Dave **Tang**

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Some stuff about me

- I grew up in Papua New Guinea
- I did my PhD in Japan through a Marie Curie training network (BrainTrain)
- I play a lot of basketball

Education

The University of Queensland — *Brisbane, Australia*
BACHELOR OF SCIENCE (HONOURS) — *2001-2005*

Vrije University — *Amsterdam, the Netherlands*
PHD IN COMPUTATIONAL BIOLOGY — *2010-2015*

Work history

The University of Western Australia — *Perth, Australia*
POST-DOCTORAL RESEARCH ASSOCIATE — *2017-now*

RIKEN Yokohama — *Yokohama, Japan*
VISITING SCIENTIST — *2015-now*

Publications

1. Rothacker, K, K Ayers, D Tang, K Joshi, J Van Den Bergen, and … (2018). A novel, homozygous mutation in desert hedgehog (DHH) in a 46, XY patient with dysgenetic testes presenting with primary amenorrhoea: a case report. *International journal of pediatric endocrinology*.
2. Hon, C, J Ramilowski, J Harshbarger, N Bertin, O Rackham, J Gough, and … (2017). An atlas of human long non-coding RNAs with accurate 5′ ends. *Nature*.
3. Roudnicky, F, L Dieterich, C Poyet, L Buser, P Wild, D Tang, and … (2017). High expression of insulin receptor on tumour‑associated blood vessels in invasive bladder cancer predicts poor overall and progression‑free survival. *The Journal of pathology*.
4. Abraham, M, D Li, D Tang, S O'Connell, F McKenzie, E Lim, and … (2017). Short stature and hypoparathyroidism in a child with Kenny-Caffey syndrome type 2 due to a novel mutation in FAM111A gene. *International journal of pediatric endocrinology*.
5. Baynam, G, N Pachter, F McKenzie, S Townshend, J Slee, C Kiraly-Borri, and … (2016). The rare and undiagnosed diseases diagnostic service–application of massively parallel sequencing in a state-wide clinical service. *Orphanet journal of rare diseases*.
6. Tang, D, D Anderson, R Francis, G Syn, S Jamieson, T Lassmann, and … (2016). Reference genotype and exome data from an Australian Aboriginal population for health-based research. *Scientific data*.
7. Hasegawa, Y, D Tang, N Takahashi, Y Hayashizaki, A Forrest, and … (2014). CCL2 enhances pluripotency of human induced pluripotent stem cells by activating hypoxia related genes. *Scientific reports*.
8. Francia, S, F Michelini, A Saxena, D Tang, M de Hoon, V Anelli, M Mione, and … (2012). Site-specific DICER and DROSHA RNA products control the DNA-damage response. *Nature*.
9. Tang, D, C Plessy, M Salimullah, A Suzuki, R Calligaris, S Gustincich, and … (2012). Suppression of artifacts and barcode bias in high-throughput transcriptome analyses utilizing template switching. *Nucleic acids research*.
10. Saxena, A, D Tang, and P Carninci (2012). piRNAs warrant investigation in Rett Syndrome: an omics perspective. *Disease markers*.
11. Thiagarajan, R, K Georgas, B Rumballe, E Lesieur, H Chiu, and … (2011). Identification of anchor genes during kidney development defines ontological relationships, molecular subcompartments and regulatory pathways. *PloS one*.

12. Thiagarajan, R, N Cloonan, B Gardiner, T Mercer, G Kolle, and ... (2011). Refining transcriptional programs in kidney development by integration of deep RNA-sequencing and array-based spatial profiling. *BMC genomics*.

13. Chiu, H, J Szucsik, K Georgas, J Jones, B Rumballe, D Tang, and ... (2010). Comparative gene expression analysis of genital tubercle development reveals a putative appendicular Wnt7 network for the epidermal differentiation. *Developmental biology*.

14. Kijas, J, D Townley, B Dalrymple, M Heaton, J Maddox, A McGrath, and ... (2009). A genome wide survey of SNP variation reveals the genetic structure of sheep breeds. *PloS one*.

15. Georgas, K, B Rumballe, M Valerius, H Chiu, R Thiagarajan, and ... (2009). Analysis of early nephron patterning reveals a role for distal RV proliferation in fusion to the ureteric tip via a cap mesenchyme-derived connecting segment. *Developmental biology*.

16. Cloonan, N, Q Xu, G Faulkner, D Taylor, D Tang, G Kolle, and ... (2009). RNA-MATE: a recursive mapping strategy for high-throughput RNA-sequencing data. *Bioinformatics*.

17. Tang, D, E Glazov, S McWilliam, W Barris, and B Dalrymple (2009). Analysis of the complement and molecular evolution of tRNA genes in cow. *BMC genomics*.