

# BÉRÉNICE A. BENAYOUN, PH.D.

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## EDUCATION

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- 2007-2011 Ph.D in Genetics and Cell Biology, Paris Diderot-Paris7 University, École doctorale GC2ID, Paris, France.  
2009 Diploma from the École Normale Supérieure (Biology major), France.  
2006-2007 M.Sc. in Genetics École Normale Supérieure/Université Paris 7, France.  
2005 B.Sc. in Biology, École Normale Supérieure, Université Paris 7, France.  
2004-2008 École Normale Supérieure (ENS), Biology Department, Paris, France.

## POSITIONS

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- 2017-present Assistant Professor of Gerontology, University of Southern California, Los Angeles, CA, USA.  
2011-2017 Post-doctoral fellow, Anne Brunet's laboratory, Department of Genetics, Stanford University School of Medicine, CA, USA.  
2007-2011 Graduate student, Reiner Veitia's laboratory, Department of Molecular and Cellular pathology, Institut Jacques Monod, CNRS UMR7592, Paris, France.  
2007 Visiting student, Daniel Vaiman's laboratory, Department of Genetics and Development, Institut Cochin, INSERM U567, CNRS UMR8104, Paris, France.  
2006 Visiting student, Robert Tjian's laboratory, University of California at Berkeley, CA, USA.  
2005 Visiting student, Richard I. Morimoto's laboratory, Northwestern University, Evanston/Chicago, IL, USA.

## ACADEMIC AND PROFESSIONAL HONORS

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- 2015 Regeneron Prize for Creative Innovation for a post-doctoral fellow, honorable mention  
2014 NIH Pathway to Independence Award (K99/R00)  
2013 Dean's postdoctoral fellowship (Stanford University School of Medicine)  
2011 Ph.D. *summa cum laude* with highest distinction, Paris Diderot-Paris7 University  
2009 Best presentation award in the Genetics Department of the Cochin Institute  
2008-2011 Ph.D. fellowship from the Research and National Education Institute/Paris 7 University  
2007 M.Sc. *summa cum laude* (ranked first), Ecole Normale Supérieure/Paris Diderot-Paris7 University  
2005 Research fellowship from the Rice Institute of Biomedical Research  
2004-2008 Student fellowship from the École Normale Supérieure of Paris

## PEER-REVIEWED PUBLICATIONS

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### Original research articles

1. Contrepois K\*, Coudereau C\*, **Benayoun BA**, Schuler N, Roux PF, Bischof O, Courbeyrette R, Carvalho C, Thuret JY, Ma Z, Derbois C, Nevers MC, Volland H, Redon C, Bonner W, Deleuze JF, Wiel C, Bernard D, Snyder MP, Rübe C, Olaso R, Fenaille F and Mann C. Histone variant H2A.J accumulates in senescent cells and promotes inflammatory gene expression (2017). *Nature Communications*, in press
2. Kurum E, **Benayoun BA**, Malhotra A, George J and Ucar D. Computational inference of a genomic pluripotency signature in human and mouse stem cells (2016). *Biology Direct*, **11**:47, doi: 10.1186/s13062-016-0148-z.
3. Valenzano D\*, **Benayoun BA\***, Singh PP\*, Zhang E, Etter PD, Hu CK, Clément-Ziza M, Willemsen D, Cui

- R, Harel I, Machado B, Lee MC, Sharp SC, Bustamente C, Beyer A, Johnson EA, and Brunet A. The African Turquoise Killifish Genome Provides Insights into Evolution and Genetic Architecture of Lifespan (2015). *Cell*, **163**, 1539-1554. \*equal contribution (highlighted in a Preview: *Cell*, **163**, 1312-1313)
4. Schaffer BE, Levin RS, Hertz NT, Maures TJ, Schoof ML, Hollstein PE, **Benayoun BA**, Banko MR, Shaw RJ, Shokat KM, Brunet A. Identification of AMPK Phosphorylation Sites Reveals a Network of Proteins Involved in Cell Invasion and Facilitates Large-Scale Substrate Prediction (2015). *Cell Metabolism*, **22**, 907-921.
  5. Pech MF, Garbuzov A, Hasegawa K, Sukhwani M, Zhang RJ, **Benayoun BA**, Brockman SA, Lin S, Brunet A, Orwig KE, and Artandi SE. High telomerase is a hallmark of undifferentiated spermatogonia and is required for maintenance of male germline stem cells (2015). *Genes and Development*, **29**, 1-15.
  6. Harel I, **Benayoun BA**, Machado B, Singh PP, Hu CK, Pech MF, Zhang E, Fullhart SC, Artandi SE, and Brunet A. Rapid exploration of aging and disease-related genes in a naturally short-lived vertebrate (2015). *Cell*, **160**, 1013-1026. (highlighted in a Preview: *Cell*, **160**, 814-815)
  7. Kareta MS, Gorges LL, Hafeez S, **Benayoun BA**, Zmoos AF, Cecchini MJ, Spacek D, Batista LFZ, O'Brien M, Ng YH, Ang CE, Vaka D, Artandi SE, Dick FA, Brunet A, Sage J, and Wernig M. Inhibition of Pluripotency Networks by the Rb Tumor Suppressor Restricts Reprogramming and Tumorigenesis (2014). *Cell Stem Cell*, **16**, 39-50.
  8. **Benayoun BA\***, Pollina EA\*, Uçar D\*, Wong ED, Mancini E, Mahmoudi S, Hitz BC, Devarajan K, Gupta R, Rando TA, Baker JC, Snyder MP, Cherry JM, and Brunet A. H3K4me3 breadth is linked to cell identity and transcriptional consistency (2014). *Cell*, **158**, 673-688. \*equal contribution. (highlighted in F1000) Correction in: *Cell*, 2015, **163**, 1281-1286.
  9. Maures TJ, Booth L, **Benayoun BA**, Izrayelit Y, Schroeder F and Brunet A. Males shorten the lifespan of *C. elegans* hermaphrodites via secreted compounds (2014). *Science*, **343**, 541-544.
  10. **Benayoun BA\***, Anttonen M\*, L'hôte D, Bailly-Bechet M, Andersson N, Heikinheimo M and Veitia RA. Adult ovarian granulosa cell tumor transcriptomics: prevalence of FOXL2 target genes misregulation gives insights into the pathogenic mechanism of the p.Cys134Trp somatic mutation (2013). *Oncogene*, **32**, 2739-2746. \*equal contribution
  11. L'hôte D, Georges A, Todeschini AL, Kim JH, **Benayoun BA**, Bae J and Veitia RA. Discovery of novel protein partners of the transcription factor FOXL2 provides insights into its physiopathological roles (2012). *Human Molecular Genetics*, **21**, 3264-3274.
  12. Georges AB, **Benayoun BA**, Marongiu M, Dipietromaria A, L'hôte D, Todeschini AL, Auer J, Crisponi L and Veitia RA. SUMOylation of the Forkhead transcription factor FOXL2 promotes its stabilization/activation through transient recruitment to PML bodies (2011). *PLoS ONE*, **6**, e25463.
  13. Greer EL, Maures TJ, Ucar D, Hauswirth A, Mancini E, Lim J, **Benayoun BA**, Shi Y and Brunet A. Transgenerational Epigenetic Inheritance of Longevity in *C. elegans* (2011). *Nature*, **479**, 365-371.
  14. Lelièvre EC, **Benayoun BA**, Mahieu L, Roger JE, Sahel JA, Sennlaub F, Veitia RA, Goureau O and Guillonnet X. A Regulatory Domain Is Required for Foxn4 Activity During Retinogenesis (2011). *Journal of Molecular Neuroscience*, **46**, 315-323.
  15. **Benayoun BA**, Georges AB, L'Hôte D, Andersson N, Dipietromaria A, Todeschini AL, Caburet S, Bazin C, Anttonen M and Veitia RA. Transcription factor FOXL2 protects granulosa cells from stress and delays cell cycle: role of its regulation by the SIRT1 deacetylase (2011). *Human Molecular Genetics*, **20**, 1673-1686.
  16. **Benayoun BA\***, Caburet S\*, Dipietromaria A, Georges AB, D'Haene B, Pandaranayaka PJE, L'Hôte D, Todeschini AL, Krishnaswamy S, Fellous M, De Baere E and Veitia RA. Functional exploration of the adult ovarian granulosa cell tumor-associated somatic FOXL2 mutation p.Cys134Trp (c.402C>G) (2010). *PLoS ONE*, **5**, e8789. \*equal contribution

17. Dipietromaria A, **Benayoun BA**, Todeschini AL, Rivals I, Bazin C and Veitia RA. Towards a functional classification of pathogenic FOXL2 mutations using transactivation reporter systems (2009). *Human Molecular Genetics*, **18**, 3324-3333.
18. Laissue P, Lakhal B, **Benayoun BA**, Dipietromaria A, Braham R, Elghezal H, Philibert P, Saâd A, Sultan C, Fellous M, and Veitia RA. Functional evidence implicating FOXL2 in non syndromic premature ovarian failure and in the regulation of the transcription factor OSR2 (2009). *Journal of Medical Genetics*, **46**, 455-457.
19. **Benayoun BA**, Batista F, Auer J, Dipietromaria A, L'hôte D, De Baere E and Veitia RA. Positive and negative feedback regulates the transcription factor FOXL2 in response to cell stress: evidence for a regulatory imbalance induced by disease-causing mutations (2009). *Human Molecular Genetics*, **18**, 632-644.
20. **Benayoun BA\***, Caburet S\*, Dipietromaria A\*, Bailly-Bechet M, Batista F, Fellous M, Vaiman D and Veitia RA. The identification and characterization of a FOXL2 response element provides insights into the pathogenesis of mutant alleles (2008). *Human Molecular Genetics*, **17**, 3118-3127. \*equal contribution
21. **Benayoun BA**, Auer J, Caburet S and Veitia RA. The post-translational modification profile of the forkhead transcription factor FOXL2 suggests the existence of parallel processive modification pathways (2008). *Proteomics*, **8**, 3118-3123.
22. Nallathambi J, Laissue P, Batista F, **Benayoun BA**, Lesaffre C, Moumné L, Pandaranayaka PJE, Usha K, Krishnaswamy S, Sundaresan P and Veitia RA. Differential Functional Effects of Novel Mutations of the Transcription Factor FOXL2 in BPES Patients (2008). *Human Mutation*, **29**, E123-E131.

## Reviews

1. **Benayoun BA\***, Pollina EA\*, and Brunet A. Epigenetic regulation of ageing: linking environmental inputs to genomic stability (2015). *Nature Reviews Molecular and Cellular Biology*, **16**, 593-610. \*equal contribution
2. **Benayoun BA** and Brunet A. Epigenetic Memory of longevity in *Caenorhabditis elegans* (2012). *Worm*, **1**, 77-81.
3. Yusuf D, Butland SL, Swanson MI, Bolotin E, Ticoll A, Cheung WA, Zhang XY, Dickman CT, Fulton DL, Lim JS, Schnabl JM, Ramos OH, Vasseur-Cognet M, de Leeuw CN, Simpson EM, Ryffel GU, Lam EW, Kist R, Wilson MS, Marco-Ferreres R, Brosens JJ, Beccari LL, Bovolenta P, **Benayoun BA**, Monteiro LJ, Schwenen HD, Grontved L, Wederell E, Mandrup S, Veitia RA, Chakravarthy H, Hoodless PA, Mancarelli M, Torbett BE, Banham AH, Reddy SP, Cullum RL, Liedtke M, Tschan MP, Vaz M, Rizzino A, Zannini M, Frieze S, Farnham PJ, Eijkelenboom A, Brown PJ, Laperriere D, Leprince D, de Cristofaro T, Prince KL, Putker M, Del Peso L, Camenisch G, Wenger RH, Mikula M, Rozendaal M, Mader S, Ostrowski J, Rhodes SJ, Van Rechem C, Boulay G, Olechnowicz SW, Breslin MB, Lan MS, Nanan KK, Wegner M, Hou J, Mullen RD, Colvin SC, Noy PJ, Webb CF, Witek ME, Ferrell S, Daniel JM, Park J, Waldman SA, Peet DJ, Taggart M, Jayaraman PS, Karrich JJ, Blom B, Vesuna F, O'Geen H, Sun Y, Gronostajski RM, Woodcroft MW, Hough MR, Chen E, Europe-Finner N, Karolczak-Bayatti M, Bailey J, Hankinson O, Raman V, Lebrun DP, Biswal S, Harvey CJ, Debruyne JP, Hogenesch JB, Hevner RF, Heligon C, Luo XM, Blank MC, Millen KJ, Sharlin DS, Forrest D, Dahlman-Wright K, Zhao C, Mishima Y, Sinha S, Chakrabarti R, Portales-Casamar E, Sladek FM, Bradley PH and Wasserman WW. The Transcription Factor Encyclopedia (2012). *Genome Biology*, **13**, R24.
4. Caburet S, Georges A, L'hôte D, Todeschini AL, **Benayoun BA** and Veitia RA. The transcription factor FOXL2: At the crossroads of ovarian physiology and pathology (2012). *Molecular and Cellular Endocrinology*, **356**, 55-64.
5. **Benayoun BA**, Caburet S and Veitia RA. Forkhead transcription factors: key players in health and disease (2011). *Trends in Genetics*, **27**, 224-232.
6. Georges AB, **Benayoun BA**, Caburet S and Veitia RA. Generic binding sites, generic DNA binding domains: where does specific promoter recognition comes from? (2010). *FASEB Journal*, **24**, 346-356.

7. **Benayoun BA**, Kalfa N, Sultan C and Veitia RA. The Forkhead transcription factor FOXL2: a novel tumor suppressor gene? (2010). *BBA reviews on Cancer*, **1805**, 1-5.
8. Kalfa N, Veitia RA, **Benayoun BA**, Boizet-Bonhoure B and Sultan C. The new molecular biology of granulosa cell tumors of the ovary (2009), *Genome Medicine*, **1**, 81.
9. **Benayoun BA** and Veitia RA. A post-translational modification code for transcription factors: sorting through a sea of signals (2009). *Trends in Cell Biology*, **19**, 189-197.
10. Moumné L, Batista F, **Benayoun BA**, Nallathambi J, Fellous M, Sundaresan P and Veitia RA. The mutations and potential targets of the forkhead transcription factor FOXL2 (2008). *Molecular and Cellular Endocrinology*, **282**, 2-11.

## BOOK CHAPTERS

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1. Duygu Ucar and **Benayoun BA**. Aging epigenetics: changes and challenges, *in* Epigenetics of Aging and Longevity, supervised by Moskalev & Vaiserman, Elsevier. (2017)
2. **Benayoun BA**, Dipietromaria A, Bazin C and Veitia RA. FOXL2: at the crossroads of female sex determination and ovarian function. Section IV: Translating vital cellular mechanisms into successful clinical care, *in* Forkhead Transcription Factors: Vital Elements in Biology and Medicine, supervised by K. Maise, Landes Biosciences. (2010-02-01)

## PRESENTATIONS

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### Oral presentations

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|---------------------------------------|---|
| <b>January 31<sup>st</sup>, 2017</b>  | <b>Rockefeller University</b> , New York, New York, USA ( <i>Invited communication</i> )<br>“Epigenomic regulation of aging in vertebrates”   |
| <b>October 13<sup>th</sup>, 2016</b>  | <b>Lewis-Sigler Institute for Integrative Genomics</b> , Princeton University, Princeton, New Jersey, USA ( <i>Invited communication</i> )<br>“Epigenomic regulation of aging in vertebrates”                                 |
| <b>September 8<sup>th</sup>, 2016</b> | <b>Department of Pathology and Laboratory Medicine, Perelman School of Medicine at University of Pennsylvania</b> , Philadelphia, Pennsylvania, USA ( <i>Invited communication</i> )<br>“Epigenomics of aging in vertebrates” |
| <b>August 22<sup>nd</sup>, 2016</b>   | <b>The Mayo Clinic</b> , Rochester, Minnesota, USA ( <i>Invited communication</i> )<br>“Epigenomics of aging in vertebrates”  |
| <b>August 16<sup>th</sup>, 2016</b>   | <b>Department of Cell and Tissue Biology</b> , University of California in San Francisco, San Francisco, California, USA ( <i>Invited communication</i> )<br>“Epigenomic regulation of aging in vertebrates”                  |
| <b>July 25<sup>th</sup>, 2016</b>     | <b>Division of Nutritional Sciences</b> , Cornell University, Ithaca, New York, USA ( <i>Invited communication</i> )<br>“Epigenomic regulation of aging in vertebrates”   |
| <b>July 20<sup>th</sup>, 2016</b>     | <b>School of Gerontology</b> , University of Southern California, Los Angeles, California, USA ( <i>Invited communication</i> )<br>“Epigenomic regulation of aging in vertebrates”  |
| <b>June 23<sup>th</sup>, 2016</b>     | <b>The Jackson Laboratory</b> , Bar Harbor, Maine, USA ( <i>Invited communication</i> )<br>“Epigenomic regulation of aging in vertebrates”  |
| <b>June 14<sup>th</sup>, 2016</b>     | <b>Lewis-Sigler Institute for Integrative Genomics</b> , Princeton University, Princeton, New Jersey, USA ( <i>Invited communication</i> )  |

- “Epigenomic regulation of aging in vertebrates”
- May 5<sup>th</sup>, 2016** **Keystone symposium on Epigenetic and Metabolic Regulation of Aging and Aging-Related Diseases**, Hilton Santa Fe Historic Plaza Hotel, Santa Fe, New Mexico, USA  
“Genome-Wide Chromatin Maps and Transcriptomes Across Tissues during Mouse Aging”
- April 29<sup>th</sup>, 2016** **Department of Pathology & Immunology**, Washington University School of Medicine, BJC Institute of Health, St. Louis, Missouri, USA (*Invited communication*)  
“Epigenomic regulation of aging in vertebrates”
- April 20<sup>th</sup>, 2016** **Department of Genetics and Complex Diseases**, Harvard T.H. Chan School of Public Health, Boston, Massachusetts, USA (*Invited communication*)  
“Epigenomic regulation of aging in vertebrates”
- December 9<sup>th</sup>, 2014** **9<sup>th</sup> Bay Area Aging Symposium**, Gladstone Institutes/University of California at San Francisco, San Francisco, California, USA  
“Exploration of the H3K4me3 breadth landscape during aging”
- September 11<sup>th</sup>, 2014** **Meeting on Epigenetics and Chromatin**, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, USA  
“H3K4me3 breadth is linked to cell identity and transcriptional consistency”
- April 8<sup>th</sup>, 2014** **Département de Biologie, Institut de Biologie de l'ENS (IBENS)**, Paris, France (*Invited communication*)  
“H3K4me3 breadth promotes transcriptional consistency at genes key for cell identity and function”
- January 30<sup>th</sup>, 2014** **14<sup>th</sup> Annual Symposium for Biomedical Computing at Stanford (BCATS 2014)**, Stanford University, Stanford, California, USA  
“Buffer Domains promote transcriptional stability at key cell identity and function genes”
- November 26<sup>th</sup>, 2012** **5<sup>th</sup> Bay Area Aging Symposium**, Gladstone Institutes/University of California at San Francisco, San Francisco, California, USA  
“*De novo* assembly of the genome and transcriptome of the short-lived African killifish *Nothobranchius furzeri*: a new model for aging research”
- October 20<sup>th</sup>, 2009** **Institut Jacques Monod, IJM2 Inauguration conference**, Paris, France (*Invited communication*)  
“FOXL2: at the crossroads of the cellular stress response and of tumor suppression”
- May 25<sup>th</sup>, 2009** **European Human Genetics Conference 2009**, Molecular bases of Mendelian disorders session, Vienna, Austria  
“Positive and negative feedback regulates the transcription factor FOXL2 in response to cell stress: evidence for a regulatory imbalance induced by disease-causing mutations”
- January 23<sup>rd</sup>, 2009** **Journées des Doctorants de l'Institut Cochin**, Paris, France  
“Implication of Forkhead transcription factor FOXL2 in the ovarian stress response”
- October 25<sup>th</sup>, 2007** **28<sup>èmes</sup> Journées Annuelles de la Société Française de Gériatrie et de Gériatrie**, Session Recherche Clinique et Fondamentale, Paris, France (*Invited communication*)  
“The transcription factor FoxL2: a molecular actor of ovarian aging?”

## Posters

- September 27<sup>th</sup>, 2016** **Meeting on Mechanisms of Aging**, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, USA  
“Genome-Wide Chromatin Maps and Transcriptomes Across Tissues during Mouse Aging”

- May 26<sup>th</sup>, 2016**      **12<sup>th</sup> Bay Area Aging Symposium**, University of California at Berkeley, California, USA  
 “Genome-Wide Chromatin Maps and Transcriptomes Across Tissues during Mouse Aging”
- May 12<sup>th</sup>, 2015**      **10<sup>th</sup> Bay Area Aging Symposium**, Buck Institute for Aging Research, California, USA  
 “Age-dependent loss of transcriptional consistency is linked to a widespread increase in the variability of H3K4me3 domain breadth”
- May 28<sup>th</sup>, 2014**      **8<sup>th</sup> Bay Area Aging Symposium**, University of California at Berkeley, California, USA  
 “*De novo* assembly and annotation of the genome of the short-lived African killifish *Nothobranchius furzeri*: a new model for aging research”
- November 25<sup>th</sup>, 2013**    **7<sup>th</sup> Bay Area Aging Symposium**, Stanford, California, USA  
 “*De novo* assembly and annotation of the genome of the short-lived African killifish *Nothobranchius furzeri*: a new model for aging research”
- November 12<sup>th</sup>, 2013**    **Chromatin Structure and Function Abcam Conference**, Grand Cayman Island, Cayman Islands  
 “Buffer Domains are associated to reduced transcriptional variability at key cell identity and function genes”
- September 29<sup>th</sup>, 2009**    **Congrès Jeunes Chercheurs Paris Descartes 2009**, Institut Cochin, Paris, France  
 “Positive and negative feedback regulates the transcription factor FOXL2 in response to cell stress”

## RESEARCH SUPPORT

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- 04/2015-03/2020    **NIH Pathway to Independence Award K99**, National Institutes of Aging  
 AG049934-01, entitled “Regulation of transcriptional consistency by broad H3K4me3 domains in young cells and during aging”.
- 01/2013-12/2013    **Dean’s Postdoctoral Fellowship (Stanford University School of Medicine).**  
 The aim of the project was to study H3K4me3 breadth in mouse neural stem cells.
- 09/2008-08/2011    **Graduate training fellowship (French Research and National Education Institute).**  
 The aim of the project was to study the role of the transcription factor FOXL2 in mammalian ovarian function.
- 06/2005-08/2005    **Visiting scholar fellowship (Rice Institute of Biomedical Research).**  
 The aim of the project was to study modulators of the heat-shock response in the *C. elegans* model.
- 09/2004-08/2008    **Pre-doctoral training fellowship (École Normale Supérieure of Paris, France).**  
 This fellowship is awarded upon a competitive exam to support the training of outstanding students in science and research at the pre-doctoral level.

## STATISTICS AND INFORMATICS TRAINING

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- April 7<sup>th</sup>, 2015**      **Statistical Learning**, Stanford University, Stanford online class (completed)
- January 8<sup>th</sup>, 2015**    **Practical Machine Learning**, Johns Hopkins University, Coursera online class (completed with distinction)
- December 17<sup>th</sup>, 2014** **The Data Scientist’s Toolbox**, Johns Hopkins University, Coursera online class (completed with distinction)
- December 17<sup>th</sup>, 2014** **Statistical Inference**, Johns Hopkins University, Coursera online class (completed with distinction)
- December 8<sup>th</sup>, 2014**    **Regression Models**, Johns Hopkins University, Coursera online class (completed with distinction)

**October 6<sup>th</sup>, 2014**    **Reproducible research**, Johns Hopkins University, Coursera online class (completed with distinction)

**February 24<sup>th</sup>, 2014**    **Introduction to object-oriented programming (in C++)**, École Polytechnique Fédérale de Lausanne, Coursera online class (completed with distinction)

**September 23<sup>rd</sup>, 2013**    **Initiation to programmation (in C++)**, École Polytechnique Fédérale de Lausanne, Coursera online class (completed with distinction)