

Xavier Robin, PhD

Current position Post-doc at Linding Lab, BRIC,
University of Copenhagen, Denmark

Personal information • Nationality : Switzerland
• Born : 9th January 1983
• Place of birth : Switzerland

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• Vesterbrogade 39.2 th
DK-1620 København V, Denmark
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Areas of expertise	<ul style="list-style-type: none"> • Systems biology, cell signaling, network analysis • High-throughput microscopy image analysis • Data analysis (ROC curves, biomarkers, supervised learning, deep learning) • Bioinformatics programming (R, perl, java, python, C++) • Web development (including database design) • Linux system administration (multi-user servers, SGI UV shared memory supercomputer)
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Scientific tools

- MIAPEGelDB: a web interface to create MIAPE-gel-compliant documents
miapgedb.expasy.org
- pROC: a package for R and S+ to build and analyze ROC curves
www.expasy.org/tools/pROC
- PanelomiX: a framework and tool to create threshold-based biomarker panels
www.panelomix.net
- DeepLearning: R package for Deep Learning
github.com/xrobin/DeepLearning

Publications

1. **X. Robin**, C. Hoogland, R. D. Appel, F. Lisacek (2008). MIAPEGelDB, a web-based submission tool and public repository for MIAPE gel electrophoresis documents. *Journal of Proteomics* 71 (2), p. 249–251. PMID: [18590991](https://pubmed.ncbi.nlm.nih.gov/18590991/). DOI: [10.1016/j.jprot.2008.06.005](https://doi.org/10.1016/j.jprot.2008.06.005). IF 2009: 3.9
2. C. Hoogland, D. Walther, P. M. Palagi, G. Bouchet, K. Mostaguir, **X. Robin**, R. D. Appel, Lisacek F. (2008). A suite of tools to analyse and publish 2-DE data. *Proteomics* 8 (23-24), p. 4907–4909. PMID: [19072735](https://pubmed.ncbi.nlm.nih.gov/19072735/). DOI: [10.1002/pmic.200800301](https://doi.org/10.1002/pmic.200800301). IF 2008: 4.6
3. A. Hainard, N. Tiberti, **X. Robin**, V. Lejon, D. M. Ngoyi, E. Matovu, J. C. Enyaru, C. Fouda, J. M. Ndung'u, F. Lisacek, M. Müller, N. Turck, J.-C. Sanchez (2009). A Combined CXCL10, CXCL8 and H-FABP Panel for the Staging of Human African Trypanosomiasis Patients. *PLoS Neglected Tropical Diseases* 3 (6), p. e459. PMID: [19554086](https://pubmed.ncbi.nlm.nih.gov/19554086/). DOI: [10.1371/journal.pntd.0000459](https://doi.org/10.1371/journal.pntd.0000459). IF 2009: 4.7
4. N. Turck, L. Vutskits, P. Sanchez-Pena, **X. Robin**, A. Hainard, M. Gex-Fabry, C. Fouda, H. Bassem, M. Mueller, F. Lisacek, L. Puybasset, J.-C. Sanchez (2010). A multiparameter panel method for outcome prediction following aneurysmal subarachnoid hemorrhage. *Intensive Care Medicine* 36 (1), p. 107–115. PMID: [19760205](https://pubmed.ncbi.nlm.nih.gov/19760205/). DOI: [10.1007/s00134-009-1641-y](https://doi.org/10.1007/s00134-009-1641-y). IF 2009: 5.2
5. **X. Robin**, N. Turck, A. Hainard, F. Lisacek, J.-C. Sanchez, M. Müller (2009). Bioinformatics for protein biomarker panel classification: What is needed to bring biomarker panels into in vitro diagnostics? *Expert Review of Proteomics* 6 (6), p. 675–689. PMID: [19929612](https://pubmed.ncbi.nlm.nih.gov/19929612/). DOI: [10.1586/EPR.09.83](https://doi.org/10.1586/EPR.09.83). IF 2009: 3.6

6. N. Tiberti, A. Hainard, V. Lejon, **X. Robin**, D. M. Ngoyi, N. Turck, E. Matovu, J. Enyaru, J. M. Ndung'u, A. Scherl, L. Dayon, J.-C. Sanchez (2010). Discovery and verification of osteopontin and beta-2-microglobulin as promising markers for staging human African trypanosomiasis. *Molecular & Cellular Proteomics*, 9 (12), p. 2783–2795. PMID: [20724469](#). DOI: [10.1074/mcp.M110.001008](#). IF 2009: 8.8
7. A. Hainard, N. Tiberti, **X. Robin**, D. M. Ngoyi, E. Matovu, J. C. Enyaru, M. Müller, N. Turck, J. M. Ndung'u, V. Lejon, J.-C. Sanchez (2011). Matrix metalloproteinase-9 and intercellular adhesion molecule 1 are powerful staging markers for human African trypanosomiasis. *Tropical Medicine and International Health*, 16 (1), p. 119–126. PMID: [20958893](#). DOI: [10.1111/j.1365-3156.2010.02642.x](#). IF 2009: 2.3
8. **X. Robin**, N. Turck, A. Hainard, N. Tiberti, F. Lisacek, J.-C. Sanchez, M. Müller (2011). pROC: an open-source package for R and S+ to analyze and compare ROC curves. *BMC Bioinformatics*, 12, p. 77. PMID: [21414208](#). DOI: [10.1186/1471-2105-12-77](#). IF 2009: 3.4; citations: >1000
9. N. Tiberti, A. Hainard, V. Lejon, B. Courtioux, E. Matovu, J. C. Enyaru, **X. Robin**, N. Turck, K. Kristensson, D. M. Ngoyi, G. M. L. Vatunga, S. Krishna, P. Büscher, S. Bisser, J. M. Ndung'u, J.-C. Sanchez (2012). Cerebrospinal fluid neopterin as marker of the meningo-encephalitic stage of *Trypanosoma brucei gambiense* sleeping sickness. *PLoS ONE*, 7 (7), p. e40909. PMID: [22815865](#). DOI: [10.1371/journal.pone.0040909](#). IF 2010: 4.4
10. N. Turck, **X. Robin**, N. Walter, C. Fouda, A. Hainard, R. Sztajzel, G. Wagner, D. Hochstrasser, J. Montaner, P. R. Burkhard, J.-C. Sanchez (2012). Blood Glutathione S-Transferase- π as a Time Indicator of Stroke Onset. *PLoS ONE*, 7 (9), p. e43830. PMID: [23028472](#). DOI: [10.1371/journal.pone.0043830](#). IF 2010: 4.4
11. J.-C. Copin, M. M. Rebetez, N. Turck, **X. Robin**, J.-C. Sanchez, K. Schaller, Y. Gasche, B. Walder (2012). MMP-9 and cellular fibronectin plasma concentrations are predictors of the composite endpoint of length of stay and death in the intensive care unit after severe traumatic brain injury. *Scandinavian Journal of Trauma, Resuscitation and Emergency Medicine*, 20 (1), p. 83. PMID: [23249478](#). DOI: [10.1186/1757-7241-20-83](#). IF 2011: 1.8
12. F. Glück, C. Hoogland, P. Antinori, **X. Robin**, A. Zufferey, C. Pasquarello, V. Fetaud, L. Dayon, F. Nikitin, M. Müller, F. Lisacek, L. Geiser, D. Hochstrasser, J.-C. Sanchez, A. Scherl (2013). Easyprot – an easy-to-use graphical platform for proteomics data analysis. *Journal of Proteomics*, 79, p. 146–160. PMID: [23277275](#). DOI: [10.1016/j.jprot.2012.12.012](#). IF 2011: 4.9
13. N. Tiberti, E. Matovu, A. Hainard, J. C. Enyaru, V. Lejon, **X. Robin**, N. Turck, D. M. Ngoyi, S. Krishna, S. Bisser, B. Courtioux, P. Büscher, K. Kristensson, J. M. Ndung'u, J.-C. Sanchez (2013). New biomarkers for stage determination in *Trypanosoma brucei rhodesiense* sleeping sickness patients. *Clinical and Translational Medicine*, 2 (1), p. 1. PMID: [23369533](#). DOI: [10.1186/2001-1326-2-1](#). IF 2011: NA; citations: 15
14. N. Tiberti, V. Lejon, A. Hainard, B. Courtioux, **X. Robin**, N. Turck, K. Kristensson, E. Matovu, J. C. Enyaru, D. Mumba Ngoyi, S. Krishna, S. Bisser, J. M. Ndung'u, P. Büscher, J.-C. Sanchez (2013). Neopterin Is a Cerebrospinal Fluid Marker for Treatment Outcome Evaluation in Patients Affected by *Trypanosoma brucei gambiense* Sleeping Sickness. *PLOS Neglected Tropical Diseases*, 7 (2), p. e2088. PMID: [23469311](#). DOI: [10.1371/journal.pntd.0002088](#). IF 2011: 4.7
15. B. Walder, **X. Robin**, M. M. L. Rebetez, J.-C. Copin, Y. Gasche, J.-C. Sanchez, N. Turck (2013). The prognostic significance of the serum biomarker H-FABP in comparison with S100b in severe traumatic brain injury. *Journal of Neurotrauma*, in press. PMID: [23590685](#). DOI: [10.1089/neu.2012.2791](#). IF 2011: 3.7

16. **X. Robin**, N. Turck, A. Hainard, N. Tiberti, F. Lisacek, J.-C. Sanchez, M. Müller (2013). PanelomiX: A threshold-based algorithm to create panels of biomarkers. *Translational Proteomics*, 1 (1), p. 57–64. DOI: [10.1016/j.trprot.2013.04.003](https://doi.org/10.1016/j.trprot.2013.04.003).
IF 2011: NA; citations: 7
17. **X. Robin**, P. Creixell, O. Radetskaya, C. C. Santini, J. Longden, R. Linding (2013). Personalized Network-Based Treatments in Oncology. *Clinical Pharmacology & Therapeutics*, 94 (6), p. 646-650. PMID: [23995267](https://pubmed.ncbi.nlm.nih.gov/23995267/). DOI: [10.1038/clpt.2013.171](https://doi.org/10.1038/clpt.2013.171)
IF 2013: 7.4
18. H. Horn, E. M. Schoof, J. Kim, **X. Robin**, M. L. Miller, F. Diella, A. Palma, G. Cesareni L. Juhl Jensen, R. Linding (2014). KinomeXplorer: an integrated platform for kinome biology studies. *Nature Methods*, 6, p. 603-604. PMID: [24874572](https://pubmed.ncbi.nlm.nih.gov/24874572/).
DOI: [10.1038/nmeth.2968](https://doi.org/10.1038/nmeth.2968) IF 2014: 32
19. M. Calderón-Santiago, F. Priego-Capote, N. Turck, **X. Robin**, B. Jurado-Gómez, J.-C. Sanchez, M. D. Luque de Castro (2015). Human sweat metabolomics for lung cancer screening. *Analytical and bioanalytical chemistry* 407 (18), p. 5381-5392. PMID: [25935675](https://pubmed.ncbi.nlm.nih.gov/25935675/). DOI: [10.1007/s00216-015-8700-8](https://doi.org/10.1007/s00216-015-8700-8) IF 2015: 3.1
20. V. Severino, J.-M. Dumonceau, M. Delhay, S. Moll, I. Annessi-Ramseyer, **X. Robin**, J.-L. Frossard, A. Farina (2017). Extracellular Vesicles in Bile as Markers of Malignant Biliary Stenoses. *Gastroenterology*, in press. DOI: [10.1053/j.gastro.2017.04.043](https://doi.org/10.1053/j.gastro.2017.04.043)
IF 2015: 18.2

Manuscripts in preparation

1. J. Longden, **X. Robin**, et al. Elucidating signaling networks driving ErbB-family drug resistance from complex cell morphologies using deep neural networks. Submitted.
2. **X. Robin**, et al. Multi-scale Sampling of Molecular Networks Underlying Colon Cancer Metastases. Manuscript in preparation.

Research Experience

2014 – present University of Copenhagen
 Postdoc at Biotech Research and Innovation Centre (BRIC) – Linding Lab

- Computational methods for data integration
- Analysis of Mass Spectrometry and NGS
- Deep Learning, Non-negative matrix factorization

2013 Technical University of Denmark
 Postdoctoral fellow, independent researcher

- Funded by the Swiss National Science Foundation
- Analysis of high-throughput microscopy images to determine the structure of the cell signaling network
- Network drugs and biomarkers

Education

2007 – 2012 University of Geneva
 PhD thesis in sciences, mention interdisciplinary

- “Panels of biomarker to improve patient classification in brain diseases”
- Committee: J.-C. Sanchez, D. Hochstrasser, R. Appel, M. Müller, J. Colinge.

2005 – 2007 University of Geneva
 Master's degree in proteomics and bioinformatics (jointly organized by the faculties of medicine and sciences and the Swiss Institute of Bioinformatics)

- Practical work “Tools for proteomic standards” (web interface for MIAPE documents)

2002 – 2005 University of Geneva
 Bachelor in biology (faculty of sciences)

- Awards and Grants**
- 2002 Federal maturity, Geneva
 - Prix Denise Lecoultre for my maturity work about prion
 - 2008 8th Siena meeting, Siena, Italy
 - Swiss Proteomics Society Grant
 - 2008 European BioAlpine Convention, Geneva
 - Award for the best poster in the session “beyond discovery in proteomics”
 - 2012 Integrative Network Biology 2012: Network Medicine, Helsingør, Denmark
 - Travel Fellowship
 - 2012 Swiss National Science Foundation
 - Post-doc fellowship
- Posters**
- 2007 Congress of the Swiss Proteomics Society, Lausanne
 - MIAPEGelDB: a web-based submission tool and public repository for MIAPE gel electrophoresis documents
 - 2008 8th Siena meeting, Siena, Italy
 - Comparison of statistical learning methods for biomarker combination
 - 2008 European BioAlpine Convention, Geneva
 - Comparison of statistical learning methods for biomarker combination
 - 2012 Integrative Network Biology 2012: Network Medicine, Helsingør, Denmark
 - pROC: an open-source package for R and S+ to analyze and compare ROC curves
 - 2013 9th q-bio Conference, Santa Fe, NM, USA
 - Genome-scale morphological mapping of the mechanisms underlying cell invasion
- Public presentations**
- 2009 UseR! conference, Rennes France
 - Combination of protein biomarkers
 - 2010 Swiss Proteomics Society PhD students' symposium, Basel
 - How to combine biomarkers?
 - 2011 HUPO Annual World Congress, Geneva
 - PanelomiX – a bioinformatic tool to build biomarker panels
 - 2012 9th Siena Meeting, Siena, Italy
 - PanelomiX: a web-based tool to create panels of biomarkers based on thresholds
 - 2013 Bioimaging Workshop, Copenhagen, Denmark
 - Genome-scale morphological mapping of the mechanisms underlying cell invasion
 - 2016 ISC High Performance, Frankfurt am Main, Germany
 - Preparing for the Next Step in Genomic Analysis; with Phong Le, SGI.
- Teaching activities**
- 2010, 2011 Masters in proteomics and bioinformatics
 - Biomarker validation part 2: statistical analysis (1h)
 - Combination of biomarkers (2h)
 - 2014 Bachelor in IT and Health, KU / DTU
 - Introduction to Systems Biology (course organizer)

- Miscellaneous** Peer-reviewed manuscripts for:
- Journal of Proteomics
 - Biomarkers
 - The Open Proteomics Journal
 - Bioinformatics
 - Journal of Statistical Software

2012–present

- Member of the editorial board of the Journal of Proteomics