Curriculum vitae

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Education

Year	Degree (Honors)	Field of Study (Thesis advisor for PhDs)	Institution
2007 - 2011	B.S.	Life Sciences	Peking University
2011-2015	Ph.D.	Biostatistics and Bioinformatics & Integrative Biology (Dr. Yang Xie)	UT Southwestern Medical Center
2012-2015	M.S.	Statistics	UT Dallas

Honors and Awards

Year	Name of Honor/Award	Awarding Organization
2014	Co-Best Performance team for sub-challenge 1	BROAD-DREAM Gene Essentiality Prediction Challenge
2013	Best Performance team for both sub-challenges	NIEHS-NCATS-UNC DREAM Toxicogenetics Challenge
2012	Best Performance team for predicting the synergistic effect of drug combinations	NCI-DREAM Drug Sensitivity Prediction Challenge

Faculty Academic Appointments

Year(s)	Academic Title	Department	Academic Institution
2015-2017	Assistant Professor (research track)	Clinical Sciences	UT Southwestern Medical Center
2015-2017	Assistant Professor (research track)	Center for the Genetics of Host Defense	UT Southwestern Medical Center
2017-Present	Assistant Professor (tenure track)	Population and Data Sciences	UT Southwestern Medical Center

2017-Present	Assistant Professor (tenure track)	Center for the Genetics of Host Defense	UT Southwestern Medical Center

Committee Service (*Member, unless noted otherwise)*

Year(s)	Name of Committee	Institution/Organization
UTSW		
2017-	Biomedical Engineering graduate program	UT Southwestern Medical Center
2019	Cancer Center Biostatistics Faculty Search Committee	UT Southwestern Medical Center
2019-	UTSW PhD Admissions Committee	UT Southwestern Medical Center
2019-Present	UTSW Simmons Cancer Center Biostatistics Core Internal Advisory Committee	UT Southwestern Medical Center
2019-2020	UTSW Computational and Systems Works-In-Progress & Journal Club organization committee	UT Southwestern Medical Center
2020-	Immunology graduate program	UT Southwestern Medical Center

Professional Societies

Dates	Society Name
2016-Present	American Statistical Association
2021-Present	American Association for Cancer Research

Grant Review Activities

Year(s)	Name of Review Committee	Organization
2021	ZCA1 RTRB-U (O2) R	NIH R03/R21
2021	ASPIRE PHASE II	Mark Foundation for Cancer Research
2021	Translational Pilot Funding Program	UTSW SCCC
2022	ZRG1 IMST-M (70) R	NIH U54

Editorial Activities

Year(s)	Journal Name
Ad Hoc Reviewer	
2016	PLOS ONE, Genome Biology, Statistics in Biopharmaceutical Research, Journal of Applied Statistics, Biostatistics, Nucleic Acids Research, Clinical Epigenetics, Fermentation, Electronic Journal of Statistics, Biometrical Journal, Contemporary Clinical Trials Communications, Quantitative Biology, FEBS Open Bio, Contemporary Clinical Trials, Biometrics & Biostatistics International Journal
2017	Nature Communications

2020	Patterns
2021	Science Immunology, Nature Methods, Nature Communications, Genome Biology
2022	Clinical Cancer Research, iScience, Genome Biology, Aging, Nature Communications, Nature Medicine, Nature Computational Science, Nature Biotechnology, Science Advances
2023	Nature Communications, Nature Machine Intelligence, Nucleic Acids Research

Grant Support

Present	**Grantor: NIAID 1U01AI156189-01**
	Title of Project: Finding the optimal balance of immunotherapy efficacy and toxicity
	Role: co-Investigator
	Goal: The major goal of this project is to determine the optimal balance between ICI efficacy and toxicity, ultimately identifying a set of biomarkers useful for selection of patients, treatment type and duration, and clinical monitoring
	Annual amount and date: $ 352,787, 6/1/2020 – 5/31/2025
	Grantor: NCI 1R01CA258584-01
	Title of Project: Applying deep learning to predict T cell receptor binding specificity of neoantigens and response to checkpoint inhibitors
	Role: PI
	Goal: This grant application seeks to apply advanced deep learning methods to predict T cell receptor binding specificity towards neoantigens, and use that prediction model as a building block to predict response to checkpoint inhibitors in cancer patients
	Annual amount and date: $253,991, 05/01/2021 – 04/30/2025
	Grantor: NCI 2P50CA070907-21A1
	Title of Project: UTSW SPORE in Lung Cancer, Data Analytics Core
	Role: co-Investigator
	Goal: The core will provide bioinformatics, biostatistics and database support for all SPORE projects and other cores.
	Annual amount and date: $194,159, 09/01/2020 – 08/30/2025
	Grantor: NIAID 1U01AI156189-01 Administrative Supplement
	Title of Project: Interpreting the TCR repertoire of lung cancers after immunotherapy treatment
	Role: PI
	Goal: To use our recently published Tessa tool to understand the functional relevance of the TCR repertoire for determining immunotherapy response, in lung cancer patients under immunotherapy treatment
	Annual amount and date: $250,000 in 03/01/2021-02/28/2022, NCE to 04/30/23
	Grantor: CPRIT RP190208
	Title of Project: Dissecting cellular heterogeneity of bulk tumors for prediction of overall survival and responsive patients to immunotherapy

	Role: PI
	Goal: To develop advanced statistical methodologies for analysis of RNA-sequencing data to deconvolute the various cell types in the tumor microenvironment of kidney cancers
	Annual amount and date: $300,000, 09/01/19-08/31/22, NCE to 08/31/23
	Grantor: 1R01CA251928-01
	Title of project: Improving hepatocellular carcinoma mouse modeling by understanding the malignant potential and biology of liver cell subpopulations
	Role: Co-I
	Goal: This grant aims to develop more faithful liver cancer models by using a new panel of CreER mouse strains.
	Annual amount and date: $325,484, 06/01/2020 - 05/31/2025
	Grantor: NIH/National Institute of Biomedical Imaging, 1R01GM140012-01
	Title of project: Developing computational algorithms for histopathological image analysis
	Role: Co-I
	Goal: To develop computational tools in order to facilitate pathology image analysis for different types of diseases.
	Annual amount and date: $250,000, 01/01/2021 – 12/31/2024
	Grantor: Southern Methodist University Dean's Research Council
	Title of project: Advanced statistical methodologies for analysis of single cell proteomics (CyTOF) data
	Role: MPI
	Goal: To develop advanced statistical methodologies for analysis of single cell proteomics (CyTOF) data
	Annual amount and date: $26,575, 04/01/2022 – 03/31/2023

Past	**Grantor: Center for Translational Medicine Pilot Grant**
	Title of Project: Building a longitudinal prognostic model to predict overall survival for patients with kidney cancer in real time
	Role: PI
	Annual amount and date: $5,000, 02/01/2017-04/01/2017
	Grantor: Kidney Cancer Coalition research award
	Title of Project: Dissect the cellular heterogeneity observed in bulk kidney cancer RNA Seq data by advanced statistical methods
	Role: PI
	Annual amount and date: $20,000, 10/01/2017-10/01/2018
	Grantor: NIH R03
	Title of Project: Development of integrative models for early liver toxicity assessment
	Role: PI
	Annual amount and date:$50,000 in 09/01/2017-08/31/2018

	Total amount of award (if multi-year) and dates:$100,000, 09/01/2015-08/31/2018
	Grantor: NIH R01
	Title of Project: Integrative Analysis to Identify Therapeutic Targets for Lung Cancer
	Role: Co-Investigator
	Annual amount and date: $207,500 in 09/01/2017-08/31/2018
	Total amount of award (if multi-year) and dates: $1,031,275, 09/26/2013-08/31/2018
	Grantor: Kidney Cancer SPORE Developmental Research Program
	Title of Project: Mining tumor neoantigens for predicting response to immunotherapies in kidney cancer
	Role: PI
	Annual amount and date: $25,000, 09/01/18-08/31/19
	Grantor: UTSW Lung cancer SPORE Developmental Research Program
	Title of Project: Mining tumor neoantigens for predicting response to immunotherapies in lung cancer
	Role: PI
	Annual amount and date: $25,000 in 01/01/2019-12/31/2019
	Grantor: NIH 3P50CA070907-20S1
	Title of Project: UTSW Lung cancer SPORE Administrative Supplement
	Role: co-Investigator
	Annual amount and date: $48,995 in 09/01/2019 – 08/31/2020
	Grantor: CPRIT RP180192
	Title of Project: Dissecting the interplay between BAP1 and PBRM1 in renal cancer
	Role: Co-PI
	Annual amount and date:$284,251 in 03/01/2018-02/28/2021
	Grantor: UT Southwestern Cancer Center
	Title of project: Leveraging a Novel Glucocorticoid Receptor Antagonist as Precision Therapy Against Lethal CHD1-def Metastatic Prostate Cancer
	Role: Co-I
	Goal: Develop novel therapeutic approaches based on heterozygous and homozygous depletions of the chromodomain helicase DNA-binding protein 1, for metastatic castration resistant prostate cancer.
	Annual amount and date: $10,000, 2/1/21-1/31/22
	Grantor: Jeanne Shelby Fund for Cancer Research
	Title of project: Enhancing precision cancer care: liquid biopsies as early markers of response in pancreatic cancers
	Role: Co-PI
	Goal: Determine whether clonal outgrowth of drug-resistant cancer cells inferred from ctDNA analyses is predictive of pathologic response and long-term benefit to treatment
	Annual amount and date: $10,000, 04/01/21-03/31/22
	Grantor: UT Southwestern Cancer Center

	Title of project: Leveraging a Novel Glucocorticoid Receptor Antagonist as Precision Therapy Against Lethal CHD1-def Metastatic Prostate Cancer
	Role: Co-I
	Goal: Develop novel therapeutic approaches based on heterozygous and homozygous depletions of the chromodomain helicase DNA-binding protein 1, for metastatic castration resistant prostate cancer.
	Annual amount and date: $10,000, 2/1/21-1/31/22

Teaching Activities

Year(s)	Activity
Medical and graduate school didactic and small group teaching	
2016-2019	Advanced Data Analysis and Statistical Learning, course instructor (~15 students/post-docs)
2020-Present	Advanced Data Analysis and Statistical Learning, course leader (~15 students/post-docs). Renamed as "Machine Learning".
2022-	scRNA-seq Genomics Nanocourse, course leader (~40 students/post-docs/faculty members)
2018	Artificial Intelligence in medicine, course instructor (~15 students/post-docs)
Graduate and Medical Student Trainees	
2017-2021	PhD: Ze Zhang (UTSW BME program, thesis: single cell sequencing analytical approaches to understanding tumor immunology)
2018-2021	PhD: Tianshi Lu (UTSW BME program, thesis: Modeling of tumor neoantigens for predicting patient outcome)
2019-Present	PhD: James Zhu (UTSW Cancer program, thesis: joint modeling of neoantigen and microbiome data)
2021-Present	PhD: Yuqiu Yang (UTSW/SMU Joint Biostatistics Program, thesis: novel methodology development for CyTOF data analysis)
2022-Present	PhD: Noah Chang (UTSW BME/CB program, thesis: to be determined)
Postdoctoral trainees	
2021-Present	Bing Song, Ph.D.
2022-Present	Yi Han, Ph.D.
PhD Thesis Committee	
2019-2020	PhD Committee for Debapriya Sinha (BME)
2020-2022	PhD Committee for Xinyi Zhang (BME)
2020-	PhD Committee for Zhuyu Wen (BME)
2019-2021	PhD Committee for Danyi Xiong (Bio-statistics)
2022-	PhD Committee for Yun Zhang (BME)

Invited Lectures

Year(s)	Title	Location

International		
2013	Estimating population-scale toxicities for environmental chemicals (Host: Dr. Gustavo Stolovitzky)	RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges, Toronto, Canada
2018	Multi-faceted modeling approaches to characterize tumor immunity (Host: Dr. Qinghua Zhou)	Huaxi Hospital, Sichuang China
2018	Multi-faceted modeling approaches to characterize tumor immunity (Host: Dr. Zhiming Luo)	Southwestern University, Chongqing, China
2018	Multi-faceted modeling approaches to characterize tumor immunity (Host: Dr. Jian Chen)	Suzhou University, Jiangsu, China
2018	Three-component dissection of tumor cellular heterogeneity by a Bayesian Hierarchical Model (Host: Dr. Jia Hua)	Joint Statistical Meetings, Vancouver, Canada
2019	Neoantigen clonal balance predicts immunotherapy outcomes and prognosis (Host: Dr. Jun Chen)	Tianjin Medical University General Hospital, Tianjin, China
2020	SClineager: A Bayesian Hierarchical Model to Perform Single Cell Lineage Tracing Based on Genetic Variants (Host: Qiongshi Lu)	2020 Joint Statistical Meetings (Virtual)
2022	Deep learning-based prediction of the T cell receptor-antigen binding specificity (Host: Victor Greiff)	iReceptor Plus (Virtual)
2022	De-noising Spatial Expression Profiling Data Based on in situ Position and Image Information (Host: Mi Deng)	Beijing Cancer Hospital
National		
2018	SCINA: Semi-Supervised Analysis of Single Cells in silico (Host: Dr. Jeremy Taylor)	University of Michigan School of Public Health Biostatistics Department, Michigan, USA
2020	TESSA, an Integrated Model for Mapping the Functional Landscape of TCR Repertoire by Single T cell Gene Expression (Host: Yi Xing)	NCI IOTN Bioinformatics and Computational Biology Working Group Meeting (Virtual)
2021	Deep learning-based prediction of the T cell receptor-antigen binding specificity (Host: Yi Xing)	NCI IOTN Bioinformatics and Computational Biology Working Group Meeting (Virtual)
2022	De-noising Spatial Expression Profiling Data Based on in situ Position and Image Information (Host: Moshe Sade-Feldman)	Drug Resistance and Sensitivity Network (DRSN) (Virtual)
Regional/Local		
2018	Three-component dissection of tumor cellular heterogeneity by a Bayesian Hierarchical Model (Host: Dr. Daniel Heitjan)	Southern Methodist University, Dallas, TX

2018	Investment Opportunities in Cancer Immunogenomics (Host: Dr. Ejun Huang)	MyBioGate, Inc., Houston, TX
2021	Deep learning-based prediction of the T cell receptor-antigen binding specificity (Host: Alexandre Reuben)	University of Texas MD Anderson Cancer Center
2022	Deep learning-based prediction of the T cell receptor-antigen binding specificity (Host: Zhongming Zhao)	UT Health, School of Biomedical Informatics
2022	Deep learning-based prediction of the T cell receptor-antigen binding specificity (Host: Peng Jiang)	NCI/NIH CDSL (Virtual)
2022	Deep learning-based prediction of the T cell receptor-antigen binding specificity (Host: Tangsheng Yi)	Gilead, Inc
2022	De-noising Spatial Expression Profiling Data Based on in situ Position and Image Information (Host: Qiwei Li)	UT Dallas

Technological and Other Scientific Innovations

Innovation
United States Letters Patent, Serial No. 62/904,268. *“HIF-2 Complex Dissociation, Target Inhibition, and Acquired Resistance with First-in-Class HIF-2 Inhibitor in Patients”*
UTSD 3738. *“pMTnet: A Deep Learning*-*based Tool for Predicting the T Cell Receptor Binding Specificity of Neoantigens”*
UTSD 3941 *“Systems And Methods To Identify Mutation And Phenotype Association”*

Service to the Community

Year(s)	Role	Organization or institution
2022	Lead organizer	2022 PKU Bio-Net Symposium in Dallas

Bibliography

Peer-Reviewed Publications

Original Research Articles

1.	**Wang T**, Xie Y, Xiao G. dCLIP: a computational approach for comparative CLIP-seq analyses. Genome biology. 2014; 15(1):R11. PubMed [journal] PMID: 24398258, PMCID: PMC4054096. (First author, pre-doctoral)
2.	**Wang T**, Chen B, Kim M, Xie Y, Xiao G. A model-based approach to identify binding sites in CLIP-Seq data. PloS one. 2014; 9(4):e93248. PubMed [journal] PMID: 24714572, PMCID: PMC3979666 (First author, pre-doctoral)
3.	Yun J, **Wang T**, Xiao G. Bayesian hidden Markov models to identify RNA-protein interaction sites in PAR-CLIP. Biometrics. 2014; 70(2):430-40. NIHMSID: NIHMS563098 PubMed [journal] PMID: 24571656, PMCID: PMC4061157 (Pre-doctoral)
4.	Kwon I, Xiang S, Kato M, Wu L, Theodoropoulos P, **Wang T**, Kim J, Yun J, Xie Y, McKnight SL. Poly-dipeptides encoded by the C9orf72 repeats bind nucleoli, impede RNA biogenesis, and kill cells. Science (New

	York, N.Y.). 2014; 345(6201):1139-45. NIHMSID: NIHMS696026 PubMed [journal] PMID: 25081482, PMCID: PMC4459787 (Pre-doctoral)
5.	Augustyn A, Borromeo M, **Wang T**, Fujimoto J, Shao C, Dospoy PD, Lee V, Tan C, Sullivan JP, Larsen JE, Girard L, Behrens C, Wistuba II, Xie Y, Cobb MH, Gazdar AF, Johnson JE, Minna JD. ASCL1 is a lineage oncogene providing therapeutic targets for high-grade neuroendocrine lung cancers. Proceedings of the National Academy of Sciences of the United States of America. 2014; 111(41):14788-93.PubMed [journal] PMID: 25267614, PMCID: PMC4205603 (Pre-doctoral)
6.	Bansal M, Yang J, Karan C, Menden MP, Costello JC, Tang H, Xiao G, Li Y, Allen J, Zhong R, Chen B, Kim M, **Wang T**, Heiser LM, Realubit R, Mattioli M, Alvarez MJ, Shen Y, Gallahan D, Singer D, Saez-Rodriguez J, Xie Y, Stolovitzky G, Califano A. A community computational challenge to predict the activity of pairs of compounds. Nature biotechnology. 2014; 32(12):1213-22. NIHMSID: NIHMS663971 PubMed [journal] PMID: 25419740, PMCID: PMC4399794 (Pre-doctoral)
7.	Chen X*, Zhao C*, Li X*, **Wang T***, Li Y, Cao C, Ding Y, Dong M, Finci L, Wang JH, Li X, Liu L. Terazosin activates Pgk1 and Hsp90 to promote stress resistance. Nature chemical biology. 2015; 11(1):19-25. NIHMSID: NIHMS681681 PubMed [journal] PMID: 25383758, PMCID: PMC4412158 (* Co-first author, pre-doctoral)
8.	**Wang T**, Zhan X, Bu CH, Lyon S, Pratt D, Hildebrand S, Choi JH, Zhang Z, Zeng M, Wang KW, Turer E, Chen Z, Zhang D, Yue T, Wang Y, Shi H, Wang J, Sun L, SoRelle J, McAlpine W, Hutchins N, Zhan X, Fina M, Gobert R, Quan J, Kreutzer M, Arnett S, Hawkins K, Leach A, Tate C, Daniel C, Reyna C, Prince L, Davis S, Purrington J, Bearden R, Weatherly J, White D, Russell J, Sun Q, Tang M, Li X, Scott L, Moresco EM, McInerney GM, Karlsson Hedestam GB, Xie Y, Beutler B. Real-time resolution of point mutations that cause phenovariance in mice. Proceedings of the National Academy of Sciences of the United States of America. 2015; 112(5):E440-9. PubMed [journal] PMID: 25605905, PMCID: PMC4321302 (First author, pre-doctoral)
9.	Yang J, Tang H, Li Y, Zhong R, **Wang T**, Wong S, Xiao G, Xie Y. DIGRE: Drug-Induced Genomic Residual Effect Model for Successful Prediction of Multidrug Effects. CPT: pharmacometrics & systems pharmacology. 2015; 4(2):e1. PubMed [journal] PMID: 26225227, PMCID: PMC4360668 (Pre-doctoral)
10.	Sei E*, **Wang T***, Hunter OV, Xie Y, Conrad NK. HITS-CLIP analysis uncovers a link between the Kaposi's sarcoma-associated herpesvirus ORF57 protein and host pre-mRNA metabolism. PLoS pathogens. 2015; 11(2):e1004652. PubMed [journal] PMID: 25710169, PMCID: PMC4339584 (* Co-first author, pre-doctoral)
11.	Chu Y*, **Wang T***, Dodd D, Xie Y, Janowski BA, Corey DR. Intramolecular circularization increases efficiency of RNA sequencing and enables CLIP-Seq of nuclear RNA from human cells. Nucleic acids research. 2015; 43(11):e75. PubMed [journal] PMID: 25813040, PMCID: PMC4477644 (* Co-first author, pre-doctoral)
12.	Zhou M*, **Wang T***, Fu J, Xiao G, Liu Y. Nonoptimal codon usage influences protein structure in intrinsically disordered regions. Molecular microbiology. 2015; 97(5):974-87. NIHMSID: NIHMS733877 PubMed [journal] PMID: 26032251, PMCID: PMC4636118 (* Co-first author, pre-doctoral)
13.	Eduati F*, Mangravite LM*, **Wang T***, Tang H*, Bare JC, Huang R, Norman T, Kellen M, Menden MP, Yang J, Zhan X, Zhong R, Xiao G, Xia M, Abdo N, Kosyk O, Friend S, Dearry A, Simeonov A, Tice RR, Rusyn I, Wright FA, Stolovitzky G, Xie Y, Saez-Rodriguez J. Prediction of human population responses to toxic compounds by a collaborative competition. Nature biotechnology. 2015; 33(9):933-40. NIHMSID: NIHMS703453 PubMed [journal] PMID: 26258538, PMCID: PMC4568441 (* Co-first author, pre-doctoral)
14.	Zang C*, **Wang T***, Deng K, Li B, Hu S, Qin Q, Xiao T, Zhang S, Meyer CA, He HH, Brown M, Liu JS, Xie Y, Liu XS. High-dimensional genomic data bias correction and data integration using MANCIE. Nature communications. 2016; 7:11305. PubMed [journal] PMID: 27072482, PMCID: PMC4833864 (* Co-first author, pre-doctoral)
15.	Sieberts SK, Zhu F, García-García J, Stahl E, Pratap A, Pandey G, Pappas D, Aguilar D, Anton B, Bonet J, Eksi R, Fornés O, Guney E, Li H, Marín MA, Panwar B, Planas-Iglesias J, Poglayen D, Cui J, Falcao AO, Suver C, Hoff B, Balagurusamy VS, Dillenberger D, Neto EC, Norman T, Aittokallio T, Ammad-Ud-Din M, Azencott CA, Bellón V, Boeva V, Bunte K, Chheda H, Cheng L, Corander J, Dumontier M, Goldenberg A, Gopalacharyulu P, Hajiloo M, Hidru D, Jaiswal A, Kaski S, Khalfaoui B, Khan SA, Kramer ER, Marttinen P, Mezlini AM, Molparia B, Pirinen M, Saarela J, Samwald M, Stoven V, Tang H, Tang J, Torkamani A, Vert JP, Wang B, **Wang T**, Wennerberg K, Wineinger NE, Xiao G, Xie Y, Yeung R, Zhan X, Zhao C, Greenberg J, Kremer J, Michaud K, Barton A, Coenen M, Mariette X, Miceli C, Shadick N, Weinblatt M, de Vries N, Tak PP, Gerlag D, Huizinga TW, Kurreeman F, Allaart CF, Louis Bridges S Jr, Bridges SL, Criswell L, Moreland L, Klareskog L, Saevarsdottir S, Padyukov L, Gregersen PK, Friend S, Plenge R, Stolovitzky G, Oliva B, Guan Y, Mangravite LM. Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. Nature communications. 2016; 7:12460. PubMed [journal] PMID: 27549343, PMCID: PMC4996969 (Pre-doctoral)

16.	Guinney J*, **Wang T***, Laajala TD*, Winner KK, Bare JC, Neto EC, Khan SA, Peddinti G, Airola A, Pahikkala T, Mirtti T, Yu T, Bot BM, Shen L, Abdallah K, Norman T, Friend S, Stolovitzky G, Soule H, Sweeney CJ, Ryan CJ, Scher HI, Sartor O, Xie Y, Aittokallio T, Zhou FL, Costello JC. Prediction of overall survival for patients with metastatic castration-resistant prostate cancer: development of a prognostic model through a crowdsourced challenge with open clinical trial data. The Lancet. Oncology. 2017; 18(1):132-142. NIHMSID: NIHMS831722 PubMed [journal] PMID: 27864015, PMCID: PMC5217180 (* Co-first author, research track faculty)
17.	Li Q, Yi F, **Wang T**, Xiao G, Liang F. Lung Cancer Pathological Image Analysis Using a Hidden Potts Model. Cancer informatics. 2017; 16:1176935117711910. PubMed [journal] PMID: 28615918, PMCID: PMC5462552 (Research track faculty)
18.	Choi JH, Wang KW, Zhang D, Zhan X, **Wang T**, Bu CH, Behrendt CL, Zeng M, Wang Y, Misawa T, Li X, Tang M, Zhan X, Scott L, Hildebrand S, Murray AR, Moresco EM, Hooper LV, Beutler B. IgD class switching is initiated by microbiota and limited to mucosa-associated lymphoid tissue in mice. Proc. Natl. Acad. Sci. U.S.A. 2017 Feb 14;114(7):E1196-E1204. PubMed ID: 28137874 (Research track faculty)
19.	Turer E, McAlpine W, Wang KW, Lu T, Li X, Tang M, Zhan X, **Wang T**, Zhan X, Bu CH, Murray AR, Beutler B. Creatine maintains intestinal homeostasis and protects against colitis. Proc. Natl. Acad. Sci. U.S.A. 2017 Feb 14;114(7):E1273-E1281. PubMed ID: 28137860 (Research track faculty)
20.	Gu YF, Cohn S, Christie A, McKenzie T, Wolff N, Do QN, Madhuranthakam AJ, Pedrosa I, **Wang T**, Dey A, Busslinger M, Xie XJ, Hammer RE, McKay RM, Kapur P, Brugarolas J. Modeling Renal Cell Carcinoma in Mice: <i>Bap1</i> and <i>Pbrm1</i> Inactivation Drive Tumor Grade. Cancer discovery. 2017; 7(8):900-917. NIHMSID: NIHMS874898 PubMed [journal] PMID: 28473526, PMCID: PMC5540776 (Research track faculty)
21.	**Wang T***, Bu CH, Hildebrand S, Jia G, Siggs OM, Lyon S, Pratt D, Scott L, Russell J, Ludwig S, Murray AR, Moresco EMY, Beutler B*. Probability of phenotypically detectable protein damage by ENU-induced mutations in the Mutagenetix database. Nature communications. 2018; 9(1):441. PubMed [journal] PMID: 29382827, PMCID: PMC5789985 (First and * co-corresponding author, tenure track faculty)
22.	McAlpine W, Wang KW, Choi JH, San Miguel M, McAlpine SG, Russell J, Ludwig S, Li X, Tang M, Zhan X, Choi M, **Wang T**, Bu CH, Murray AR, Moresco EMY, Turer EE, Beutler B. The class I myosin MYO1D binds to lipid and protects against colitis. Dis Model Mech 2018 Sep 27;11(9). PubMed ID: 30279225 (Tenure tack faculty)
23.	Wang S, Khera R, Das S, Vigen R, **Wang T**, Luo X, Lu R, Zhan X, Xiao G, Vongpatanasin W, Xie Y. Usefulness of a Simple Algorithm to Identify Hypertensive Patients Who Benefit From Intensive Blood Pressure Lowering. The American Journal of Cardiology. 122(2): 248-254. PMCID: PMC29880288. (Tenure track faculty)
24.	Wang Y, Cao L, Lee C, Matsuo T, Wu K, Asher G, Tang L, Saitoh T, Russell J, Klewe-Nebenius D, Wang L, Soya S, Hasegawa E, Chérasse Y, Zhou J, Li Y, **Wang T**, Zhan X, Miyoshi C, Irukayama Y, Cao J, Meeks J, Gautron L, Wang Z, Sakurai K, Funato H, Sakurai T, Yanagisawa M, Nagase H, Kobayakawa R, Kobayakawa K, Beutler B, Liu Q. Large-scale forward genetics screening identifies Trpa1 as a chemosensor for predator odor-evoked innate fear behaviors. Nature Communications. 2018; 9(1):-. (Tenure track faculty)
25.	**Wang T***, Lu R, Kapur P, Jaiswal BS, Hannan R, Zhang Z, Pedrosa I, Luke JJ, Zhang H, Goldstein LD, Yousuf Q, Gu YF, McKenzie T, Joyce A, Kim MS, Wang X, Luo D, Onabolu O, Stevens C, Xie Z, Chen M, Filatenkov A, Torrealba J, Luo X, Guo W, He J, Stawiski E, Modrusan Z, Durinck S, Seshagiri S*, Brugarolas J*. An Empirical Approach Leveraging Tumorgrafts to Dissect the Tumor Microenvironment in Renal Cell Carcinoma Identifies Missing Link to Prognostic Inflammatory Factors. Cancer discovery. 2018; PubMed [journal] PMID: 29884728 (First and * co-corresponding author, tenure track faculty)
26.	Zhang M, **Wang T**, Sirianni R, Shaul P, Xie Y. Identifying genes with tri-modal association with survival and tumor grade in cancer patients. BMC Bioinformatics. 2018. PubMed PMID: 30621577; PubMed Central PMCID: PMC6323748. (Tenure track faculty)
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