

Giulio Ferrero's Curriculum Vitae

Affiliation: University of Torino
Institutions: Department of Computer Science
Working Address: Corso Svizzera 185
Zip Code: I-10149
City: Torino
State: Italy

Education

- 25/01/2016 **Ph.D** in Complex Systems for Life Sciences, University of Torino
Thesis: *"Functional characterization of the human noncoding genome by integrative analysis of High-Throughput data."*
Supervisors: Dr. Francesca Cordero (Department of Computer Science), Prof. Michele De Bortoli (Department of Clinical and Biological Sciences), and Prof. Gianfranco Balbo (Department of Computer Science)
- 17/10/2012 **M.A.** Cellular and Molecular Biology, University of Torino
Thesis: *"A new data processing pipeline for the bioinformatic analysis of transcription factor genomic binding events."*
Supervisors: Dr. Francesca Cordero (Department of Computer Science) and Prof. Michele De Bortoli (Department of Clinical and Biological Sciences)
Marks: 110/110 cum laude
- 06/10/2010 **B.A.** Biological Science, University of Torino
Thesis: *"ChIA-PET: Analysis and prospects of a novel technique to study chromatin architecture."*
Supervisors: Dr. Santina Cutrupi (Department of Clinical and Biological Sciences) and Prof. Michele De Bortoli (Department of Clinical and Biological Sciences)
Marks: 100/110

Grants and scholarships

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| 2020-ongoing | Research grant - Assegno di ricerca: <i>"Setting bioinformatics pipelines for omics data integration in human diseases"</i> . Department of Clinical and Biological Sciences, University of Torino. Duration: 12 months. |
| 2019 | FIRC-AIRC Fellowship - Borsa di ricerca: <i>"Host-gut microbiome small RNA cross-talk: an innovative source of biomarkers for an accurate colorectal cancer detection"</i> . Department of Computer Science, University of Torino. Duration: 12 months. |
| 2018 | Scholarship - Borsa di ricerca: <i>"Definition of new pipelines to analyze transcriptome data for the identification of diagnostic and prognostic tumor biomarkers"</i> . Department of Computer Science, University of Torino. Duration: 6 months. |
| 2017 | Research grant - Assegno di ricerca: <i>"Development of algorithms for the identification of biomarkers in cancer"</i> . Department of Computer Science, University of Torino. Duration: 12 months.
Scholarship - Borsa di ricerca: <i>"Development of computational workflow for the identification of tumor biomarkers"</i> . Department of Computer Science, University of Torino. Duration: 3 months. |

- 2016 | Scholarship - Borsa di ricerca: "*Integrative bioinformatic analysis of genomic, epigenomic, and transcriptomic data*". Department of Clinical and Biological Science, University of Torino. Duration: 6 months.
Scholarship - Borsa di ricerca: "*Development of algorithms for the integration of heterogeneous biological and clinical data*". Department of Computer Science, University of Torino. Duration: 6 months.

Projects

- 2019 | Researcher - Bioinformatic tasks - '*Host-gut microbiome small RNA cross-talk: an innovative source of biomarkers for an accurate colorectal cancer detection*' - (Federazione Italiana Ricerca sul Cancro Associazione Italiana Ricerca sul Cancro - FIRC-AIRC).
2018 | Researcher - Bioinformatic tasks - "*Validation of clinical biomarkers based on non-coding RNAs and intestinal microbiota for colorectal cancer.*"- (Lega Italiana Lotta contro i Tumori - LILT).
Researcher - Bioinformatic tasks - "*Biomarker-box: an economic and efficient computer system for analyzing biological data in real time*"- (Fondazione CRT).
2017 | Researcher - Bioinformatic tasks - "*Small noncoding RNA biomarker discovery for Colorectal cancer.*"- (Lega Italiana Lotta contro i Tumori - LILT).
2015 | Researcher - Bioinformatic tasks - "*Unliganded activity of estrogen receptor alpha.*" - (Associazione Italiana Ricerca sul Cancro - AICR-IG 2015).

Awards

- 2016 | SIBBM Travel Grants for attendance to International Conferences.
BITS Travel Grants.
2015 | BITS Travel Grants for attendance to International Conferences.
2015 | BITS Travel Grants.
2013 | Best Master's degree thesis 2011-2012. Thesis: "*A new data processing pipeline for the bioinformatic analysis of transcription factor genomic binding events*".

Teaching Experiences

- 2018-2020 | Teacher of the course "*Informatics (INT0639B)*" of the Bachelor Degree Course in Biotechnology (L-2), University of Torino.
2016-2020 | Teaching Assistant for *Bioinformatic module* of the course "*Advanced Molecular Biology (SVB0041)*" of the Master Degree Course in Cellular and Molecular Biology (LM-6), University of Torino.
2015-2017 | Teaching Assistant for *R programming module* of the course "*Computational Processing of Experimental Data (MFN1306)*" of the undergraduate Degree Course in Biology (L-13), University of Torino.
2013-2015 | Teaching Assistant for the *Bioinformatic module* of the course "*Biomolecular Laboratory (MFN1294)*" of the undergraduate Degree Course in Biology (L-13), University of Torino.

Nonacademic scientific experiences

2019-ongoing | External bioinformatic consultant of Bactell inc (US) to predict antibiotic resistance from bacterial whole-genome sequencing.

Professional memberships

Società Italiana di Biofisica e Biologia Molecolare (SIBBM).
The Bioinformatics Italian Society (BITS).
International Society of Computational Biology (ISCB).
EuroScience.

Certified professional developments

2019 | *"Machine Learning A-Z: Hands-On Python & R In Data Science"* through Udemy.
"Whole genome sequencing of bacterial genomes - tools and applications." by the Technical University of Denmark through Coursera.
"Metagenomics applied to surveillance of pathogens and antimicrobial resistance." by the Technical University of Denmark through Coursera.
"Introduction to Machine Learning" through DataCamp.
"Data visualization with ggplot2" through DataCamp.
"Reporting with R Markdown" through DataCamp.

2017 | *"Python for Genomic Data Science"* by the Johns Hopkins University through Coursera.

2016 | *"Bioinformatic Methods II"* by the University of Toronto through Coursera.

2015 | *"Big Data Science with the BD2K-LINCS Data Coordination and Integration Center"* by the Icahn School of Medicine at Mount Sinai through Coursera.
"Case Study: ChIP-seq data analysis" by the Harvard University through edX.
"Data Analysis and Statistical Inference" by the Duke University through Coursera.
"Bioinformatic Methods I" by the University of Toronto through Coursera.
"Statistics and R for the Life Sciences" by the Harvard University through edX.
"Data Mining with Weka" by the University of Waikato.
"Genomic and Precision Medicine" by the University of California, San Francisco through Coursera.
"Network Analysis in Systems Biology" by the Icahn School of Medicine at Mount Sinai through Coursera.

2014 | *"R Programming"* by the Johns Hopkins Bloomberg School of Public Health through Coursera.
"An Introduction to Interactive Programming in Python" by the Rice University through Coursera.
"Intro to Computer Science" through Udacity.

2013 | *"Csama 2013: computational statistics for genome biology (11th edition)"* at Bressanone-Brixen, Italy.

Publications in refereed journals

Dr Ferrero has published his results on a wide range of topics in scientific peer-reviewed journal and conferences. He authored **22 articles** published in international ISI indexed peer-reviewed journals and in the proceedings of international conferences of the field. His H-index in Scopus is **8** with **255 citations**, while his H-index in Google Scholar is **10** with **336 citations**.

20. Ferrero, G., Licheri, N., Coscujuela Tarrero, L., De Intinis, C., Miano, V., Calogero, R. A., Cordero, F., De Bortoli, M., and Beccuti, M. (2020). Docker4circ: A framework for the reproducible characterization of circrnas from rna-seq data. *International Journal of Molecular Sciences*, 21(1):293. [IF=4.18, Q1: Computer Science Applications; Medicine (miscellaneous), Q2: Molecular Biology]
19. Elhasnaoui, J., Miano, V., Ferrero, G., Doria, E., Leon, A. E., Fabricio, A. S., Annaratone, L., Castellano, I., Sapino, A., and De Bortoli, M. (2020). Dscam-as1-driven proliferation of breast cancer cells involves regulation of alternative exon splicing and 3'-end usage. *Cancers*, 12(6):1453, [IF=6.16, Q1: Cancer Research; Oncology]
18. Mandili, G., Follia, L., Ferrero, G., Katayama, H., Hong, W., Momin, A. A., Capello, M., Giordano, D., Spadi, R., Satolli, M. A., et al. (2020). Immune-complexome analysis identifies immunoglobulin-bound biomarkers that predict the response to chemotherapy of pancreatic cancer patients. *Cancers*, 12(3):746. [IF=6.16, Q1: Cancer Research; Oncology]
17. Tarallo, S., Ferrero, G., Gallo, G., Francavilla, A., Clerico, G., Realis Luc, A., Manghi, P., Thomas, A. M., Vineis, P., Segata, N., Pardini, B., Naccarati, A., and Cordero, F. (2019). Altered fecal small rna profiles in colorectal cancer reflect gut microbiome composition in stool samples. *mSystems*, 4(5):e00289–19. [IF=6.52, Q1: Computer Science Applications; Microbiology; Genetics; Molecular Biology]
16. Thomas, A. M., Manghi, P., Asnicar, F., Pasolli, E., Armanini, F., Zolfo, M., Beghini, F., Manara, S., Karcher, N., Pozzi, C., Gandini, S., Serrano, D., Tarallo, S., Francavilla, A., Gallo, G., Trompetto, M., Ferrero, G., Mizutani, S., Shiroma, H., Shiba, S., Shibata, T., Yachida, S., Yamada, T., Wirbel, J., Schrotz-King, P., Ulrich, C. M., Brenner, H., Arumugam, M., Bork, P., Zeller, G., Cordero, F., Dias-Neto, E., Setubal, J. C., Tett, A., Pardini, B., Rescigno, M., Waldron, L., Naccarati, A., and Segata, N. (2019). Metagenomic analysis of colorectal cancer datasets identifies cross-cohort microbial diagnostic signatures and a link with choline degradation. *Nature medicine*, 25:334–339, [IF=30.64. Q1: Biochemistry, Genetics and Molecular Biology (miscellaneous); Medicine (miscellaneous)]
15. Follia, L., Ferrero, G., Mandili, G., Beccuti, M., Giordano, D., Spadi, R., Satolli, M. A., Evangelista, A., Katayama, H., Hong, W., Momin, A. A., Capello, M., Hanash M, S., Novelli, F., and Cordero, F. (2019). Integrative analysis of novel metabolic subtypes in pancreatic cancer fosters new prognostic biomarkers. *Frontiers in Oncology*, 9:115. [IF=4.14. Q1: Cancer Research; Oncology]
14. Kulkarni, N., Alessandri, L., Panero, R., Arigoni, M., Olivero, M., Ferrero, G., Cordero, F., Beccuti, M., and Calogero, R. A. (2018). Reproducible bioinformatics project: A community for reproducible bioinformatics analysis pipelines. *BMC Bioinformatics*, 19(Suppl10):211–219. [IF=2.51. Q1: Computer Science Applications; Applied Mathematics; Biochemistry]
13. Ferrero, G., Cordero, F., Tarallo, S., Arigoni, M., Riccardo, F., Gallo, G., Ronco, G., Allasia, M., Kulkarni, N., Matullo, G., Vineis, P., Calogero, R. A., Pardini, B., and Naccarati, A. (2018). Small non-coding RNA profiling in human biofluids and surrogate tissues from healthy individuals: Description of the diverse and most represented species. *Oncotarget*, 9(3):3097. [IF=0. Q1: Oncology]
12. Tarrero, L. C., Ferrero, G., Miano, V., De Intinis, C., Ricci, L., Arigoni, M., Riccardo, F., Annaratone, L., Castellano, I., Calogero, R. A., Beccuti, M., Cordero, F., and De Bortoli, M. (2018). Luminal breast

- cancer-specific circular RNAs uncovered by a novel tool for data analysis. *Oncotarget*, 9(18):14580. [IF=0. Q1: Oncology]
11. Miano, V., Ferrero, G., Rosti, V., Manitta, E., Elhasnaoui, J., Basile, G., and De Bortoli, M. (2018). Luminal lncRNAs regulation by ER α -controlled enhancers in a ligand-independent manner in breast cancer cells. *International journal of molecular sciences*, 19(2):593. [IF=4.18. Q1: Computer Science Applications; Medicine (miscellaneous), Q2: Molecular Biology]
 10. Iannello, A., Rolla, S., Maglione, A., Ferrero, G., Bardina, V., Inaudi, I., De Mercanti, S., Novelli, F., D'Antuono, L., Cardaropoli, S., Todros, T., Turrini, M. V., Cordioli, C., Puorro, G., Marsili, A., Lanzillo, R., Morra, V. B., Cordero, F., De Bortoli, M., Durelli, L., Visconti, A., Cutrupi, S., and Clerico, M. (2018). Pregnancy epigenetic signature in t helper 17 and t regulatory cells in multiple sclerosis. *Frontiers in Immunology*, 9:3075. [IF=4.72. Q1: Immunology; Immunology and Allergy]
 9. Miglio, U., Berrino, E., Panero, M., Ferrero, G., Coscujuela, L., Miano, V., Dell'Aglio, C., Sarotto, I., Annaratone, L., Marchiò, C., Comoglio, P., De Bortoli, M., Pasini, B., Venesio, T., and Sapino, A. (2018). The expression of LINE1-MET chimeric transcript identifies a subgroup of aggressive breast cancers. *International Journal of Cancer*, pages 1–11. [IF=4.98. Q1: Cancer Research; Oncology]
 8. Ferrero, G., Miano, V., Beccuti, M., Balbo, G., De Bortoli, M., and Cordero, F. (2017). Dissecting the genomic activity of a transcriptional regulator by the integrative analysis of omics data. *Scientific reports*, 7(1):8564. [IF=4.01. Q1: Multidisciplinary]
 7. Miano, V., Ferrero, G., Reineri, S., Caizzi, L., Annaratone, L., Ricci, L., Cutrupi, S., Castellano, I., Cordero, F., and De Bortoli, M. (2016). Luminal long non-coding RNAs regulated by estrogen receptor alpha in a ligand-independent manner show functional roles in breast cancer. *Oncotarget*, 7(3):3201. [IF=0. Q1: Oncology]
 6. Guglielmo, M., Reineri, S., Iannello, A., Ferrero, G., Vanzan, L., Miano, V., Ricci, L., Tamagno, E., De Bortoli, M., and Cutrupi, S. (2016). E2 regulates epigenetic signature on neuroglobin enhancer-promoter in neuronal cells. *Frontiers in cellular neuroscience*, 10:147. [IF=3.90. Q1: Cellular and Molecular Neuroscience]
 5. Rosso, M. C., Badino, P., Ferrero, G., Costa, R., Cordero, F., and Steidler, S. (2016). Biologic data of cynomolgus monkeys maintained under laboratory conditions. *PloS one*, 11(6):e0157003. [IF=2.78. Q1: Agricultural and Biological Sciences (miscellaneous); Biochemistry, Genetics and Molecular Biology (miscellaneous)]
 4. Cordero, F., Ferrero, G., Polidoro, S., Fiorito, G., Campanella, G., Sacerdote, C., Mattiello, A., Masala, G., Agnoli, C., Frasca, G., Panico, S., Palli, D., Krogh, V., Tumino, R., Vineis, P., and Naccarati, A. (2015). Differentially methylated microRNAs in prediagnostic samples of subjects who developed breast cancer in the European prospective investigation into nutrition and cancer (epic-Italy) cohort. *Carcinogenesis*, 36(10):1144–1153. [IF=4.87. Q1: Cancer Research; Medicine (miscellaneous)]
 3. Misale, C., Ferrero, G., Torquati, M., and Aldinucci, M. (2014). Sequence alignment tools: one parallel pattern to rule them all? *BioMed research international*, 2014. [IF=2.20. Q1: Biochemistry, Genetics and Molecular Biology (miscellaneous); Medicine (miscellaneous)]
 2. Caizzi, L., Ferrero, G., Cutrupi, S., Cordero, F., Ballarè, C., Miano, V., Reineri, S., Ricci, L., Friard, O., Testori, A., Cora, D., Caselle, M., Di Croce, L., and De Bortoli, M. (2014). Genome-wide activity of unliganded estrogen receptor- α in breast cancer cells. *Proceedings of the National Academy of Sciences*, page 201315445. [IF=9.58. Q1: Multidisciplinary]
 1. Cutrupi, S., Ferrero, G., Reineri, S., Cordero, F., and De Bortoli, M. (2014). Genomic lens on neuroglobin transcription. *IUBMB life*, 66(1):46–51. [IF=3.05. Q1: Clinical Biochemistry]

Contributions in refereed conferences - Conference papers and proceedings

2. Piaggieschi G.B., Licheri N., Romano G., Pernice S., Follia L., and Ferrero G. MethylFASTQ: a tool simulating bisulfite sequencing data. (2019) PDP2019. Pavia, Italy 13-15 Febr 2019.
1. Follia L., Tordini F., Romano G., Pernice S., Piaggieschi G.B. and Ferrero G. ParallNormal: an efficient variant calling pipeline for unmatched sequencing data. (2018) PDP2018. Cambridge, England 21-23 March 2018.

Contributions in refereed conferences - Conference abstract

10. Mandili G., Follia L., Ferrero G., Katayama H., Wang H., Momin A. A., Capello M., Cordero F., Hanash S. M. and Novelli F. Chemotherapy effects on immune-complexes in pancreatic ductal adenocarcinoma patients serum. International Proteomics and Metabolomics conference. High-throughput MS-based proteomics and metabolomics: from cells to clinic. Novara, Italy, June 25, 2018.
9. Bulfamante S., Mandili G., Principe M., Giordano D., Mazza E., Curcio C., Follia L., Ferrero G., Evangelista A, Satolli M.A., Cappello P., Novelli F. Antibody and T cell response profiling in pancreatic cancer patients before and after chemotherapy identify tumor associated antigens suitable for immunotherapy. AACR Annual Meeting 2018; 2018 Apr 14-18; Chicago, IL. Philadelphia (PA): Cancer Res 2018;78(13 Suppl). 2017
8. Pardini B., Cordero B., Naccarati A., Ferrero G., Viberti C., Oderda M., Arigoni M., Calogero R.A., Sacerdote C., Gontero P., Vineis P., Matullo G. Urine microRNA profiling in bladder cancer by next-generation sequencing. (2017). AACR Annual Meeting 2017; 1-5 Apr 2017; Washington, DC. Philadelphia (PA): AACR; Cancer Res 2017;77(13 Suppl).
7. De Bortoli M., Miano V., Ferrero G., Annaratone L., Coscujuela L., Castellano I., Cordero F., Sapino A. DSCAM-AS1, a breast cancer specific and Estrogen receptor α -dependent long noncoding RNA, is a key component of the pathway controlling cell growth and migration. (2017) Proceedings of the 2016 San Antonio Breast Cancer Symposium; 2016 Dec 6-10; San Antonio, TX. Philadelphia (PA): AACR; Cancer Res 2017;77(4 Suppl).
6. Catarsi P., Cordero F., Ferrero G., Beccuti M., Poletto V., Bonetti E., Villani L., Massa M., Fois G., Campanelli R., Magrini U., Rosti V., Barosi G. (2017). Deregulated Genes in Hematopoietic Stem Cells Isolated from Spleen of Patients with Myelofibrosis. Blood, 128(22), 4279.
5. Gallo G., Tarallo S., Cordero F., Pardini B., Ferrero G., Vineis P., Clerico G., Realis Luc A., Naccarati A., Trompetto M. Next-generation sequencing for miRNA profiling of stool and plasma samples of patients with colorectal cancer or precancerous lesions. (2017). European Journal of Cancer. 72, Supplement 1, Page S62. Conference proceeding
4. Clerico M., Cutrupi S., De Mercanti S., Rolla S., Iannello A., Ferrero G., De Bortoli M., Durelli L. Estrogen Receptor Alpha Regulates Key Genomic Regions of Thelper 17 and T Regulatory Cells in Multiple Sclerosis: A New Potential Biomarker of Disease Activity. (2016). Neurology. 86 P5.348. Conference proceeding
3. Gallo G., Clerico G., Tarallo S., Cordero G., Pardini B., Vineis P., Ferrero G., Naccarati A., Realis Luc A., Trompetto M. Next-generation sequencing miRNA profiling in stool and plasma samples of patients with colorectal cancer or precancerous lesions. (2016). European Journal of Surgical Oncology, Vol. 42, Issue 9, S143. Conference proceeding

2. Clerico M., Cutrupi S., Iannello A., Ferrero G., Cordero F., Rolla S., Annibali V., De Bortoli M., Durelli L. Estrogen receptor-alpha regulates epigenetic changes on genomic regulatory regions: potential biomarkers in multiple sclerosis outcomes. (2016). MULTIPLE SCLEROSIS JOURNAL, 22, 479-480.
1. Naccarati A., Polidoro S., Fiorito G., Cordero F., Ferrero G., Campanella G., Sacerdote C., Mattiello A., Panico S., Masala G., Palli D., Agnoli C., Krogh V., Frasca G., Tumino, R., Vineis, P. Epigenome-wide study in prediagnostic samples from the European Prospective Investigation into Nutrition and Cancer (EPIC-Italy) cohort: Differentially methylated microRNAs in subjects who developed breast cancer. (2015). Proceedings of the 106th Annual Meeting of the AACR; 18-22 Apr. Philadelphia, Pennsylvania.

Oral presentation in refereed conferences

3. Ferrero G., Tarallo S., Francavilla A., Gallo G., Clerico G., Manghi P., Thomas A., Segata N., Pardini B., Naccarati A., Cordero F. Gut microbiome composition and small RNA spectra in human stool for colorectal cancer detection. (2018). BITS Annual Meeting 2018. 27-29 June. Turin, Italy.
2. Ferrero G., Miano V., Balbo G., De Bortoli M., Beccuti M., Cordero F. An integrative strategy to functional analysis of the noncoding genome. (2015). EMBL | STANFORD CONFERENCE: "Personalised Health". 16-19 Nov. Heidelberg, Germany.
1. Ferrero G., Miano V., Balbo G., De Bortoli M., Beccuti M., Cordero F. Integrative strategy for omics data: ERα cistrome and epigenome case-study. (2014). NETTAB 2014, "From structural bioinformatics to integrative systems biology", 15-17 Oct. Torino, Italy.

Contributions in refereed conferences - Posters

33. Tarallo S., Ferrero G., Francavilla A., Gallo G., Clerico G., Manghi P., Thomas A., Segat N., Cordero F., Pardini B., Naccarati A. Small RNA profiles in human stool reflect gut microbiome composition and together provide high accuracy to detect colorectal cancer. (2019). SIBBM Frontiers in Molecular biology, Nucleic acid immunity: from cellular mechanisms to new technologies. 11-13 June. Bologna, Italy.
32. Follia L., Ferrero M., Ferrero G., Pernice S., Dalmaso G., Visentin L., Sirovich R. and Cordero F. Mathematical evolutionary cancer models: a new frontier for cancer treatment. (2019). BITS annual meeting 2019. 26-28 June Palermo, Italy.
31. Coscujuela TL. Ferrero G., Doria E., Miano V., De Bortoli M. ACDYL circularizing exon involved in luminal breast cancer cell survival. (2019). SIBBM Frontiers in Molecular biology, Nucleic acid immunity: from cellular mechanisms to new technologies. 11-13 June. Bologna, Italy.
30. Maglione A., Iannello A., Ferrero G., Carello S., Rolla S., Cordero F., Clerico M., Cutrupi S. Integrative analysis of -omic data reveals estrogen-responsive genomic regions in T helper cell plasticity. (2019). SIBBM Frontiers in Molecular biology, Nucleic acid immunity: from cellular mechanisms to new technologies. 11-13 June. Bologna, Italy.
29. Tarallo S., Ferrero G., Francavilla A., Gallo G., Clerico G., Manghi P., Thomas A., Segat N., Cordero F., Pardini B., Naccarati A. Gut microbiome composition and small RNA spectra in human stool for colorectal cancer detection. (2018). EMBO | EMBL Symposium: The Human Microbiome. 16-19 Sept. Heidelberg, Germany.

28. Follia L., Ferrero G., Mandili G., Beccuti B., Katayama H., Hong W., Momin A.M., Capello M., Hanash S.M., Novelli F., Cordero F. An integrative transcriptomic analysis of glycolytic genes reveals different metabolic subtypes in pancreatic cancer. (2018). BITS Annual Meeting 2018. 27-29 June. Turin, Italy.
27. Elhasnaoui J., Ferrero G., Miano V., De Bortoli M. A transcript-level analysis of breast cancer RNA-Seq data revealed a widespread hormone-independent activity of ER α on RNA alternative splicing. (2018). BITS Annual Meeting 2018. 27-29 June. Turin, Italy.
26. Maglione A, Ferrero G., Iannello A., Cordero F., Clerico M., Cutrupi S. Integrative analysis of -omics data reveals estrogen-responsive regions in Th17 and Treg genomes. (2018). BITS Annual Meeting 2018. 27-29 June. Turin, Italy.
25. Coscujuela T.L., Ferrero G., Miano V., Ricci L., De Intinis C., Arigoni M., Riccardo F., Calogero R.A., Beccuti M., Cordero F. De Bortoli M. CircRNA characterisation in MCF-7 breast cancer cell line. (2017) ISMB/ECCB 2017. 21-25 July. Prague, Czech Republic.
24. Follia L., Mandili G., Ferrero G., Beccuti M., Cordero F., Katayama H., Wang H., Momin A.A., Capello M., Hanash S. M. and Novelli F. Proteomic data analysis of pancreatic cancer patient sera revealed how chemotherapy shapes the immunogenicity of developing tumors. (2017) ISMB/ECCB 2017. 21-25 July. Prague, Czech Republic.
23. Coscujuela T.L., Ferrero G., Miano V., Ricci L., De Intinis C., Arigoni M., Riccardo F., Calogero R.A., Beccuti M., Cordero F. and De Bortoli M. CircRNA characterisation in MCF-7 breast cancer cell line. (2017) ISFMS 2017. Basel, Switzerland 21-23 June 2017.
22. Catarsi P., Cordero F., Ferrero G., Beccuti M., Poletto V., Bonetti E., Villani L., Massa M., Fois G., Campanelli R., Magrini U., Rosti V., Barosi G. Deregulated Genes in Hematopoietic Stem Cells Isolated from Spleen and Peripheral Blood of Patients with Myelofibrosis. (2017). qPCR dPCR item NGS 2017. 3-7 Apr. Freising-Weihenstephan, Germany.
21. Follia L., Ferrero G., Totis N., Riganti C., Novelli F., Balbo G., Beccuti M., Cordero F. Inspecting Energy Releasing Pathways by combination of genomics data and mechanistic approach. (2016). EMBO Conference: From Functional Genomics to Systems Biology. 12-15 Nov. Hiedelberg, Germany.
20. Follia L., Ferrero G., Totis N., Riganti C., Novelli F., Balbo G., Beccuti M., Cordero F. Inspecting Energy Releasing Pathways by combination of genomics data and mechanistic approach. (2016). ECCB 2016, 15th European Conference on Computational Biology. The Hague, Netherland.
19. Ferrero G., Beccuti M., Balbo G., Holstein P., Cordero F. Detecting critical nodes in the analysis of cancer integrative networks. (2016). BITS Annual Meeting 2016. 15-17 June. Salerno, Italy.
18. Ferrero G., Tordini F., Holstein P., Miano V., Coscujuela L., Ricci L., Aldinucci M., Beccuti M., De Bortoli M, Cordero F. Identification of critical enhancers by network modeling of long-range chromatin interactions. (2016). SIBBM Frontiers in Molecular biology, From Single Cell Analysis to Precision Medicine. 16-18 June. Naples, Italy.
17. Iannello A., Ferrero G., Cordero F., Rolla S., Durelli L., Clerico M., Cutrupi S. Epigenetic control of Th17 and Treg cells balance upon E2 treatment. (2016). SIBBM Frontiers in Molecular biology, From Single Cell Analysis to Precision Medicine. 16-18 June. Naples, Italy.
16. Miano V., Ferrero G., Coscujuela T.L., Ricci L., Cordero F., De Bortoli M. Estrogen receptor α -dependent, luminal subtype-specific long noncoding RNAs in breast cancer cells (2016). SIBBM Frontiers in Molecular biology, From Single Cell Analysis to Precision Medicine. 16-18 June. Naples, Italy.

15. Coscujuela T.L., Ricci L., Ferrero G., Miano V., De Intinis C., Arigoni M., Calogero R., Cordero F., De Bortoli M. CircRNAs characterization in MCF-7 breast cancer cells (2016). SIBBM Frontiers in Molecular biology, From Single Cell Analysis to Precision Medicine. 16-18 June. Naples, Italy.
14. Ferrero G., Miano V., Balbo G., De Bortoli M., Beccuti M., Cordero F. An integrative strategy to functional analysis of the noncoding genome. (2015). EMBL | STANFORD CONFERENCE: "Personalised Health". 16-19 Nov. Heidelberg, Germany.
13. Miano V., Ferrero G., Cordero F., Cutrupi S., Di Croce L., De Bortoli M. Estrogen receptor α -dependent, luminal subtype-specific long noncoding RNAs in breast cancer cells. (2015). EMBO/EMBL Symposium "The non-coding genome". 18-20 Nov. Heidelberg, Germany.
12. Ferrero G., Miano V., Balbo G., De Bortoli M., Beccuti M., Cordero F. Integrative strategies for omics data: ER α cistrome and epigenome case-study. (2015). SIBBM Frontiers in Molecular biology, "From Genomes to Functions". 1-3 Jul. Torino, Italy.
11. Ricci L., Ferrero G., Arigoni M., Riccardo F., Cordero F., Annaratone L., Calogero R., De Bortoli M. Detection and role of circular RNAs in breast cancer. (2015). SIBBM Frontiers in Molecular biology, "From Genomes to Functions", 1-3 Jul. Torino, Italy.
10. Iannello A., Ferrero G., Tamaddon E., Rolla S., Inaudi I., Bardina V., Durelli L., Clerico M., Cutrupi S. Estrogen receptor alpha role in Th17 and Treg cells balance during pregnancy of multiple sclerosis patients. (2015). SIBBM Frontiers in Molecular biology, "From Genomes to Functions". 1-3 Jul. Torino, Italy.
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