***Curriculum vitae***

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| **Date Prepared:** | 08/21/2019 |
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**Education**

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| --- | --- | --- | --- |
| 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**

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| --- | --- | --- |
| 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**

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| --- | --- | --- | --- |
| 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 |

**Major Administrative/Leadership Positions**

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| --- | --- | --- |
| Year(s) | Position Title | Institution |
| 2017-2020 | Bioinformatics Co-Leader | UTSW Kidney Cancer Program |
| 2017-2020 | Data analytics Core co-director | UTSW Kidney Cancer SPORE |

**Committee Service (***Member, unless noted otherwise)*

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| --- | --- | --- |
| 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 |
| 2019-2020 | PhD Committee for Debapriya Sinha (BME) | UT Southwestern Medical Center |
| 2019- | UTSW PhD Admissions Committee | UT Southwestern Medical Center |
| 2019- | 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- | PhD Committee for Xinyi Zhang (BME) | UT Southwestern Medical Center |
| 2020- | Immunology graduate program | UT Southwestern Medical Center |
| 2019-2021 | PhD Committee for Danyi Xiong (Bio-statistics) | UT Southwestern Medical Center/ Southern Methodist University |

**Professional Societies**

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

**Grant Review Activities**

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| Year(s) | Name of Review Committee | Organization |
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**Editorial Activities**

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| --- | --- |
| 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 |

**Grant Support**

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| --- | --- |
| 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 |
|  | Grantor: NCI 2P50CA070907-21A1 |
|  | Title of Project: UTSW SPORE in Lung Cancer |
|  | Role: co-Investigator |
|  | Goal: The core will provide bioinformatics, biostatistics and database support for all SPORE projects and other cores. |
|  | Grantor: NIAID 1U01AI156189-01 Administrative Supplement |
|  | Title of Project: Interpreting the TCR repertoire of lung cancers after immunotherapy treatment |
|  | Role: PI |
|  | Annual amount and date: $250,000 in 03/01/2021-02/28/2022 |
|  | Grantor: CPRIT RP190208 |
|  | Title of Project: Dissecting cellular heterogeneity of bulk tumors for prediction of overall survival and responsive patients to immunotherapy |
|  | Role: PI |
|  | Annual amount and date: $300,000, 09/01/19-08/31/22 |
|  | 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. |
|  | 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 |
|  | 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: NIH/National Cancer Institute, 5R01CA258584-02 |
|  | Title of project: Applying deep learning to predict T cell receptor binding specificity of neoantigens and response to checkpoint inhibitors |
|  | Role: PI |
|  | Goal: To develop deep learning-based algorithm for prediction of TCR-pMHC pairing |
|  | Annual amount and date: $229,010, 05/01/2021 – 04/30/2025 |

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| Past | Grantor: Center for Translational Medicine Service Package 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 |

**Teaching Activities**

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| Year(s) | Activity |
| Medical and graduate school didactic and small group teaching |
| 2016-2019 | Advanced Data Analysis and Statistical Learning, course instructor  |
| 2020-Present | Advanced Data Analysis and Statistical Learning, course leader |
| 2018-Present | AI in medicine, course instructor |
| Graduate student rotations |
| 2016 | Ze Zhang |
| 2016 | Tuozhi Huang |
| 2017 | Yujing Cheng |
| 2017 | Tianshi Lu |
| 2018 | Zhuoyu Wen |
| 2019 | James Zhu |
| 2019 | Xinke Wen |
| Graduate student trainees |
| 2017-Present | PhD: Ze Zhang (UTSW BME program, thesis: single cell sequencing analytical approaches to understanding tumor immunology) |
| 2018-Present | 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) |

**Invited Lectures**

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| 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 |
| 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 |
| 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 |

**Technological and Other Scientific Innovations**

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| 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”* |

**Bibliography**

**Peer-Reviewed Publications**

Original Research Articles

|  |  |
| --- | --- |
|  | **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) |
|  | **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) |
|  | 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) |
|  | 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) |
|  | 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) |
|  | 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) |
|  | 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) |
|  | **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) |
|  | 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) |
|  | 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) |
|  | 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) |
|  | 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) |
|  | 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) |
|  | 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) |
|  | 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) |
|  | 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) |
|  | 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) |
|  | 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) |
|  | 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)  |
|  | 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) |
|  | **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) |
|  | 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) |
|  | 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) |
|  | 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) |
|  | **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 last author, tenure track faculty) |
|  | 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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|  | **Wang T**, Lu R, Lai S, Schiller J, Zhou F, Ci B, Wang S, Gao X, Yao B, Gerber D, Johnson D, Xiao G, and Xie Y. Development and Validation of a Nomogram Prognostic Model for Patients with Advanced Non-Small-Cell Lung cancer. Cancer Informatics 18:1176935119837547. PMCID: PMC6452590. 2019 (First author, tenure track faculty) |
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