

# TOMAS BABAK

Assistant Professor

Department of Biology, Queen's University

Kingston ON K7L 3N6

Tel: 613-533-6131

E-Mail: [tomas.babak@queensu.ca](mailto:tomas.babak@queensu.ca) (updated May 2015)

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## EDUCATION

Nov 2007	University of Toronto, Toronto ON CAN	Ph.D.	Molecular Genetics
May 2002	Queen's University, Kingston ON CAN	Hon. B.Sc.	Biology

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## PROFESSIONAL EXPERIENCE

Jul 2014 – Present	Assistant Professor	Department of Biology, Queen's University, Kingston ON CAN
Jan 2012 – Jun 2014	Research Fellow	Lab of Hunter B. Fraser, Ph.D., Department of Biology Stanford University, Stanford CA USA
Feb 2012 – July 2012	Consultant	Molecular Methods Development Group, NuGen, San Carlos CA USA
Nov 2009 – Dec 2011	Head	Sequencing Methods Development Lab, Merck Research Laboratories, Boston MA USA
Oct 2008 – Oct 2009	Sr. Research Scientist	Department of Informatics and Analysis, Merck Research Laboratories, Boston MA USA
Feb 2007 – Sept 2008	Postdoctoral Fellow	Supervisor: Lee P. Lim, Ph.D. Rosetta Inpharmatics, Seattle WA USA

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## HONOURS AND AWARDS

Nov 2014	Junior Investigator Grant Panel Travel Award – Canadian Cancer Society
Nov 2014	Faculty Travel Award – Queen's University
2006 – 2007	University of Toronto Open Fellowship
2004 – 2006	National Sciences and Engineering Research Council Doctoral Award (PGS-D)
2002 – 2004	National Sciences and Engineering Research Council Award (PGS-A)
2002	Beth Parker Memorial Bursary: Summer student research grant from Epilepsy Canada
1998-2002	Chernoff Family Award Undergraduate Scholarship, Queen's University
2000	Wallace Near Prize in Biology, Queen's University
1999	William I. Chischolm Scholarship in Biology, Queen's University
1999	Annie Bentley Lillie Prize, Queen's University
1999	WT MacClement Memorial Prize, Queen's University

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## GRANTS

2015-2018	CBCF Ontario Operating Grant. <i>Characterizing cis-regulatory drivers of breast cancer.</i>	\$446,575 (applied)
2015-2017	CQDM/OCE Explore Program. <i>Establishing efficacious drug targets through single-cell genetic interactions in human cells.</i>	\$297,307 (applied)
2015-2019	Canada Foundation for Innovation (JELF). <i>Nextgen sequencing laboratory for methods development and deciphering genomic and epigenetic causes of complex disease.</i>	\$300,000
2015-2016	RAC Computing Grant (Compute Canada Resource Allocation). 1 CPU hour valued at \$1-\$3 commercially.	1 million CPU hours
2014-2019	Research Initiation Grant. Faculty of Arts & Science, Queen's University.	\$100,000
2011-2012	McLaughlin Accelerator Grant in Genomic Medicine. <i>Identifying cis-acting effects associated with Schizophrenia and Bipolar disorder by mapping allele-specific expression.</i>	\$70,000
2010-2012	NIH R21 Grant (HG005240-01A1) awarded to Hunter B. Fraser and Tomas Babak. <i>Genome-wide discovery of allele-specific chromatin states and gene expression.</i>	\$276,500
2009-2010	Canadian School of Energy and Environment Grant, awarded to Gordon Chua and Tomas Babak. <i>Genomic characterization of hydrocarbon-producing algae.</i>	\$50,000

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## FORMAL TEACHING EXPERIENCE

<u>YEAR</u>	<u>QTR</u>	<u>COURSE</u>	<u>LECTURES/HOURS</u>
2015	Winter	4 <sup>th</sup> Year, Era of Big Data	36 lectures
2014	Fall	Bioinformatics Graduate Club – Next Gen Sequencing	10 lectures
2014	Fall	3 <sup>rd</sup> Year, Cell Biology (BIO330) – Co-taught	10 lectures
2003 – 2006	Fall & Winter	Teaching Assistant; 2 <sup>nd</sup> Year Biology (BIO250) University of Toronto.	180 hrs/year
2000 – 2002	Fall & Winter	Teaching Assistant; 1 <sup>st</sup> Year Physics (PHYS106) Queen's University.	80 hrs/year
2002	Spring	Student Practicum, High School Physics. Regiopolis-Notre Dame Secondary School.	2 weeks

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## PROFESSIONAL ASSOCIATIONS & ACTIVITIES

2014 – present	Advanced Computing & Analytics Committee, Queen's University (Planning committee for creating a high throughput computing-oriented institute for teaching and research)
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2014 – present	Graduate student committee member (contribute to graduate student policies and education)
2013 – 2014	Faculty 1000 Member
2006 – 2007	President: Graduate Student Association, Dept. of Molecular Genetics, University of Toronto (Elected position, represented ~200 graduate students in political and social mandates, implemented a 'time-to-completion' program)
2006	Faculty Search Committee, Dept. of Molecular Genetics, University of Toronto (Graduate student representative with voting privileges)
2001 – 2002	Don, Queen's University Residences, Leonard Hall

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## PUBLICATIONS (citations; May 2015)

1. Tehranchi A, Fraser HB, **Babak T.** (in preparation) mRNA-capture for sequencing the expressed genome.
2. DeVeale B, York R, Zhou Y, Fraser HB, **Babak T.** (in preparation) Differential alternative splicing of glutamate receptors predicts their cellular localization and schizophrenia.
3. **Babak T,** Fraser HB. (in preparation) trueASE: a method for reliably estimating confidence of allele-specific expression measured with RNA-Seq.
4. **Babak T,** DeVeale B, Tsang EK, Zhou Y, Li X, Smith KS, Kukurba KR, Zhang R, Li JB, van der Kooy D, Montgomery SB, Fraser HB. (2015) Genetic conflict reflected in tissue-specific maps of genomic imprinting in human and mouse. **Nature Genetics** April 13; 47:544-9. **(1 citation)**
5. DeVeale B, Brokhman I, Mohseni P, **Babak T,** Yoon C, Lin A, Onishi K, Tomilin A, Pevny L, Zandstra PW, Nagy A, van der Kooy D. (2014) Oct4 is required ~E7.5 for proliferation in the primitive streak. **PLoS Genetics** Nov;9(11):e1003957. **(9 citations)**
6. DeVeale B, van der Kooy D, **Babak T.** (2012) Critical evaluation of imprinted gene expression by RNA-Seq: a new perspective. **PLoS Genetics** Mar;8(3):e1002600. **(106 citations)**  
  
Featured In:
  - Imprinted Genes ... and the Number Is? *PLoS Genetics* e1002600, Kelsey G, Bartolomei M. (2012).
  - Fewer imprinted genes at re-count. *Nature* 484: 145, Shen H. (2012).
  - RNA studies under fire. *Nature* 484: 428, Hayden EC. (2012).
7. Derti A, Garrett-Engle P, Macisaac KD, Stevens RC, Sriram S, Chen R, Rohl CA, Johnson JM, **Babak T.** (2012) A quantitative atlas of polyadenylation in five mammals. **Genome Research** Jun;22(6):1173-83. **(102 citations)**

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Featured In: Sequencing the end. *Nature Methods* 9, 534 (2012). | doi:10.1038/nmeth.2050

8. **Babak T.** (2012) Imprinting Discovery from RNA-Seq Data. **Methods Mol Biol** 925:79-88 (**2 citation**)
9. Singh-Babak SD, **Babak T**, Diezmann S, Hill JA, Xie JL, Chen YL, Poutanen SM, Rennie RP, Heitman J, Cowen LE. (2012) Global Analysis of the Evolution and Mechanism of Echinocandin Resistance in *Candida glabrata*. **PLoS Pathogens** e1002718 (**32 citations**)
10. Fraser HB, **Babak T**, Tsang J, Zhang B, Mehrabian M, Schadt EE. (2011) Systematic detection of polygenic cis-regulatory evolution. **PLoS Genetics** Mar;7(3):e1002023 (**31 citations**)
11. Vignali M, Armour CD, Chen J, Morrison R, Castle JC, Biery MC, Bouzek H, Moon W, **Babak T**, Fried M, Raymond CK, Duffy PE. (2011) NSR-seq transcriptional profiling enables identification of a gene signature of *Plasmodium falciparum* parasites infecting children. **J Clin Invest** 121(3):1119-29 (**16 citations**)
12. **Babak T**, Garret-Engle P, Armour C, Raymond C, Johnson JM, Fraser HA,\* Schadt EE\*, (2010) Genetic validation of whole-transcriptome sequencing for mapping expression affected by cis-regulatory variation. **BMC Genomics** 13;11:473 (**27 citations**)
13. Yang F, **Babak T**, Shendure J, Disteche CM. (2010) Global survey of escape from X inactivation by RNA-sequencing in mouse. **Genome Research** 20(5):614-622 (**137 citations**)
14. Khanna M, Van Bakel H, Tang X, Calarco JA, **Babak T**, Guo G, Emili A, Greenblatt JF, Hughes TR, Krogan NJ et al. (2009) A systematic characterization of Cwc21, the yeast ortholog of the human spliceosomal protein SRm300. **RNA** 15:2174-2185 (**17 citations**)
15. Armour CD, Castle JC, Chen R, **Babak T**, Loerch P, Jackson S, Shah JK, Dey J, Rohl C, Johnson JM, Raymond CK. (2009) Digital profiling of whole transcriptomes using selective hexamer priming for cDNA synthesis. **Nature Methods** 6(9):647-9 (**119 citations**)
16. Chan ET, Quon, GT, Chua G, **Babak T**, Trochesset M, Zirngibl RA, Aubin J, Ratcliffe M, Wilde A, Brudno M, Morris QD, Hughes TR. (2009) Conservation of core gene expression in vertebrate tissues. **Journal of Biology** 8:33 (**98 citations**)
17. Coughlin DJ, **Babak T**, Nihrazn C, Hughes TR, Engelke DR. (2009) Prediction and verification of mouse tRNA gene families. **RNA Biology** 31:6(2) (**12 citations**)
18. **Babak T,\*** DeVeale B,\* Armour CD, Raymond CK, Cleary MA, van der Kooy DD, Johnson JM, Lim LP. (2008) Global survey of genomic imprinting by transcriptome sequencing. **Current Biology**, 18: 1735-1741 (**117 citations**)

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19. Marcon E, **Babak T**, Chua G, Hughes T, Moens PB. (2008) miRNA and piRNA localization in the male mammalian meiotic nucleus. **Chromosome Research** 16(2):243-60 (**70 citations**)
20. Huang JC\*, **Babak T\***, Corson TW, Chua G, Khan S, Gallie BL, Hughes TR, Blencowe BJ, Frey BJ, Morris QD. (2007) Using expression profiling data to identify human miRNA targets. **Nature Methods** 4(12):1045-9 (**271 citations**)
21. Lecuyer E, Yoshida H, Parthasarathy N, Alm C, **Babak T**, Cerovina T, Hughes TR, Tomancak P, Krause HM. (2007) Global analysis of mRNA localization reveals a prominent role in organizing cellular architecture and function. **Cell** 131(1):174-87 (**437 citations**)
22. Fagnani M, Barash Y, Ip JY, Misquitta C, Pan Q, Saltzman AL, Shai O, Lee L, Rozenhek A, Mohammad N, Willaime-Morawek S, **Babak T**, Zhang W, Hughes TR, van der Kooy D, Frey BJ, Blencowe BJ. (2007) Functional coordination of alternative splicing in the mammalian central nervous system. **Genome Biology** 8(6):R108 (**71 citations**)
23. **Babak T**, Blencowe BJ, Hughes TR. (2007) Considerations in the identification of functional RNA structural elements in genomic alignments. **BMC Bioinformatics** 8:33 (**52 citations**)
24. Tadros W, Goldman AL, **Babak T**, Menzies F, Vardy L, Orr-Weaver T, Hughes TR, Westwood JT, Smibert CA, Lipshitz HD. (2007) SMAUG is a major regulator of maternal mRNA destabilization in *Drosophila* and its translation is activated by the PAN GU kinase. **Developmental Cell** 12(1):143-55 (**140 citations**)
25. Hughes TR, Hiley SL, Saltzman AL, **Babak T**, Blencowe BJ. (2006) Microarray analysis of RNA processing and modification. **Methods Enzymology** 410:300-16 (**21 citations**)
26. **Babak T**, Blencowe BJ, Hughes TR. (2005) A systematic search for new mammalian noncoding RNAs indicates little conserved intergenic transcription. **BMC Genomics** 6:104 (**59 citations**)
27. Hiley SL, **Babak T**, Hughes TR. (2005) Global analysis of yeast RNA processing identifies new targets of RNase III and uncovers a link between tRNA 5' end processing and tRNA splicing. **Nucleic Acids Research** 33(9):3048-56 (**22 citations**)
28. Hiley SL, Jackman J, **Babak T**, Trochesset M, Morris QD, Phizicky E, Hughes TR. (2005) Detection and discovery of RNA modifications using microarrays. **Nucleic Acids Research** 33(1):e2 (**31 citations**)
29. Pan Q, Shai O, Misquitta C, Zhang W, Saltzman AL, Mohammad N, **Babak T**, Siu H, Hughes TR, Morris QD, Frey BJ, Blencowe BJ. (2004) Revealing global regulatory features of mammalian alternative splicing using a quantitative microarray platform. **Molecular Cell** 16(6):929-41 (**292 citations**)
30. **Babak T**, Zhang W, Morris Q, Blencowe BJ, Hughes TR. (2004) Probing microRNAs with microarrays: tissue specificity and functional inference. **RNA** 10(11):1813-9 (**336 citations**)

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## PRESENTATIONS (\*Invited)

<u>DATE</u>	<u>MEETING/INSTITUTION</u>	<u>LOCATION</u>
Nov 25 2014	*Department of Pathology & Medicine, Queen's University. <i>Linking gene expression to phenotype with allele-specific expression: genomic imprinting as a case study.</i>	Kingston, ON CAN
Jun 12 2014	Society for Molecular Biology and Evolution. <i>Genetic conflict reflected in tissue specific maps of genomic imprinting.</i>	San Juan, Puerto Rico USA
Oct 15 2013	*Institute of Molecular Life Sciences. <i>Elucidating evolutionary origins of genomic imprinting through a cross-species transcriptome comparison</i>	University of Zurich, Switzerland
Oct 9 2013	*Next-Generation Sequencing and Bioinformatics Summit. <i>Integrating RNA-Seq features to understand schizophrenia and bipolar disease</i>	Berlin, Germany
Jun 19 2013	*RNA-Seq Summit, Hanson-Wade Meeting. <i>Global mapping of allele-specific expression to understand complex disease.</i>	Boston, MA USA
June 21 2013	*Next Generation Sequencing: GTC-Bio Meeting. <i>Global mapping of allele-specific expression to understand complex disease</i>	San Francisco, CA USA
Feb 20 2013	*University of Pittsburgh Lecture. <i>Integrating RNA-Seq features to understand non-mendelian phenotypes</i>	Pittsburgh, PA USA
Feb 13 2012	*Epigenetics of Common Diseases - Wellcome Trust Scientific Meeting. <i>Elucidating evolutionary origins of genomic imprinting through a cross-species transcriptomic comparison.</i>	Baltimore, MD USA
Apr 13 2011	*NuGEN Technical Symposium. <i>Spectrum of RNA-Seq applications: the next five years.</i>	San Francisco, CA USA
Nov 15 2010	*Oxford Global Next Generation Sequencing Congress. <i>Digital gene expression and global mapping of polyadenylation sites with PolyA-Seq.</i>	London, UK
Aug 2 2010	*Next Generation Sequencing & Genomic Medicine	San Francisco, CA USA

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Applications Summit (IBC). *Leveraging allele specific genomics for drug target identification.*

Oct 16 2009 \*40<sup>th</sup> Anniversary of the Department of Molecular Genetics – Toronto, ON CAN  
Scientific Symposium. *Mapping the causes of complex disorders through allele-specific expression.*

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