



*Unit Director*  
Emmanuel Barillot

**Teams in this computational unit study several aspects of the cancer pathology through observation of the underlying molecular and cellular mechanisms: initiation (etiology, through the modelling of gene and environment interaction), development and tumor progression (inferring and modelling the gene and protein networks involved, analysis of phenotypes through bioimaging), and improvement in therapeutic strategies (diagnosis, prognosis, design and analysis of clinical trials, identification of therapeutic targets, virtual selection of therapeutic molecules).**

Research projects are conducted in close collaboration with biologists and clinicians and always involved a mix of experimental and theoretical approaches, in iterative cycles from the wet biology to the mathematical model and back, which ultimately lead to validated and thus predictive models. They take advantage of new high throughput biological technologies at both the molecular and cellular levels (spectrometry, microarrays, high-throughput cellular phenotyping, deep sequencing) and use state-of-the-art and innovative methods of data integration and systems biology, statistical analysis, high dimension statistical learning, study of complexity, network modeling, virtual screening and bioimaging.

## Key publications

#### Year of publication 2017

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Manuela Portoso, Roberta Ragazzini, Živa Brenčič, Arianna Moiani, Audrey Michaud, Ivaylo Vassilev, Michel Wassef, Nicolas Servant, Bruno Sargueil, Raphaël Margueron (2017 Feb 8)

**PRC2 is dispensable for HOTAIR-mediated transcriptional repression.**

*The EMBO journal* : [DOI : e201695335](https://doi.org/10.1038/e201695335)

Maud Borensztein, Laurène Syx, Katia Ancelin, Patricia Diabangouaya, Christel Picard, Tao Liu, Jun-Bin Liang, Ivaylo Vassilev, Rafael Galupa, Nicolas Servant, Emmanuel Barillot, Azim Surani, Chong-Jian Chen, Edith Heard (2017 Jan 31)

**Xist-dependent imprinted X inactivation and the early developmental consequences of its failure.**

*Nature structural & molecular biology* : [DOI : 10.1038/nsmb.3365](https://doi.org/10.1038/nsmb.3365)

#### Year of publication 2016

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Daniela Chmiest, Nanaocha Sharma, Natacha Zanin, Christine Viaris de Lesegno, Massiullah Shafaq-Zadah, Vonick Sibut, Florent Dingli, Philippe Hupé, Stephan Wilmes, Jacob Piehler, Damarys Loew, Ludger Johannes, Gideon Schreiber, Christophe Lamaze (2016 Dec 6)

**Spatiotemporal control of interferon-induced JAK/STAT signalling and gene transcription by the retromer complex.**

*Nature communications* : 13476 : [DOI : 10.1038/ncomms13476](https://doi.org/10.1038/ncomms13476)

Wael Jdey, Sylvain Thierry, Christophe Russo, Flavien Devun, Muthana Al Abo, Patricia Noguez-Hellin, Jian-Sheng Sun, Emmanuel Barillot, Andrei Zinovyev, Inna Kuperstein, Yves Pommier, Marie Dutreix (2016 Aug 26)

**Drug Driven Synthetic Lethality: bypassing tumor cell genetics with a combination of Dbait and PARP inhibitors.**

*Clinical cancer research : an official journal of the American Association for Cancer Research* : [DOI : clincanres.1193.2016](https://doi.org/10.1158/1078-0432.CCR.151982)

#### Year of publication 2015

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Natasha Zamudio, Joan Barau, Aurélie Teissandier, Marius Walter, Maté Borsos, Nicolas Servant, Déborah Bourc'his (2015 Jun 26)

**DNA methylation restrains transposons from adopting a chromatin signature permissive for meiotic recombination.**

*Genes & development* : 1256-70 : [DOI : 10.1101/gad.257840.114](https://doi.org/10.1101/gad.257840.114)

#### Year of publication 2014

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Elsa Bernard, Laurent Jacob, Julien Mairal, Jean-Philippe Vert (2014 May 9)



U900 – Bioinformatics, Biostatistics, Epidemiology and  
Computational Systems. Biology of Cancer  
**Integrative Tumour Biology, Immunology and Environment**

**Efficient RNA isoform identification and quantification from RNA-Seq data with network flows.**

*Bioinformatics (Oxford, England)* : 2447-55 : [DOI : 10.1093/bioinformatics/btu317](https://doi.org/10.1093/bioinformatics/btu317)