

Zichen Wang, Ph.D.

Principal Scientist
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Education

- 2016 **Ph.D. Biomedical Science**
Icahn School of Medicine at Mount Sinai, New York, NY
- 2012 **B.S. Biochemistry and Molecular Biology**
China Agricultural University, Beijing, China

Work Experience

- 09/2019 - present **Principal Scientist**
Clinical Informatics
Sema4, Stamford, CT
- 06/2017 - 09/2019 **Assistant Professor**
Department of Pharmacological Sciences
Icahn School of Medicine at Mount Sinai, New York, NY
- 01/2017 - 06/2017 **Postdoctoral Fellow**
Department of Pharmacological Sciences
Icahn School of Medicine at Mount Sinai, New York, NY
- 05/2013 - 12/2016 **Doctoral Student**
Department of Genetics and Genomic Sciences
Icahn School of Medicine at Mount Sinai, New York, NY
- 11/2011 - 05/2012 **Research Assistant**
Institute of Biophysics
Chinese Academy of Sciences, Beijing, China

Publications

Research Articles

1. Keenan AB, Torre D, Lachmann A, Leong AK, Wojciechowicz ML, Utti V, Jagodnik KM, Kropiwnicki E, **Wang Z**, Ma'ayan A: ChEA3: transcription factor enrichment analysis by orthogonal omics integration. *Nucleic Acids Research* 2019, 47(W1):W212-W224
2. Nakahara F, Borger DK, Wei Q, Pinho S, Maryanovich M, Zahalka A, Suzuki M, Greally J, Cruz C, **Wang Z**, Ma'ayan A, Xu C, Boulais P, Frenette PS: Engineering a haematopoietic stem cell niche by revitalizing mesenchymal stromal cells. *Nature Cell Biology* 2019, 21: 560-567
3. Ellis RJ, **Wang Z**, Genes N, Ma'ayan A: Predicting opioid dependence from electronic health records with machine learning. *BioData Mining* 2019, 12(3)

4. Mok KW, Saxena N, Heitman N, Grisanti L, Srivastava D, Muraro M, Jacob T, Sennett R, **Wang Z**, Su Y, Yang LM, Ma'ayan A, Ornitz DM, Kasper M, Rendl M: Dermal Condensate Niche Fate Specification Occurs Prior to Formation and Is Placode Progenitor Dependent. **Developmental Cell** 2019, 48(1):32-48.e5
5. Breen MS, Ozcan S, Ramsey JM, **Wang Z**, Ma'ayan A, Rustogi N, Gottschalk MG, Webster MJ, Weickert CS, Buxbaum JD, Bahn S: Temporal proteomic profiling of postnatal human cortical development. **Translational Psychiatry** 2018, 8(1) 267
6. Gomes AM, Kurochkin I, Chang B, Daniel M, Law K, Satija N, Lachmann A, **Wang Z**, Ferreira L, Ma'ayan A, Chen BK, Papatsenko D, Lemischka IR, Moore KA, Pereira CF: Cooperative Transcription Factor Induction Mediates Hemogenic Reprogramming. **Cell Reports** 2018, 25(10) 2821-2835.e7
7. **Wang Z**, He E, Sani K, Jagodnik KM, Silverstein M, Ma'ayan A: Drug Gene Budger (DGB): An application for ranking drugs to modulate a specific gene based on transcriptomic signatures. **Bioinformatics** 2018, bty763
8. Strub T, Ghiraldini FG, Carcamo S, Li M, Wroblewska A, Singh R, Goldberg MS, Hasson D, **Wang Z**, Gallagher SJ, Hersey P, Ma'ayan A, Long GV, Scolyer RA, Brown B, Zheng B, Bernstein E: SIRT6 haploinsufficiency induces BRAF V600E melanoma cell resistance to MAPK inhibitors via IGF signalling. **Nature Communications** 2018, 9(3440)
9. Guo Y, Pace J, Li Z, Ma'ayan A, **Wang Z**, Revelo MP, Chen E, Gu X, Attalah A, Yang Y, Estrada C, Yang VW, John C, He JC, Mallipattu SK: Podocyte-Specific Induction of Krüppel-Like Factor 15 Restores Differentiation Markers and Attenuates Kidney Injury in Proteinuric Kidney Disease. **Journal of the American Society of Nephrology** 2018, ASN.2018030324
10. Clarke DJB, Kuleshov MV, Schilder BM, Torre D, Duffy ME, Keenan AB, Lachmann A, Feldmann AS, Gundersen GW, Silverstein MC, **Wang Z**, Ma'ayan A: eXpression2Kinases (X2K) Web: linking expression signatures to upstream cell signaling networks. **Nucleic Acids Research** 2018, gky450
11. Harel A, Sperling D, Petracca M, Ntranos A, Kats-Sand I, Krieger S, Lublin F, **Wang Z**, Liu Y, Inglese M: Brain microstructural injury occurs in patients with RRMS despite 'no evidence of disease activity'. **Journal of Neurology, Neurosurgery & Psychiatry** 2018
12. Torre D, Krawczuk P, Jagdonik KM, Lachmann A, Kuleshov MV, **Wang Z**, Wang L, Kuleshov MV, Ma'ayan A: Datasets2Tools, repository and search engine for bioinformatics datasets, tools and canned analyses. **Scientific Data** 2018, 5:180023
13. **Wang Z**, Lachmann A, Keenan AB, Ma'ayan A: L1000FWD: Large-scale visualization of drug-induced transcriptomic signatures. **Bioinformatics** 2018, bty060
14. Fu J, **Wang Z**, Lee K, Wei G, Liu Z, Zhang M, Zhou M, Zhang W, Chuang P, Ma'ayan A, He JC, Liu Z: Transcriptomic analysis uncovers novel synergistic mechanisms in combination therapy for lupus nephritis. **Kidney International** 2018, 93(2):416-429
15. Hodos R, Zhang P, Duan Q, **Wang Z**, Clark NR, Ma'ayan A, Wang F, Lee HC, Kidd B, Sontag D, Hu J, Dudley JT: Prediction of drug-induced gene expression profiles using tensor completion. **Pacific Symposium on Biocomputing** 2018, 32-43
16. **Wang Z**, Li L, Glicksberg BS, Israel A, Dudley JT, Ma'ayan A: Predicting Age by Mining Electronic Medical Records with Deep Learning Characterizes Differences between Chronological and Physiological Age. **Journal of Biomedical Informatics** 2017, 76:59-68
17. Niepel M, Hafner M, Duan Q, **Wang Z**, Paull EM, Chung M, Lu X, Stuart JM, Golub TR, Subramanian A, Ma'ayan A, Sorger PK: Common and cell-type specific responses to anti-cancer drugs revealed by high throughput transcript profiling. **Nature Communications** 2017, 8(1):1186

18. Asada N, Kunisaki Y, Pierce H, **Wang Z**, Fernandez N, Birbrair A, Ma'ayan A, Frenette P: Differential cytokine contributions of perivascular haematopoietic stem cell niches. **Nature Cell Biology** 2017, 19 (3), 214-223
19. **Wang Z**, Monteiro CD, Jagodnik KM, Fernandez NF, Gundersen GW, Rouillard AD, Jenkins SL, Feldmann AS, Hu KS, McDermott MG *et al*: Extraction and analysis of signatures from the gene expression omnibus by the crowd. **Nature Communications** 2016, 7, 12846.
20. von Schimmelmann M, Feinberg PA, Sullivan JM, Ku SM, Badimon A, Duff MK, **Wang Z**, Lachmann A, Dewell S, Ma'ayan A, Han M-H, Tarakhovsky A, Schaefer A: Polycomb repressive complex 2 (PRC2) silences genes responsible for neurodegeneration. **Nature Neuroscience** 2016, 19, 1321-1330
21. Duan Q, Reid SP, Clark NR, **Wang Z**, Fernandez NF, Rouillard AD, Readhead B, Tritsch SR, Hodos R, Hafner M, Niepel M, Sorger PK, Dudley JT, Bavari S, Panchal RG, Ma'ayan A: L1000CDS2: LINCS L1000 characteristic direction signatures search engine. **Npj Systems Biology And Applications** 2016, 2:16015.
22. Kuleshov MV, Jones MR, Rouillard AD, Fernandez NF, Duan Q, **Wang Z**, Koplev S, Jenkins SL, Jagodnik KM, Lachmann A *et al*: Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. **Nucleic Acids Research** 2016, 44 (W1): W90-W97.
23. **Wang Z**, Clark NR, Ma'ayan A: Drug-induced adverse events prediction with the LINCS L1000 data. **Bioinformatics** 2016, 32(15):2338-2345.
24. Rezza A, **Wang Z**, Sennett R, Qiao W, Wang D, Heitman N, Mok Ka W, Clavel C, Yi R, Zandstra P *et al*: Signaling Networks among Stem Cell Precursors, Transit-Amplifying Progenitors, and their Niche in Developing Hair Follicles. **Cell Reports** 2016, 14(12):3001-3018.
25. Kong D-S, Kim J, Lee I-H, Kim ST, Seol HJ, Lee J-I, Park W-Y, Ryu G, **Wang Z**, Ma'ayan A, Nam D-H: Integrative radiogenomic analysis for multicentric radiophenotype in glioblastoma. **Oncotarget** 2016, 7(10), 11526.
26. **Wang Z**, Ma'ayan A: An open RNA-Seq data analysis pipeline tutorial with an example of reprocessing data from a recent Zika virus study [version 1; referees: 3 approved]. **F1000Research** 2016, 5(1574).
27. Rouillard AD, Gundersen GW, Fernandez NF, **Wang Z**, Monteiro CD, McDermott MG, Ma'ayan A: The harmonizome: a collection of processed datasets gathered to serve and mine knowledge about genes and proteins. **Database** 2016, baw100.
28. Morgan DJ, Poolman TM, Williamson AJK, **Wang Z**, Clark NR, Ma'ayan A, Whetton AD, Brass A, Matthews LC, Ray DW: Glucocorticoid receptor isoforms direct distinct mitochondrial programs to regulate ATP production. **Scientific Reports** 2016, 6:26419.
29. Pfau ML, Purushothaman I, Feng J, Golden SA, Aleyasin H, Lorsch ZS, Cates HM, Flanigan ME, Menard C, Heshmati M, **Wang Z**, Ma'ayan A, Shen L, Hodes GE, and Russo SJ: Integrative analysis of sex-specific microRNA networks following stress in mouse nucleus accumbens. **Frontiers in Molecular Neuroscience** 2016, 9:144
30. Clark NR, Szymkiewicz M, **Wang Z**, Monteiro CD, Jones MR, Ma'ayan A: Principal Angle Enrichment Analysis (PAEA): Dimensionally Reduced Multivariate Gene Set Enrichment Analysis Tool. **Proceedings IEEE International Conference on Bioinformatics and Biomedicine** 2015, 2015:256-262.
31. Sennett R, **Wang Z**, Rezza A, Grisanti L, Roitershtein N, Sicchio C, Mok Ka W, Heitman Nicholas J, Clavel C, Ma'ayan A *et al*: An Integrated Transcriptome Atlas of Embryonic Hair Follicle Progenitors, Their Niche, and the Developing Skin. **Developmental Cell** 2015, 34(5):577-591.
32. **Wang Z**, Clark N, Ma'ayan A: Dynamics of the discovery process of protein-protein interactions from low content studies. **BMC Systems Biology** 2015, 9(1):26.

33. Yu Z, Zhou X, Wang W, Deng W, Fang J, Hu H, **Wang Z**, Li S, Cui L, Shen J *et al*: Dynamic Phosphorylation of CENP-A at Ser68 Orchestrates Its Cell-Cycle-Dependent Deposition at Centromeres. **Developmental Cell** 2015, 32(1):68-81.
34. Duan Q, **Wang Z**, Fernandez NF, Rouillard AD, Tan CM, Benes CH, Ma'ayan A: Drug/Cell-line Browser: interactive canvas visualization of cancer drug/cell-line viability assay datasets. **Bioinformatics** 2014, 30(22):3289-3290.
35. Duarte LF, Young ARJ, **Wang Z**, Wu H-A, Panda T, Kou Y, Kapoor A, Hasson D, Mills NR, Ma'ayan A, Narita M, Bernstein E: Histone H3.3 and its proteolytically processed form drive a cellular senescence programme. **Nature Communications** 2014, 5, 5210.
36. Chen E, Tan C, Kou Y, Duan Q, **Wang Z**, Meirelles G, Clark N, Ma'ayan A: Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. **BMC Bioinformatics** 2013, 14(1):128.
37. Wang W, Wang L, Chen C, Xiong G, Tan X-Y, Yang K-Z, **Wang Z-C**, Zhou Y, Ye D, Chen L-Q: Arabidopsis CSLD1 and CSLD4 are required for cellulose deposition and normal growth of pollen tubes. **Journal of Experimental Botany** 2011, 62(14):5161-5177.

Review Articles

38. Keenan AB, Wojciechowicz ML, **Wang Z**, Jagodnik KM, Jenkins SL, Lachmann A, Ma'ayan A: Connectivity Mapping: Methods and Applications. **Annual Review of Biomedical Data Science** 2019, 2: 69-92
39. **Wang Z**, Lachmann A, Ma'ayan A: Mining data and metadata from the gene expression omnibus. **Biophysical Reviews** 2019, 11(1) 103-110
40. Keenan AB, Jenkins SL, Jagodnik KM, Koplev S, He E, Torre D, **Wang Z**, *et al*: The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. **Cell Systems** 2017, 6(1):13-24
41. Rouillard AD, **Wang Z**, Ma'ayan A: Reprint of "Abstraction for data integration: Fusing mammalian molecular, cellular and phenotype big datasets for better knowledge extraction". **Computational Biology and Chemistry** 2015, 59, Part B:123-138.
42. Ma'ayan A, Rouillard AD, Clark NR, **Wang Z**, Duan Q, Kou Y: Lean Big Data integration in systems biology and systems pharmacology. **Trends in Pharmacological Sciences** 2014, 35(9): 450-460.

Other Publications (accepted/submitted/in revision/preprints)

43. Edwards JJ, Rouillard AD, Fernandez NF, **Wang Z**, Lachmann A, Shankaran SS, Bisgrove BW, Demarest B, Turan N, Srivastava D, Bernstein D, Deanfield J, Giardini A, Porter G, Kim R, Roberts AE, Newburger JW, *et al*: Systems analysis implicates WAVE2 in the pathogenesis of left-sided obstructive heart defects. **Circulation: Cardiovascular Genetics** (in revision)
44. Ochsner S, Abraham D, Martin K, Ding W, McOwiti A, **Wang Z**, Andreano K, Hamilton R, Chen Y, Hamilton A, Gantner M, Dehart M, Qu D, Hilsenbeck S, Bechel L, Bridges D, Ma'ayan A, Huss J, Stossi F, Foulds C, Kralli A, McDonnell D, McKenna N: The Signaling Pathways Project: an integrated 'omics knowledgebase for mammalian cellular signaling pathways. **bioRxiv** 2018 doi: <https://doi.org/10.1101/401729>

Invited Presentations

- 03/2019 Single-cell Approaches for the Dissection of Cell Lineage
Computational Genomics guest lecture at Weill Cornell Medicine
New York, NY
- 12/2018 L1000 data analysis and visualization using machine learning
LINCS Connectivity Map Workshop Series
Cambridge, MA
- 10/2018 Pharmacometrics in Big Data Era - Mission possible to find the needle in a haystack
American Conference on Pharmacometrics (ACoP9)
San Diego, CA
- 03/2018 Towards Large-scale Predictive Drug Safety: A Systems Pharmacology Perspective
American Medical Informatics Association (AMIA) Informatics Summit
San Francisco, CA

Ad-hoc Peer-Review Service

Bioinformatics, PLoS Computational Biology, Statistical Methods in Medical Research, Nature Communications, Oncogene, Scientific Reports, IEEE International Conference on Bioinformatics and Biomedicine, Bulletin of Mathematical Biology, Gene, Meta Gene, Algorithms, EBioMedicine, BMC Medical Informatics and Decision Making, CPT: Pharmacometrics & Systems Pharmacology, Nucleic Acids Research, Royal Society Open Science, Frontiers in Genetics

Advising and Supervision

Kevin Sani	Visiting undergraduate student	Harvard University, Cambridge, MA	2016
Daniel Clarke	Visiting undergraduate student	Fairleigh Dickinson University, Teaneck, NJ	2016
Jennifer Lin	Visiting high school student	Oceanside High School, Oceanside, NY	2016
Damon Pham	Visiting undergraduate student	Indiana University, Bloomington, IN	2017, 2019
Charlotte Zuber	Visiting undergraduate student	Rutgers University, New Brunswick, NJ	2017
Randall Ellis	Rotation PhD student	Icahn School of Medicine at Mount Sinai, New York, NY	2017-2018
Katherine Chew	Visiting undergraduate student	Massachusetts Institute of Technology, Cambridge, MA	2018
Vivek Sriram	Visiting undergraduate student	Duke University, Durham, NC	2018
David Szanto	Visiting undergraduate student	Harvard University, Cambridge, MA	2019