

CURRICULUM VITAE

François Robert, Ph.D.

Institut de recherches cliniques de Montreal (IRCM)
 110 Avenue des Pins Ouest
 Montreal, Qc, Canada, H2W 1R7
 tel: 514-987-5737
 email: francois.robert@ircm.qc.ca
 web: <http://robertlab.org>

Degrees

1991/09 – 1994/06 B.Sc. (Biology), Université de Sherbrooke
 1994/09 – 1999/08 Ph.D. (Molecular Biology), Université de Sherbrooke
 Thesis: *Étude de la structure du complexe transcriptionnel de l'ARN polymérase II*
 Supervisor : Benoit Coulombe, Ph.D.

Postdoctoral training

1999/06 – 2003/07 Whitehead Institute for Biomedical Research (MIT)
 Research focus: Genome-wide Studies of Protein-DNA Interactions
 Supervisor: Richard A. Young, Ph.D.

Employment

Since 2003/07 Director, Laboratory of Chromatin and Genomic Expression, IRCM
 Since 2004/01 Accredited Member, *Programmes de biologie moléculaire*, Faculté des études supérieures, Université de Montréal
 Since 2016/07 Full IRCM Research Professor, IRCM
 Since 2017/06 Full Research Professor, Département de médecine, Faculté de médecine, Université de Montréal
 Since 2018/07 Accredited Member, Division of Experimental Medicine, Department of Medicine, McGill University
 Since 2018/08 Part-time Adjunct Professor, Department of Medicine, McGill University
 2011/05 – 2017/05 Associate Research Professor, Département de médecine, Faculté de médecine, Université de Montréal
 2010/07 – 2016/06 Associate IRCM Research Professor, IRCM
 2004/01 – 2011/05 Adjunct Researcher, Département de médecine, Faculté de médecine, Université de Montréal
 2004/11 – 2015/10 Scientific Advisor, Molecular Biology and Functional Genomics core facility, IRCM
 2011/11 – 2015/10 Director, Systems Biology and Medicinal Chemistry Research Division, IRCM
 2006/09 – 2009/09 Associate Professor, Département de biologie, Faculté des sciences, Université de Sherbrooke

Honors and awards

1996/07 – 1999/06 Ph.D. Scholarship, Fonds pour la formation de chercheurs et l'aide à la recherche (FCAR)
 1999 Dean's list, Faculté des Sciences de l'Université de Sherbrooke
 1999/07 – 2001/06 Postdoctoral Fellowship, Natural Sciences and Engineering Research Council of Canada (NSERC) – declined

1999/07 – 2001/06	Postdoctoral Fellowship, Fonds pour la formation de chercheurs et l'aide à la recherche (FCAR) – declined
1999/07 – 2002/06	Postdoctoral Fellowship, Medical Research Council of Canada (MRC) – declined
1999/07 – 2002/06	Postdoctoral Fellowship, National Cancer Institute of Canada (NCIC)
2004/07 – 2007/06	<i>Bourse de chercheur-boursier "Junior 1"</i> , Fonds de la recherche en santé du Québec (FRSQ) – declined
2004/07 – 2009/06	Young Investigator Award, Canadian Institutes of Health Research (CIHR)
2008/10	Maud Menten New Principal Investigator Prize (Biomedical Research), Institute of Genetics, Canadian Institutes of Health Research (CIHR)
2009/07 – 2011/06	<i>Bourse de chercheur-boursier "Junior 2"</i> , Fonds de la recherche en santé du Québec (FRSQ)
2012/07 – 2015/06	<i>Bourse de chercheur-boursier "Sénior Volet Fondamental"</i> , Fonds de la recherche en santé du Québec (FRSQ)
2017/07 – 2021/06	<i>Chaire de recherche FRQS</i> , Fonds de recherche du Québec — Santé (FRQS)

Grant and Program Review Committees

2009 – 2011	Member, Panel D (Nuclear signaling and transcriptional regulation), Operating grants, National Cancer Institute of Canada (NCIC)
2011	Member, Genomics Panel, Operating grants, Canadian Institutes of Health Research (CIHR)
2013 – 2015	Member, Evaluation committee, <i>Chercheur Boursier Junior 1</i> , Fonds de recherche du Québec — Santé (FRQS)
2015 – 2017	Member, Evaluation committee, Postdoctoral fellowships, Canadian Institutes of Health Research (CIHR)
2019 – Ongoing	Member, Biochemistry and Molecular Biology – B Panel, Operating grants, Canadian Institutes of Health Research (CIHR)

Meeting organization

2007/03	Co-organisor, 1 st IRCM Meeting on Systems Biology: Molecular Networks, Montreal, March 12-13, 2007
2008/03	Co-organisor, 2 nd IRCM Meeting on Systems Biology: Molecular Networks, Montreal, March 11-12, 2008
2009/10	Co-organisor, 3 rd IRCM Meeting on Systems Biology: Molecular Networks, Montreal, October 26-27, 2009
2010/05	Co-organisor, Colloque 106 on <i>L'expression et la fonction du génome au 78e Congrès de l'Association francophone pour le savoir</i> (ACFAS), Montréal, May 12, 2010

Infrastructure grants

2004/04 – 2005/03	Genome-Wide Aspects of Nuclear Activities, CFI, 146 673 \$ per year
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Operating grants

2003/04 – 2006/03	Regulatory Networks in Gene Expression: From the Genome to the Organism, Genome Québec/Canada, 3 666 667 \$ per year, PI: Benoit Coulombe, My role: co-investigator
2003/10 – 2006/09	Genome-Wide Contributions of Chromatin Regulators to Nuclear Functions (MOP64230), CIHR, 141 323 \$ per year
2004/07 – 2005/06	Genome-Wide Contributions of Chromatin Regulators to Nuclear Functions, FRSQ, 15 000 \$ per year
2005/07 – 2007/06	Deciphering the Protein-Protein and Protein-DNA Interactions Engaging AICD, Alzheimer Society of Canada, 74 524 \$ per year

2006/07 – 2009/06	Dissecting the Role of Histone Variant H2A.Z in Gene Expression, Cellular Senescence, and Cancer (017350), NCIC, 124 243 \$ per year, PI: Luc Gaudreau, My role: co-investigator
2007/04 – 2012/03	The Role of Chromatin in Cell Cycle Gene Transcription and DNA Replication (MOP82891), CIHR, 154 937 \$ per year
2008/10 – 2009/09	Systematic characterization of the proteome associated with specific genomic loci: A proof of concept (MOP89842), CIHR, 137 699 \$ per year
2009/04 – 2014/03	Shaping the euchromatic and heterochromatic landscapes by p400 complex-mediated incorporation of H2A.Z within the chromatin (MOP191732), CIHR, 151 354 \$ per year, PI: Luc Gaudreau, My role: co-investigator
2010/04 – 2014/03	<i>Programme de recherche IRCM sur l'interactome : Comprendre l'assemblage des machines moléculaires humaines et ses dérèglements lors de maladies</i> , FRSQ, 499 00 \$ per year, PI: Benoit Coulombe, My role: co-investigator
2010/10 – 2015/09	Deciphering epigenetics plasticity during hematopoietic stem cell differentiation, (MOP106427), CIHR, 176 515 \$ per year
2013/04 – 2018/05	Regulation of RNA polymerase II by the deubiquitinase Ubp15 (435833-2013), NSERC, 30 000\$ per year
2014/04 – 2019/03	Dissecting the writers, readers and function of the RNAPII CTD code (MOP133648), CIHR, 111 025 \$ per year
2015/04 – 2018/03	<i>Caractérisation du protéome associé à des loci génétiques d'intérêt</i> (2016-PR-191341), Fonds de recherche Nature et technologies (FRQNT), 47 450 \$ per year
2016/09 – 2018/08	Investigating the role of H2A.Z-mediated cryptic transcription in cancers (21388), Cancer Research Society (CRS), 60 000 \$ per year
2018/04 – 2023/03	Dissecting the function and mechanisms of the Mediator Kinase module (MOP156383), CIHR, 169 065 \$ per year
2018/04 – 2023/03	The role of Mediator in post-initiation events (2018-04518), NSERC, 37 000\$ per year
2019/04 – 2024/03	Disentangling the intricate functions of the RNA polymerase II CTD (MOP-162334), CIHR, 155 295\$ per year

Publications – Refereed research article

1. Robert F, Forget D, Li J, Greenblatt J, Coulombe B. Localization of subunits of transcription factors IIE and IIF immediately upstream of the transcriptional initiation site of the adenovirus major late promoter. *J Biol Chem.* 1996 Apr 12;271(15):8517-20.
2. Forget D, Robert F, Grondin G, Burton ZF, Greenblatt J, Coulombe B. RAP74 induces promoter contacts by RNA polymerase II upstream and downstream of a DNA bend centered on the TATA box. *Proc Natl Acad Sci U S A.* 1997 Jul 8;94(14):7150-5.
3. Robert F, Douziech M, Forget D, Egly JM, Greenblatt J, Burton ZF, Coulombe B. Wrapping of promoter DNA around the RNA polymerase II initiation complex induced by TFIIIF. *Mol Cell.* 1998 Sep;2(3):341-51.
4. Ren B, Robert F, Wyrick JJ, Aparicio O, Jennings EG, Simon I, Zeitlinger J, Schreiber J, Hannett N, Kanin E, Volkert TL, Wilson CJ, Bell SP, Young RA. Genome-wide location and function of DNA binding proteins. *Science.* 2000 Dec 22;290(5500):2306-9.
5. Adam M, Robert F, Larochelle M, Gaudreau L. H2A.Z is required for global chromatin integrity and for recruitment of RNA polymerase II under specific conditions. *Mol Cell Biol.* 2001 Sep;21(18):6270-9.
6. Robert F, Blanchette M, Maes O, Chabot B, Coulombe B. A human RNA polymerase II-containing complex associated with factors necessary for spliceosome assembly. *J Biol Chem.* 2002 Mar 15;277(11):9302-6.
7. Ng HH, Robert F, Young RA, Struhl K. Genome-wide location and regulated recruitment of the RSC nucleosome-remodeling complex. *Genes Dev.* 2002 Apr 1;16(7):806-19.
8. Lee TI, Rinaldi NJ, Robert F, Odom DT, Bar-Joseph Z, Gerber GK, Hannett NM, Harbison CT, Thompson CM, Simon I, Zeitlinger J, Jennings EG, Murray HL, Gordon DB, Ren B, Wyrick JJ, Tagne JB, Volkert TL,

- Fraenkel E, Gifford DK, Young RA. Transcriptional regulatory networks in *Saccharomyces cerevisiae*. *Science*. 2002 Oct 25;298(5594):799-804.
9. Ng HH, Robert F, Young RA, Struhl K. Targeted recruitment of Set1 histone methylase by elongating Pol II provides a localized mark and memory of recent transcriptional activity. *Mol Cell*. 2003 Mar;11(3):709-19.
 10. Bar-Joseph Z, Gerber GK, Lee TI, Rinaldi NJ, Yoo JY, Robert F, Gordon DB, Fraenkel E, Jaakkola TS, Young RA, Gifford DK. Computational discovery of gene modules and regulatory networks. *Nat Biotechnol*. 2003 Nov;21(11):1337-42.
 11. Robert F, Pokholok DK, Hannett NM, Rinaldi NJ, Chandy M, Rolfe A, Workman JL, Gifford DK, Young RA. Global position and recruitment of HATs and HDACs in the yeast genome. *Mol Cell*. 2004 Oct 22;16(2):199-209.
 12. Laganière J, Deblois G, Lefebvre C, Bataille AR, Robert F, Giguère V. From the Cover: Location analysis of estrogen receptor alpha target promoters reveals that FOXA1 defines a domain of the estrogen response. *Proc Natl Acad Sci U S A*. 2005 Aug 16;102(33):11651-6.
 13. Guillemette B, Bataille AR, Gévry N, Adam M, Blanchette M, Robert F, Gaudreau L. Variant histone H2A.Z is globally localized to the promoters of inactive yeast genes and regulates nucleosome positioning. *PLoS Biol*. 2005 Dec;3(12):e384.
 14. Nourani A, Robert F, Winston F. Evidence that Spt2/Sin1, an HMG-like factor, plays roles in transcription elongation, chromatin structure, and genome stability in *Saccharomyces cerevisiae*. *Mol Cell Biol*. 2006 Feb;26(4):1496-509.
 15. Blanchette M, Bataille AR, Chen X, Poitras C, Laganière J, Lefebvre C, Deblois G, Giguère V, Bergeron D, Coulombe B, Robert F. Genome-wide computational prediction of transcriptional regulatory modules reveals new insights into human gene expression. *Genome Res*. 2006 May;16(5):656-68.
 16. Larochelle M, Drouin S, Robert F, Turcotte B. Oxidative stress-activated zinc cluster protein Stb5 has dual activator/repressor functions required for pentose phosphate pathway regulation and NADPH production. *Mol Cell Biol*. 2006 Sep;26(17):6690-701.
 17. Ferretti V, Poitras C, Bergeron D, Coulombe B, Robert F, Blanchette M. PReMod: a database of genome-wide mammalian cis-regulatory module predictions. *Nucleic Acids Res*. 2007 Jan;35(Database issue):D122-6.
 18. Sonoda J, Laganière J, Mehl IR, Barish GD, Chong LW, Li X, Scheffler IE, Mock DC, Bataille AR, Robert F, Lee CH, Giguère V, Evans RM. Nuclear receptor ERR alpha and coactivator PGC-1 beta are effectors of IFN-gamma-induced host defense. *Genes Dev*. 2007 Aug 1;21(15):1909-20.
 19. Rufiange A, Jacques PE, Bhat W, Robert F, Nourani A. Genome-wide replication-independent histone H3 exchange occurs predominantly at promoters and implicates H3 K56 acetylation and Asf1. *Mol Cell*. 2007 Aug 3;27(3):393-405.
 20. Soontornngun N, Larochelle M, Drouin S, Robert F, Turcotte B. Regulation of gluconeogenesis in *Saccharomyces cerevisiae* is mediated by activator and repressor functions of Rds2. *Mol Cell Biol*. 2007 Nov;27(22):7895-905.
 21. Harada R, Vadnais C, Sansregret L, Leduy L, Bérubé G, Robert F, Nepveu A. Genome-wide location analysis and expression studies reveal a role for p110 CUX1 in the activation of DNA replication genes. *Nucleic Acids Res*. 2008 Jan;36(1):189-202.
 22. Znaidi S, Weber S, Al-Abdin OZ, Bomme P, Saidane S, Drouin S, Lemieux S, De Deken X, Robert F, Raymond M. Genomewide location analysis of *Candida albicans* Upc2p, a regulator of sterol metabolism and azole drug resistance. *Eukaryot Cell*. 2008 May;7(5):836-47.
 23. Truscott M, Harada R, Vadnais C, Robert F, Nepveu A. p110 CUX1 cooperates with E2F transcription factors in the transcriptional activation of cell cycle-regulated genes. *Mol Cell Biol*. 2008 May;28(10):3127-38.
 24. Gévry N, Hardy S, Jacques PE, Laflamme L, Svtelias A, Robert F, Gaudreau L. Histone H2A.Z is essential for estrogen receptor signaling. *Genes Dev*. 2009 Jul 1;23(13):1522-33.

25. Ghazal G, Gagnon J, Jacques PE, Landry JR, Robert F, Elela SA. Yeast RNase III triggers polyadenylation-independent transcription termination. *Mol Cell*. 2009 Oct 9;36(1):99-109.
26. Hardy S, Jacques PE, Gévry N, Forest A, Fortin ME, Laflamme L, Gaudreau L, Robert F. The euchromatic and heterochromatic landscapes are shaped by antagonizing effects of transcription on H2A.Z deposition. *PLoS Genet*. 2009 Oct;5(10):e1000687.
27. Turcotte B, Liang XB, Robert F, Soontorngun N. Transcriptional regulation of nonfermentable carbon utilization in budding yeast. *FEMS Yeast Res*. 2010 Feb;10(1):2-13.
28. Szilard RK, Jacques PE, Laramée L, Cheng B, Galicia S, Bataille AR, Yeung M, Mendez M, Bergeron M, Robert F, Durocher D. Systematic identification of fragile sites via genome-wide location analysis of gamma-H2AX. *Nat Struct Mol Biol*. 2010 Mar;17(3):299-305.
29. Hardy S, Robert F. Random deposition of histone variants: A cellular mistake or a novel regulatory mechanism? *Epigenetics*. 2010 Jul 1;5(5):368-72.
30. Drouin S, Laramée L, Jacques PÉ, Forest A, Bergeron M, Robert F. DSIF and RNA polymerase II CTD phosphorylation coordinate the recruitment of Rpd3S to actively transcribed genes. *PLoS Genet*. 2010 Oct 28;6(10):e1001173.
31. Gonsalves SE, Moses AM, Razak Z, Robert F, Westwood JT. Whole-genome analysis reveals that active heat shock factor binding sites are mostly associated with non-heat shock genes in *Drosophila melanogaster*. *PLoS One*. 2011 Jan 14;6(1):e15934.
32. Ivanovska I, Jacques PÉ, Rando OJ, Robert F, Winston F. Control of chromatin structure by spt6: different consequences in coding and regulatory regions. *Mol Cell Biol*. 2011 Feb;31(3):531-41.
33. Poschmann J, Drouin S, Jacques PE, El Fadili K, Newmarch M, Robert F, Ramotar D. The peptidyl prolyl isomerase Rrd1 regulates the elongation of RNA polymerase II during transcriptional stresses. *PLoS One*. 2011;6(8):e23159.
34. Bataille AR, Jeronimo C, Jacques PÉ, Laramée L, Fortin MÈ, Forest A, Bergeron M, Hanes SD, Robert F. A universal RNA polymerase II CTD cycle is orchestrated by complex interplays between kinase, phosphatase, and isomerase enzymes along genes. *Mol Cell*. 2012 Jan 27;45(2):158-70.
35. Soontorngun N, Baramée S, Tangsombatvichit C, Thepnok P, Cheevadhanarak S, Robert F, Turcotte B. Genome-wide location analysis reveals an important overlap between the targets of the yeast transcriptional regulators Rds2 and Adr1. *Biochem Biophys Res Commun*. 2012 Jul 13;423(4):632-7.
36. Sansó M, Lee KM, Viladevall L, Jacques PÉ, Pagé V, Nagy S, Racine A, St Amour CV, Zhang C, Shokat KM, Schwer B, Robert F, Fisher RP, Tanny JC. A positive feedback loop links opposing functions of P-TEFb/Cdk9 and histone H2B ubiquitylation to regulate transcript elongation in fission yeast. *PLoS Genet*. 2012;8(8):e1002822.
37. Woo S, Zhang X, Sauteraud R, Robert F, Gottardo R. PING 2.0: an R/Bioconductor package for nucleosome positioning using next-generation sequencing data. *Bioinformatics*. 2013 Aug 15;29(16):2049-50.
38. Jeronimo C, Bataille AR, Robert F. The writers, readers, and functions of the RNA polymerase II C-terminal domain code. *Chem Rev*. 2013 Nov 13;113(11):8491-522.
39. Praktijnjo SD, Llamas B, Scott-Boyer MP, Picard S, Robert F, Langlais D, Haibe-Kains B, Faubert D, Silversides DW, Deschepper CF. Novel effects of chromosome Y on cardiac regulation, chromatin remodeling, and neonatal programming in male mice. *Endocrinology*. 2013 Dec;154(12):4746-56.
40. Jeronimo C, Robert F. Kin28 regulates the transient association of Mediator with core promoters. *Nat Struct Mol Biol*. 2014 May;21(5):449-55. <https://www.ncbi.nlm.nih.gov/pubmed/?term=24704787>.
41. Coulombe C, Poitras C, Nordell-Markovits A, Brunelle M, Lavoie MA, Robert F, Jacques PÉ. VAP: a versatile aggregate profiler for efficient genome-wide data representation and discovery. *Nucleic Acids Res*. 2014 Jul;42(Web Server issue):W485-93.
42. Shahbaban K, Jeronimo C, Forget A, Robert F, Chartrand P. Co-transcriptional recruitment of Puf6 by She2 couples translational repression to mRNA localization. *Nucleic Acids Res*. 2014 Jul;42(13):8692-704.

43. Gasmi N, Jacques PE, Klimova N, Guo X, Ricciardi A, Robert F, Turcotte B. The switch from fermentation to respiration in *Saccharomyces cerevisiae* is regulated by the Ert1 transcriptional activator/repressor. *Genetics*. 2014 Oct;198(2):547-60.
44. Burugula BB, Jeronimo C, Pathak R, Jones JW, Robert F, Govind CK. Histone deacetylases and phosphorylated polymerase II C-terminal domain recruit Spt6 for cotranscriptional histone reassembly. *Mol Cell Biol*. 2014 Nov 15;34(22):4115-29.
45. Cheng X, Auger A, Altaf M, Drouin S, Paquet E, Utley RT, Robert F, Côté J. Eaf1 Links the NuA4 Histone Acetyltransferase Complex to Htz1 Incorporation and Regulation of Purine Biosynthesis. *Eukaryot Cell*. 2015 Jun;14(6):535-44.
46. Jeronimo C, Watanabe S, Kaplan CD, Peterson CL, Robert F. The Histone Chaperones FACT and Spt6 Restrict H2A.Z from Intragenic Locations. *Mol Cell*. 2015 Jun 18;58(6):1113-23.
47. Jeronimo C, Robert F. Histone chaperones FACT and Spt6 prevent histone variants from turning into histone deviants. *Bioessays*. 2016 May;38(5):420-6.
48. Hönes JM, Botezatu L, Helness A, Vadnais C, Vassen L, Robert F, Hergenhan SM, Thivakaran A, Schütte J, Al-Matary YS, Lams RF, Fraszczak J, Makishima H, Radivoyevitch T, Przychodzen B, da Conceição Castro SV, Görgens A, Giebel B, Klein-Hitpass L, Lennartz K, Heuser M, Thiede C, Ehninger G, Dührsen U, Maciejewski JP, Möröy T, Khandanpour C. GFI1 as a novel prognostic and therapeutic factor for AML/MDS. *Leukemia*. 2016 Jun;30(6):1237-45.
49. Gaudreau MC, Grapton D, Helness A, Vadnais C, Fraszczak J, Shooshtarizadeh P, Wilhelm B, Robert F, Heyd F, Möröy T. Heterogeneous Nuclear Ribonucleoprotein L is required for the survival and functional integrity of murine hematopoietic stem cells. *Sci Rep*. 2016 Jun 7;6:27379.
50. Jeronimo C, Collin P, Robert F. The RNA Polymerase II CTD: The Increasing Complexity of a Low-Complexity Protein Domain. *J Mol Biol*. 2016 Jun 19;428(12):2607-2622.
51. Fraszczak J, Helness A, Chen R, Vadnais C, Robert F, Khandanpour C, Möröy T. Threshold Levels of Gfi1 Maintain E2A Activity for B Cell Commitment via Repression of Id1. *PLoS One*. 2016 Jul 28;11(7):e0160344.
52. Botezatu L, Michel LC, Helness A, Vadnais C, Makishima H, Hönes JM, Robert F, Vassen L, Thivakaran A, Al-Matary Y, Lams RF, Schütte J, Giebel B, Görgens A, Heuser M, Medyouf H, Maciejewski J, Dührsen U, Möröy T, Khandanpour C. Epigenetic therapy as a novel approach for GFI136N-associated murine/human AML. *Exp Hematol*. 2016 Aug;44(8):713-726.e14.
53. Jeronimo C, Langelier MF, Bataille AR, Pascal JM, Pugh BF, Robert F. Tail and Kinase Modules Differently Regulate Core Mediator Recruitment and Function In Vivo. *Mol Cell*. 2016 Nov 3;64(3):455-466.
54. Steunou AL, Cramet M, Rossetto D, Aristizabal MJ, Lacoste N, Drouin S, Côté V, Paquet E, Utley RT, Krogan N, Robert F, Kobor MS, Côté J. Combined Action of Histone Reader Modules Regulates NuA4 Local Acetyltransferase Function but Not Its Recruitment on the Genome. *Mol Cell Biol*. 2016 Oct 28;36(22):2768-2781.
55. Uwimana N, Collin P, Jeronimo C, Haibe-Kains B, Robert F. Bidirectional terminators in *Saccharomyces cerevisiae* prevent cryptic transcription from invading neighboring genes. *Nucleic Acids Res*. 2017 Jun 20;45(11):6417-6426.
56. Jeronimo C, Robert F. The Mediator Complex: At the Nexus of RNA Polymerase II Transcription. *Trends Cell Biol*. 2017 Oct;27(10):765-783.
57. Robert F. Spt6 Gets in the Way of Polycomb to Promote ESC Pluripotency. *Mol Cell*. 2017 Oct 19;68(2):263-264.
58. Robert F. Bidirectional terminators: an underestimated aspect of gene regulation. *Curr Genet*. 2018 Apr;64(2):389-391.
59. Collin P, Jeronimo C, Poitras C, Robert F. (2019) RNA Polymerase II CTD Tyrosine 1 Is Required for Efficient Termination by the Nrd1-Nab3-Sen1 Pathway. *Mol Cell*. 2019 Feb 21;73(4):655-669.
60. Jeronimo C, Poitras C, Robert F. (2019) Histone Recycling by FACT and Spt6 during Transcription Prevents the Scrambling of Histone Modifications. *Cell Rep*. 2019 Jul 30;28(5):1206-1218.

61. Eyboulet F, Jeronimo C, Côté J, Robert F (2020) The deubiquitylase Ubp15 couples transcription to mRNA export. *Elife*. 2020 Nov 23;9:e61264.

Publications – Book chapters

1. Robert, F. and Coulombe, B. Use of site-specific protein-DNA photocrosslinking to analyze the molecular organization of the RNA polymerase II initiation complex. In: Tom Moss, éd. *Methods Mol Biol Totowa, NJ: Humana Press, 2001; 148:383-393.*
2. Bataille, A.R. and Robert, F. Profiling Genome-wide Histone Modifications and Variants by ChIP-chip on Tiling Microarrays in *S. cerevisiae*. In: Tom Moss and Benoît Leblanc, éd. *Protein-DNA Interactions, Third Edition, Methods Mol Biol. Totowa, NJ: Humana Press, 2009; 543:267-279.*
3. Brunelle, M., Coulombe, C., Poitras, C., Robert, M-A., Markovits, A.N., Robert, F. and Jacques, P-E. Aggregate and heatmap representations of genome-wide localization data using VAP, a versatile aggregate profiler. In: Benoît Leblanc and Sébastien Rodrigue, éd. *DNA-Protein Interactions: Principles and Protocols, Methods Mol Biol. Springer Science+Business Media New York, 2015; 1334:273-98.*
4. Jeronimo, C. and Robert, F. A Spiking Strategy for ChIP-chip Data Normalization in *S. cerevisiae*. In: Benoit Guillemette and Luc Gaudreau, éd. *Histones: Methods and Protocols, Methods Mol Biol. Springer Science+Business Media New York, 2017; 1528:211-227.*

Patents

1. Author: John Wyrick, Richard A. Young, Bing Ren, François Robert
Title: Chromosome-wide Analysis of Protein-DNA Interactions
Date: June 25, 2002
U.S. Patent No.: 6,410,243 B1
European Patent No.: 00959909.3-2402
Owner: Whitehead Institute for Biomedical Research, Cambridge, MA (USA)
2. Author: John Wyrick, Richard A. Young, Bing Ren, François Robert, Itamar Simon
Title: Genome-Wide location and function of DNA binding proteins
Date: December 30, 2008
U.S. Patent No.: 7,470,507 B2
Owner: Whitehead Institute for Biomedical Research, Cambridge, MA (USA)
3. Author: John Wyrick, Richard A. Young, Bing Ren, François Robert, Itamar Simon
Title: Genome wide location and function of DNA binding proteins
Date: August 18, 2009
U.S. Patent No.: 7,575,869 B2
Owner: Whitehead Institute for Biomedical Research, Cambridge, MA (USA)

Presentations, lectures and workshops (since 2003)

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| 2003/01 | Département de biologie, Université de Sherbrooke, QC, Canada
Title: Genome-Wide Location Analysis: From Galactose Utilization in Yeast to New Targets for Alzheimer's Disease |
| 2003/03 | FASEB Research conferences: Chromatin and Transcription. Snowmass, CO, USA
Title: Global Position and Recruitment of Chromatin-Modifying Complexes in the Yeast Genome |
| 2003/06 | Northeast Regional Yeast Meeting (NERY), Montréal, QC, Canada
Title: Global Position and Recruitment of Chromatin-Modifying Complexes in the Yeast Genome |
| 2003/07 | 22 nd Summer Symposium in Molecular Biology: Chromatin Structure and Function, State College, PA, USA
Title: Global Position and Recruitment of Chromatin-Modifying Complexes in the Yeast Genome |

- 2004/03 *Retraite scientifique des chercheurs de l'IRCM, St-Jean-de-Matha, QC, Canada*
Title: Genome-wide Aspects of Chromatin structure and Function
- 2004/06 Réunion annuelle de l'Initiative en Génomique du Ministère d'Agriculture et Agroalimentaire
Canada, Ottawa, ON, Canada
Title: Genome-Wide Aspects of Chromatin Structure and Function
- 2005/03 Montreal Microarray Symposium, Biotechnology Research Institute (BRI), Montréal, QC, Canada
Title: Genome-wide Location Analysis of DNA-Binding Proteins: from Yeast to Mammals
- 2005/08 Agilent Innovative Microarray Technology Meeting, Agilent Technologies, Toronto, ON, Canada
Title: Variant Histone H2A.Z is Globally Localized to the Promoters of Inactive Yeast Genes and
Regulates Nucleosome Positioning
- 2005/08 Mechanisms of Eukaryotic Transcription, Cold Spring Harbor, NY, USA
Title: Variant Histone H2A.Z is Globally Localized to the Promoters of Inactive Yeast Genes and
Regulates Nucleosome Positioning
- 2006/01 McGill University Health Center, Division of Urology, Montréal, QC, Canada
Title: Chipping away chromatin: Genome-wide aspects of chromatin function
- 2006/03 University of Toronto at Mississauga Biology Seminar Series, Mississauga, ON, Canada
Title: Dissecting chromatin function using CHIP-chip
- 2006/04 *Retraite scientifique des chercheurs de l'IRCM, St-Jean-de-Matha, QC, Canada*
Title: Genome-wide Aspects of Chromatin Functions
- 2006/11 Department of Medical Genetics and Microbiology, University of Toronto, ON, Canada
Title: Dissecting gene networks and chromatin function using CHIP-chip
- 2006/11 Inaugural and Founding Meeting of the Canadian Society for Systems Biology, National Research
Council, Ottawa, ON, Canada
Title: Integrating Multiple Data Sources: Towards a Complete Understanding of Nuclear
Functions
- 2007/03 1st IRCM Meeting on Systems Biology: Molecular Networks, Montréal, QC, Canada
Title: Special chromatin structure primes promoters for gene activation
- 2007/10 *Centre de recherche du CHU Sainte-Justine, Montréal, QC, Canada*
Title: Mapping chromatin structure and dynamics at the genomic level
- 2007/12 *Institut de recherche en immunologie et en oncologie (IRIC), Université de Montréal, QC, Canada*
Title: Genome-wide mapping of chromatin structure and dynamics in yeast and mammals
- 2008/02 Keystone Symposia – Regulatory Mechanisms in Eukaryotic Transcription, Keystone, CO, USA
Title: Human H2A.Z modulates early events in the process of transcription and is required for
estrogen receptor signaling
- 2008/03 2nd IRCM Meeting on Systems Biology: Molecular Networks, Montréal, QC, Canada
Title: Genome-wide mapping of yeast gammaH2AX reveals an interplay between chromatin
structure and replisome progression
- 2008/03 Terrence Donnelly Centre for Cellular and Biomolecular Research (Donnelly CCBR), University of
Toronto, ON, Canada
Title: Mapping chromatin structure and dynamics at the genomic scale
- 2008/04 *Retraite scientifique des chercheurs de l'IRCM, Ste-Adèle, QC, Canada*
Title: The role of chromatin in the regulation of nuclear processes in yeast and mammals
- 2008/07 Department of Biochemistry, University of Alberta, Edmonton, AB, Canada
Title: The role of chromatin in the regulation of nuclear processes in yeast and mammals
- 2008/11 Maud Menten Award (IG-CIHR), 7th Annual New Principal Investigators Meeting, Jackson Point,
ON, Canada
Title: Variant Histone H2A.Z Shapes the Euchromatic and Heterochromatic Landscapes
- 2009/06 Keystone Symposium on Dereglulation of Transcription in Cancer: Controlling Cell Fate Decisions,
Killarney, Co. Kerry, Ireland

- Title: Shaping the euchromatic and heterochromatic landscapes by reciprocal antagonizing effects of transcription and H2A.Z deposition
- 2009/08 Mechanisms of Eukaryotic Transcription, Cold Spring Harbor, NY, USA
Title: Genome-wide localization of RNA polymerase II phospho-isoforms reveals cross-talk between phosphorylation events
- 2009/12 OISB, Faculty of Medicine, University of Ottawa, ON, Canada
Title: Probing chromatin function using functional genomics
- 2010/03 *Retraite scientifique des chercheurs de l'IRCM*, Orford, QC, Canada
Title: Chronicle on the complex relationship between chromatin and the transcription machinery
- 2010/03 Lady Davis Institute, General Hospital, Montréal, QC, Canada
Title: The role of the variant histone H2A.Z in gene expression
- 2010/09 ASBMB Special Symposium on Transcription Regulation by Chromatin and RNA Polymerase II, Tahoe City, CA, USA
Title: DSIF and RNA polymerase II CTD phosphorylation coordinate the recruitment of RPD3S to actively transcribed genes
- 2011/03 Dartmouth College, Department of Genetics, Hanover, NH, USA
Title: Dissection of the RNA polymerase II CTD phosphorylation cycle using genome-wide methods
- 2011/03 Stowers Institute for Medical Research, Kansas City, MO, USA
Title: Dissection of the RNA polymerase II CTD phosphorylation cycle using genome-wide methods
- 2011/06 Michigan State University, Summer Symposium on Transcriptional Dynamics, Evolution, and Systems Biology, East Lansing, MI, USA
Title: A universal RNA polymerase II CTD cycle is orchestrated by complex interplays between kinase, phosphatase and isomerase enzymes along genes
- 2011/08 Mechanisms of Eukaryotic Transcription, Cold Spring Harbor, NY, USA
Title: A universal RNA polymerase II CTD cycle is orchestrated by complex interplays between kinase, phosphatase and isomerase enzymes along genes
- 2012/06 *Retraite scientifique des chercheurs de l'IRCM*, Estérel, QC, Canada
Title: A proteomic pipeline for the dissection of the CTD code
- 2013/06 Ottawa Institute for Systems Biology Symposium, Mont-Tremblant, QC, Canada
Title: Establishing the H2A.Z genomic landscape: The unexpected role of histone chaperones
- 2013/08 Mechanisms of Eukaryotic Transcription, Cold Spring Harbour, NY, USA
Title: Establishing the H2A.Z genomic landscape: The unexpected role of histone chaperones
- 2013/10 Oakland University, Department of Biological Sciences, Rochester, MI, USA
Title: Loaded in / triaged out: The journey of a histone variant.
- 2014/06 *Retraite scientifique des chercheurs de l'IRCM*, Estérel, QC, Canada
Title: Selective co-transcriptional removal of H2A.Z by FACT and Spt6 prevents cryptic transcription
- 2014/06 EMBO Conference Series, Gene Transcription in Yeast: From regulatory networks to mechanisms, Sant Feliu de Guixols, Spain
Title: FACT and Spt6 play key roles in the establishment of the H2A.Z genomic landscape
- 2014/10 ASBMB Transcription Symposium, Snowbird, UT, USA
Title: Spt6 and FACT prevent cryptic transcription by impeding SWR-C-dependent H2A.Z loading in gene bodies
- 2015/01 Département de biologie, Université de Sherbrooke, QC, Canada
Title: H2A.Z: the light and the dark side of a histone variant
- 2015/03 The First joint Conference on Biomedical Research organized by the IRCM and IMRIC (Institute for Medical Research Israel-Canada) from Hebrew University of Jerusalem, Montréal, QC, Canada
Title: Transcription-associated histone chaperones: guardians of the epigenome?

- 2015/07 Penn State's 34th Summer Symposium in Molecular Biology: Chromatin and Epigenetic Regulation of Transcription, State College, PA, USA
Title: Transcription-associated histone chaperones: guardians of the epigenome?
- 2015/08 Mechanisms of Eukaryotic Transcription, Cold Spring Harbor, NY, USA
Title: Histone Chaperones FACT and Spt6: Guardians of the Epigenome?
- 2016/06 2016 IRCM Scientific Forum, Hôtel & Spa Mont Gabriel, QC, Canada
Title: Epigenetic Editing and Surveillance: An Emerging Paradigm in Chromatin and Gene Expression
- 2016/06 Instituto de Biomedicina de Sevilla, Sevilla, Spain
Title: Histone chaperones FACT and Spt6 play roles in epigenetic editing and surveillance
- 2016/06 EMBO Conference Series, Gene Transcription in Yeast: From Chromatin to RNA and Back, Sant Feliu de Guixols, Spain
Title: Association of Mediator with the pre-initiation complex is Tail module-independent and involves the release of the Kinase module
- 2016/10 ASBMB Special Symposia Series: Transcriptional Regulation by Chromatin and RNA Polymerase II, Snowbird, UT, USA
Title: Histone chaperones FACT and Spt6 play roles in epigenetic editing and surveillance
- 2017/02 York University, Biology Department, Toronto, ON, Canada
Title: Dissecting the function of Mediator in living cells
- 2017/08 Mechanisms of Eukaryotic Transcription, Cold Spring Harbor, NY, USA
Title: Transcription-associated Histone Chaperones Prevent the Scrambling of Histone Modifications
- 2017/10 Centre de Recherche CHU de Québec, Québec, QC, Canada
Title: Dissecting the dynamic composition of Mediator during transcription
- 2017/11 Centre de Recherche CHU-Ste Justine, Montréal, QC, Canada
Title: Histone chaperones prevent transcription from scrambling the epigenetic information
- 2017/12 Fred Hutchinson Cancer Research Center, Seattle, WA, USA
Title: The complex interplay between Mediator and gene promoters
- 2018/05 Département de Microbiologie et Infectiologie, Université de Sherbrooke, Sherbrooke, QC, Canada.
Title: Preserving epigenetic information in the face of transcription: a key function for histone chaperones
- 2018/06 EMBO Conference Series, Gene Transcription in Yeast: From global analyses to single cells, Sant Feliu de Guixols, Spain.
Title: RNA Polymerase II CTD Tyrosine 1 is Required for Termination by the Nrd1-Nab3-Sen1 Pathway
- 2018/10 ASBMB Special Symposia Series: Transcriptional Regulation by Chromatin and RNA Polymerase II, Snowbird, UT, USA.
Title: FACT and Spt6 Prevent the Scrambling of Histone Modifications during Transcription
- 2019/08 Mechanisms of Eukaryotic Transcription, Cold Spring Harbor, NY, USA.
Title: RNA polymerase II CTD tyrosine 1 is required for efficient termination by the Nrd1-Nab3-Sen1 pathway
- 2019/11 Department of Biochemistry & Molecular Biology, Louisiana State University Health Sciences Center, LA, USA.
Title: Transcribing through nucleosomes: A delicate task aided by histone chaperones
- 2020/01 Keystone Symposium on Gene Regulation: From Mechanisms to Disease, Keystone, Colorado, USA.
Title: Transcribed chromatin, rather than RNA polymerase II itself, recruits FACT to active genes

- 2020/05 Colloque 107 on *Organisation des chromosomes et stabilité du génome* at the 88^{ième} congrès de l'Association Canadienne-Française pour l'Avancement des Sciences (ACFAS), Sherbrooke, Canada. –Meeting cancelled dur to COVID-19 pandemic–.
Title: *Le chaperon d'histones FACT est recruté au nucléosome +1 des gènes transcrits et s'étale le long des gènes avec l'aide du remodeleur de chromatine Chd1*
- 2020/06 Chromatin Structure and Function Gordon Research Conference: Chromatin Modifications, RNA and Metabolism, Castelldefels, Spain. –Meeting cancelled dur to COVID-19 pandemic–.
Title: FACT is recruited to the +1 nucleosome of transcribed genes and spreads in a Chd1-dependent manner
- 2020/06 Max-Planck-Institut für molekulare Genetik, Dahlem Colloquia in Molecular Genetics seminar series, Berlin, Germany. –Visit cancelled dur to COVID-19 pandemic–.
Title: FACT is recruited to the +1 nucleosome of transcribed genes and spreads in a Chd1-dependent manner
- 2020/06 CNRS Workshop Conference: Gene transcription in yeast: From single molecules to phase separation, San Feliu, Spain. –Meeting cancelled dur to COVID-19 pandemic–.
Title: FACT is recruited to the +1 nucleosome of transcribed genes and spreads in a Chd1-dependent manner
- 2020/10 ASBMB Special Symposium on Transcriptional Regulation by RNA Polymerase II and Chromatin. – Meeting cancelled dur to COVID-19 pandemic–.
- 2020/11 Fragile Nucleosome Seminar Series.
Title: Transcription and chromatin remodeler Chd1 join forces to convey FACT to genes

Teaching

BIM-7020: *Lectures en biologie moléculaire*. I teach this class since 2004. Mandatory class for PhD students in the *Programmes de biologie moléculaire* at Université de Montréal. A small group of student discuss scientific articles. 12 to 15 students. 9 hours.

BIM-6025, SMC-6041: *Biologie moléculaire et cellulaire: Génomique*. I taught in this class from 2005 to 2012. Class given to students in the *Programmes de biologie moléculaire* and students from the Département de médecine at Université de Montréal. The class also includes students from McGill University. I taught them “Modern genomics technologies”. About 30 students. 2 hours.

BIM-6030: *Biologie moléculaire - sujets d'actualité, Bloc 3: Protéomique et génomique fonctionnelle*. I teach this class since 2006. Mandatory class for Master students in the *Programmes de biologie moléculaire* at Université de Montréal. I teach modern “Genomics technologies”. About 30 students. 2 hours.

BCM-6023: *Régulation de l'expression génétique I*. I teach this class since 2006 to graduate students from the Département de biochimie at Université de Montréal. From 2006 to 2016, I was lecturing about “Gene regulatory networks” but since 2017 I teach “High throughput sequencing technologies”. 20-30 students. 2 hours.

BIM-6026: *Biologie moléculaire et cellulaire: Structure et fonctions des chromosomes et de la chromatine*. I teach this class since 2013 to graduate students in the *Programmes de biologie moléculaire* at Université de Montréal and students from McGill University. I teach the “Structure and functions of chromatin”. About 30 students. 2 hours.

BIM-6073: *Pratique en recherche translationnelle*. I teach this class since 2013 to graduate students from the Molecular and Cellular Medicine option from the *Programmes de biologie moléculaire* at Université de Montréal. I teach “Gene expression” and “The genomics tools to study gene expression”. About 6 students. 6 hours.

MMD-6001: *Médecine moléculaire: Régulation de l'expression génique*. I teach this class since 2016 to graduate students from the *Programme en Sciences biomédicales* at Université de Montréal. I teach the "Regulation of gene expression". About 10 students. 3 hours, twice a year.

BIM6028 – EXMD604D: *Biologie moléculaire et cellulaire II*. I am the coordinator of this class from the *Programmes de biologie moléculaire* at Université de Montréal since 2013. I am responsible for identifying and inviting Professors to give lectures on various aspects of molecular biology. A different topic is taught each week from a different Professor.

Postdoc supervision

Marco Belfiore. 2005/02 – 2006/05. Identification and characterization of novel histone modifying enzymes in *S. cerevisiae*.

Sara Hardy. 2006/01 – 2009/12. Genomic localization of variant histone H2A.Z in mammalian cells.

Josette-Renée Landry. 2007/08 – 2008/10. Transcriptional regulatory network of hematopoietic cells.

Pierre-Étienne Jacques. 2005/10 – 2010/07. Investigating the role of chromatin in gene expression co-regulation: a computational approach.

Célia Jeronimo. 2010/01 – 2013/08. Characterization of the role of H2A.Z in heterochromatin functions.

Émelyne Dejeux. 2010/10 – 2011/11. Mapping the human methylasome.

Vivianne Calabrese. 2012/10 – 2013/04. The role of H2A.Z in heterochromatin function during differentiation.

Anton Lebedev. 2011/01 – 2013/08. Hematopoiesis and leukemogenesis: investigation of epigenetic reprogramming during hematopoietic stem cell differentiation.

Malika Aid. 2012/12 – 2014/01. Developing new algorithms to study pervasive transcription using high throughput sequencing.

Anne Helness. 2012/09 – 2015/09. Investigation of epigenetic reprogramming during hematopoietic stem cell differentiation.

Fanny Eyboulet. 2015/01 – 2020/03. The role of deubiquitinase Ubp15 in the regulation of RNA polymerase II.

Ashok Reddy. 2016/08 – 2017/10. Investigating the role of H2A.Z-mediated cryptic transcription in cancers.

Graduate student supervision – PhD students

Alain Bataille. 2003/10 - 2011/09. The role of the variant histone H2A.Z in gene expression.

Simon Drouin. 2004/01 - 2011/04. The role of the histone deacetylase Rpd3 in the regulation of cell cycle in yeast.

Pierre Collin. 2013/09 - 2019/04. Investigating the relationship between CTD phosphorylation and transcriptional elongation.

Elie Lambert. 2019/09 – ongoing. The role of Mediator in post-initiation events.

Noe Seija. 2019/09 – ongoing. The role of Spt6 in AID function.

Graduate student supervision – Master students (with thesis)

Maxime Bergeron. 2007/05 - 2009/01. The role of H2A.Z in nucleosome positioning in yeast and mammals.

Lorelei Durand. 2010/09 - 2013/05. Characterization of the Set3C complex.

Nicole Uwimana. 2014/09 - 2016/09. Identification of cryptic transcripts by strand-specific RNA-seq.

Jin Zhi Goh. 2018/09 – withdraw. Identification and characterization of the substrates of Cdk8.

Marjorie Aleman. 2019/01 – ongoing. The role of CTD-Tyr1 phosphorylation in the recruitment of the elongation factor Paf1C.

Micaela Miyauchi. 2019/01 – ongoing. A high-resolution map of protein interactions along the RNA polymerase II CTD in vivo using a site-specific protein crosslinking technique combined with mass spectrometry.

Kavindu Puwakdannawa. 2020/01 – ongoing. Identification and characterization of the substrates of Cdk8.

Graduate student supervision – Master students (non-thesis)

Elie El-Skaf. 2013/05 - 2014/05. Swr1-independent functions of histone variant H2A.Z.

Olivier Rocheleau-Leclair. 2015/09 - 2015/12. Development of BioID in *Saccharomyces cerevisiae*.

Karthik Eswara. 2016/09 - 2016/12. Dissecting the Med13-Med19 interaction linking Cdk8 to Mediator.

Meruert Sarsenova. 2018/01 - 2018/05. Determine the effect of *chd1* catalytic dead mutation (K407R) on FACT occupancy.

Noé Seija Desivo. 2018/09 - 2019/08. The role of Spt6 in AID function.

Undergraduate student supervision

Martin Pearson, Joanie Proulx, Stéphanie Naud, Rachim Saïd, Lorelei Durand, Joannie Connell, Lora Tzaneva, Gwendellyn Espedido, Trevor Lau, Ngawan Dhargyal, Shraddha Solanki, Hang Nguyen, Olivier Rocheleau-Leclerc, Louis Parent, Claudine Tessier, Marie Harel, Noemie Lemaire, Chaïma Benaksas, Anna Axakova, Amélie Lachance, Ali Almail, Yi Fei Tao.