

Matteo D'Antonio, Ph.D.

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Profile

I am an Assistant Project Scientist in Dr. Kelly Frazer's laboratory at UC San Diego, Department of Pediatrics. Working at UC San Diego, I have been involved in the iPSCORE study, a project that seeks to link molecular phenotypes to genotypes through the generation of iPSC-derived cell types, including cardiovascular progenitor cells (iPSC-CVPCs), pancreatic progenitor cells (iPSC-PPCs) and retinal pigment epithelium (RPE). Within this project, I have investigated multiple aspects of iPSCs, iPSC-CVPCs and RPE using whole genome sequence data, RNA-seq, ATAC-seq, ChIP-seq (H3K27ac and NKX2-5), single-cell RNA-seq and Hi-C.

I am skilled in conducting genomic, transcriptomic, and epigenomic analyses, which will allow me to analyze and integrate human genetic variation with multiple molecular phenotypes to examine their effects on complex traits and disease.

Research experience

University of California, San Diego

- 2019 – present Assistant Project Scientist, Department of Pediatrics, University of California, San Diego.
Supervisor: Kelly Frazer, Ph.D.
- 2018 – 2019 Genomics Computational Scientist, Institute for Genomic Medicine, University of California, San Diego.
Supervisor: Kelly Frazer, Ph.D.
- 2013 – 2018 Postdoctoral scholar, Moores Cancer Center, University of California, San Diego.
Supervisor: Kelly Frazer, Ph.D.

Determine the associations between genetic variation, molecular phenotypes and complex traits:

- Performed QTL analysis on 180 iPSC-CVPCs and compared it to GTEx cardiac tissues to detect genetic variants that act in a fetal-specific context and are associated with cardiac traits
- Developed a computational approach to determine the associations between HLA types and gene expression and their disease implications
- Detected and analyzed the effects of somatic mutations in iPSCs using whole genome sequencing

Detect driver mutations outside coding regions in breast cancer:

- Identified somatic mutations in 97 breast cancer samples from TCGA and developed a pipeline to discriminate between driver and passenger mutations
- Validated novel driver regulatory mutations based on their effects on gene expression and by targeted sequencing

European Institute of Oncology

2012 – 2013 Postdoctoral scholar, European Institute of Oncology, Milan, Italy.
Supervisor: Francesca Ciccarelli, Ph.D.

2008 – 2012 PhD student in Molecular Medicine, European School of Molecular Medicine, European Institute of Oncology, Milan, Italy.
Supervisor: Francesca Ciccarelli, Ph.D.

Understand how protein interaction networks evolve to detect novel cancer genes:

- Analyzed protein interaction networks from multiple organisms to study how gene duplicability changed during evolution from prokaryotes to mammals
- Integrated protein interaction network and duplicability properties to detect novel driver mutations for ovarian cancer
- Developed a database (<http://ncg.kcl.ac.uk/ncg4/>) that contains information about duplicability, evolution, protein-protein interactions and mutations for > 1,500 cancer genes

Other research experience

2007 Undergraduate Researcher, Department of Electronics and Information, Politecnico di Milano, Italy
Supervisor: Marco Masseroli, Ph.D.

2005 – 2006 Undergraduate Researcher, Center for Biological Sequence Analysis, Technical University of Denmark, Lyngby, Denmark
Supervisors: Søren Brunak, Ph.D.; Anne Mølgaard, Ph.D.

2003 Internship, LAFAS, Department of Human Anatomy, Università degli Studi di Milano, Italy

2000 Internship, CNR – Center for Microbiological Studies on Milk, Università degli Studi di Milano, Italy

Skills

- Analysis of next-generation sequencing data: whole genome sequencing, RNA-seq, ATAC-seq, ChIP-seq and single-cell RNA-seq (10X Genomics)
- Software for sequencing analysis:
 - Whole genome sequencing: GATK, bcftools, SnpEff, SnpSift, CADD
 - RNA-seq: STAR, WASP, MBASED
 - ATAC-seq and ChIP-seq: MACS2, HOMER

- Single-cell RNA-seq and single nuclei ATAC-seq: CellRanger, Seurat, Signac, Demuxlet
- Other: bedtools, clustal, blast, vt
- Programming tools: R, Perl, Jupyter notebook, HTML, PHP
- QTL analysis: fastqtl, MatrixEQTL, limix, lmer package (R), coxme package (R)
- Cancer genomics and analysis of somatic mutations: Mutect, Strelka
- Integration and analysis of publicly available data:
 - Gene expression: MSigDB, GSEA
 - eQTL analysis: GTEX
 - Epigenomics: ENCODE, Roadmap Epigenomics
 - Genome-wide association studies: GWAS Catalog, LDHub, UK Biobank, Haploreg
 - Genome Browsers: UCSC Genome Browser, WashU Epigenome Browser
 - Cancer genomics: the Cancer Genome Atlas (TCGA), International Cancer Genomics Consortium (ICGC), Broad GDAC Firehose
 - Protein interaction networks: BioGRID, STRING, IntAct, MINT, HPRD
 - Genomics: Gencode, LNCipedia, Noncode

Education

- 2012 **Ph.D., Molecular Medicine – Bioinformatics and Evolutionary Genomics of Cancer**, European School of Molecular Medicine, European Institute of Oncology, Milan, Italy.
Thesis: Evolution of protein interaction networks through gene duplication
Supervisor: Francesca Ciccarelli, Ph.D.
- 2008 **MSc., Biomedical Engineering**, Politecnico di Milano, Italy.
Thesis: PASS: a Web application for extraction, integration and analysis of Alternative Splicing and Protein Structure distributed information
Supervisor: Marco Masseroli, Ph.D.
- 2006 **MSc., Bioinformatics**, Technical University of Denmark, Lyngby, Denmark.
Thesis: Linking Alternative Splicing and Protein Structures
Supervisors: Søren Brunak, Ph.D.; Anne Mølgaard, Ph.D.
- 2004 **BSc., Biomedical Engineering**, Politecnico di Milano, Italy.
Thesis: Ultrasound instruments for odontoiatric purposes
Supervisor: Gabriele Dubini, Ph.D.

Honors and Awards

- 2015 Runner-up award, Genome Research poster competition, Biology of Genomes Meeting, Cold Spring Harbor
- 2008 – 2011 Fondazione Umberto Veronesi Ph.D. scholarship, European School of Molecular Medicine
- 2010 Oral presentation selected from abstracts, Seventh Annual General Meeting of the Bioinformatics Italian Society (BITS)
- 2009 Best poster award, EMBO practical course “Networks in biology analysis, modelling and reverse engineering”

- 2008 Oral presentation selected from abstracts, Network Tools and Applications in Biology (NETTAB) Meeting, Varenna, Italy
- 2004-2006 Top Industrial Managers for Europe (TIME) double Master's degree program, Politecnico di Milano and Technical University of Denmark
- 2005 Erasmus scholarship, European Commission - Education & Training
- 2005 Integration of Erasmus scholarship, Politecnico di Milano

Teaching Experience

- 2012 Programming Course for PhD students, European Institute of Oncology, Milan, Italy

Other Professional Experience

- 2006 – 2008 Translator of Medical Books (English to Italian), McGraw-Hill Publishing Group, Milan, Italy

Publications

Published articles are available at https://scholar.google.com/citations?hl=en&user=ufaal_MAAAAJ

1. **D'Antonio, M.**, and Masseroli, M. (2009). Extraction, integration and analysis of alternative splicing and protein structure distributed information. *BMC Bioinformatics* 10 Suppl 12, S15.
2. Syed, A.S., **D'Antonio, M.**, and Ciccarelli, F.D. (2010). Network of Cancer Genes: a web resource to analyze duplicability, orthology and network properties of cancer genes. *Nucleic Acids Research* 38, D670-675.
3. **D'Antonio, M.**, and Ciccarelli, F.D. (2011). Modification of gene duplicability during the evolution of protein interaction network. *PLoS Computational Biology* 7, e1002029.
4. **D'Antonio, M.**, Pendino, V., Sinha, S., and Ciccarelli, F.D. (2012). Network of Cancer Genes (NCG 3.0): integration and analysis of genetic and network properties of cancer genes. *Nucleic Acids Research* 40, D978-983.
5. **D'Antonio, M.**, and Ciccarelli, F.D. (2013). Integrated analysis of recurrent properties of cancer genes to identify novel drivers. *Genome Biology* 14, R52.
6. **D'Antonio, M.**, Guerra, R.F., Cereda, M., Marchesi, S., Montani, F., Nicassio, F., Di Fiore, P.P., and Ciccarelli, F.D. (2013). Recessive cancer genes engage in negative genetic interactions with their functional paralogs. *Cell Reports* 5, 1519-1526.
7. An, O., Pendino, V., **D'Antonio, M.**, Ratti, E., Gentilini, M., and Ciccarelli, F.D. (2014). NCG 4.0: the network of cancer genes in the era of massive mutational screenings of cancer genomes. *Database: the journal of biological databases and curation*. 2014; 2014. bau015.
8. Smith, E.N., Jepsen, K., Khosroheidari, M., Rassenti, L.Z., **D'Antonio, M.**, Ghia, E.M., Carson, D.A., Jamieson, C.H., Kipps, T.J., and Frazer, K.A. Biased estimates of clonal evolution and subclonal heterogeneity can arise from PCR duplicates in deep sequencing experiments. *Genome Biology*. 2014; 15, 420.
9. **D'Antonio, M.**, Tamayo, P., Mesirov, J.P., and Frazer, K.A. Kataegis Expression Signature in Breast Cancer Is Associated with Late Onset, Better Prognosis, and Higher HER2 Levels. *Cell Reports*. 2016; 16. 672-683.

10. **D'Antonio, M.**, Woodruff, G., Nathanson, J.L., D'Antonio-Chronowska, A., Arias, A., Matsui, H., Williams, R., Herrera, C., Reyna, S.M., Yeo, G.W., Panopoulos, A. D., Goldstein, J. S. B., and Frazer, K. A. High-throughput and cost-effective characterization of induced pluripotent stem cells. *Stem Cell Reports*. 2017; 8. 1101-1111.
11. Panopoulos, A.D., **D'Antonio, M.**, Arias, A., Benaglio, P., DeBoever, C., Williams, R., Garcia, M., Nelson, B., Harismendy, O., Grinstein, J.D., Drees, F., Okubo, J., Diffenderfer, K., Hishida, Y., McGarry, T. J., Matsui, H., Reyna, J., Aguirre, A., Rao, F., O'Connor, D. T., Yeo, G. W., Evans, S. M., Chi, N. C., Goldstein, J. S. B., Izpisua Belmonte, J. C., Berggren, W. T., Adler, E., D'Antonio-Chronowska, A., Smith, E. N., and Frazer, K. A. iPSCORE: A resource of 222 iPSC lines enabling functional characterization of genetic variation across a variety of cell types. *Stem Cell Reports*. 2017; 8. 1086-1100.
12. DeBoever, C., Li, H., Jakubosky, D., Arias, A., Olson, K.M., Huang, H., Biggs, W., Sandoval, E., Matsui, H., Ren, B., Benaglio, **D'Antonio, M.**, P., Nariai, N., Smith, E.N., D'Antonio-Chronowska, A., Farley, E.K., and Frazer, K. A. Genetic Regulation of Gene Expression in Human Induced Pluripotent Stem Cells. *Cell stem cell*. 2017; 20. 533-546.
13. **D'Antonio, M.**, Weghorn, D., D'Antonio-Chronowska, A., Coulet, F., Olson, K. M. DeBoever, C., Drees, F., Arias, A., Alakus, A., Richardson, A.L., Schwab, R. B., Farley, E. K., Sunyaev, S. R., and Frazer, K. A. Identification of driver distal regulatory elements in breast cancer. *Nature Communications*. 2017; 8. 436.
14. Zanca, C., Villa, G., Benitez, J.A., Thorne, A.H., Koga, T., **D'Antonio, M.**, Ikegami, S., Ma, J., Boyer, A., Eliseeva, O.V., Barnabe, G., Liu, F., Wu, S., Young, H., Wykosky, J., Frazer, K. A., Verkusha, V., Isagulians, M. G., Weiss, W. A., Gahman, T., Shiau, A., Mischel, P., Cavenee, W., and Furnari, F. Inter-clonal cell communication in glioblastoma attenuates sensitivity to EGFR kinase inhibitors. *Genes & Development*. 2017; 31. 1212-1227.
15. Benitez, J.A., Ma, J., **D'Antonio, M.**, Boyer, A., Camargo, M.F., Zanca, C., Kelly, S., Khodadadi-Jamayran, A., Jameson, N.M., Andersen. M., Miletic, H., Saberli, S., Frazer, K. A., Cavenee, W., and Furnari, F. DAXX inhibition suppresses PTEN-deficient glioblastoma oncogenicity through histone H3.3 chromatin regulation. *Nature Communications*. 2017; 8. 15223.
16. **D'Antonio, M.**, Benaglio, P., Jakubosky, D., Greenwald, W.W., Matsui, H., Donovan, M.K.R., Li, H., Smith, E.N., D'Antonio-Chronowska, A., and Frazer, K. A. Insights into the mutational burden of human induced pluripotent stem cells using an integrative omics approach. *Cell Reports*. 2018; 24. 883-894.
17. Biswas, P., Chekuri, A.K., Ear, J., Boroah, S., Matsui, H., **D'Antonio, M.**, Frazer, K.A., Devalaraja, S., Khan, S.Y., Naeem, M.A., Riazuddin, S., Akram, J., Hejtmancik, J.F., Ghosh, P., Riazuddin, S.A., and Ayyagari, R. A homozygous mutation in the novel gene ARFGAP2 is associated with non-syndromic recessive inherited retinal degeneration (IRD). *Investigative Ophthalmology & Visual Science*. 2018; 59. 5383-5383.
18. Smith, E.N., D'Antonio-Chronowska, A., Greenwald, W.W., Borja, V., Ribeiro Aguiar, L., Pogue, R., Matsui, H., Boorah, S., **D'Antonio, M.**, Ayyagari, R., and Frazer, K. A. Human iPSC-derived retinal pigment epithelium: a model system for identifying and functionally characterizing causal variants at AMD risk loci. *Stem Cell Reports*. 2019; 12. 1342-1353.
19. Greenwald, W.W., Li, H., Benaglio, P., Jakubosky, D., Matsui, H., Schmitt, A., Selvaraj, S., **D'Antonio, M.**, D'Antonio-Chronowska, A., Smith, E.N., and Frazer, K. A. Subtle changes in chromatin loop contact propensity are associated with differential gene regulation and expression. *Nature Communications*. 2019. 1054.
20. Benaglio, P., D'Antonio-Chronowska, A., Greenwald, W.W., DeBoever, C., Li, H., Drees, F., Singhal, S., Matsui, H., **D'Antonio, M.**, Smith, E.N., and Frazer, K. A. Allele-specific NKX2-5 binding underlies multiple genetic associations with human EKG traits. *Nature Genetics*. 2019. Oct;51(10):1506-1517.

21. D'Antonio-Chronowska, A.*, Donovan, M.K.R.*, Benaglio, P., Greenwald, W.W., Ward, M.C., Matsui, H., Hashem, S., Soncin, F., Parast, M., Adler, E., Smith, E.N., **D'Antonio, M.**, and Frazer, K. A. Ground state expression differences and X chromosome dosage impact differentiation potential of human induced pluripotent stem cells. *Stem Cell Reports*. 2019. Nov 12;13(5):924-938.
22. **D'Antonio M**, Reyna J, Jakubosky D, Donovan MK, Bonder MJ, Matsui H, Stegle O, Nariai N, D'Antonio-Chronowska A, Frazer KA. Systematic genetic analysis of the MHC region reveals mechanistic underpinnings of HLA type associations with disease. *Elife*. 2019 Nov 20;8.
23. D'Antonio-Chronowska A, **D'Antonio M**, Frazer KA. In vitro Differentiation of Human iPSC-derived Retinal Pigment Epithelium Cells (iPSC-RPE). *Bio-Protocol*. 2019 Dec 20. Vol. 9, Iss. 24.
24. Koga T, Chaim IA, Benitez JA, Markmiller S, Parisian AD, Hevner RF, Turner KM, Hessenauer FM, **D'Antonio M**, Nguyen ND, Saberi S, Ma J, Miki S, Boyer AD, Ravits J, Frazer KA, Bafna V, Chen CC, Mischel PS, Yeo GW, Furnari FB. Longitudinal assessment of tumor development using cancer avatars derived from genetically engineered pluripotent stem cells. *Nature Communications*. 2020 Jan 28;11(1):550.
25. Donovan MKR, D'Antonio-Chronowska A, **D'Antonio M**, Frazer KA. Cellular deconvolution of GTEx tissues powers discovery of disease and cell-type associated regulatory variants. *Nature Communications*. 2020 Feb 19;11(1):955.
26. Kanchan K, Iyer K, Yanek RL, Carcamo-Orive I, Taub MB, Malley C, Baldwin K, Becker LC, Broeckel U, Cheng L, Cowan C, **D'Antonio M**, Frazer KA, Quertermous T, Mostoslavsky G, Murphy G, Rabinovitch M, Raderj DJ, Steinberg MH, Topol E, Yang W, Knowles JW, Jaquish CE, Ruczinski I, Mathias, RA. *Stem Cell Research*, 2020; 46, 101803.
27. Jakubosky D, Smith EN, **D'Antonio M**, Bonder MJ, Smail C, Young Greenwald WW, D'Antonio-Chronowska A, Matsui H, Stegle O, Montgomery SB, DeBoever C, Frazer KA, i2QTL Consortium. Discovery and Quality Analysis of a Comprehensive Set of Structural Variants and Short Tandem Repeats. *Nature Communications*. 2020; 11 (1), 1-15.
28. Jakubosky D, **D'Antonio M**, Bonder MJ, Smail C, Donovan MKR, Young Greenwald WW, D'Antonio-Chronowska A, Matsui H, Stegle O, Smith EN, Montgomery SB, DeBoever C, Frazer KA, i2QTL Consortium. Genomic properties of structural variants and short tandem repeats that impact gene expression and complex traits in humans. *Nature Communications*. 2020; 11 (1), 1-15.
29. **D'Antonio M**, D'Antonio-Chronowska A, Frazer KA. Revealing Instability: Genetic Variation Underlies Variability in mESC Pluripotency. *Cell Stem Cell*, 2020; 27 (3), 347-349.
30. D'Antonio-Chronowska A, **D'Antonio M**, Frazer KA. In vitro Differentiation of Human iPSC-derived Cardiovascular Progenitor Cells (iPSC-CVPCs). *Bio-protocol*, 2020; 10 (18), e3755-e3755.
31. D'Antonio-Chronowska A, Donovan MKR, Fujita K, Salgado BM, Matsui H, Arthur TA, Nguyen JP, **D'Antonio M**, Frazer KA. iPSC-derived pancreatic progenitors are an optimal model system to study T2D regulatory variants active during fetal development of the pancreas. *Biorxiv*, 2021.
32. **D'Antonio M**, Nguyen JP, Arthur TA, Matsui H, Donovan MKR, D'Antonio-Chronowska A, Frazer KA. In heart failure reactivation of RNA-binding proteins drives the transcriptome into a fetal state. *Biorxiv*, 2021.
33. **D'Antonio M**, Arthur TA, Nguyen JP, Matsui H, D'Antonio-Chronowska A, Frazer KA. Insights into genetic factors contributing to variability in SARS-CoV-2 susceptibility and COVID-19 disease severity. *Medrxiv*, 2021.
34. Bonder MJ, Smail C, Gloudemans MJ, Frésard L, Jakubosky D, **D'Antonio M**, Li X, Ferraro NM, Carcamo-Orive I, Mirauta B, Seaton DD, Cai N, Vakili D, Horta D, Zhao C, Zastrow DB, Bonner DE, Wheeler MT, Kilpinen K, Knowles JW, Smith EN, Frazer KA, Montgomery SB, Stegle O. Identification of rare and common regulatory variants in pluripotent cells using population-scale transcriptomics. *Nature Genetics*, 2021; 53 (3), 313-321.

35. Oh S, Shao J, Mitra J, Xiong F, **D'Antonio M**, Wang R, Garcia-Bassets I, Ma Q, Zhu X, Lee JH, Nair SJ, Yang F, Ohgi K, Frazer KA, Zhang ZD, Li W, Rosenfeld MG. Enhancer release and retargeting activates disease-susceptibility genes. *Nature*, 2021: 1-6.

Other Presentations, Posters and Abstracts

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| May 2019 | Biology of Genomes (Cold Spring Harbor, NY): Poster presentation |
| October 2018 | American Society of Human Genetics (San Diego, CA): Poster presentation |
| March 2018 | 10X Genomics User Group Meeting (La Jolla, CA): Invited speaker |
| January 2018 | Cancer Genomics Cross-Laboratory Meeting at The University of California, San Diego (La Jolla, CA): Oral presentation |
| April 2017 | San Diego Chromatin Club Series at Sanford Consortium for Regenerative Medicine: Oral presentation |
| November 2016 | Postdoctoral Symposium at The University of California, San Diego (La Jolla, CA): Poster presentation |
| October 2016 | American Society of Human Genetics (Vancouver, BC, Canada): Poster presentation |
| November 2015 | Postdoctoral Symposium at The University of California, San Diego (La Jolla, CA): Poster presentation |
| May 2015 | Biology of Genomes (Cold Spring Harbor, NY): Poster presentation |
| September 2010 | European Conference on Computational Biology (ECCB) (Gent, Belgium): Poster presentation |
| May 2010 | 4 th International PhD student Cancer Conference (Milan, Italy): Poster presentation |
| April 2010 | 7 th Annual General Meeting of the Bioinformatics Italian Society (BITS) (Bari, Italy): Oral presentation |
| September 2009 | EMBO practical course "Networks in biology analysis, modelling and reverse engineering" (Bologna, Italy): Poster presentation |
| May 2008 | 8th International Workshop on Network Tools and Applications in Biology (NETTAB) (Varenna, Italy): Oral presentation Matteo D'Antonio, Ph.D. |

Referee Services

- Journal articles: Nucleic Acids Research, Frontiers, PLoS One and Proteomics
 Grant proposals: Italian Ministry of Health, Department of Public Health and Innovation, Applied clinical and biomedical research;