

## 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

Affiliated Member, Institute for Data Science in Oncology 11/2023–

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, GDAN m<sup>6</sup>A methylation Working Group, **National Cancer Institute**, USA 8/2023–

Member, **Damon Runyon Quantitative Biology Fellowship Award Committee** 8/2023–

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

Elected Fellow, **American Institute for Medical and Biological Engineering** (2024)  
R. Lee Clark Prize in Basic Research, **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** (2017-2024)  
Signaling Breakthrough of the Year, **Science Signaling** (2015)  
STARS Award, **The University of Texas System** (2015)  
R. Lee Clark Fellow Award for Junior Faculty, **MD Anderson Cancer Center** (2014)  
Uterine SPORE Career Development Award, **NIH/NCI** (2012, 2013)  
SMBE Conference Travel Award, **Society of Molecular Biology and Evolution** (2008)  
RNA Conference Travel Fellowship, **RNA Society** (2007)  
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 PI/PD grants

**Core Director**, The University of Texas MD Anderson Cancer Center SPORE in Ovarian Cancer (Bioinformatics and Biostatistics Core), NIH/NCI, P50CA281701, 9/19/2023-7/31/2028 (\$226,800/year)  
PI: Anil Sood and Robert Bast (UTMDACC)

**MPI**, Systematic Characterization and Targeting of Neomorphic Drivers in Cancer, NIH/NCI, U01CA281902, 9/19/2023-8/31/2028, \$1,399,680 (MDACC subaward amount, 279,936/year)  
Other PI: Gordon Mills (contact PI, OHSU) and Ben Deneen (Baylor)

**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)

## Completed PI/PD grants

Core Director, 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)

Principal Investigator (subaward), 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)

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

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, (supplementary fund), 3U24CA209851-02S, NIH/NCI, 9/1/2017-8/31/2019, \$160,000 (\$80,000/year)

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, 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)

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, The Role of RNA Editing in Endometrial Tumorigenesis, 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)

## PUBLICATIONS

Google H index = 91, total citations 59,577

Career summary: 196 papers, including 69 first or corresponding authorship research papers

PI summary: 174 papers, including 54 corresponding authorship research papers

### Top 50 Corresponding-authorship Research Papers in the last 12 years (2012-) as PI

1. Luo Y, **Liang H.** (2024) Developmental-status-aware transcriptional decomposition establishes a cell state panorama of human cancers. **Genome Medicine** 16(1): 124
2. Li J, Liu W, Mojumdar K, Kim H, Zhou Z, Ju Z, Kumar SV, Ng P, Chen, H, Davies MA, Lu Y, Akbani R, Mills GB, **Liang H.** (2024) A protein expression atlas on tissue samples and cell lines from cancer patients provides insights into tumor heterogeneity and dependencies. **Nature Cancer** 5(10):1579-1595
3. Luo Y, Xia Y, Liu D, Li X, Li H, Liu J, Zhou D, Dong Y, Li X, Qian Y, Xu C, Tao K, Li G, Pan W, Zhong Q, Liu X, Xu S, Wang Z, Liu R, Zhang W, Shan W, Fang T, Wang S, Peng Z, Jin P, Jin N, Shi S, Chen Y, Wang M, Jiao X, Luo M, Gong W, Wang Y, Yao Y, Zhao Y, Huang X, Ji X, He Z, Zhao G, Liu R, Wu M, Chen G, Hong L, the COCPO Consortium, Ma D, Fang Y, **Liang H<sup>#</sup>**, Gao G. (2024) Neoadjuvant PARPi or

chemotherapy in ovarian cancer Informs targeting effector treg cells for tumors with homologous recombination deficiency. **Cell** 187(18):4905-4925

*#lead corresponding author*

4. Lin W, Luo Y, Wu J, Zhang H, Jin G, Guo C, Zhou H, **Liang H**<sup>#</sup>, Xu X. (2023) Loss of ADAR1 in macrophages in combination with interferon gamma suppresses tumor growth by remodeling the tumor microenvironment. **Journal for ImmunoTherapy of Cancer** 11(11): e007402.  
*#co-corresponding author*
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**<sup>#</sup>, Wang L. (2023) Cxxc finger protein 1 maintains homeostasis and function of intestinal group 3 innate lymphoid cells with aging. **Nature Aging** 3(8):965-981  
*#co-corresponding author*
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**<sup>#</sup>, 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  
*#co-corresponding author*
8. 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**<sup>#</sup>, 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  
*#co-corresponding author*
9. 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
10. 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
11. 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
12. 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.
13. 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
14. Zong X, Zhang Y, Peng X, Cao D, Yu M, Wang J, Li H, Guo X, **Liang H**<sup>#</sup>, Yang J. (2021) Analysis of the genomic landscape of yolk sac tumors reveals mechanisms of evolution and chemoresistance. **Nature Communications** 12:3579  
*#co-corresponding author*

15. Li J, Chen H, Wang Y, Chen MM, **Liang H.** (2021) Next-generation analytics for omics data. **Cancer Cell** 39(1), 3-6
16. 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
17. 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
18. 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<sup>#</sup>,** Ji J. (2020) Multi-omics characterization of molecular features of gastric cancer correlated with response to neoadjuvant chemotherapy. **Science Advances** 6(9): e4211  
*#co-corresponding author*
19. 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
20. Chen H, Li J, Wang Y, Ng PK, Tsang TH, Shaw KR, Mills GB, **Liang H.** (2020) Comprehensive assessment of computational algorithms in predicting cancer driver mutations. **Genome Biology** 21 (1): 43
21. Yuan Y, Ju YS, Kim Y, Li J, Wang Y, Yoon CJ, Yang Y, Martincorena I, Creighton CJ, Weinstein JN, Xu Y, Han L, Kim H-L, Nakagawa H, Park K, Campbell PJ, **Liang H;** PCWAG Consortium. (2020) Comprehensive molecular characterization of mitochondrial genomes in human cancers. **Nature Genetics** 52(3):342-352
22. Xu X, Wang Y, Mojumdar K, Zhou Z, Jeong K, Mangala LS, Yu S, Tsang YH, Lu Y, Lopez-Berestein G, Sood AK, Mills GB, **Liang H.** (2019) A-to-I edited miRNA-379-5p inhibits cell proliferation through CD97-induced apoptosis. **The Journal of Clinical Investigation** 129(12): 5343-5356
23. Gao GF, Parker JS, Reynolds SM, Silva TC, Wang L, Zhou W, Akbani R, Bailey M, Balu S, Berman BP, Brooks D, Chen H, Cherniack AD, Demchok JA, Ding L, Felau I, Gaheen S, Gerhard DS, Heiman DI, Hernandez KM, Hoadley KA, Jayasinghe R, Kemal A, Knijnenburg TA, Laird PW, Mensah MK, Mungall AJ, Robertson G, Shen H, Tarnuzzer R, Wang Z, Wyczalkowski M, Yang L, Zenklusen JC, Zhang Z, The Genomic Data Analysis Network, **Liang H<sup>#</sup>,** Noble MS. (2019) Before and after: a comparison of legacy and harmonized TCGA data at the Genomic Data Commons. **Cell Systems** 9(1):24-34.e10  
*#co-corresponding author*
24. Chen M, Li J, Wang Y, Akbani R, Lu Y, Mills GB, **Liang H.** (2019) TCPA v3.0: An integrative platform to explore the pan-cancer analysis of functional proteomic data. **Mol & Cell Proteomics** 18(8 suppl 1):S15-S25
25. Ye Y, Hu Q, Chen H, Liang K, Yuan Y, Xiang Y, Ruan H, Zhang Z, Song A, Zhang H, Liu L, Diao L, Lou Y, Zhou B, Wang L, Zhou S, Gao J, Jonasch E, Lin SH, Xia Y, Lin C, Yang L, Mills GB, **Liang H<sup>#</sup>,** Han L. (2019) Characterization of hypoxia-associated molecular features to aid hypoxia-targeted therapy. **Nature Metabolism** 1: 431-444  
*#co-corresponding author*
26. Wang Y, Xu X, Maglic D, Dill MT, Mojumdar K, Ng P, Jeong KJ, Tsang YH, Moreno D, Bhavana VH, Peng X, Ge Z, Chen H, Li J, Chen Z, Zhang H, Han L, Du D, Creighton CJ, Mills GB, The Cancer Genome Atlas Research Network, Camargo F, **Liang H.** (2018) Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. **Cell Reports** 25(5):1304-1317

27. Zhang H, Wang Y, Li J, Chen H, He X, Zhang H, **Liang H<sup>#</sup>**, Lu J. (2018) Biosynthetic energy cost for amino acids decreases in cancer evolution. **Nature Communications** 9(1):4124  
*#co-corresponding author*
28. Chen H, Li C, Zhou Z, **Liang H.** (2018) Fast-evolving human-specific enhancers are associated with aging-related diseases. **Cell Systems** 6(5):604-611
29. Peng X, Xu X, Wang Y, Hawke D, Yu S, Han L, Zhou Z, Jeong KJ, Tsang YH, Zhang M, Lu Y, Hwu P, Scott KL, **Liang H<sup>#</sup>**, Mills GB. (2018) A-to-I RNA editing contributes to proteomic diversity in Cancer. **Cancer Cell** 33(5): 817-828  
*#lead corresponding author*
30. Chen H, Li C, Peng X, Zhou Z, Weinstein JN, The Cancer Genome Atlas Research Network, **Liang H.** (2018) A pan-cancer analysis of enhancer expression in nearly 9000 patient samples. **Cell** 173(2):386-399
31. Peng X, Chen Z, Farshidfar F, Xu X, Lorenzi PL, Wang Y, Cheng F, Tan L, Mojumdar K, Du D, Ge Z, Li J, Thomas GV, Birsoy K, Liu L, Zhang H, Zhao Z, Marchand C, Weinstein JN, The Cancer Genome Atlas Research Network, Bathe OF, **Liang H.** (2018) Molecular characterization and clinical relevance of metabolic expression subtypes in human cancers. **Cell Reports** 23(1):255-269
32. Ge Z, Leighton JS, Wang Y, Peng X, Chen Z, Chen H, Sun Y, Yao F, Li J, Zhang H, Liu J, Shriver CD, Hu H, The Cancer Genome Atlas Research Network, Piwnicka-Worms H, Ma L, **Liang H.** (2018) Integrated genomic analysis of the ubiquitin pathway across cancer types. **Cell Reports** 23(1):213-226
33. Ng P, Li J, Jeong KJ, Shao S, Chen H, Tsang YH, Sengupta S, Wang Z, Bhavana VH, Tran R, Soewito S, Minussi DC, Moreno D, Kong K, Dogruluk T, Lu H, Gao J, Tokheim C, Zhou DC, Johnson AM, Zeng J, Ip C, Ju Z, Wester M, Yu S, Li Y, Vellano C, Schultz N, Karchin R, Ding L, Lu Y, Cheung L, Chen K, Shaw KR, Meric-Bernstam F, Scott KL, Yi S, Sahni N, **Liang H<sup>#</sup>**, Mills GB. (2018) Systematic functional annotation of somatic mutations in cancer. **Cancer Cell** 33, 450-462  
*#lead corresponding author*
34. Deng J, Chen H, Zhou D, Zhang J, Chen Y, Liu Q, Ai D, Zhu H, Chu L, Ren W, Zhang X, Xia Y, Sun M, Zhang H, Li J, Peng X, Li L, Han L, Lin H, Cai X, Xiang J, Chen S, Sun Y, Zhang Y, Zhang J, Chen H, Zhang S, Zhao Y, Liu Y, **Liang H<sup>#</sup>**, Zhao K. (2017) Comparative genomic analysis of esophageal squamous cell carcinoma between Asian and Caucasian patient populations. **Nature Communications** 8(1):1533  
*#co-corresponding author*
35. Li J, Akbani R, Zhao W, Lu Y, Weinstein JN, Mills GB, **Liang H.** (2017) Explore, visualize and analyze functional cancer proteomic data using the cancer proteome atlas. **Cancer Research** 77(21): e51-54
36. Wang Y, Xu X, Yu S, Jeong KJ, Zhou Z, Han L, Tsang YH, Li J, Chen H, Mangala LS, Yuan Y, Eterovic AK, Lu Y, Sood AK, Scott KL, Mills GB, **Liang H.** (2017) Systematic characterization of A-to-I RNA editing hotspots in microRNAs across human cancers. **Genome Research** 27(7):1112-1125 (Cover story)
37. Li J, Zhao W, Akbani R, Liu W, Ju Z, Ling S, Vellano CP, Roebuck P, Yu Q, Eterovic AK, Byers LA, Davies MA, Deng W, Vashisht Gopal YN, Chen G, von Euw EM, Slamon D, Conklin D, Heymach JV, Minna JD, Myers JN, Lu Y, Mills GB, **Liang H.** (2017) Characterization of human cancer cell lines by reverse phase protein arrays. **Cancer Cell** 31(2): 225-239
38. Yuan Y, Liu L, Chen H, Wang Y, Xu Y, Mao H, Li J, Mills GB, Shu Y, Li L, **Liang H.** (2016) Comprehensive characterization of molecular differences in cancer between male and female patients. **Cancer Cell** 29 (5): 711-722

39. Chang HR, Nam S, Kook MC, Kim KT, Liu X, Yao H, Jung HR, Lemos R Jr, Seo HH, Park HS, Gim Y, Hong D, Huh I, Kim YW, Tan D, Liu CG, Powis G, Park T, **Liang H<sup>#</sup>**, Kim YH. (2016) HNF4 $\alpha$  is a therapeutic target that links AMPK to WNT signaling in early-stage gastric cancer. **Gut** 65(1):19-32  
*#co-corresponding author*
40. Han L, Diao L, Yu S, Xu X, Li J, Zhang R, Yang Y, Werner HM, Eterovic AK, Yuan Y, Li J, Nair N, Minelli R, Tsang Y, Cheung LW, Jeong KJ, Roszik J, Ju Z, Woodman SE, Lu Y, Scott KL, Li JB, Mills GB, **Liang H**. (2015) The genomic landscape and clinical relevance of A-to-I RNA editing in human cancers. **Cancer Cell** 28(5):515-528
41. Yang JY, Werner HM, Li J, Westin SN, Lu Y, Halle MK, Trovik J, Salvesen HB, Mills GB, **Liang H**. (2015) Integrative protein-based prognostic model for early-stage endometrioid endometrial cancer. **Clinical Cancer Research** 22(2): 513-523
42. Li J, Han L, Roebuck P, Diao L, Liu L, Yuan Y, Weinstein JN, **Liang H**. (2015) TANRIC: an interactive open platform to explore the function of lncRNAs in cancer. **Cancer Research** 75(18):3728-37
43. Han L, Yuan Y, Zheng S, Yang Y, Li J, Edgerton ME, Diao L, Xu Y, Verhaak RG, **Liang H**. (2014) The Pan-Cancer analysis of pseudogene expression reveals biologically and clinically relevant tumor subtypes. **Nature Communications** 5:3963
44. Yuan Y, Van Allen EM, Omberg L, Wagle N, Amin-Mansour A, Sokolov A, Byers LA, Xu Y, Hess KR, Diao L, Han L, Huang X, Lawrence MS, Weinstein JN, Stuart JM, Mills GB, Garraway LA, Margolin AA, Getz G, **Liang H**. (2014) Assessing the clinical utility of cancer genomic and proteomic data across tumor types. **Nature Biotechnology** 32(7):644-52
45. Yang Y, Han L, Yuan Y, Li J, Hei N, **Liang H**. (2014) Gene co-expression network analysis reveals common system-level properties of prognostic genes across cancer types. **Nature Communications** 5: 3231
46. Li J, Lu Y, Akbani R, Ju Z, Roebuck PL, Liu W, Yang JY, Broom BM, Verhaak RG, Kane DW, Wakefield C, Weinstein JN, Mills GB, **Liang H**. (2013) TCPA: a resource for cancer functional proteomics data. **Nature Methods** 10(11): 1046-47
47. Li Y, Zhang L, Ball RL, Liang X, Li J, Lin Z, **Liang H**. (2012) Comparative analysis of somatic copy-number alterations across different human cancer types reveals two distinct classes of breakpoint hotspots. **Human Molecular Genetics** 21(22):4957-65.
48. **Liang H**, Cheung LW, Li J, Ju Z, Yu S, Stemke-Hale K, Dogruluk T, Lu Y, Liu X, Gu C, Guo W, Scherer SE, Carter H, Westin SN, Dyer MD, Verhaak RG, Zhang F, Karchin R, Liu CG, Lu KH, Broaddus RR, Scott KL, Hennessy BT, Mills GB. (2012) Whole-exome sequencing combined with functional genomics reveals novel candidate driver cancer genes in endometrial cancer. **Genome Research** 22(11): 2120-29.
49. Li J, Roebuck P, Grünwald S, **Liang H**. (2012) SurvNet: a web server for identifying network-based biomarkers that most correlate with patient survival data. **Nucleic Acids Research** 40(W): W123-126.
50. Yuan Y, Xu Y, Xu J, Ball RL, **Liang H** (2012) Predicting the lethal phenotype of knockout mouse by integrating comprehensive genomic data. **Bioinformatics** 28(9): 1246-1252.

#### **Top 10 Research Papers as Ph.D. student or postdoctoral fellow**

1. **Liang H**, Li WH. (2009) Functional compensation by duplicated genes in mouse. **Trends in Genetics** 25(10): 441-442
2. **Liang H**, Li WH. (2009) Lowly expressed human microRNA genes evolve rapidly. **Molecular Biology and Evolution** 26(6): 1195-1198

3. **Liang H**, Lin YS, Li WH. (2008) Fast evolution of core promoters in primate genomes. **Molecular Biology and Evolution** 25(6): 1239-1244
4. **Liang H**, Li WH. (2007) MicroRNA regulation of human protein-protein interaction network. **RNA** 13(9): 1402-1408
5. **Liang H**, Li WH. (2007) Gene essentiality, duplicability and protein connectivity in human and mouse. **Trends in Genetics** 23(8): 375-378
6. **Liang H**, Landweber LF. (2007) Hypothesis: RNA editing of microRNA target sites in humans? **RNA** 13(4): 463-467
7. **Liang H**, Zhou W, Landweber LF. (2006) SWAKK: a web server for detecting positive selection in proteins using a sliding window substitution rate analysis. **Nucleic Acids Research** 34: W382-384
8. **Liang H**, Landweber LF. (2006) A genome-wide study of dual coding regions in human alternatively spliced genes. **Genome Research** 16(2): 190-196
9. **Liang H**, Landweber LF. (2005) Molecular mimicry: quantitative methods to study structural similarity between protein and RNA. **RNA** 11(8):1167-1172
10. **Liang H**, Cavalcanti AR, Landweber LF. (2005) Conservation of tandem stop codons in yeasts. **Genome Biology** 6(4): R31

### Top 10 Bioinformatics Tools

1. **DrBioRight**, a LLM-based chatbot for bioinformatic data analysis  
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. **MCLP**, a data portal for accessing, visualizing, and analyzing functional proteomics of cancer cell lines  
Website: <https://bioinformatics.mdanderson.org/public-software/mclp>
6. **TANRIC**, an integrative analytic platform for lncRNAs in cancer  
Website: <http://bioinformatics.mdanderson.org/public-software/tanric>
7. **The Cancer Proteome Atlas**, a data portal for cancer RPPA-based functional proteomics data  
Website: <http://tcpaportal.org>
8. **BM-Map**, a software package for mapping multireads of RNA-seq data  
Website: <http://bioinformatics.mdanderson.org/public-software/bm-map>
9. **SurvNet**, a webserver for identifying network biomarkers that most correlate with patient survival data  
Website: <http://bioinformatics.mdanderson.org/public-software/survnet>
10. **SWAKK**, a webserver for detecting coding positive selection using sliding window substitution rate analysis  
Website: <http://bioinformatics.mdanderson.org/public-software/swakk>



## EDUCATIONAL EXPERIENCE

### Teaching

- Leading Clinical Research Faculty Learning Series, **MD Anderson Cancer Center** 2021- present
- QCB Journal Club, Baylor College of Medicine, 2019- present
- Lecturer "Introduction to Bioinformatics", Division of Cancer Medicine Hematology/Oncology Fellow's UTMDACC, 2018- present
- 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 the **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** (2012-2021)
- 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 Medicinal 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 (PhD, Kuming Institute of Zoology, 2/2012-8/2015, current position: Associate Professor, Texas A&M University); Jun Li (PhD, CAS-PIBS, 9/2013-); Yuan Yuan (PhD, 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 (PhD, Ohio State University, 7/2016-8/2018); Kamalika Mojumdar (PhD, All India Institute of Medical Sciences, 1/2017-); Mei-Ju Chen (PhD, Taiwan University, 8/2017-11/2020); Yumeng Wang (PhD, Baylor College of Medicine, 3/2018-7/2019); Ming-chu Xu (PhD, Baylor College of Medicine, 5/2018-11/2019); Wei Zhao (PhD, The University of North Carolina at Chapel Hill, PhD, 2018/4-2018/10); Parisa Imanriad (2018/4-2019/2), Hu Chen (PhD, Baylor College of Medicine, 12/2020-12/2022); Wei Liu (PhD, Huazhong University of Science and Technology, 2/2022-); Zhenzhen (Shanghai JiaoTong University, PhD, 10/2023-)
- 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-); Liudeng Zhang (BCM, 3/2024-); Yining Zhao (BCM, 3/2024-)

## 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, 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, 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)
- Organizer, Research Town Hall on Computational Biology, 5/2024
- Review Committee Chair, Faculty Mid-term evaluation, 7/2024 (Ying-Nai Wang)

## PEER REVIEW EXPERIENCE

### 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

### 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)

DOD Congressionally Directed Medical Research Programs (CDMRP) PRCRP (10/2023)

NIEHS Epigenetics and Stem Cell Laboratory Board of Scientific Counselors Review (12/2023)

Damon Runyon Quantitative Biology Fellowship (2/2023, 2/2024)

La Caixa Foundation (2/2023, 2/2024)

NIH study section DP2 (12/2023)

NIH study section F09A (3/2024)

## OTHER ACTIVITIES

- Theoretical and Computational Biophysics Summer School, **UIUC**, Illinois, USA 6/2003
- 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, 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
- 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,USA, 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)
- American Institute for Medical and Biological Engineering (2024-present)