

**Dr. Simon Robert Vincent Knott**  
**Curriculum Vitae**

***Present Address***

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***Education***

- 1996-2001: B.Sc. (Hon)- Life Sciences, Queen's University, Canada
- 2002-2004: B.Sc. (Hon)- Computer Sciences, Queen's University, Canada
- 2004-2006: M.Sc.-Computer Science, Queen's University, Canada
- 2006-2011: Ph.D.-Computational Biology, University of Southern California

***Professional Experience***

- 2004-2006: M.Sc. Student at Queen's University, Canada. Machine learning and gene regulatory network inference
- 2006-2011: Ph.D. Student at University of Southern California. Computational and molecular analysis of genome-wide DNA-synthesis
- 2011-2014: Postdoctoral Fellow at Cold Spring Harbor Laboratory. Optimization of RNAi screening technology, tumor heterogeneity and metastasis
- 2014-2016: Research Investigator at Cold Spring Harbor Laboratory. Tumor heterogeneity, metastasis, *in vivo* RNAi screens and nanobody production
- 2014-2016: Visiting Scientist at CRUK, Cambridge Institute, United Kingdom. Target characterization and development of CRISPR/Cas9 tools for functional genomics
- 2016-: Research Scientist I, Cedars Sinai Medical Center. Associate Director of the Center for Bioinformatics and Functional Genomics.

***Professional Activities***

- 2012-: TransOMIC Technologies. Consultant
- 2012-: Pfizer Oncology. Played a primary role in transferring RNAi technologies into the company target identification pipeline
- 2013-: National Breast Cancer Coalition's Artemis Project for a Preventative Vaccine
- 2014-: National Breast Cancer Coalition's Artemis Project Prevention of Metastasis
- 2015-: Hope Funds for Cancer Research Scientific Advisory Committee

***Honors and Awards***

- 2006-2010: Center of Excellence in Genomics Ph.D. Fellowship
- 2010: Harrison M. Kurtz Memorial Award for most outstanding Ph.D.
- 2012-2015: Hope Funds For Cancer Postdoctoral Fellowship

***Invited Lectures and Presentations***

- 2005: IEEE International Conference on Control Applications, Toronto, ON, Canada
- 2008: DNA Replication and Genome Integrity, La Jolla, CA

- 2014: Discovery on Target Boston, MA
- 2015: Discovery on Target Boston, MA

***Supervisory and Teaching Experience***

- 2005: Teaching Assistant-Introduction to Computer Science I at Queen's University, Canada
- 2006: Teaching Assistant-Advanced Artificial Neural Networks at Queen's University, Canada
- 2012-: Supervisor of students and technicians at Cold Spring Harbor Laboratory, NY

### **Research Papers-Peer Reviewed**

1. Fernald GH, **Knott SRV**, Pachner A, Caillier S, Narayan K, Oksenberg JR, Mousavi P, Baranzini SE. Genome-wide network analysis reveals the global properties of IFN-beta immediate transcriptional effects in humans. *J Immunol.* 2007, 178(8): 5076-5085.
2. Szyjka SJ, Aparicio JG, Viggiani CJ, **Knott SRV**, Xu W, Tavaré S, Aparicio OM. Rad53 regulates replication fork restart after DNA damage in *S. cerevisiae*. *Genes Dev.* 2008, 22(14):1906-1920.
3. **Knott SRV**, Viggiani CV, Tavaré S, Aparicio OM. Genome-wide replication profiles indicate an expansive role for Rpd3L in regulating replication initiation timing or efficiency, and reveal genomic loci of Rpd3 function in *Saccharomyces cerevisiae*. *Genes Dev.* 2009, 23(9):1077-1090.
4. **Knott SRV**, Viggiani CV, Aparicio OM, Tavaré S. Strategies for analyzing highly enriched IP-chip datasets. *BMC Bioinformatics.* 2009, 10:305.
5. Viggiani CJ, **Knott SRV**, Aparicio OM. Genome-wide analysis of DNA synthesis by BrdU immunoprecipitation on tiling microarrays (BrdU-IP-chip) in *Saccharomyces cerevisiae*. *CSH Protoc* 2010, 2:2010.
6. **Knott SRV**, Mostafavi S, Mousavi P. A neural network based modeling and validation approach for identifying gene regulatory networks. *Neurocom.* 2010, 73(13-15):2419-2429.
7. Dalton JE, Kacheria TS, **Knott SRV**, Lebo MS, Nishitani A, Sanders LE, Stirling EJ, Winbush A, Arbeitman MN. Dynamic, mating-induced gene expression changes in female head and brain tissues of *Drosophila melanogaster*. *BMC Genomics.* 2010, 11:541.
8. **Knott SRV**, Peace JM, Ostrow AZ, Gan Y, Rex AE, Viggiani CJ, Tavaré S, Aparicio OM. Forkhead transcription factors establish origin timing and long-range clustering in *S. cerevisiae*. *Cell.* 2012, 148(1-2):99-111.
9. Ipsaro JJ, Haase AD, **Knott SRV**, Joshua-Tor L, Hannon GJ. The structural biochemistry of Zucchini implicates it as a nuclease in piRNA biogenesis. *Nature.* 2012, 491(7423):279-283.
10. Zhong Y, Nellimoottil T, Peace JM, **Knott SRV**, Villwock SK, Yee JM, Jancuska JM, Rege S, Tecklenburg M, Sclafani RA, Tavaré S, Aparicio OM. The level of origin firing inversely affects the rate of replication fork progression. *J Cell Biol.* 2013, 201(3):373-383.
11. Dalton JE, Fear JM, **Knott SRV**, Baker BS, McIntyre LM, Arbeitman MN. Male-specific Fruitless isoforms have different regulatory roles conferred by distinct zinc finger DNA binding domains. *BMC Genomics.* 2013, 27:14:659.
12. Ostrow AZ, Nellimoottil T, **Knott SRV**, Fox CA, Tavaré S, Aparicio OM. Fkh1 and Fkh2 bind multiple chromosomal elements in the *S. cerevisiae* genome with distinct specificities and cell cycle dynamics. *PLoS One.* 2014, 9(2):e87647.

13. **Knott SRV**, Maceli A, Erard N, Chang K, Marran K, Zhou X, Gordon A, El Demerdash O, Wagenblast E, Kim S, Fellmann C, Hannon GJ. A computational algorithm to predict shRNA potency. *Mol Cell*. 2014, 56(6):796-807.
14. Wagenblast E, Soto M, Gutiérrez-Ángel S, Hartl CA, Gable AL, Maceli AR, Erard N, Williams AM, Kim SY, Dickopf S, Harrell CJ, Smith AD, Perou CM, Wilkinson JE, Hannon GJ & **Knott SRV**. A model of breast cancer heterogeneity reveals vascular mimicry as a driver of metastasis. *Nature*. 2015, 520:358-362.
15. Wasik KA, Tam OH, **Knott SRV**, Falcioni I, Hammell M, Vagin VV, Hannon GJ. RNF17 blocks promiscuous activity of PIWI proteins in mouse testes. *Genes Dev*. 2015, 29(13):1403-1415.

***Research Papers-Peer Reviewed (Submitted)***

1. Knott SRV, Wagenblast E, Kim SY, Soto M, Khan S, Gable AL, Maceli AR, Dickopf S, Erard N, Harrell C, Perou CM, Wilkinson JE, Hannon GJ. Asparagine availability governs metastasis in a model of breast cancer. ***In review***.

### ***Research Papers-Non-Peer Reviewed***

1. **Knott SRV**, Mostafavi S, Mousavi P, Glasgow J. Genetic network inference via gene set stochastic sampling and sensitivity analysis. *IEEE International Conference on Control applications* (2005), Toronto, ON, Canada.
2. **Knott SRV**, Mostafavi S, Mousavi P. A neural network based approach for inference and verification of transcriptional regulatory interactions. *IEEE Engineering in Medicine and Biology Society Conference* (2006), New York, NY, USA.
3. **Knott SRV**, Mousavi P, Baranzini S. A systematic approach for identifying regulatory interactions in large temporal gene expression datasets from peripheral blood. *IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology* (2006), Toronto, ON, Canada.

## **Reviews**

1. **Knott SRV**, Viggiani CV, Aparicio OM. To promote and protect: Coordinating DNA replication and transcription for genome stability. *Epigenetics*. 2009, 4(6):362-365.

## **Papers in Preparation**

1. Knott SRV, Erard N, Khan S, Hannon GJ. An optimized CRISPR/Cas9 library for functional screens in mammalian cells. *In preparation*

## **Abstracts**

1. Mostafavi S, **Knott SRV**, Mousavi P. Inference of regulatory genetic interactions by neural networks. *Canadian Student Conference on Biomedical Computing* (2006), Kingston, ON, Canada.
2. Szyjka SS, Aparicio JG, Viggiani CJ, **Knott SRV**, Xu W, Tavaré S, Aparicio OM. Rad53 regulates replication restart after DNA damage in *S. cerevisiae*. *DNA Replication and Genome Integrity* (2008), La Jolla, CA, USA.
3. **Knott SRV**, Viggiani CJ, Tavaré S, Aparicio OM. Whole-genome replication timing profiles of Rpd3 complex mutants reveal distinct roles of Rpd3S and Rpd3L in regulating the initiation timing of replication origins in *S. cerevisiae*. *DNA Replication and Genome Integrity* (2008), La Jolla, CA, USA.
4. Zhong Y, Peace JM, **Knott SRV**, Tecklenburg M, Sclafani RA, Aparicio OM. Cdc7 regulates replication fork progression through damaged DNA. *Cold Spring Harbor Meeting on Eukaryotic DNA Replication & Genome Maintenance* (2009), Cold Spring Harbor, NY, USA.
5. **Knott SRV**, Viggiani CJ, Nellimooti T, Ostrow AZ, Tavaré S, Aparicio OM. Forkhead transcription factors as broad regulators of replication origin efficiency and/or timing in *S. cerevisiae*. *Cold Spring Harbor Meeting on Eukaryotic DNA Replication & Genome Maintenance* (2009), Cold Spring Harbor, NY, USA.
6. Aparicio OM, **Knott SRV**, Ostrow AZ, Peace JM, Gan Y, Kalhor R, Chen L, Tavaré S. Forkhead (Fox) transcription factors open a new dimension in understanding the epigenetic control of replication origins in *S. cerevisiae*. *FASEB* (2013), 27, 200.1.
7. **Knott SRV**. Optimized shRNA designs in combination with an improved mir backbone allows for more effective RNAi screening. *Discovery On Target* (2014), Boston, MA, USA.
8. **Knott SRV**. A computational algorithm to predict shRNA potency. *Discovery On Target* (2014), Boston, MA, USA.