2018)

41. How to maximize the utility of the Teasbig cancer genomic data? [invited speaker] Cancer and Big Data Medicine Symposium, Georgia Institute of Technology, Atlanta, USA (4/26/2018)
42. Big Data Mining in Precision Cancer Medicine. [Invited Talk] 2018 China Gynecologic Oncology Annual Meeting, Chongqing, China (4/22/2018)
43. The Cancer Proteome Atlas, TCPA: An Integrated Bioinformatics Resource for Functional Cancer Proteomic Data. [Invited speaker] AACR Annual Meeting 2018, Chicago, IL USA (4/14/2018)
44. Systematic Characterization of A-to-I RNA Editing in Cancer Development. [Poster presentation] AACR Annual Meeting 2018, Chicago, IL USA (4/16/2018)
45. Systematic Functional Annotation of Somatic Mutations in Cancer. [Poster presentation] AACR Annual Meeting 2018, Chicago, IL USA (4/17/2018)
46. Big Cancer Genomics Data Mining for Precision Medicine. 2018 Enmore BioConference [Invited Speaker], Suzhou, China (3/9/2018)
47. How to maximize the utility of big cancer genomics data? 2nd International Conference on Genomic Medicine" (GeneMed-2018) [Keynote Speaker], Houston, Texas, USA (2/26/2018)
48. Systematic Functional Annotation of Somatic Mutations in Clinically Actionable Genes. [Invited talk] Molecular Medicine Tri-conference 2018, San Francisco, CA, USA (2/12/2018)
49. Maximize the Power of Cloud Computing for Precision Oncology. [Invited talk] Molecular Medicine Tri-conference 2018, San Francisco, CA, USA (2/12/2018)
50. Big data mining in precision cancer medicine [invited talk] International Symposium on Gastric Cancer, Hangzhou, China (11/4/2017)
51. Big data mining in precision cancer medicine [invited talk] The 2nd International Symposium of Lung and Esophageal Cancers, Shanghai, China (10/14/2017)
52. The Pan-Cancer Analysis using TCGA data. [Invited talk] The 2017 International Bioinformatics Workshop (IBW), Harbin, China (8/6/2017)
53. The Cancer Proteome Atlas, TCPA: An Integrated Bioinformatics Resource for Functional Cancer Proteomic Data. [Contributed talk] ITCR 2017 Annual Meeting. Santa Cruz, CA, USA (6/1/2017)
54. Systematic characterization of A-to-I RNA editing hotspots in microRNAs across human cancers. [Poster presentation] AACR Annual Meeting 2017, Washington DC, USA (4/3/2017)
55. Integrating multi-Omics data for clinical actions. [Invited talk] Molecular Medicine Tri-conference 2017, San Francisco, CA, USA (2/20/2017)
56. Functional Proteomics as a major approach for precision cancer medicine. [invited talk] The 2016 International Conference on Intelligent Biology and Medicine (ICIBM'16), Houston, TX, USA (12/10/2016)
57. Big data mining in precision cancer medicine [invited talk] World Precision Medicine (China) Summit, Shanghai, China (12/4/2016)
58. Big data mining in precision cancer medicine [invited talk] International Symposium on Gastric Cancer, Hangzhou, China (11/12/2016)

59. How to maximize the utility of the big cancer genomic data? [invited talk] China-US Biomedical Symposium on Oncology & Immunology, Baoding, China (10/15/2016)
60. Functional proteomics as a major approach for precision cancer medicine [contributed talk] The 7th National Conference on Bioinformatics and Systems Biology and International Workshop on Advanced Bioinformatics and Precision, Chengdu, China (10/7/2016)
61. An evolutionary origin of aging-related diseases. The Genomics of Common Diseases 2016. [poster presentation]. Baltimore, DM, USA (9/26/2016)
62. Comprehensive Characterization of the Mitochondrial Genome across Cancers. [oral presentation] The 12th ICGC Scientific Workshop, Boston, USA (9/21/2016)
63. How to maximize the utility of the big cancer genomic data? [invited talk] 2016 Precision Medicine Summit: Personalized Diagnostics and Treatment of Human Diseases, Shanghai, China (6/24/2016)
64. How to maximize the utility of the big cancer genomic data? [keynote speaker] Precision Cancer Medicine Symposium, Seoul, Korea (6/15/2016)
65. The genomic landscape and clinical relevance of A-to-I RNA editing in human cancers. [oral presentation] AACR Annual Meeting 2016, New Orleans, USA (4/18/2016)
66. Comprehensive Characterization of the Mitochondrial Genome across Cancers. [oral presentation] ICGC PCAWG F2F meeting, Barcelona, Spain (4/8/2016)
67. The genomic landscape and clinical relevance of A-to-I RNA editing in human cancers. [poster presentation] Keystone Symposium on The Cancer Genome, Banff, Canada (2/10/2016)
68. TANRIC: An Interactive Open Platform to Explore the Function of LncRNAs in Cancer. [contributed talk] TCGA Network Meeting, Bethesda, MD, USA (10/14/2015)
69. Improve Cancer Treatments by Incorporating the NGS Data of Tumor Samples. [invited talk] Next Generation Dx Summit 2015, Washington D.C., USA (8/20/2015)
70. Precision Cancer Medicine and Precision Academic Development. [invited talk] 2015 PKU Bio-Net Reunion Meeting, Boston, IL, USA (07/25//2015)
71. Maximizing the Utility of TCGA Genomic Data. [invited talk] The 2015 International Bioinformatics Workshop (IBW), Harbin, China (7/9/2015)
72. Maximizing the Utility of TCGA Genomic Data. [invited talk] The Second Worldwide Chinese Translational Biomedical Informatics Workshop (WC-TBIW2015), Harbin, China (7/4/2015)
73. Dissecting Novel Genetic Elements in Cancer. [invited talk] Tongji University Bioinformatics Workshop, Shanghai, China (7/2/2015)
74. Maximizing the Utility of TCGA Genomic Data. [invited talk] Bioinformatics and Brain Science Frontier Forum, Xi'an, China (6/29/2015)
75. Improve the prognostic estimation of cancer patients by incorporating the molecular data of tumor samples. [oral presentation] CSH-Asia Conference: Precision Cancer Biology & Medicine, Suzhou, China (5/7/2015)
76. Integrative protein-marker prognostic model for early-stage endometrioid endometrial carcinoma. [poster presentation] 2015 AACR Annual Meeting, Philadelphia, PA, USA (4/22/2015)

77. The genomic landscape and clinical relevance of A-to-I RNA editing in human cancer. [poster presentation] Gordon Research Conference on RNA Editing, Luccs, Italy (3/11/2015)
78. Maximizing the Utility of TCGA Genomic Data. [invited talk] 2015 Molecular Medicine Tri-Conference, San Francisco USA (2/18/2015)
79. Maximizing the Utility of TCGA Genomic Data. [highlighted talk] The 2014 International Conference on Intelligent Biology and Medicine (ICIBM'14), San Antonio, TX USA (12/6/2014)
80. Progress summary of PCAWG-15 working group. [invited talk] ICGC PanCancer Analysis of Whole Genomes (PCAWG) Face-to-Face meeting. Boston, USA (11/4/2014)
81. Maximizing the Utility of TCGA Genomic Data. [invited talk] China-US Biomedical Symposium on Oncology. Shijiazhuang, China (10/20/2014)
82. Improve the Prognostic Estimation of Cancer Patients by Incorporating the Molecular Data of Tumor Samples. [poster presentation] Quantitative Biology: From Genes, Cells to Networks. Cold Spring Harbor Asian Conference. Suzhou, China (10/14/2014)
83. Maximizing the Utility of TCGA Genomic Data. [invited talk] The 4th International Workshop on Cancer Systems Biology. Changchun, China (6/20/2014)
84. Maximizing the Utility of TCGA Genomic Data. [invited talk] Young Scholar Forum for Interdisciplinary Research of Mathematics, Computer Science, and Life Sciences. Beijing, China (5/25/2014)
85. Overview and Plans for the Mitochondrial Genome Working Group. [invited talk]. The 9th International Cancer Genome Consortium Scientific Workshop. Beijing, China (5/20/2014)
86. Systematic Functional Annotation of Somatic Mutations in Clinically Actionable Cancer Genes. [poster presentation] The Cancer Genome Atlas 3rd Annual Symposium, Bethesda, MD, USA (5/13/2014)
87. Dissecting the Clinical Utility of Cancer Genomic Data across Tumor Types. [poster presentation] 2014 AACR Annual Meeting, San Diego, CA, USA (4/8/2014)
88. From Complete Catalogs to "Actionable" Shortlists: Integrative Analysis of Next-generation Sequencing Data in Cancer Research. [invited talk] BIO-IT World Asia Conference, Singapore (5/30/2013)
89. eFISMIC: a Comprehensive Database of Experimental-evidence-based Functional Impact of Somatic Mutations. [poster presentation] Cancer Target Discovery and Development (CTD²) Network Annual Steering Committee Meeting, Bethesda, MD, USA (5/23/2013)
90. From Complete Catalogs to "Actionable" Shortlists: Integrative Analysis of Next-generation Sequencing Data in Cancer Research. [invited talk] Select Biosciences Next-Gen Sequencing track at our Genomics Research 2013 Conference, Boston, MA, USA (5/10/2013)
91. Pseudogene Expression Defines Biologically and Clinically Relevant Cancer Subtypes [contributed talk]; Clinical Utility of TCGA Genomic Data [contributed talk]; The Cancer Proteome Atlas [poster presentation] The Cancer Genome Atlas (TCGA) Semi-Annual Steering Committee Meeting, Seattle, WA, USA (5/1-2/2013)
92. Comparative Analysis of Somatic Copy-number Alterations across Different Human Cancer Types Reveals Two Distinct Classes of Breakpoint Hotspots. [poster presentation] The Cancer Genome Atlas 2nd Annual Symposium, Crystal City, VA, USA (11/2012)

93. Network Properties of Biomarkers in the Gene Co-expression Networks of Human Cancer. [contributed Talk] The TCGA PanCancer Workshop, Santa Cruz, CA, USA (10/2012).
94. On the Evolution of Somatic Copy-number Alteration Breakpoint Hotspots in Human Cancer. [poster presentation] International Conference on Stochastic Processes in Systems Biology, Genetics & Evolution, Houston, TX, USA (8/2012)
95. Comparative Analysis of Somatic Copy-number Alterations across Different Human Cancer Types Reveals Two Distinct Classes of Breakpoint Hotspots. [poster presentation] The Cancer Genome Atlas Semi-Annual Steering Committee Meeting, Houston, TX, USA (4/2012)
96. BM-Map: an Efficient Software Package for Accurately Allocating Multireads of RNA-sequencing Data. [contributed talk] The 2012 International Conference on Intelligent Biology and Medicine (ICIBM'12), Nashville, Tennessee, USA (4/2012)
97. A Systematical View on Key Genetic Factors Affecting Somatic Copy Number Alterations in Different Cancers. [poster presentation] AACR Annual Meeting, Chicago, IL, USA (4/2012)
98. Multilayer and Integrative Analysis of the Whole Transcriptome in Gastric Cancer. [invited talk] Cambridge Healthtech Institute Second Annual X-GEN Congress and Expo, San Diego, CA, USA. (3/2011)
99. BM-Map: Bayesian Mapping of Multireads for Next-Generation Sequencing Data. [contributed talk] Cold Spring Harbor Asia Computational Biology Meeting, Suzhou, China (10/2010)
100. Protein Interaction Network Architecture and Gene Duplication. [contributed talk] 2008 Society of Molecular Biology and Evolution conference, Barcelona, Spain (06/2008)
101. MicroRNA Regulation of Human Protein-Protein Interaction Network. [poster presentation] The 1st Annual Midwest Symposium on Computational Biology and Bioinformatics, Chicago, IL, USA (10/2007)
102. MicroRNA Regulation of Human Protein-Protein Interaction Network. [contributed talk] The Twelfth Annual Meeting of the RNA Society, Madison, WI, USA (5/2007)
103. Coordination between Regulation at the Transcriptional and Post-transcriptional Levels. [contributed talk] SWAKK: a Web Server for Detecting Positive Selection in Proteins Using a Sliding Window Substitution Rate Analysis. [poster presentation] The 2006 Society of Molecular Biology and Evolution Annual Conference, Tempe, AZ, USA (2006)
104. A Genome-wide Study of Dual Coding Regions in Human Alternatively Spliced Genes. [contributed talk] The 24th Summer Symposium in Molecular Biology, State College, PA, USA (2005)
105. Molecular Mimicry and the RNA World. [poster presentation] Are Stop Codons Recognized by Triplets in the Large Ribosomal RNA Subunit? [poster presentation] The 14th International Conference on the Origin of Life, Beijing, China (2005)
106. A Genome-wide Study of Dual Coding Regions in Human Alternatively Spliced Genes. [contributed talk] Are Stop Codons Recognized by Triplets in the Large Ribosomal RNA Subunit? [poster presentation] The Tenth Annual Meeting of the RNA Society, Banff, Alberta, Canada (2005)
107. Tandem Stop Codon Analysis in Yeasts. [contributed talk] The 2004 Society of Molecular Biology and Evolution Annual Conference, State College, PA, USA (2004)
108. Computational Tests of Molecular Mimicry between tRNA and Protein Translation Factors. [contributed talk] The Ninth Annual Meeting of the RNA Society, Madison, WI, USA (2004)

109. Computational Tests of Molecular Mimicry between tRNA and Protein Translation Factors. [contributed talk] 2003 Society of Molecular Biology and Evolution Conference, Newport Beach, CA, USA (2003)
110. Emergent Genetic Codes: Variations on a Theme. [conference abstract] The 13th International Conference on the Origin of Life, Oaxaca, Mexico (2002)

INVITED LECTURES

1. Fill the gap between cancer omics data and precision cancer medicine. [invited talk] **Peking Union Medical College Hospital**, Beijing, China (7/4/2023)
2. Fill the gap between cancer omics data and precision cancer medicine. [invited talk] **Zhejiang University 2nd Affiliated Hospital**, Hangzhou, China (6/30/2023)
3. Fill the gap between cancer omics data and precision cancer medicine. [invited talk] **Cancer Hospital of Harbin Medical University**, Harbin, Hangzhou, China (6/27/2023)
4. Artificial Intelligence, Big Data and Cancer Systems, Department of Systems Biology, **The University of Texas MD Anderson Cancer Center**, Houston, TX, USA (5/11/2023)
5. Introduction to The Cancer Proteome Atlas. Webinar for the NCI, (5/9/2023)
6. Artificial Intelligence, Big Data and Cancer Systems, the Bioscience Program Seminar, **King Abdullah University of Science and Technology (KAUST)**, Thuwal, Kingdom of Saudi Arabia (3/21/2023)
7. Trade-off effects in cancer evolution. Light of Evolution Symposium. **Chinese Society of Genetics** (3/11/2023)
8. Fill the gap between big cancer data and precision cancer medicine. Englander Institute for Precision Medicine, **Weill Cornell Medicine College**, New York City, NY, USA (2/7/2023)
9. Fill the gap between big data and precision cancer medicine. **Peking-Tsinghua University Center for Life Sciences**, Beijing, China (11/21/2022)
10. Artificial Intelligence, Big Data and Cancer Systems, CNRCS Seminar Series, Center for Nuclear Receptors and Cell Signaling, **The University of Houston**, Houston, TX USA (11/4/2022)
11. The role of enhancer RNAs in cancer. [Invited Talk] Small non-coding RNA bioinformatics club. (1/10/2022)
12. Fill the gap between big data and precision cancer medicine. CCSG/MCO Distinguished Speaker Seminar, **UT MD Anderson**, Houston, TX, USA (12/1/2021)
13. Artificial Intelligence, Big Data and Cancer Systems, **Clinical and Translational Science Institute Distinguished Speaker Series**, David Geffen School of Medicine, **UCLA**, CA, USA (5/5/2021)
14. Comprehensive assessment of computational algorithms in predicting cancer driver mutations, CTD² D-HIP webinar, Office of Cancer Genomics, **NIH/NCI** (4/8/2021)
15. Artificial Intelligence, Big Data and Cancer Systems, **Department of Computational Medicine and Bioinformatics**, School of Medicine, The University of Michigan at Ann Arbor, MI, USA (2/10/2021)
16. Artificial Intelligence, Big Data and Cancer Systems, Oncology R&D, **AstraZeneca**, Waltham, MA, USA (1/29/2021)

17. How AI helps address the challenge of big cancer genomic data? Department of Biomedical Informatics, **University of Pittsburgh**, Pittsburgh, PA, USA (1/22/2021)
18. How AI helps address the challenge of big cancer genomic data? Center for Individualized Medicine – Precision Cancer Therapeutics, tics, **Mayo Clinic**, Jacksonville, FL, USA (12/11/2020)
19. Large-scale characterization of drug responses of clinically relevant proteins in cancer cell lines. Research Town Hall, **UT MD Anderson**, Houston, TX, USA (12/4/2020)
20. How AI helps address the challenge of big cancer genomic data? [Invited Talk] , Center for Applied Bioinformatics, **St. Jude Children’s Research Hospital**, Memphis, TN, USA (10/16/2020)
21. How AI helps address the challenge of big cancer genomic data? [Invited Talk] Enjoy Science Series, **UT MD Anderson**, Houston, TX, USA (4/24/2020)
22. Novel Insights into Immunotherapy by Deep Mining of Big Cancer Genomic Data. **Institute of Zoology**, Chinese Academy of Science, Beijing, China (11/18/2019)
23. Novel Insights into Immunotherapy by Deep Mining of Big Cancer Genomic Data. Institute for Biomedical Informatics, **University of Pennsylvania**, Philadelphia, USA (11/6/2019)
24. The Cancer Proteome Atlas: A Comprehensive Bioinformatics Resource for Functional Cancer Proteomic Data. [Invited talk] NCI Webniar, (10/29/2019)
25. Novel Insights into Immunotherapy by Deep Mining of Big Cancer Genomic Data. Cancer Hospital/National Cancer Center, **Chinese Medical College**, Beijing, China (8/1/2019)
26. Novel Insights into Immunotherapy by Deep Mining of Big Cancer Genomic Data. Science of Medicine Seminar Series, **Mayo Clinic**, Scottsdale, AZ, USA (5/9/2019)
27. The role of enhancers in cancer development: From evolutionary origin to immunotherapy. 2nd affiliated hospital, **Zhejiang University**, Hangzhou, China (11/25/2018)
28. Mining of Big Cancer Genomic Data for Precision Medicine. Cancer Hospital//National Cancer Center, **Chinese Medical College**, Beijing, China (10/9/2018)
29. Maximize the Unity of Big Cancer Genomic Data. Department of Pharmacology & Chemical Biology, **Baylor College of Medicine**, Houston, TX (8/7/2018)
30. The role of A-to-I RNA editing in cancer development. Department of Molecular and Cellular Biology, **Baylor College of Medicine**, Houston, TX (11/1/2017)
31. Maximize the utility of TCGA data: Tools, Analysis and Discovery. **The University of Texas MD Anderson Cancer Center**, Department of Experimental Therapeutics, Houston, TX (9/6/2017)
32. Big data mining in precision cancer medicine. **Peking University Cancer Hospital**, Beijing, China (8/7/2017)
33. The role of RNA editing in noncoding RNAs in cancer. **The University of Texas MD Anderson Cancer Center**, Institutional Grand Rounds, Houston, TX (5/19/2017)
34. The role of A-to-I RNA editing in human cancer. Human Genetics Center, **The University of Texas Health Science Center at Houston**, Houston, TX (3/27/2017)

35. How to maximize the utility of the big cancer genomic data? College of Life Sciences, **Tsinghua University**, Beijing, China (12/8/2016)
36. An evolutionary origin of human aging-related diseases. Department of Ecology and Evolutionary Biology, **Princeton University**, Princeton, NJ, USA (12/2/2016)
37. How to maximize the utility of the big cancer genomic data? **Southern Medical University**, Guangzhou, China (11/14/2016)
38. How to maximize the utility of the big cancer genomic data? Department of Biochemistry and Molecular Biology, **The University of Texas Health Science Center at Houston**, TX, USA (10/24/2016)
39. How to maximize the utility of the big cancer genomic data? Epigenetic Translational Program, **Mayo Clinic**, Rochester, MN, USA (8/18/2016)
40. How to maximize the utility of the big cancer genomic data? **Hôpital de la Pitié-Salpêtrière**, Paris, French (7/6/2016)
41. How to maximize the utility of the big cancer genomic data? **Beijing 301 Hospital**, Beijing, China (6/23/2016)
42. How to maximize the utility of the big cancer genomic data? **Peking University School of Oncology, Beijing Cancer Hospital & Institute**, Beijing, China (6/22/2016)
43. How to maximize the utility of the big cancer genomic data? **Beijing Institute of Genomics**, Chinese Academy of Sciences, Beijing, China (6/22/2016)
44. How to maximize the utility of the big cancer genomic data? School of Life Sciences, **Peking University**, Beijing, China (6/21/2016)
45. How to maximize the utility of the big cancer genomic data? Innovative Cancer Medicine Institute, **Samsung Medical Center**, Seoul, Korea (6/16/2016)
46. The Role of RNA Editing in Cancer. Department of Cancer Biology, **The University of Texas MD Anderson Cancer Center**, Houston, TX (5/25/2016)
47. Maximizing the Utility of TCGA Data, **The University of Miami Sylvester Comprehensive Cancer Center**, Miami, FL (5/20/2016)
48. Maximizing the Utility of TCGA Data. **Computational Cancer Biology Training Program**, Rice University, Houston, TX (4/29/2016)
49. Maximizing the Utility of The Cancer Genome Atlas. Department of Computer Sciences, **The University of Southern California**, Los Angeles, CA (1/15/2016)
50. Maximizing the Utility of The Cancer Genome Atlas. Interdepartmental Bioinformatics Seminar, **UCLA**, Los Angeles, CA (1/14/2016)
51. Maximizing the Utility of TCGA Genomic Data. College of Computer Science and Engineering, **Harbin Institute of Technology**, Harbin, China (7/8/2015)
52. Maximizing the Utility of TCGA Genomic Data. State Key Laboratory of Cancer Biology, **The Fourth Military Medical University**, Xi'an, China (6/29/2015)

53. Identification of Novel Genetic Elements in Human Cancer, **Institute of Zoology**, Chinese Academy of Science, Beijing, China (5/22/2015)
54. Maximizing the Utility of TCGA Genomic Data, Department of Genetics, **The University of Texas Health Science Center**, Houston, TX, USA (3/2/2015)
55. Maximizing the Utility of TCGA Genomic Data, College of Life Sciences, **Sun Yat-sen University**, Guangzhou, China (10/23/2014)
56. Maximizing the Utility of TCGA Genomic Data, College of Life Sciences, **Tsinghua University**, Beijing, China (10/21/2014)
57. Maximizing the Utility of TCGA Genomic Data, DKFZ-MDACC workshop, **DKFZ**, Heidelberg, German (10/9/2014)
58. Maximizing the Utility of TCGA Genomic Data, **Department of Computational Medicine and Bioinformatics**, School of Medicine, The University of Michigan at Ann Arbor, MI, USA (8/19/2014)
59. Maximizing the Utility of TCGA Genomic Data, **Institute of Zoology**, Chinese Academy of Science, Beijing, China (6/18/2014)
60. Maximizing the Utility of TCGA Genomic Data, Center for Life Sciences, **Peking University**, Beijing, China (6/17/2014)
61. Maximizing the Utility of TCGA Genomic Data, **Institute of Applied Mathematics**, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China (6/11/2014)
62. Maximizing the Utility of TCGA Genomic Data, College of Life Sciences, **Tongji University**, Shanghai, China (5/28/2014)
63. Maximizing the Utility of TCGA Genomic Data, Center for Systems Biology, **Soochow University**, Suzhou, China (5/27/2014)
64. Dissecting the Clinical Utility of Cancer Genomic Data across Tumor Types, Department of Bioengineering, **University of California at San Diego**, CA, USA (4/11/2014)
65. FASMIC: A Revolutionary Tool Facilitating Clinical Decisions for Personalized Cancer Therapy, Sixth Street Showcase (Keynote speech), **The University of Texas System**, Austin, USA (3/9/2014)
66. Dissecting the Clinical Utility of Cancer Genomic Data across Tumor Types, Human Genetics Seminar, **The University of Texas Health Science Center at Houston**, TX, USA (3/3/2014)
67. Dissecting the Clinical Utility of Cancer Genomic Data across Tumor Types, Department of Systems Biology, **UT MD Anderson Cancer Center**, Houston, TX, USA (10/31/2013)
68. From Complete Catalogs to “Actionable” Shortlists: Integrative Analysis of NGS Data for Target Identification, GCC Keck Seminar Series, **Rice University**, Houston, TX, USA (3/8/2013)
69. Cancer Genomics of Gastric Cancer: Insights from TCGA, **National Cancer Center**, Korean (11/22/2012)
70. On the Evolution of Somatic Copy-Number Alteration Breakpoints in Human Cancers, Department of Ecology and Evolutionary Biology, **Rice University**, Houston, TX, USA (11/19/2012)

71. A Personal Journey in US Academia & Bioinformatics for Personalized Cancer Therapy. 2012 PKU Bio-Net Reunion Meeting, Boston, MA, USA (07/14/2012).
72. From Complete Catalogs to “Actionable” Shortlists: Integrative Analysis of NGS Data for Target Identification, Ben May Department of Cancer Research, **The University of Chicago**, Chicago, IL, USA (04/05/2012)
73. RNA-Seq Analysis in Cancer Research, Department of Internal Medicine, **The University of Iowa**, Iowa City, IA, USA (04/05/2011)
74. BM-Map: Bayesian Mapping of Multireads for Next-Generation Sequencing Data, Centre for Bioinformatics, **Peking University**, Beijing, China (10/11/2010)
75. Bioinformatics Analysis and Computational Challenges of Next-Generation Sequencing, Making Cancer History: A New Alliance with Sandia National Laboratories, **UT MD Anderson Cancer Center**, Houston, TX, USA (11/2009)
76. Job interview talk, Department of Bioinformatics and Computational Biology, **UT MD Anderson Cancer Center, Houston, TX, USA** (8/2008)
77. Job interview talk, Systems Immunology and Infectious Disease Modeling Program, **The National Institute of Allergy and Infectious Diseases**, Bethesda, MD, USA (8/2008)
78. Job interview talk, Center for RNA Molecular Biology, School of Medicine, **Case Western Reserve University**, Cleveland, OH, USA (7/2008)
79. Job interview talk, Department of Biomedical Informatics, **The Ohio State University Medical Center**, Columbus, OH, USA (6/2008)
80. Job interview talk, Program in Computational Biology, **Fred Hutchinson Cancer Research Center**, Washington, WA, USA (3/2008)
81. Job interview talk, Department of Statistics, **The University of Chicago**, IL, Chicago, USA. (3/2008)
82. Job interview talk, Lane Center for Computational Biology, **Carnegie Mellon University**, PA, USA (3/2008)
83. Job interview talk, Department of Biology, **University of Rochester**, NY, USA (2/2008)
84. Job interview talk, School of Biology, **Georgia Institute of Technology**, GA, USA (2/2008)
85. Job interview talk, Human Molecular Genetics Program, Feinberg School of Medicine, **Northwestern University**, Chicago, IL, USA (11/2007)
86. Small RNAs with a Big Impact: MicroRNA Regulation in Humans. Bioinformatics Seminar, Department of Computer Science, **University of Illinois, Urbana-Champaign**, IL, USA (10/2007)

EDUCATIONAL EXPERIENCE

Teaching

- Leading Clinical Research Faculty Learning Series, UTMDACC 5/2021
- QCB Journal Club, Baylor College of Medicine, 2/2019
- Lecturer *“Introduction to Bioinformatics”*, Division of Cancer Medicine Hematology/Oncology Fellow’s UTMDACC, 4/2018, 5/2019, 4/2020, 6/2021, 4/2022
- Lecturer in *Dragon Star Course “Translational Bioinformatics in Precision Cancer Medicine”* at **Harbin Medicinal University**, sponsored by National Science Foundation of China (7/2015)

- Co-lecturer in *Introduction to Bioinformatics* GS011143 at **University of Texas GSBS** (10/2012, 10/2013, 11/2014, 11/2015, 11/2016, 11/2017, 12/2018, 11/2019, 4/2021, 5/2022)
- Guest lecturer in *SCBMB Advanced Topics* at **Baylor College of Medicine** (9/2012, 11/2015, 11/2016, 9/2017, 3/2018, 11/2019; 8/2020, 10/2021)
- Co-lecturer in *Biostatistics* 505 at **Rice University** (3/2010, 3/2014)
- Teaching Assistant for *Molecular Evolutionary Genetics*, Department of Ecology and Evolutionary Biology, **Princeton University** (1/2005–5/2005)
- Teaching Assistant for *General Chemistry Laboratory*, Department of Chemistry, **Princeton University** (9/2003–1/2004)

Mentoring

- Junior Faculty: Han Xu (Assistant Professor Department of Epigenetics, UTMDACC, 2/2016-), Jun Li (Assistant Professor, Department of Bioinformatics and Computational Biology, 4/2018-), Zhicheng Zhou (Instructor, Department of Bioinformatics and Computational Biology 3/2021-), Han Chen (Instructor, Department of Bioinformatics and Computational Biology 11/2021)
- Visiting scholar: Yudong Li (Instructor at Zhejiang Gongshang University, 8/2011-9/2012); Lingxiang Liu (Associate Professor, Nanjing Medical University, 8/2014-8/2015); Xiaoyan Xu (Associate Professor at Chinese Medical University, 11/2014-11/2017); Chunyan Li (Assistant Professor at Beijing Institute of Genomics, 6/2016-12/2017); Ke Chen (Assistant Professor at Beijing Institute of Genomics, 6/2018-9/2019)
- Postdoctoral research Fellow: Han Leng (Ph.D., Kuming Institute of Zoology, 2/2012-8/2015, current position: Assistant Professor, Department of Molecular Biology and Biochemistry, The University of Texas Health Center at Houston); Jun Li (Ph.D., CAS-PIBS, 9/2013-); Yuan Yuan (Ph.D., Baylor College of Medicine, 1/2015-12/2015); Hussein Abbas (co-advisee with Elsa Flores, 9/2014-6/2016), Zhicheng Zhou (PhD. UT MD Anderson, 5/2015-3/2020), Xinxin Peng (PhD. Wuhan University of Technology, 8/2015-8/2018), Han Chen (NLM postdoc fellowship, PhD. Sun Yat-sen University, 3/2016-); Zhongqi Ge (Ohio State University, PhD., 7/2016-8/2018); Kamalika Mojumdar (All India Institute of Medical Sciences, PhD, 1/2017-); Mei-Ju Chen (Taiwan University, PhD., 8/2017-11/2020); Yumeng Wang (Baylor College of Medicine, PhD, 3/2018-7/2019); Ming-chu Xu (5/2018-11/2019); Wei Zhao (The University of North Carolina at Chapel Hill 2018/4-2018/10); Parisa Imanriad (2018/4-2019/2), Hu Chen (Baylor, PhD., 12/2020-12/2022); Wei Liu (HUST, PhD 2/2022-)
- Ph.D. Student: Yuan Yuan (SCBMB, Baylor College of Medicine, 9/2010-1/2015); Robyn L. Ball (Department of Statistics, Texas A&M University, 5/2011-7/2012); Jun Li (CAS-PIBS, 8/2011-9/2013); Yang Yang (UT Health Center School of Public Health, 9/2012-8/2013); Yumeng Wang (SCBMB, Baylor College of Medicine, 2/2015-3/2018); Hu Chen (SCBMB, Baylor College of Medicine, 4/2015-11/2020); Zhongyuan Chen (Department of Statistics, Rice University, 1/2016-7/2019); Yikai Luo (QCB, Baylor College of Medicine, 6/2019-); Xin Peng (Tianjin Medical University, 9/2019-2/2021), Yitao Tang (UTGSBS, 8/2020-)
- Rotation/intern Student: Howard Rosoff (Ph.D. student, UTGSBS, 3/2010-6/2010); Meng Liu (Master Student, University of Houston, 11/2010-05/2011); Kevin Farquhar (Ph.D. student UTGSBS, 6/2012-8/2012); Yumeng Wang (SCBMB, Baylor College of Medicine, 7/2012-9/2012); Aayush Raman (SCBMB, Baylor College of Medicine, 8/2013-12/2013); Hu Chen (SCBMB, Baylor College of Medicine, 10/2014-12/2014); Zhenna Xiao (Ph.D. student, UTGSBS, 1/2015-4/2015); Zhongyuan Chen (Master student, Rice University, 9/2015-12/2015); Tapsi Seth (Master Student, 9/2015-12/2015); Darlan C Minussi (PhD. Student, UTGSBS, 9/2016-12/2016); Jake S Leighton (PhD. Student, UTGSBS, 1/2017-3/2017); Weijiang Zhou (PhD. Student, QCB, Baylor College of Medicine, 3/2017-5/2017); Yipeng Gao (SCBMB, Baylor College of Medicine, 10/2017-12/2017); Yikai Luo (QCB, Baylor College of Medicine, 1/2019-3/2019); Tian Xia (QCB, Baylor College of Medicine, 10/2019-12/2019), Zian Liu (QCB, Baylor College of Medicine, 1/2020-3/2020), Yitao Tang (UT GSBS, 5/2020-8/2020), Yupei Lin (QCB, Baylor, 10/2020-12/2020); Jiajinlong Kang (UT GSBS, 9/2021-12/2021); Xiang Wang (QCB, Baylor, 10/2021-12/2021); Varshini Vakulabharanam (University of Houston, 7/2022-8/2022); Palacios, Daniel Mauricio (BCM, 1/2023-3/2023)

- Member in Advisory committee: Gang Peng (Ph.D. student, UTGSBS, 8/2011-8/2015); Han Chen (Master student, UTGSBS, 6/2012-8/2013); Kevin Farquhar (Ph.D. student, UTGSBS, 12/2012-04/2019); Guoshui Cai (Ph.D. student, UTGSBS, 9/2012-8/2013); Samir Amin (Ph.D. student, SCBMB, Baylor College of Medicine, 2/2013-12/2016); Lukas Simon (Ph.D. student, SCBMB, Baylor College of Medicine, 2/2013-3/2016); Jialu Li (Ph.D. student, UTGSBS, 1/2014-4/2017), Aaron Taylor (Ph.D. student, SCBMB, Baylor College of Medicine, 2/2014-5/2019); Tenghui Chen (Ph.D. student, UTGSBS, 3/2015-4/2016), Yang Yang (UT Health Center School of Public Health, 9/2013-11/2015), Jianfeng Xu (Ph.D. student, SCBMB, Baylor College of Medicine, 1/2017-6/2020); Dhvani Rupani (PhD. Student, UTGSBS, 10/2017-8/2022); Jake S Leighton (PhD. Student, UTGSBS, 10/2017-12/2022); Akash Mitra (Ph.D. student, UTGSBS, 10/2017-6/2021); Lang Dong (PhD Baylor, 9/2020-); Manrong Wu (PhD. student, Baylor QCB, 3/2021-), Matthew Montierth (QCB, Baylor, 6/2021-); Recep Bayraktar (PhD. Student, UTGSBS, 9/2021-); Jiajinlong Kang (UT GSBS, 9/2022-)
- Member in candidacy/qualifying exam committee/PhD thesis: Philip Boune (Ph.D student, Baylor College of Medicine, 9/2010); Guoshui Cai (Ph.D. student, UTGSBS, 2/2012); Lukas Simon (Ph.D. student, SCBMB, Baylor College of Medicine, 9-10/2012); Samir Amin (Ph.D. student, SCBMB, Baylor College of Medicine, 9/2012); Gang Peng (Ph.D. student, UTGSBS, 12/2011); Aaron Taylor (Ph.D. student, SCBMB, Baylor College of Medicine, 9/2013); Tenghui Chen (Ph.D. student, UTGSBS, 3/2015); Daniel Konecki (Ph.D. student, SCBMB, Baylor College of Medicine, 11/2015); Lillian Ashmore (Ph.D. student, SCBMB, Baylor College of Medicine, 11/2015); Kyle Chang (Ph.D. student, UTGSBS, 12/2015); Jianfeng Xu (Ph.D. student, SCBMB, Baylor College of Medicine, 11/2016); Selma Elsarrag (Ph.D. student, SCBMB, Baylor College of Medicine, 11/2017); Kenneth Eagle (Ph.D. student, SCBMB, Baylor College of Medicine, 12/2017); Jake S Leighton (PhD. Student, UTGSBS, 12/2018); Jiayang Li (Ph.D. student, QCB, Baylor College of Medicine, 11/2018); Yingyuan Hu (Ph.D. student, QCB, Baylor College of Medicine, 12/2018); Vinayak Bhandari (University of Toronto, Department of Medical Physics 6/2019); Wen Jiang (Ph.D. student, QCB, Baylor College of Medicine, 11/2019); Jiasheng Wang (Ph.D. student, QCB, Baylor College of Medicine, 12/2019); Brian Ho (Ph.D. student, QCB, Baylor College of Medicine, 12/2019); Matthew Montierth (Ph.D. student, QCB, Baylor College of Medicine, 12/2021), Swati Mohapatra (Ph.D. student, UTGSBS, 4/2022); TaeHyung Kim (University of Toronto, Department of Computer Science, 12/2022)

Trainee Honors

- Hu Chen, Travel award for the 2022 ITCR Annual Meeting, 9/2022
- Wei Liu, Travel award for the 2022 ITCR Annual Meeting, 9/2022
- Yikai Luo, the First Prize in Trainee Presentation Competition in 2022 SCBA-TX Annual Symposium, 4/2022
- Han Chen, the 2022 Odyssey Fellowship Outstanding Research Publication Awards in Cancer Research, MD Anderson, 2/2022
- Hu Chen, CPRIT Computational Biology Training Grant Postdoc Fellowship, 12/2020
- Han Chen, Lupe C. Garcia Fellowship in Cancer Research, MD Anderson, 7/2020
- Mei-Ju Chen, CPRIT Computational Biology Training Grant Postdoc Fellowship, 12/2019
- Mei-Ju Chen, Travel award for the 2019 ITCR Annual Meeting, 5/2019
- Han Chen, Maryanne Rosenstein Family Fellowship in Cancer Research, MDAnderson, 4/2019
- Yumeng Wang, CPRIT Computational Biology Training Grant Postdoc Fellowship, 7/2018 (renewed)
- Yumeng Wang, The 2018 Chinese Government Award for Outstanding Self-Financed Students Abroad, 5/2018
- Parisa Imanriad, NLM biomedical informatics postdoc fellowship, 4/2018
- Jun Li, The Ben F. Love Fellowship in Innovative Cancer Therapies, 5/2017
- Yumeng Wang, the First Prize in Trainee Presentation Competition in 2017 SCBA-TX Annual Symposium, 4/2017
- Jun Li, The Ben F. Love Fellowship in Innovative Cancer Therapies, 5/2016
- Yang Yang, The 2016 Chinese Government Award for Outstanding Self-Financed Students Abroad, 5/2016
- Han Chen, NLM biomedical informatics postdoc fellowship, 3/2016

- Leng Han, The Recruitment Award of First-Time, Tenure-Track Faculty Members from Cancer Prevention & Research Institute of Texas (CPRIT), 8/2015
- Yuan Yuan, The 2014 Chinese Government Award for Outstanding Self-Financed Students Abroad 6/2015
- Leng Han, The Ben F. Love Fellowship in Innovative Cancer Therapies, 5/2015
- Leng Han, the Second Prize in Trainee Presentation Competition in 2015 SCBA-TX Annual Symposium, 5/2015
- Yuan Yuan, the Trainee Excellence Award winner (2015 Cycle 1), UTMDCC, 3/2015
- Yuan Yuan, Best Post Award, SCBMB Annual Retreat, Baylor College of Medicine 2/2014
- Yuan Yuan, John Trentin Award in the GSBS Symposium 2012 of Baylor College of Medicine
- Jun Li, Finalist in the Poster Competition of Trainee Research Day 2012, UTMDACC, 6/2012
- Yuanxun Xu (coauthored with Han Liang), BM-Map: Bayesian Mapping of Multireads for Next-Generation Sequencing Data, the International Biometric Society's Eastern North American Region (ENAR) Distinguished Student Paper Awards for the 2011 ENAR Spring Meetings

INSTITUTIONAL SERVICE

- Internal reviewer for the Technology Review Committee 4/2010
- Chair, Departmental Postdoctoral Fellow Search Committee 10/2010-
- Reviewer for 2011 RNA Center-Laura and John Arnold Foundation Award Proposal 1/2011
- UTGSBS Award Committee, Reviewer for the City Federation of Women's Clubs Endowed Scholarship in the Biomedical Sciences, 10/2011
- Faculty Senate, 1/2011-08/2012
- Member, Departmental Faculty Search Committee 3/2013-
- Chair, External speaker seminars, 8/2013-
- Member, Department of Systems Biology, Faculty Search Committee 8/2013-
- Committee Member, Research Data Storage Planning & Governance, 10/2014
- Deputy Chair, Department of Bioinformatics and Computational Biology, 1/2015-
- Reviewer for INTEREST, UTMDACC, 4/2015, 9/2015, 6/2016, 9/2018
- Reviewer for CPRIT High-risk High rewarding LOI selection, 8/2015
- Internal start-up fund reviewer, 9/2015
- Reviewer Committee Member, Faculty Mid-term evaluation, 7/2016 (Liuqing Yang and Chunru Lin)
- Member, Institutional Bridge Fund Advisory Committee, 10/2016-
- Reviewer, the NCI R25T Postdoctoral Fellowship in Cancer Prevention, 11/2016
- Review Committee Chair, Faculty Mid-term evaluation, 5/2018 (Yiwen Chen)
- Departmental Faculty Search Committee, Chair 8/2018-
- Member, Core Facility Oversee Committee, 9/2020-12/2021
- Member, Promotion and Tenure Committee, 9/2022-8/2025
- Member, TMP T32 Curriculum Committee, 12/2022-
- Member, Data Science Faculty Recruitment Committee, 1/2023

COMMUNITY SERVICE

- Panelist, Texas-Israel Summit on Healthcare Innovation, Houston, TX USA (11/14/2022)
- Panelist, 2022 PKU Bio-Net Reunion Meeting, Dallas, TX, USA (11/5/2022).
- Session Chair, The 18th Society of Chinese Bioscientists in America (SCBA) International Symposium, Boston, MA, USA (7/30/22)
- Session Chair, Cell-NCI Symposium: beyond cancer genomics toward precision oncology, virtual, USA (10/5/2021)
- Steering Committee of NLM Biomedical Informatics Training grant, 12/2019-
- Executive Committee of QCB program, Baylor College of Medicine, 6/2018-
- QCB Qualifying Exam Chair Committee, Baylor College of Medicine, 6/2018-
- NLM Trainee Fellowship Review Committee, 5/2018

- Program committee member (both Genomics and Bioinformatics subcommittee), 2018 AACR Meeting, 4/2017
- Session Chair, China-US Biomedical Symposium on Oncology & Immunology, Baoding, China (10/15/2016)
- Moderator, the roundtable discussion “Big Data and Precision Medicine”, The G-Summit Conference, San Francisco, CA, USA (9/27/2016)
- Steering Committee, The 2016 International Conference on Intelligent Biology and Medicine (12/2016)
- Minisymposium Chair, “Epigenetic Alterations in Cancer”, AACR 2016 Annual Meeting (4/2016)
- Steering Committee, The 2015 International Conference on Intelligent Biology and Medicine (11/2015)
- Member, Faculty Search Committee, The University of Texas Health Science Center at Houston, School of Biomedical Informatics (8-9/2015)
- Session Chair, The 2015 International Bioinformatics Workshop (7/2015)
- Program Committee, Pacific Symposium Biocomputing (PSB)-Cancer Panomics Session (8/2014)
- Session Chair, The Cancer Genome Atlas 3rd Annual Symposium, Bethesda, MD, USA (5/2014)
- Leader of the Scientific Working Group of Mitochondrial Genome and HLA, the ICGC/TCGA Pan-Cancer Whole Genome Analysis Project (3/2014-)
- Chair, TCGA Pan-Cancer Clinical/Predictor Group (4/2013-)
- Session Chair, Select Biosciences Next-Gen Sequencing track at Genomics Research 2013 Conference, Boston, MA, USA (5/2013)
- Member, Program Committee, The 1st International Conference on Translational Biomedical Informatics (ICTBI 2012), Suzhou, Jiangsu, China (12/2012)
- Session Chair, The 2012 International Conference on Intelligent Biology and Medicine (ICIBM’12), The 2012 International Conference on Intelligent Biology and Medicine, Vanderbilt, TN, USA. (4/2012)
- Organizer, Bioinformatics Workshop, The 2011 PKU Bio-net Annual Conference, New York, NY (7/2011)
- Session Chair, The Cancer Genome Atlas: an Extraordinary Enterprise, Houston, TX, USA (4/2011)

PEER REVIEWER

Ad Hoc grant reviewer

Nature Science Foundation of China (5/2012)
 Cancer Research, United Kingdom (6/2012; site visit 7/2017)
 European Research Council (ERC) (2/2013)
 NIH Study Section ZRG1 1MST-U (2/2017)
 The Israel Science Foundation (3/2017, 6/2018)
 NIH study section CBSS (2/2018)
 Czech Science Foundation (7/2018)
 Japan Agency for Medical Research and Development (AMED) (6/2019; 5/2020)
 The Florida Department of Health Biomedical Research Programs (11/2019, 10/2021, 10/2022)
 NIH study section IMT U50 (6/2020)
 Pennsylvania Department of Health (7/2020)
 The Singapore Ministry of Education (11/2021)
 FWO Bio1 panel member (1/2022-12/2024)
 NCI study section CAMP (2/2022)
 NCI study section ZCA1 RPRB-L (O1) P50 (6/2022)
 Science Foundation Ireland (POI) (6/2022)
 NIH study section GRIC (10/2022)
 NIH study section ZCA1 RPRB-L (J1) S P50 (10/2022)

Editorial Broad Member

Scientific Reports (4/2015-3/2019)
 Genome Biology (6/2019-)
 The Innovation Journal (3/2020-)
 Cancer Cell (5/2020-)

Cancer Innovation (6/2022-)

Ad Hoc journal reviewer

Science; Nature; Nature Biotechnology; Nature Medicine; Nature Methods; Nature Genetics; Nature Cancer; Nature Communications; Cell; Cancer Cell; Cell Systems; Cancer Discovery; PNAS; JNCI, Trends in Genetics; Genome Research; Genome Biology; Molecular Systems Biology; Cancer Research; PLoS Genetics; PLoS Computational Biology; Nucleic Acids Research; RNA; Molecular Cancer Therapy; Bioinformatics; BMC Genomics; BMC Bioinformatics; BMC Systems Biology; Journal of Molecular Evolution; Biology Direct; Cell Research; OMICS; Gene; Wiley Interdisciplinary Reviews: Systems Biology and Medicine; International Journal of Systems and Synthetic Biology; Genome Biology and Evolution; Molecular Biology and Evolution; PLoS One; Proteins Infection, Genetics and Evolution; Cancer Prevention Research; Genome; Human Genetics; Journal of Proteome Research; Cancer Letters; Database; The American Journal of Human Genetics; Human Mutation; mAbs; Oncogene; Wiley Interdisciplinary Reviews: RNA; Oncotarget; Briefs in Bioinformatics; Oncotarget and Therapy; Trends in Cancer; Current Biology; Cell Death & Disease; National Science Review; Genomics, Bioinformatics and Proteomics; Human Genetics; Advanced Science

OTHER ACTIVITIES

- Theoretical and Computational Biophysics Summer School, **UIUC**, Illinois, USA 6/2003
- Consultant, Bone Disease Program of Texas, **Baylor College of Medicine** 2012
- Advisor, New Experimental Therapeutic Branch, **National Cancer Center of Korean** 2012-2014
- Bioinformatics Intern, **Rosetta Inpharmatics (Merck)**, Seattle, WA, USA 7/2004–9/2004
- President, Association of Chinese Students and Scholars, **Princeton University** 8/2003–6/2004
- Vice President, Chinese Association of Students and Scholars, Greater New York Area 8/2003–6/2004
- Consultant, INFOTECH Soft Inc 11/2016-12/2017
- Co-founder and Chief Scientific Advisor, Precision Scientific (Beijing) Ltd., 7/2017–
- Co-founder and Chief Scientific Advisor, Eagle Nebula Inc, Princeton, NJ 9/2017–12/2019

MEMBERSHIPS

- New York Computational Biology Society (2002-2006)
- RNA Society (2003-2009)
- Sigma Xi Society (2006-2007)
- Society of Molecular Biology and Evolution (2006-2009)
- American Association of Cancer Research (2011-present)
- International Society of Computational Biology (2012-present)
- Society of Chinese Bioscientists in American (2014-present)
- The American Association for the Advancement of Science (2016-present)