MING TANG

Senior Scientist
Department of Data Science
Dana-Farber Cancer Institute
Boston, MA, 02215

EMPLOYMENT

2015 | 2017	**Postdoctoral Fellow** MD Anderson Cancer Center	TX, USA
2017 | 2018	**Research Scientist** MD Anderson Cancer Center	TX, USA
2018 | 2020	**Senior Bioinformatics Scientist** Harvard FAS informatics	MA, USA
2020-	**Senior Scientist** Dana-Farber Cancer Institute	MA, USA

EDUCATION

2008	**Shanghai Jiaotong University** B.S. in Biotechnology	Shanghai, China
2014	**University of Florida** Ph.D. in Genetics and Genomics	FL, USA

HONORS AND AWARDS

2006	**People's Scholarship** Shanghai Jiaotong University	China
2007	**National Stipend for Academic Excellence** Shanghai Jiao Tong University	China
2007	**National Scholarship for Academic Excellence** Shanghai Jiao Tong University	China
2012	**Outstanding International Student** University of Florida	USA
2013	**Genetics & Genomics program Travel Grant** University of Florida	USA
2014	**Next Generation Sequencing course certificate** Michigan State University	USA
2015	**Summer Institutes in Statistics for Big Data Scholarship** University of Washington	USA
2018	**USC BD2K Data Science Road-Trip fellow** University of Southern California	USA

CONTACT INFO

✉ tangming2005@gmail.com

github.com/crazyhottommy

📞 +1 352-226-9384

website:

divingintogeneticsandgenomics.rbind.io/

For more information, please contact me via email.

SKILLS

Extensive experience with next generation sequencing data analysis and pipeline/workflow development.

Experienced in Single-cell data analysis.

Highly skilled in R, Bash and Python.

Great communication skills.

*This resume was made with the R package **pagedown**.*

Last updated on 2021-01-11.

2019   **Bioconductor annual meeting Travel award**
Bioconductor   📍 NYC, USA

2019   **Top 75 Bioinformatics Blogs and Websites for Bioinformaticians**
feedspot.com   📍 USA

2020   **Bioconductor annual meeting Travel award**
Bioconductor, virtual due to COVID19, waived registration fee.   📍 Boston, USA

📄 PUBLICATIONS (* FOR CO-FIRST AUTHOR)

2011   **Restraint of angiogenesis by zinc finger transcription factor CTCF-dependent chromatin insulation.**
Proc Natl Acad Sci USA. 2011 Sep 13;108(37):15231-6. PubMed PMID: 21896759
Tang M, Chen B, Lin T, Li Z, Pardo C, et al.

2012   **CTCF-dependent chromatin insulator as a built-in attenuator of angiogenesis.**
Transcription. 2012 Mar-Apr;3(2):73-7. PubMed PMID: 22414750; PubMed Central PMCID: PMC3337828.
Lu J and **Tang M**.

2013   **The malignant brain tumor (MBT) domain protein SFMBT1 is an integral histone reader subunit of the LSD1 demethylase complex for chromatin association and epithelial-to-mesenchymal transition.**
J Biol Chem 2013 Sep 20;288(38):27680-91. PubMed PMID: 23928305;PubMed Central PMCID: PMC3779763.
Tang M, Shen H, Jin Y, Lin T, Cai Q, et al

2014   **TRIM29 suppresses TWIST1 and invasive breast cancer behavior.**
Cancer Res. 2014 Sep 1;74(17):4875-87. PubMed PMID: 24950909.
Ai L, Kim WJ, Alpay M, **Tang M**, Pardo CE, et al.

2014   **Genomic and proteomic analysis of transcription factor TFII-I reveals insight into the response to cellular stress.**
Nucleic Acids Res. 2014;42(12):7625-41. PubMed PMID:24875474; PubMed Central PMCID: PMC4081084.
Fan AX, Papadopoulos GL, Hossain MA, Lin IJ, Hu J, **Tang M**, et al.

2016   **MOF Acetylates the Histone Demethylase LSD1 to Suppress Epithelial-to-Mesenchymal transition.**
Cell Reports. 2016.PMID: 27292636
Luo HC, Shenoy AK, Li X, Jin Y, Jin L, Cai Q, **Tang M**, Liu Y, Chen H et.al.

2016   **A Molecular Take on Malignant Rhabdoid Tumors.**
Trends in Cancer 2016. May;2(5):217-218
Tang M and Verhaak R.

2016   **Suppression of type I IFN signaling in tumors mediates resistance to anti-PD-1 treatment that can be overcome by radiotherapy.**
Cancer Res. 2016. Nov 7. pii: canres.3142.2015.
Wang X, Schoenhals JE, Li A, Valdecanas DR, Ye H, Zhang F, Tang C, **Tang M**, Liu CG, LiuX, Krishnan S, Allison JP, Sharma P, Hwu P, Komaki R, Overwikjk WW, Gomez DR, Chang JY, Hahn SM, Cortez Mam Welsh JW

2016   **Epithelial-to-mesenchymal transition confers pericyte properties on cancer cells.**
Journal of Clinical Investigation. 2016. Nov 1;126(11):4174-4186. doi: 10.1172/JCI86623
Shenoy AK, Jin Y, Luo H, **Tang M**, Pampo C, Shao R, Siemann DW, Wu L, Heldermon C, Law BK, Chang LJ, Lu J.

2017 ● **Systematic Analysis of Telomere Length, Telomerase and Telomere Maintenance across 31 cancer types.**
Nature Genetics. 2017. doi:10.1038/ng.3781

Barthel FP, Wei W, **Tang M**, Martinez-Ledesma E, Hu X, Amin S, Seth S, Song X, Lichtenberg T, Hu J, Zhang J, Zheng S, Verhaak R.

2017 ● **Synthetic essentiality of chromatin remodeling factor CHD1 in PTEN-deficient cancer**
Nature. 2017. doi:10.1038/nature21357

Zhao D, Lu X, Wang G, Lan Z, Liao W, Li J, Liang X Chen J, Shah S, Shang X, **Tang M**, Deng P, Dey P, Chakravarti D, Chen P, Spring D, Navone N, Troncoso P, Zhang j, Wang YA, DePinho RA

2017 ● **Integrative Analysis identifies Four Molecular and Clinical Subsets in Uveal Melanoma**
Cancer Cell. 2017.32:2:p204-220.e15

Robertson AG, Shih J, Yau C, Gibb EA, Mungall KL, Hess JM, Uzunangelov V, Walter V, Danilova L, Lichtenberg TM, Kucherlapati M, Kimes PK, **Tang M**, Penson A, Babur O, Bristow CA, Hoadley KA, Iype L, Chang MT, Oba J, The Cancer Genome Atlas (TCGA) Network, Cherniack AD, Benz C, Verhaak R, Griewank KG, Felau I, Zenklusen JC, Gershenwald JE, Schoenfield L, Lazar AJ, Abdel-Rahman M, Roman-Roman S, Stern, MH, Cebulla CM, Williams MD, Jager MJ, Coupland S, Esmaeli B, Kandoth C, Woodman SE

2017 ● **TFII-I interacts with E2F transcription factors and regulates their association with the cooccupied ATF3 gene locus.**
Jounral of Cellular Biochemistry. 2017. Doi:10.1002/jcb.26235

Fan A, Aryan M, Shen Y, Hossain M, **Tang M**, Lu J, Strouboulis J, Bungert J.

2017 ● **TumorFusions: an integrative resource for reporting cancerassociated transcript fusion in 33 tumor types.**
Nucleic Acids Research. 2017.Doi:10.1093/nar/gkx1018/4584571

Hu X, Wang Q, **Tang M**, Barthel FP, Amin S, Yoshihara K, Lang FM, Lee SH, Zheng S, Verhaak R.

2018 ● **An Integrated Platform for Genome-wide Mapping of Chromatin States Using Highthroughput ChIP-sequencing In Tumor Tissues**
Journal of Visualized Experiments. 2018.(134),e56972,doi:10.3791/56972.

Terranova C, **Tang M**, Orouji E, Maitituoheti M, Raman A, Amin S, Liu Z, Rai K.

2018 ● **The Tandem Duplicator Phenotype Is a Prevalent Genome-Wide Cancer Configuration Driven by Distinct Gene Mutations**
Cancer Cell. 2018. 13;34(2)197-210.e5 doi:10.1016/j.ccell.2018.06.008

Menghi F, Barthel FP, Yadav V, **Tang M**, Ji B, Tang Z, Cater GW, Ruan Y, Scully R, Verhaak R, Jonkers J, Liu E.

2018 ● **Positive Regulation of Transcription by Human ZMYND8 through Its Association with PTEFb Complex.**
Cell Reports. 2018. Aug21;24(8):21441-2154.e6 doi:10.1016/j.celrep.2018.07.064

Ghosh K, **Tang M**, Kumari N, Nandy A, Basu S, Mall DP, Rai K, Biswas D

2018 ● **Histone deacetylase inhibitor targets CD123/CD47-positive cells and reverse chemoresistance phenotype in acute myeloid leukemia.**
Leukemia. 2018. Doi:1038/s41375-018-0279-6.

Yan B, Chen Q, Shimada K, **Tang M**, Li H, Gurumurthy A, Khoury JD, Xu B, Huang S, Qiu Y

2018

Landscape of EGFR-Dependent and -Independent Resistance Mechanisms to Osimertinib and Continuation Therapy Beyond Progression in EGFR-Mutant NSCLC.
Clin Cancer Res. 2018 Dec 15;24(24):6195-6203. doi: 10.1158/1078-0432.CCR-18-1542.

Le X, Puri S, Negrao M, Nilsson M, Robichaux J, Boyle T, Hicks J, Lovinger K, Roarty E, Rinsurongkawong W,**Tang M**, Sun H, Elamin Y, Lacerda L, Lewis J, Roth J, Swisher S, Lee J, William W, Glisson B, Zhang J, Papadimitrakopoulou V, Gray J, Heymach J.

2019

KRAS-IRF2 Axis Drives Immune Suppression and Immune Therapy Resistance in Colorectal Cancer.
Cancer Cell. 2019 Apr 15;35(4):559-572.e7. doi: 10.1016/j.ccell.2019.02.008.

Liao W, Overman M, Boutin A, Shang X, Zhao D, Dey P, Li J, Wang G, Lan Z, Li J, **Tang M**, Jiang S, Ma X, Chen P, Katkhuda R, Korphaisarn K, Chakravarti D, Chang A, Spring D, Chang Q, Zhang J, Maru D, Maeda D, Zebala J, Kopetz S, Wang Y, Depinho R.

2019

Distinct Co-Acquired Alterations and Genomic Evolution During TKI Treatment in Non-Small-Cell Lung Cancer Patients With or Without Acquired T790M Mutation
Oncogene. 2020 Feb;39(9):1846-1859. doi: 10.1038/s41388-019-1104-z.

Jin Y, Bao H, Le X, Fan X, **Tang M**, Shi X, Zhao J, Yan J, Xu Y, Quek K, Elamin Y, Zhan J, Futreal A, Wistuba I, Heymach J, Lou G, Shao L, He Q, Lin C, Wu X, Shao Y, Wang X, He J, Chen Y, Stebbing J, Chen M, Zhang J, Yu X.

2020

LATS kinase–mediated CTCF phosphorylation and selective loss of genomic binding.
Science Advances . 2020 Feb 19;6(8):eaaw4651. doi: 10.1126/sciadv.aaw4651.

Luo H, Yu Q, Liu Y, **Tang M**, Liang M, Zhang D, Xiao T, Wu L, Tan M, Ruan Y, Bungert J, Lu J.

2020

Fast analysis of scATAC-seq data using a predefined set of genomic regions.
F1000Research. 2020, 9:199 (https://doi.org/10.12688/f1000research.22731.2)

Valentina Giansanti, **Ming Tang**, Davide Cittaro.

2020

KMT2D Deficiency Impairs Super-Enhancers to Confer a Glycolytic Vulnerability in Lung Cancer.
Cancer Cell. 2020 Apr 13;37(4):599-617.e7. doi: 10.1016/j.ccell.2020.03.005.

Alam H*, **Tang M***, Maitituoheti M, Dhar S, Kumar M, han C, Ambati C, Amin S, Gu B, Chen T, Lin Y, Chen J, Muller F, Putluri N, Flores E, Demayo F, Baseler L, Rai K, Lee M.

2020

Tumor microenvironment remodeling enables bypass of oncogenic KRAS dependency in pancreatic cancer
Cancer Discovery. 2020 Apr 27. doi: 10.1158/2159-8290.CD-19-0597.

Hou P, Kapoor A, Zhang Q, Li J, Wu C, Li J, Lan Z, **Tang M**, Ma X, Ackroyd J, Kalluri R, Zhang J, Jiang S, Spring D, Wang Y, DePinho R.

2020

Integrative analyses of single-cell transcriptome and regulome using MAESTRO
Genome Biology. 2020 Aug 7;21(1):198. doi: 10.1186/s13059-020-02116-x.

Chenfei Wang, Dongqing Sun, Xin Huang, Changxin Wan, Ziyi Li, Ya Han, Qian Qin, Jingyu Fan, Xintao Qiu, Yingtian Xie, Clifford A Meyer, Myles Brown, **Ming Tang**, Henry Long, Tao Liu, X Shirley Liu.

2020

Evaluating single-cell cluster stability using the Jaccard similarity index.
Bioinformatics 2020 Nov 09. doi: https://doi.org/10.1093/bioinformatics/btaa956

Tang M, Kaymaz Y, Logeman B, Eichhorn S, Liang Z, Dulac C, Sackton T.

PREPRINT (* FOR CO-FIRST AUTHOR)

2019

Bivalent and Broad Chromatin Domains Regulate Pro-metastatic Drivers in Melanoma.
BioRxiv 2019 doi: https://doi.org/10.1101/721480

Terranova C*, **Tang M***, Maitituoheti M, Raman A, Schulz J, Amin S, Orouji E, Tomczak K, Sarkar S, Oba J, Crasy C, Wu C, Zhao D, Chen K, Haydu L, Wang W, Lazar A, Woodman S, Bernatchez C, Rai K.

2020

HieRFIT: Hierarchical Random Forest for Information Transfer
BioRxiv 2020 doi: https://doi.org/10.1101/2020.09.16.300822

Kaymaz Y, Ganglberger F, **Tang M**,Fernandez-Albert F, Lawless N, Sackton T.

2021

The histologic phenotype of lung cancers may be driven by transcriptomic features rather than genomic characteristics
BioRxiv 2021 doi: https://doi.org/10.1101/2021.01.01.425056

Tang M, Abbas H, Negrao M, Ramineni M, Hu X, Fujimoto J, Reuben A, Varghese S, Zhang J, Li J, Chow CW, Mao X, Song X, Lee W, Wu J, Little L, Gumbs C, Behrens C, Moran C, Weissferdt A, Lee J, Sepesi B, Swisher S, Heymach J, Wistuba I, Futreal A, Kalhor N, Zhang J.

BOOK CHAPTERS

2016

Genetically altered cancer epigenome.
Epigenetic Gene Expression and Regulation. 2016. Elsevier, Inc. Edited by Suming Huang, Michael Litt, and Cynthia Ann Blakey

Tang M, Luo HC and Lu J

2017

The biostar Handbook: A Beginner's Guide to Bioinformatics.
https://read.biostarhandbook.com/ 2017. Edited by Istvan Albert.

Sebastian A, Albert R, Leipzig J, Kelkar H, **Tang M**, Shen W, Coster WD

2018

Computational analysis of epigenetic modifications in melanoma cancer
Computational Epigenetics and Diseases. 2017. Elsevier,Inc

Rai K, **Tang M**.

SOFTWARE

2017

pyflow-ChIPseq, a snakemake workflow for processing ChIP-seq data.
github link https://github.com/crazyhottommy/pyflow-ChIPseq

2017

pyflow-ATACseq, a snakemake workflow for processing ATAC-seq data.
github link https://github.com/crazyhottommy/pyflow-ATACseq

2017

pyflow-RNAseq, a snakemake workflow for processing RNA-seq data.
github link https://github.com/crazyhottommy/pyflow-RNAseq

2018

pyflow-DNAseq, a snakemake workflow for processing DNA-seq data.
gitlab link https://gitlab.com/tangming2005/snakemake_DNAseq_pipeline/tree/multiRG

2018

pyflow-RRBS, a snakemake workflow for processing RRBS data.
gitlab link https://gitlab.com/tangming2005/pyflow-RRBSeq

2019

pyflow-scATACseq, a snakemake workflow for post-processing single-cell ATAC-seq data.
github link https://github.com/crazyhottommy/pyflow-scATACseq

2019   **scATACutils, an R package for analyzing single-cell ATAC-seq data.**
github link https://github.com/crazyhottommy/scATACutils

2019   **scclusteval, an R package for evaluating single-cell RNA-seq cluster stability**
github link https://github.com/crazyhottommy/scclusteval

🖳 TEACHING EXPERIENCE

2014   **Software Carpentry 2-day workshop.**
Instructor of R and bash for the software carpentry workshop held in the University of Miami. https://divingintoge-neticsandgenomics.rbind.io/talk/2015-miami-carpentry/

📍 FL, USA

2017   **GS01 1143 Introduction to Bioinformatics course.**
I taught the ChIP-seq bioinformatics lab for the GS01 1143 Introduction to Bioinformatics course to ~30 people with diverse background in MD Anderson Cancer Center. https://divingintogeneticsandgenomics.rbind.io/talk/2017-gsbs-chipseq-class/

📍 TX, USA

2018   **Next-Gen Sequence Analysis Workshop.**
I taught the ChIP-seq lesson for 2018 ANGUS Next-Gen Sequence Analysis Workshop held in UC Davis from 7/1/2018 to 7/14/2018, and TAed for the rest of the sessions.
https://divingintogeneticsandgenomics.rbind.io/talk/2018-dibsi-course/

📍 CA, USA

2019   **Harvard FAS informatics nanocourse**
In this 2-week long Harvard FAS informatics nanocourse, I co-taught snakemake for one afternoon and lead-in-structed scRNAseq analysis for a full day. https://divingintogeneticsandgenomics.rbind.io/talk/2019-harvard-fas-workshop/

📍 MA, USA

2020   **Liu Lab new hire bioinformatics training**
I TAed a 5-week long bioinformatics training for the Liu lab new hires using materials from Harvard course STAT115/215: Introduction to Computational Biology and Bioinformatics

📍 MA, USA

🎤 INVITED TALK

2018   **From cell line to command line: my journey to bioinformatics**
I was invited to give a talk to my PhD Genetics and Genomics program at the University of Florida. I talked about my personal experience on how I started doing bioinformatics and shared tips and resources to get the students started their own journey into bioinformatics. https://divingintogeneticsandgenomics.rbind.io/talk/2018-uf-talk/

📍 FL, USA

2019   **Reproducible research in bioinformatics**
I was invited to give a talk on reproducible bioinformatics research to the students in the Bunker Hill Community College in Boston. https://divingintogeneticsandgenomics.rbind.io/talk/2019-bunkerhill-talk/

📍 MA, USA

2020   **Reproducible computing for your own benifit.**
I was invited to give a talk on reproducible computing at Center for Functional Cancer Epigenetics(CFCE) in Dana-Farber Cancer Institute.

📍 MA, USA

2020   **MAESTRO: Model-based Analyses of Single-cell Transcriptome and Regulome**
I gave a talk on our single-cell RNA-seq and single-cell ATAC-seq analysis tool MAESTRO in the Broad Institute CC&E Seminar Series.

📍 MA, USA

2020 ● **PACT meeting update: single-cell and bulk ATAC-seq analysis pipelines**
In the joint Partnership for Access to Clinical Trials (PACT) and CIMAC-CIDC Network Fall meeting. I presented the update for our bulk ATAC-seq pipeline and the MAESTRO single-cell workflow. I led the discussion of the adoption of single-cell ATAC-seq in the CIMAC trails afterwards.

📍 MA, USA

2020 ● **Biological data science in a nutshell.**
I was invited to give a zoom talk on data science for students in the Palm Beach State Colleage in Florida.

📍 FL, USA

✎ PROFESSIONAL SERVICE

● **Reviewer for journals**

- Clinical Cancer Research.
- GigaScience.
- Bioinformatics
- Aging
- Cancer Research
- F1000 Research

- Cancer Letters
- Cell Reports
- BMC genetics
- Oncogene
- PLOS ONE
- Oncotarget

💼 PROFESSIONAL MEMBERSHIP

2016 ● **Member, Society for Neuro-Oncology (SNO)**

2017 ● **Genomics Advisory committee member for Data Carpentry, USA**

2017 - ● **Certified Instructor, Software Carpentry, Data Carpentry, USA**

2017 ● **Member, American Society of Clinical Oncology (ASCO)**

2020 ● **Member, Bioinformatics Organization.**