

Curriculum Vitae for Alistair R R Forrest

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Nationality: Australian/British **email:** alistair.forrest@gmail.com
Phone: 81-45-503-9220 (ext.3119) **fax:** 81-45-503-9216 **Date of Birth:** 23rd May 1971
ScholarProfile: <http://scholar.google.com.au/citations?user=lxBtOAoAAAAJ> **H-index:** 31

Degrees:

PhD in Bioinformatics, Institute for Molecular Bioscience, University of Queensland, 2006
Master of Information Technology, Queensland University of Technology, 2001
BSc (Hons first class) in Biotechnology, Murdoch University, 1993

Employment:

2013 – present Team Leader, Genome Information Analysis Team, RIKEN, CLST, Yokohama, Japan
2012 – 2013 Director, Bioinformatics Core Facility, RIKEN, OSC, Yokohama, Japan
2010 – 2013 Unit Leader, Genome Profiling Technology Unit, RIKEN, OSC, Yokohama, Japan
2009 – 2010 Senior Scientist, RIKEN, OSC, Yokohama, Japan
2007 – 2009 CJ Martin travelling Fellow, Visiting Senior Scientist, RIKEN, OSC, Yokohama, Japan;
Research Fellow Grade 2, The Eskitis Institute for Cell and Molecular Therapies, Griffith University
2006 – 2007 Research Officer, Institute for Molecular Biology, University of Queensland
2001 – 2006 Research Assistant, Institute for Molecular Biology, University of Queensland
1997 – 2001 Research Assistant, Joint Oncology Program, QLD Institute for Medical Research (QIMR)
1992 – 1993 Research Assistant, Murdoch University, Western Australia

Refereed journal articles (H-index - Google scholar 31, total citations > 6798. Underlining indicates first and corresponding authorships respectively)

[AF64] Forrest ARR *et al.* A promoter level expression atlas. *Nature* <http://dx.doi.org/10.1038/nature13182> (2014)

[AF63] Severin J *et al.* ZENBU: secured scientific collaborations, data integration and omics visualization. *Nature Biotechnology* <http://dx.doi.org/10.1038/nbt.2840> (2014)

[AF62] Andersson R *et al.* An atlas of active enhancers across human cell types and tissues *Nature* <http://dx.doi.org/10.1038/nature12787> (2014)

[AF61] Motakis E *et al.* Redefinition of the human mast cell transcriptome by deep sequencing *Blood* <http://dx.doi.org/10.1182/blood-2013-02-483792> (2014)

[AF60] Dimont, E. *et al.* CAGExploreR: an R package for the analysis and visualization of promoter dynamics across multiple experiments. *Bioinformatics* <http://dx.doi.org/10.1093/bioinformatics/btu125> (2014)

[AF59] Davis M *et al.* Transcriptional profiling of the human fibrillin/LTBP gene family, key regulators of mesenchymal cell functions. *Molecular Genetics and Metabolism* <http://dx.doi.org/10.1016/j.ymgme.2013.12.006> (2014)

[AF58] Rye M *et al.* Chromatin states reveal functional associations for globally defined transcription start sites in four human cell lines. *BMC Genomics* <http://dx.doi.org/10.1186/1471-2164-15-120> (2014)

[AF57] Arner E *et al.* Ceruloplasmin is a Novel Adipokine Which is Overexpressed in Adipose Tissue of Obese Subjects and in Obesity-Associated Cancer Cells *PLoS ONE* <http://dx.doi.org/10.1371/journal.pone.0080274> (2014)

[AF56] Rönnerblad M *et al.* Analysis of the DNA methylome and transcriptome in granulopoiesis reveal timed changes and dynamic enhancer methylation *Blood* <http://dx.doi.org/10.1182/blood-2013-02-482893> (2014)

[AF55] Schmidl C. *et al.* Transcription and enhancer profiling in human monocyte subsets *Blood* <http://dx.doi.org/10.1182/blood-2013-02-484188> (2014)

[AF54] Prasad P *et al.* High-throughput transcription profiling identifies putative epigenetic regulators of hematopoiesis *Blood* <http://dx.doi.org/10.1182/blood-2013-02-483537> (2014)

- [AF53] Morikawa *et al.* CAGE profiling and epigenetic factor reveal distinct gene network feature of regulatory T-cell *PNAS* <http://dx.doi.org/10.1073/pnas.1312717110> (2014)
- [AF52] Schmidl C. *et al.* The enhancer and promoter landscape of human regulatory and conventional T cell subpopulations <http://dx.doi.org/10.1182/blood-2013-02-486944> (2014)
- [AF51] Sandar A *et al.* The Evolution of Human Cells in terms of Protein Innovation *Molecular Biology and Evolution* <http://dx.doi.org/10.1093/molbev/mst139> (2014)
- [AF50] Kawaji H *et al.* Comparison of CAGE and RNA-seq transcriptome profiling using a clonally amplified and single molecule next generation sequencing *Genome Research* <http://dx.doi.org/10.1101/gr.156232.113> (2014)
- [AF49] Medvedeva Y *et al.* Effects of cytosine methylation on transcription factor binding sites *BMC Genomics* <http://dx.doi.org/10.1186/1471-2164-15-119> (2014)
- [AF48] Carrieri C, Cimatti L, Biagioli M, Beugnet A, Zucchelli S, Fedele S, Pesce E, Ferrer I, Collavin L, Santoro C, **Forrest ARR**, Carninci P, Biffo S, Stupka E, Gustincich S: Long non-coding antisense RNA controls Uchl1 translation through an embedded SINEB2 repeat. *Nature* doi:10.1038/nature11508 (2012)
- [AF47] Itoh M, Kojima M, Nagao-Sato S, Saijo E, Lassmann T, Kanamori-Katayama M, Kaiho A, Lizio M, Kawaji H, Carninci P, **Forrest ARR**, Hayashizaki Y. Automated Workflow for Preparation of cDNA for Cap Analysis of Gene Expression on a Single Molecule Sequencer., *PLoS ONE* 7(10): e30809. doi:10.1371/journal.pone.0030809 (2012)
- [AF46] Kanamori-Katayama M, Kaiho A, Ishizu Y, Okamura-Oho Y, Hino O, Abe M, Kishimoto T, Sekihara H, Nakamura Y, Suzuki H, **Forrest ARR**, Hayashizaki Y. LRRN4 and UPK3B are markers of primary mesothelial cells., *PLoS ONE* 6(10): e25391. doi:10.1371/journal.pone.0025391 (2011)
- [AF45] Hasegawa Y, Takahashi N, **Forrest ARR**, Shin JW, Kinoshita Y, Suzuki H, Hayashizaki Y CC chemokine ligand 2 and LIF cooperatively promote pluripotency in mouse induced pluripotent cells. *Stem Cells* doi: 10.1002/stem.673 (2011)
- [AF44] Kanamori-Katayama M, Itoh M, Hideya K, Lassmann T, Katayama S, Kojima M, Bertin N, Kaiho A, Ninomiya N, Daub CO, Carninci P, **Forrest ARR**, Hayashizaki Y. Unamplified Cap Analysis of Gene Expression on a single molecule sequencer. *Genome Research* doi: 10.1101/gr.115469.110 (2011)
- [AF43] Kawaji H, Severin J, Lizio M, **Forrest AR**, van Nimwegen E, Rehli M, Schroder K, Irvine K, Suzuki H, Carninci P, Hayashizaki Y, Daub CO. Update of the FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. *Nucleic Acids Res* 2010 Nov 12
- [AF42] Vitezic M, Lassmann T, **Forrest AR**, Suzuki M, Tomaru Y, Kawai J, Carninci P, Suzuki H, Hayashizaki Y, Daub CO. Building promoter aware transcriptional regulatory networks using siRNA perturbation and deepCAGE. *Nucleic Acids Res* (2010) doi: 10.1093/nar/gkq729
- [AF41] Kubosaki A, Lindgren G, Tagami M, Simon C, Tomaru Y, Miura H, Suzuki T, Arner E, **Forrest AR**, Irvine KM, et al. The combination of gene perturbation assay and CHIP-chip reveals functional direct target genes for IRF8 in THP-1 cells. *Mol Immunol.* (2010) 10.1016/j.molimm.2010.05.289
- [AF40] Ravasi T, Cannistraci C, Katayama S, Bajic V, Tan K, Akalin A, Schmeier S, Kamburov A, Kanamori M, Bertin N, Carninci P, Daub C, **Forrest A**, Gough J, Grimmond S, Han J, Hashimoto T, Hide W, Hofmann O, Kaur M, Kawaji H, Kubosaki A, Lassmann T, van Nimwegen E, MacPherson C, Ogawa C, Radovanovic A, Schwartz A, Teasdale R, Tegnér J, Lenhard B, Teichmann S, Hume D, Ideker T, Arakawa T, Ninomiya N, Murakami K, Tagami M, Fukuda S, Imamura K, Kai C, Ishihara R, Kitazume Y, Kawai J, Suzuki H, Hayashizaki Y. An atlas of combinatorial transcriptional regulation in mouse and man. *Cell* Mar 5;140(5):744-52 (2010)
- [AF39] **Forrest ARR**, Kanamori-Katayama M, Tomaru Y, Lassmann T, Ninomiya N, Takahashi Y, de Hoon MJL, Kubosaki A, Kaiho A, Suzuki M, Yasuda J, Kawai J, Hayashizaki Y, Hume DA, Suzuki H. Induction of microRNAs mir-155, mir-222, mir-424 and mir-503, promotes monocytic differentiation through combinatorial regulation. *Leukemia* 24: 460-466 (2010)
- [AF38] Tomaru Y, Simon C, **Forrest ARR**, Miura H, Kubosaki A, Hayashizaki Y, Suzuki M. Regulatory interdependence of myeloid transcription factors revealed by Matrix RNAi Analysis. *Genome Biology* 10:R121 (2009)
- [AF37] **Forrest ARR**, Abdelhamid RF, Carninci P. Annotating non-coding transcription using functional genomics strategies. *Brief Funct Genomic Proteomic* 8: 437-443 (2009); doi:10.1093/bfgp/elp041

[AF36] Takahashi Y, **Forrest A**, Maeno E, Hashimoto T, Daub C, Yasuda J. MiR-107 and miR-185 can induce cell cycle arrest in human non small cell lung cancer cell lines, *PLoS One* 4, 2009-08-18

[AF35] Suzuki H, **Forrest ARR**, van Nimwegen E, *et al.*: The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. *Nature Genetics* doi:10.1038/ng.375 (2009)

[AF34] Faulkner G, Kimura Y, Daub C, Wani S, Plessy C, Irvine K, Schroder K, Cloonan N, Steptoe A, Lassmann T, Waki K, Hornig N, Arakawa T, Takahashi H, Kawai J, **Forrest ARR**, Suzuki H, Hayashizaki Y, Hume D, Orlando V, Grimmond S, Carninci P: The regulated retrotransposon transcriptome of mammalian cells. *Nature Genetics* doi:10.1038/ng.368 (2009)

[AF33] Taft R, Glazov E, Cloonan N, Simons C, Stephen S, Faulkner G, Lassmann T, **Forrest ARR**, Grimmond S, Schroder K, Irvine K, Arakawa T, Nakamura M, Kubosaki A, Hayashida K, Kawazu C, Murata M, Nishiyori H, Fukuda S, Kawai J, Daub C, Hume D, Suzuki H, Orlando V, Carninci P, Hayashizaki Y, Mattick J: Tiny RNAs associated with transcription start sites in animals. *Nature Genetics* doi:10.1038/ng.312 (2009)

[AF32] Severin JM, Waterhouse AM, Kawaji H, Lassmann T, van Nimwegen E, Balwierz PJ, de Hoon MJL, Hume DA, Carninci P, Hayashizaki Y, Suzuki H, Daub CO, **Forrest ARR**: FANTOM4 EdgeExpressDB: an integrated database of genes, microRNAs, their promoters, expression dynamics and regulatory interactions. *Genome Biology*. 10:R39 (2009)

[AF31] Kawaji H, Severin JM, Lizio M, Waterhouse AM, Katayama S, Irvine KM, Hume DA, **Forrest ARR**, Suzuki H, Carninci P, Hayashizaki Y, Daub CO: The FANTOM Web Resource: from mammalian transcriptional landscape to its dynamic regulation. *Genome Biology*. 10:R40 (2009)

[AF30] **Forrest ARR**, Carninci P. Whole genome transcriptome analysis *RNA Biology* Apr-Jun;6(2):5-8 (2009)

[AF29] Cloonan N, Brown MK, Steptoe AL, Wani S, Chan WL, **Forrest AR**, Kolle G, Gabrielli B, Grimmond SM. The miR-17-5p microRNA is a key regulator of the G1/S phase cell cycle transition. *Genome Biology* 9(8):R127 (2008)

[AF28] Cloonan N, **Forrest ARR**, Kolle G, Gardiner BA, Faulkner GJ, Brown MK, Taylor DF, Steptoe AL, Wani S, Bethel G, Robertson AJ, Perkins AC, Bruce SJ, Lee CC, Ranade SS, Peckham HE, Manning JM, McKernan KJ, Grimmond SM. Stem cell transcriptome profiling via massive-scale mRNA sequencing *Nature Methods* doi:10.1038/nmeth.1223 (2008)

[AF27] Faulkner GJ, **Forrest AR**, Chalk AM, Schroder K, Hayashizaki Y, Carninci P, Hume DA, Grimmond SM. A rescue strategy for multimapping short sequence tags refines surveys of transcriptional activity by CAGE. *Genomics*. 91(3):281-8 (2008)

[AF26] Pagan JK, Arnold J, Hanchard KJ, Kumar R, Bruno T, Jones MJ, Richard DJ, **Forrest A**, Spurdle A, Verdin E, Crossley M, Fanciulli M, Chenevix-Trench G, Young DB, Khanna KK: A novel corepressor, BCoR-L1, represses transcription through an interaction with CtBP. *J. Biol. Chem.* 282(20), 15248-15257 (2007)

[AF25] Carninci P, Sandelin A, Lenhard B, *et al.*: Genome-wide analysis of mammalian promoter architecture and evolution. *Nature Genetics* 38(6): 626-635 (2006)

[AF24] **Forrest ARR**, Taylor D, Fink L, Gongora M, Flegg C, Teasdale R, Suzuki H, Kanamori M, Kai C, Hayashizaki Y, Grimmond S: PhosphoregDB: The tissue and sub-cellular distribution of mammalian protein kinases and phosphatases. *BMC Bioinformatics* 7(82): 1-11 (2006)

[AF23] **Forrest ARR**, Taylor D, Crowe M, Chalk A, Waddell N, Kolle G, Faulkner G, Kodzius R, Katayama S, Wells C, Kai C, Kawai J, Carninci P, Hayashizaki Y, Grimmond S: Genome wide review of transcriptional complexity in mouse protein kinases and Phosphatases. *Genome Biology* 7(1):R5 (2006)

[AF22] Wells C, Chalk A, **Forrest A**, Taylor D, Waddell N, Schroder K, Himes R, Faulkner G, Lo S, Kasukawa T, Kawaji H, Kai C, Kawai J, Katayama S, Carninci P, Hayashizaki Y, Hume D, Grimmond S: Alternate transcription of the Toll-like receptor signalling cascade. *Genome Biology* 7(2):R10 (2006)

[AF21] Frith M, **Forrest A**, Nourbaksh E, Pang K, Kai C, Kawai J, Carninci P, Hayashizaki Y, Bailey T, Grimmond S: The abundance of short proteins in the mammalian proteome. *Plos Genetics* 2(4):e52 (2006)

[AF20] Frith M, Wilming L, **Forrest A**, Kawaji H, Tan S, Wahlestedt C, Bajic V, Kai C, Kawai J, Carninci P, Hayashizaki Y, Bailey T, Huminiecki L: Pseudo-Messenger RNA: Phantoms of the Transcriptome. *Plos Genetics* 2(4): e23 (2006)

[AF19] Maeda N, Kasukawa T, Oyama R, Gough J, Frith M, Engström P, Lenhard B, Aturaliya R, Batalov S, Beisel K, Bult C, Fletcher C, **Forrest A**, Furuno M, Hill D, Itoh M, Kanamori-Katayama M, Katayama S, Katoh M, Kawashima T, Quackenbush J, Ravasi T, Ring B, Shibata K, Sugiura K, Takenaka Y, Teasdale R, Wells C, Zhu Y, Kai C, Kawai J, Hume D, Carninci P, Hayashizaki Y: Transcript annotation in FANTOM3-Mouse gene catalog based on physical cDNAs. *Plos Genetics* 2(4): e62 (2006)

- [AF18] Aturaliya R, Fink JL, Davis M, Teasdale M, Hanson K, Miranda K, **Forrest AR**, Grimmond S, Suzuki H, Kanamori M, Kai C, Hayashizaki Y, Teasdale T: Subcellular Localization of Mammalian Type II Membrane Proteins. *Traffic* 7(5): 613-625 (2006)
- [AF17] McGlinn E, van Bueren KL, Fiorenza S, Mo R, Poh AM, **Forrest A**, Soares MB, Bonaldo MD, Grimmond S, Hui CC, Wainwright B, Wicking C: Pax9 and Jagged1 act downstream of Gli3 in vertebrate limb development. *Mech. Dev.* 122(11): 1218-33 (2005)
- [AF16] Carninci P, Kasukawa T, Katayama S, *et al.*: The transcriptional landscape of the mammalian genome. *Science* 309(5740):1559-63 (2005)
- [AF15] Rae FK, Martinez G, Gillinder KR, Smith A, Shooter G, **Forrest AR**, Grimmond SM, Little MH: Analysis of complementary expression profiles following WT1 induction versus repression reveals the cholesterol/fatty acid synthetic pathways as a possible major target of WT1. *Oncogene*. 23(17):3067-79 (2004)
- [AF14] **Forrest AR**, Ravasi T, Taylor D, Huber T, Hume DA, Grimmond S; RIKEN GER Group; GSL Members: Phosphoregulators: protein kinases and protein phosphatases of mouse. *Genome Res.* 13(6B):1443-54 (2003)
- [AF13] **Forrest AR**, Taylor D, Grimmond S; RIKEN GER Group; GSL Members: Exploration of the cell-cycle genes found within the RIKEN FANTOM2 data set. *Genome Res.* 13(6B):1366-75 (2003)
- [AF12] Giles N, **Forrest A**, Gabrielli B: 14-3-3 acts as an intramolecular bridge to regulate cdc25B localization and activity. *J Biol Chem.* 278(31):28580-7 (2003)
- [AF11] Ravasi T, Huber T, Zavolan M, **Forrest A**, Gaasterland T, Grimmond S, Hume DA; RIKEN GER Group; GSL Members: Systematic characterization of the zinc-finger-containing proteins in the mouse transcriptome. *Genome Res.* 13(6B):1430-42. (2003)
- [AF10] Sousa-Nunes R, Rana AA, Kettleborough R, Brickman JM, Clements M, **Forrest A**, Grimmond S, Avner P, Smith JC, Dunwoodie SL, Beddington RS: Characterizing embryonic gene expression patterns in the mouse using nonredundant sequence-based selection. *Genome Res.* 13(12):2609-20 (2003)
- [AF9] Okazaki Y, Furuno M, Kasukawa T, *et al.*: Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. *Nature* 420(6915):563-73. (2002)
- [AF8] Ravasi T, Wells C, **Forrest A**, Underhill DM, Wainwright BJ, Aderem A, Grimmond S, Hume DA: Generation of diversity in the innate immune system: macrophage heterogeneity arises from gene-autonomous transcriptional probability of individual inducible genes. *J Immunol.* 168(1):44-50. (2002)
- [AF7] Ingram WJ, Wicking CA, Grimmond SM, **Forrest AR**, Wainwright BJ: Novel genes regulated by Sonic Hedgehog in pluripotent mesenchymal cells. *Oncogene*. 21(53):8196-205. (2002)
- [AF6] Maguire, T.L., Grimmond, S., **Forrest, A.**, Iturbe-Ormaetxe, I., Meksem, K., and Gresshoff, PM: cDNA microarray analysis of soybean (Glycine max): tissue-specific gene expression. *Journal of Plant Physiology* 159:1361-1374. (2002)
- [AF5] **Forrest A**, Gabrielli B: Cdc25B activity is regulated by 14-3-3. *Oncogene*. 20(32):4393-401. (2001)
- [AF4] Goldstone S, Pavey S, **Forrest A**, Sinnamon J, Gabrielli B: Cdc25-dependent activation of cyclin A/cdk2 is blocked in G2 phase arrested cells independently of ATM/ATR. *Oncogene*. 20(8):921-32. (2001)
- [AF3] Davezac N, Baldin V, Gabrielli B, **Forrest A**, Theis-Febvre N, Yashida M, Ducommun B: Regulation of CDC25B phosphatases subcellular localization. *Oncogene*. 19(18):2179-85. (2000)
- [AF2] **Forrest, ARR**, McCormack A, DeSouza C, Sinnamon J, Tonks I, Hayward N, Ellem K, Gabrielli B: Multiple Splicing Variants of cdc25B Regulate G2/M Progression. *BBRC*. 260:510-515 (1999)
- [AF1] **Forrest AR**, Carnegie PR: Identification of gourmet meat using FINS (forensically informative nucleotide sequencing). *Biotechniques* 17(1):24, 26. (1994)

Databases/websites

ZENBU	http://fantom.gsc.riken.jp/zenbu
The FANTOM web resource	http://fantom.gsc.riken.jp
FANTOM4 EdgeExpressDB	http://fantom.gsc.riken.jp/4/edgeexpress
Phosphoregulator Database	http://Phosphoreg.imb.uq.edu.au

Prizes:

- 2010 – OSCAWARD - FANTOM4 Project, Group Member
- 2007 – Dean’s commendation for outstanding Research Higher Degree Thesis 2006
- 2006 – Queensland Premier’s Awards for Health and Medical Research, Finalist Postgraduate student Award
- 2005 – 19th International Mouse Genome Conference – “Genomics” outstanding research poster
- 2005 – 19th International Mouse Genome Conference – Conference scholarship

- 2005 – Australian Microarray and Associated Technologies Association, travel bursary
- 2005 – 26th Lorne genome Promega student talk award
- 2004 – Australian Society for Medical Research Postgraduate Conference Poster award
- 2004 – 25th Lorne genome student poster prize
- 2003 – 3rd Australian Microarray conference student poster prize
- 2003 – University of Queensland Graduate School Scholarship (UQGSS)
- 2002 – Institute for Molecular Bioscience Symposium poster prize

Invitations:

- 2014 – TBD, Prion2014, Trieste, Italy
- 2014 – TBD, UT-ORNL-KBRIN Bioinformatics Summit 2014, Kentucky, USA
- 2014 – *FANTOM5: a mammalian promoter and enhancer atlas*, Institute for Molecular Bioscience, Brisbane, Australia
- 2014 – *FANTOM5: a promoter level expression atlas*, 13th Asian Conference on Transcription, Melbourne, Australia
- 2013 – *FANTOM5: a promoter level expression atlas*, Molecular biology Society of Japan MBSJ2013, Kobe, Japan
- 2013 – *FANTOM5: a promoter level expression atlas*, Combio2013, Perth, Australia
- 2013 – *FANTOM5: a promoter level expression atlas*, RIKEN-McGill University Joint workshop, Montreal, Canada
- 2013 – *FANTOM5: a promoter level expression atlas*, The 24th RIKEN CDB Meeting: Genomics and Epigenomics with Deep Sequencing, Kobe, Japan
- 2012 – A promoter level expression atlas using single molecule sequencing. 7th International Chick Meeting, Nagoya, Japan
- 2012 – Plenary: *The FANTOM5 Project – A promoter level expression atlas using single molecule sequencing*. 8th International Conference on Bioinformatics of genome regulation and structure\Systems Biology BGRS\SB'2012, Novosibirsk, Russia
- 2011 – *FANTOM5: A complete catalog of promoters used to regulate distinct cellular states*. 84th Japanese Biochemical Society meeting, Kyoto, Japan, (speaker and symposium co-organiser)
- 2008 – *Systems biology - lessons learnt from FANTOM4*, Adult stem cells – biology and clinical applications, Brisbane, Australia
- 2007 – Plenary: *SOLiD Sequencing of the mammalian transcriptome* MGED10, Sep 5, Brisbane, Australia
- 2006 – FANTOM4 meeting, RIKEN GSC, Yokohama, JAPAN
- 2006 – *Functional annotation of protein kinases and phosphatases* The Otago Genomics Facility Microarray Meeting, NZ
- 2005 – *Defining the components of protein phosphorylation systems Sub-cellular localization, tissue restriction and alternative transcripts of mouse protein kinases and phosphatases* The Salk Institute, San Diego, USA
- 2005 – *Alternate splicing array optimisation using the CombiMatrix CustomArray*, Australian Microarray Conference 2005, Barossa, Australia
- 2004 – FANTOM3 Harvest meeting, RIKEN GSC, Wako, JAPAN
- 2004 – FANTOM3 Tanabata meeting, RIKEN GSC, Yokohama, JAPAN
- 2004 – *Phosphoregulators meet functional genomics: characterisation of novel protein kinases and protein phosphatases using reverse transfection arrays and megaprime PCR*, GATAAG seminar series, University of Queensland, Australia
- 2003 – *Microarray Informatics*, Sir Charles Gardner Hospital, Perth, Australia
- 2002 – FANTOM2 Cherry blossom meeting, RIKEN GSC, Yokohama, JAPAN

Professional skills:

Reviewing

- 'Science', 'Acta Hematologica', 'BMC systems biology', 'Bioinformatics', 'BMC Genomics', 'Genome Biology', 'Molecular Biosystems', 'JMCB', 'PLoS ONE' and 'Genomics'
- Associate Editor – Frontiers in non-coding RNA
- Editorial board – Biology Direct (Non-coding DNA and RNA section)
- PhD theses examined – 2

Conference organization:

International Conference on Genome Informatics (GIW 2013) Singapore 2013

- Program committee

FANTOM5 consortium meetings – Yokohama 2011

- Overall organizer for the Ume blossom meeting (Feb 2011) and the Koyo meeting (Oct 2011)

Intelligent Systems for Molecular Biology (ISMB 2003)

- Student volunteer, reviewed abstracts
- This is the annual meeting of the International Society for Computational Biology (ISCB) and as such is the largest International Bioinformatics meeting.

Australian Microarray and Associated Technology Association (AMATA 2002)

- Student volunteer/organizer, assisted in review and collation of abstracts

Society affiliations:

2010–	Member, International Society of Differentiation
2009–	Member, Molecular Biology Society of Japan
2005–07	Member, American Association for the Advancement of Science
2005-07	Member, International Mammalian genome Society
2005-07	Member, Australian Society for Medical Research
2002-07	Member, Australian Microarray and Associated Technologies Association

Previous Funding:

2007 – 2009	Transcriptional complexity in mammalian genome networks. \$542,069 Australian NHMRC, CJ Martin fellowship; RegKey: 428261
2010 – 2011	“Gene activating RNAs based on naturally occurring promoter associated RNAs” Japanese MEXT grants-in-aid (Kakenhi) – “Challenging exploratory research” Grant number: 22651077; Funding ¥3,200,000 Applicant: <u>FORREST ARR</u> Role: Primary Investigator
2010 – 2013	Characterization of Haemopoietic Lineage Determining Genes Australian NHMRC project grant; RegKey: 634494; Funding: \$608,500 Applicants: <u>KLINKEN SP</u> , FORREST ARR, BOND CS, WINTERINGHAM LN Role: Chief investigator B

Intellectual property:

- Provisional Patent Application in the U.S.A -Serial No. 61/469,399: *Functional Nucleic Acid Molecule and use thereof*; Inventors: Stefano Gustincich, Claudia Carrieri & Silvia Zucchelli (SISSA), Piero Carninci & Alistair Forrest (RIKEN)
- Provisional Patent Application in Japan Serial No.: 2011-077473: *The Chemical which enhances and maintenances pluripotency and use thereof*. Yuki Hasegawa, Alistair Forrest, Harukazu Suzuki (RIKEN)