Dave Ting Pong Tang

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Education

2010–2015	PhD Candidate, Vrije University, the Netherlands
2001–2005	BSc (Honours) in biochemistry and microbiology, University of Queensland, Australia

Past Scientific Positions

2010–2015	Research Associate in the lab of Piero Carninci at RIKEN Yokohama, Japan
2008–2010	Research Assistant in the lab of Sean Grimmond at The University of Queensland, Australia
2006–2008	Research Assistant in the lab of Brian Dalrymple at the Commonwealth Scientific and Industrial Research Organisation, Australia
2005–2006	Research Assistant in the lab of Mark Ragan at the University of Queensland, Australia

Research Interests

- Genomics and transcriptomics; in particular the study of non-coding RNAs and transposable elements expression

- Open science and reproducible research

- The application of bioinformatics, in particular machine learning and data mining methods, to biological problems

Bioinformatic Skills

- Data analysis of high-throughput sequencing data from various *Seq protocols

- Knowledge and the ability to use various bioinformatic databases, repositories, and tools

- Biostatistics for the analysis of high-throughput sequencing data

Computer Skills

- Programming/scripting languages: Perl, R, SQL, bash, PHP, JavaScript, Python, and C

- Operating systems: Linux/Unix, OS X, and Windows

- Pre Web 2.0: CGI, PHP, HTML, MySQL, Apache2, and JavaScript

- Open science and reproducible research tools: git, GitHub, WordPress, Jekyll, and R Markdown/Markdown

Honours and Awards

2010	CSIRO Chairman's Medal
2008	CSIRO Partnership Excellence Award

Academic and Administrative Experience

2015	MODHEP Workshop presenter on analysing CAGE data using R
2013–2014	Organiser of the Chat with Guest sessions at RIKEN CLST DGT
2013–2014	Organiser of the Student Journal club at RIKEN CLST DGT
2013	Organising committee for the BrainTrain conference
2013	Organiser of the BrainTrain workshop: Identifying regulatory elements in the genome

Workshop and Course Attendances

2014	KI/RIKEN Doctoral Course: Employing Genome-wide Technologies for Functional Regulation in Development and Disease
2013	AMATA Conference ECR workshop
2013	Courseras Data Analysis from Johns Hopkins University
2013	BrainTrain courses and workshops
2013	RIKEN/KI Doctoral Course: Epigenomics: Methods and Applications to Disease and Development
2012	SISSA Summer School on Dopaminergic Neurons
2012	RIKEN/KI Doctoral Course: Functional regulation in development and disease
2011	UQ Winter School in Mathematical and Computational Biology
2011	RIKEN/EBI Bioinformatics Roadshow

Hobbies and Interests

Sports (especially basketball), cycling, blogging, self study, and computer games.

Academic references

Brian Dalrymple
Queensland Bioscience Precinct
306 Carmody Road
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Piero Carninci
RIKEN Yokohama Campus
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Publications

[1] **Tang, Dave** and Piero Carninci. The regulated expression of repetitive elements across human cell types and tissues. *In preparation*, 2015.

[2] **Tang, Dave**, Ana Maria Suzuki, Raffaella Calligaris, Stefano Gustincich, and Piero Carninci. Deep transcriptome sequencing of whole blood samples from Parkinson's disease patients. *In preparation*, 2015.

[3] Y. Hasegawa, **Tang, D.**, N. Takahashi, Y. Hayashizaki, A. R. Forrest, et al. CCL2 enhances pluripotency of human induced pluripotent stem cells by activating hypoxia related genes. *Sci Rep*, 4:5228, 2014. URL: http://www.ncbi.nlm.nih.gov/pubmed/24957798.

[4] **Tang, D. T.**, C. Plessy, M. Salimullah, A. M. Suzuki, R. Calligaris, S. Gustincich, and P. Carninci. Suppression of artifacts and barcode bias in high-throughput transcriptome analyses utilizing template switching. *Nucleic Acids Res.*, 41(3):e44, Feb 2013. URL: http://www.ncbi.nlm.nih.gov/pubmed/23180801.

[5] A. Saxena, **Tang, D.**, and P. Carninci. piRNAs warrant investigation in Rett Syndrome: an omics perspective. *Dis. Markers*, 33(5):261–275, 2012. URL: http://www.ncbi.nlm.nih.gov/pubmed/22976001.

[6] S. Francia, F. Michelini, A. Saxena, **Tang, D.**, M. de Hoon, V. Anelli, M. Mione, P. Carninci, and F. d'Adda di Fagagna. Site-specific DICER and DROSHA RNA products control the DNA-damage response. *Nature*, 488(7410):231–235, Aug 2012. URL: http://www.ncbi.nlm.nih.gov/pubmed/22722852.

[7] R. D. Thiagarajan, N. Cloonan, B. B. Gardiner, T. R. Mercer, G. Kolle, E. Nourbakhsh, S. Wani, **Tang, D.**, K. Krishnan, K. M. Georgas, B. A. Rumballe, H. S. Chiu, J. A. Steen, J. S. Mattick, M. H. Little, and S. M. Grimmond. Refining transcriptional programs in kidney development by integration of deep RNA-sequencing and array-based spatial profiling. *BMC Genomics*, 12:441, 2011. URL: http://www.ncbi.nlm.nih.gov/pubmed/21888672.

[8] R. D. Thiagarajan, K. M. Georgas, B. A. Rumballe, E. Lesieur, H. S. Chiu, D. Taylor, **Tang, D. T.**, S. M. Grimmond, and M. H. Little. Identification of anchor genes during kidney development defines ontological relationships, molecular subcompartments and regulatory pathways. *PLoS ONE*, 6(2):e17286, 2011. URL: http://www.ncbi.nlm.nih.gov/pubmed/21386911.

[9] H. S. Chiu, J. C. Szucsik, K. M. Georgas, J. L. Jones, B. A. Rumballe, **Tang, D.**, S. M. Grimmond, A. G. Lewis, B. J. Aronow, J. L. Lessard, and M. H. Little. Comparative

gene expression analysis of genital tubercle development reveals a putative appendicular Wnt7 network for the epidermal differentiation. *Dev. Biol.*, 344(2):1071–1087, Aug 2010. URL: http://www.ncbi.nlm.nih.gov/pubmed/20510229.

[10] N. Cloonan, Q. Xu, G. J. Faulkner, D. F. Taylor, **Tang, D. T.**, G. Kolle, and S. M. Grimmond. RNA-MATE: a recursive mapping strategy for high-throughput RNA-sequencing data. *Bioinformatics*, 25(19):2615–2616, Oct 2009. URL: http://www.ncbi.nlm.nih.gov/pubmed/19648138.

[11] K. Georgas, B. Rumballe, M. T. Valerius, H. S. Chiu, R. D. Thiagarajan, E. Lesieur, B. J. Aronow, E. W. Brunskill, A. N. Combes, **Tang, D.**, D. Taylor, S. M. Grimmond, S. S. Potter, A. P. McMahon, and M. H. Little. 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. *Dev. Biol.*, 332(2):273–286, Aug 2009. URL: http://www.ncbi.nlm.nih.gov/pubmed/19501082.

[12] **Tang, D. T.**, E. A. Glazov, S. M. McWilliam, W. C. Barris, and B. P. Dalrymple. Analysis of the complement and molecular evolution of tRNA genes in cow. *BMC Genomics*, 10:188, 2009. URL: http://www.ncbi.nlm.nih.gov/pubmed/19393063.

[13] J. W. Kijas, D. Townley, B. P. Dalrymple, M. P. Heaton, J. F. Maddox, A. McGrath, P. Wilson, R. G. Ingersoll, R. McCulloch, S. McWilliam, **Tang, D.**, J. McEwan, N. Cockett, V. H. Oddy, F. W. Nicholas, and H. Raadsma. A genome wide survey of SNP variation reveals the genetic structure of sheep breeds. *PLoS ONE*, 4(3):e4668, 2009. URL: http://www.ncbi.nlm.nih.gov/pubmed/19270757.