

Christopher L Plaisier, PhD

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Education:

Postdoctoral Fellow, Institute for Systems Biology, August 2009 – August 2012. Advisor: Nitin Baliga.

Doctor of Philosophy in Human Genetics, University of California, Los Angeles, June 2009. Advisor: Paivi Pajukanta, Dissertation Title: *Genetical Genomics Approaches to Familial Combined Hyperlipidemia*.

Masters of Science in Bioinformatics, University of California, Los Angeles, June 2009. Advisor: Steve Horvath, Thesis Title: *Transcription Factor Binding in a Familial Combined Hyperlipidemia Weighted Gene Co-expression Network*.

Bachelor of Science in Biology, University of Utah, May 2000.



Fellowships and Awards:

Science Communication Fellowship, Pacific Science Center, August 2015 – Present.

American Cancer Society Research Scholar Postdoctoral Fellowship, Institute for Systems Biology, July 2012 – July 2014. *Project Title: Constructing a Glioma Gene Regulatory Network*.

Genomic Analysis and Interpretation Training Grant, University of California, Los Angeles, June 2005 – July 2007.

Advanced Gene Mapping/Linkage Analysis Course Travel Stipend, Rockefeller University, Laboratory of Statistical Genetics, December 2006.



Research Experience:

Plaisier Lab Principal Investigator 2017-Current (School of Biological and Health Systems Engineering, Arizona State University).

Baliga Lab Senior Research Scientist 2012-2017 & Postdoctoral Fellow 2009-2012 (Institute for Systems Biology).

Pajukanta Lab Graduate Student 2004-2009 (UCLA).

Drews Lab Lab Technician / Lab Manager 2002-2004 (University of Utah).



Grant Support:

Ongoing Support

Pilot Grant ACE/NIH 06/01/18 – 05/31/19 Christopher L Plaisier (PI)
National Institutes of Health

“Quantifying population substructure to achieve adaptive therapeutic success”

This pilot project aims to develop single cell transcriptomic (sci-RNA-seq) technologies within my lab and the Arizona Cancer Evolution Center so that we can use this information to guide cancer patient treatment and diagnose why it failed.

Completed support

1U19AI106761-01: Pilot Research Grant 06/1/2016 – 05/31/2017 Christopher L Plaisier (PI)
National Institutes of Health

“Discovery of molecular switches mediating the transition to dormancy in *Mycobacterium tuberculosis*”

This project aims to systematically define network motifs in Mtb and how they contribute to the adaptation of Mtb to diverse environmental conditions during infection in the human host.

Specifically, this pilot project will advance and generalize algorithms to characterize network motifs in Mtb, particularly those that act as molecular switches and mediate global physiological state transitions, such as entry and exit from non-proliferating states.

PF-12-264-01-DMC 07/01/12 – 06/30/14 Christopher L Plaisier (PI)

To construct a global transcriptional regulatory network (GTRN) from glioma patient tumors to identify disease related co-regulated gene clusters and the transcriptional regulatory factors driving their expression.



Peer Reviewed Research Papers: (* = Corresponding Author)

31 Total Co-Authored; 1 Corresponding Author; 7 First Author; 7 Second Author

1. Thorsson V, Gibbs DL, Brown SD, Wolf D, Bortone DS, Ou Yang TH, Porta-Pardo E, Gao GF, **Plaisier CL**, Eddy JA, Ziv E, Culhane AC, Paull EO, Sivakumar IKA, Gentles AJ, Malhotra R, Farshidfar F, Colaprico A, Parker JS, Mose LE, Vo NS, Liu J, Liu Y, Rader J, Dhankani V, Reynolds SM, Bowlby R, Califano A, Cherniack AD, Anastassiou D, Bedognetti D, Rao A, Chen K, Krasnitz A, Hu H, Malta TM, Noushmehr H, Pedamallu CS, Bullman S, Ojesina AI, Lamb A, Zhou W, Shen H, Choueiri TK, Weinstein JN, Guinney J, Saltz J, Holt RA, Rabkin CE; Cancer Genome Atlas Research Network, Lazar AJ, Serody JS, Demicco EG, Disis ML, Vincent BG, Shmulevich L. [The Immune Landscape of Cancer](#). *Immunity*. 2018 Apr 17;48(4):812-830.e14. doi: 10.1016/j.immuni.2018.03.023. Epub 2018 Apr 5. PubMed PMID: 29628290.
2. Keller MP, Paul PK, Rabaglia ME, Stapleton DS, Schueler KL, Broman AT, Ye SI, Leng N, Brandon CJ, Neto EC, **Plaisier CL**, Simonett SP, Kebede MA, Sheynkman GM, Klein MA, Baliga NS, Smith LM, Broman KW, Yandell BS, Kendziorski C, Attie AD. The Transcription Factor Nfatc2 Regulates β -Cell Proliferation and Genes Associated with Type 2 Diabetes in Mouse and Human Islets. *PLoS Genet*. 2016 Dec 9;12(12):e1006466. doi: 10.1371/journal.pgen.1006466. PubMed PMID: 27935966
3. Rothchild AC, Sissons JR, Shafiani S, **Plaisier C**, Min D, Mai D, Gilchrist M, Peschon JJ, Larson RP, Bergthaler A, Baliga N, Urdahl KB, Aderem A. [A miR-155-regulated molecular network orchestrates cell fate in the innate and adaptive immune response to Mycobacterium tuberculosis](#). *Proc Natl Acad Sci U S A*. 2016 Sep 28. pii: 201608255. [Epub ahead of print] PubMed PMID: 27681624
4. **Plaisier CL***, O'Brien S, Bernard B, Reynolds S, Simon Z, Toledo CM, Ding Y, Reiss DJ, Paddison PJ, Baliga NS. [Causal Mechanistic Regulatory Network for Glioblastoma Deciphered Using Systems Genetics Network Analysis](#). *Cell Syst*. 2016 Jul 14. pii: S2405-4712(16)30189-2. doi: 10.1016/j.cels.2016.06.006. [Epub ahead of print] PubMed PMID: 27426982
5. Toledo CM, Ding Y, Hoellerbauer P, Davis RJ, Basom R, Girard EJ, Lee E, Corrin P, Hart T, Bolouri H, Davison J, Zhang Q, Hardcastle J, Aronow BJ, **Plaisier CL**, Baliga NS, Moffat J, Lin Q, Li XN, Nam DH, Lee J, Pollard SM, Zhu J, Delrow JJ, Clurman BE, Olson JM, Paddison PJ. [Genome-wide CRISPR-Cas9 Screens Reveal Loss of Redundancy between PKMYT1 and WEE1 in Glioblastoma Stem-like Cells](#). *Cell Rep*. 2015 Dec 22;13(11):2425-39. doi:10.1016/j.celrep.2015.11.021. Epub 2015 Dec 7. PubMed PMID: 26673326
6. Danziger SA, Reiss DJ, Ratushny AV, Smith JJ, **Plaisier CL**, Aitchison JD, Baliga NS. [Bicluster Sampled Coherence Metric \(BSCM\) provides an accurate environmental context for phenotype predictions](#). *BMC Syst Biol*. 2015;9 Suppl 2:S1. doi: 10.1186/1752-0509-9-S2-S1. Epub 2015 Apr 15. PubMed PMID: 25881257
7. Reiss DJ, **Plaisier CL**, Wu WJ, Baliga NS: [cMonkey2: Automated, systematic, integrated detection of co-regulated gene modules for any organism](#). *Nucleic Acids Res*. 2015 Apr 14. pii: gkv300. [Epub ahead of print] PMID: 25873626
8. **Plaisier CL**, Lo FY, Ashworth J, Brooks AN, Beer KD, Kaur A, Pan M, Reiss DJ, Facciotti MT, Baliga NS. [Evolution of context dependent regulation by expansion of feast/famine regulatory proteins](#). *BMC Syst Biol*. 2014 Nov 14;8(1):122. [Epub ahead of print] PMID: 25394904
9. Ashworth J, Bernard B, Reynolds S, **Plaisier CL**, Shmulevich I, Baliga NS. [Structure-based predictions broadly link transcription factor mutations to gene expression changes in cancers](#). *Nucleic Acids Res*. 2014 Dec 1;42(21):12973-83. doi: 10.1093/nar/gku1031. Epub 2014 Nov 5. PMID: 25378323

10. Ashworth J, **Plaisier CL**, Lo FY, Reiss DJ, Baliga NS. [Inference of expanded Lrp-like feast/famine transcription factor targets in a non-model organism using protein structure-based prediction](#). *PLoS One*. 2014 Sep 25;9(9):e107863. doi:10.1371/journal.pone.0107863. eCollection 2014. PubMed PMID: 25255272
11. Peterson EJ, Reiss DJ, Turkarslan S, Minch KJ, Rustad T, **Plaisier CL**, Longabaugh WJ, Sherman DR, Baliga NS. [A high-resolution network model for global gene regulation in *Mycobacterium tuberculosis*](#). *Nucleic Acids Res*. 2014 Oct;42(18):11291-303. doi: 10.1093/nar/gku777. Epub 2014 Sep 17. PubMed PMID:25232098
12. Brooks AN, Reiss DJ, Allard A, Wu WJ, Salvanha DM, **Plaisier CL**, Chandrasekaran S, Pan M, Kaur A, Baliga NS. [A system-level model for the microbial regulatory genome](#). *Mol Syst Biol*. 2014 Jul 15;10(7):740. doi: 10.15252/msb.20145160. PubMed PMID: 25028489.
13. **Plaisier CL**, Bennett BJ, He A, Guan B, Lusic AJ, Reue K, Vergnes L: [Zbtb16 has a role in brown adipocyte bioenergetics](#). *Nutr Diabetes*. 2012 Sep 17;2:e46. doi:10.1038/nutd.2012.21. PubMed PMID: 23446662
14. **Plaisier CL**, Pan M, Baliga NS: [A miRNA-regulatory network explains how dysregulated miRNAs perturb oncogenic processes across diverse cancers](#). *Genome Res*. 2012 Nov;22(11):2302-14. doi: 10.1101/gr.133991.111. Epub 2012 Jun 28. PubMed PMID: 22745231
15. Turkarslan S, Reiss DJ, Gibbins G, Su WL, Pan M, Bare JC, **Plaisier CL**, Baliga NS: [Niche adaptation by expansion and reprogramming of general transcription factors](#). *Mol Syst Biol*. 2011 Nov 22;7:554. doi: 10.1038/msb.2011.87. PMID: 22108796
16. **Plaisier CL**, Bare JC, Baliga NS: [miRvestigator: web application to identify miRNAs responsible for co-regulated gene expression patterns discovered through transcriptome profiling](#). *Nucleic Acids Res*. 2011 Jul;39 Suppl 2:W125-31. Epub 2011 May 20. PMID: 21602264 (<http://mirvestigator.systemsbio.net>)
17. Romanoski CE, Lee S, Kim MJ, Ingram-Drake L, **Plaisier CL**, Yordanova R, Tilford C, Guan B, Guan B, He A, Gargalovic P, Kirchgessner T, Berliner JA, Lusic AJ: [Systems Genetics Analysis of Gene-by-Environment Interactions in Human Cells](#). *Am J Hum Genet*. 2010 Mar 12;86(3):399-410. Epub 2010 Feb 17. PMID: 20170901
18. Weissglas-Volkov D, **Plaisier CL**, Huertas-Vazquez A, Cruz-Bautista I, Riano-Barros D, Herrera-Hernandez M, Riba L, Cantor RM, Sinsheimer JS, Aguilar-Salinas CA, Tusie-Luna T, Pajukanta P: [Identification of two common variants contributing to serum apolipoprotein B levels in Mexicans](#). *Arterioscler Thromb Vasc Biol*. Epub 2009 Dec 3. PMID: 19965785
19. Huertas-Vazquez A, **Plaisier CL**, Geng R, Haas BE, Lee J, Greevenbroek MM, van der Kallen C, de Bruin TWA, Taskinen M-R, Alagramam KN, Pajukanta P: [A nonsynonymous SNP within PCDH15 is associated with lipid traits in Familial Combined Hyperlipidemia](#). *Hum Genet*. Epub 2009 Oct 9. PMID: 19816713
20. **Plaisier CL**, Horvath S, Huertas-Vazquez A, Cruz-Bautista I, Herrera M, Tusie-Luna T, Aguilar-Salinas C, Pajukanta P: [A Systems Genetics Approach Implicates USF1, FADS3, and Other Causal Candidate Genes for Familial Combined Hyperlipidemia](#). *PLoS Genetics*. 2009 Sep;5(9):e1000642. Epub 2009 Sep 11. PMID: 19750004
21. Aldave AJ, Vivek SY, Vo RC, Kamal KM, Rayner SA, **Plaisier CL**, Chen MC, Damani MR, Pham MN, Gorin MB, Papp J, Sobel E: [Exclusion of Positional Candidate Gene Coding Region Mutations in the Common Posterior Polymorphous Corneal Dystrophy 1 Candidate Gene Interval](#). *Cornea*. 2009 Aug;28(7): 801-7. PMID: 19574904
22. **Plaisier CL**, Kyttälä M, Weissglas-Volkov D, Sinsheimer JS, Huertas-Vazquez A, Riba L, Ramírez-Jiménez S, de BruinTWA, Tusié-Luna T, Aouizerat BE, Pullinger CR, Malloy MJ, Kane JP, Cruz-Bautista I, Herrera MF, Aguilar-Salinas C, Kuusisto J, Laakso M, Taskinen M-R, van der Kallen CJH, Pajukanta P: [Galanin is associated with elevated plasma triglycerides](#). *Arterioscler Thromb Vasc Biol*. 2009 Jan;29(1):147-52. PMID: 18988886
23. Lee JC, Weissglas-Volkov D, Kyttälä M, Dastani Z, Cantor RM, Sobel EM, **Plaisier CL**, Engert JC, van Greevenbroek MMJ, Kane JP, Malloy MJ, Pullinger CR, Huertas-Vazquez A, Aguilar-Salinas CA, Tusié-Luna T, de BruinTWA, Aouizerat BE, van der Kallen CJH, Croce CM, Aqeilan RI, Marcil M, Viikari JSA, Lehtimäki T, Raitakari OT, Kuusisto J, Laakso M, Taskinen M-R,

Genest J, Pajukanta P: [Identification of WW domain-containing oxidoreductase as a novel HDL-C susceptibility gene](#). *Am J Hum Genet*. 2008 Aug;83(2):180-92. PMID: 18674750

24. Presson AP, Sobel EM, Pajukanta P, **Plaisier C**, Weeks DE, Aberg K, Papp JC: [Merging microsatellite data: enhanced methodology and software to combine genotype data for linkage and association analysis](#). *BMC Bioinformatics*. 2008 Jul 21;9(1):317 pg-1-16. PMID: 18644149
25. Mar-Heyming R, Miyazaki M, Weissglas-Volkov D, Kolaitis N, Sadaat N, **Plaisier C**, Pajukanta P, Cantor RM, de Bruin TW, Ntambi JM, Lusis AJ: [Association of Stearoyl-CoA Desaturase 1 Activity With Familial Combined Hyperlipidemia](#). *Arterioscler Thromb Vasc Biol*. 2008 Jun;28(6):1193-9. PMID: 18340007
26. Sinsheimer JS, **Plaisier CL**, Huertas-Vazquez A, Aguilar-Salinas C, Tusié-Luna T, Pajukanta P, Lange K: [Estimating Ethnic Admixture from Pedigree Data](#). *Am J Hum Genet*. 2008 Mar;82(3):748-55. PMID: 18319077
27. Huertas-Vazquez A, **Plaisier C**, Weissglas-Volkov D, Sinsheimer J, Canizales-Quinteros S, Cruz-Bautista I, Nikkola E, Herrera-Hernandez M, Davila-Cervantes A, Tusié-Luna T, Taskinen M-R, Aguilar-Salinas C, Pajukanta P: [TCF7L2 is associated with high serum triacylglycerol and differentially expressed in adipose tissue in families with familial combined hyperlipidaemia](#). *Diabetologia*. 2008 Jan;51(1):62-9. PMID: 17972059
28. Ghazalpour A, Doss S, Zhang B, Wang S, **Plaisier C**, Castellanos R, Brozell A, Schadt EE, Drake TA, Lusis AJ, Horvath S: [Integrating Genetic and Network Analysis to Characterize Genes Related to Mouse Weight](#). *PLoS Genet*. 2006 Aug 18;2(8):e130 pg-1182-92. PMID: 16934000
29. Weissglas-Volkov D, Huertas-Vazquez A, Suviolahti E, Lee J, **Plaisier C**, Canizales-Quinteros S, Tusié-Luna T, Aguilar-Salinas C, Taskinen MR, Pajukanta P: [Common hepatic nuclear factor-4alpha variants are associated with high serum lipid levels and the metabolic syndrome](#). *Diabetes*. 2006 Jul;55(7):1970-7. PMID: 16804065
30. Dastani Z, Quiogue L, **Plaisier C**, Engert JC, Marcil M, Genest J, Pajukanta P: [Evidence for a Gene Influencing High-Density Lipoprotein Cholesterol on Chromosome 4q31.21](#). *Arterioscler Thromb Vasc Biol*. 2006 Feb;26(2):392-7. PMID: 16322534
31. Lloyd A, **Plaisier CL**, Carroll D, Drews GN: [Targeted mutagenesis using zinc-finger nucleases in Arabidopsis](#). *Proc Natl Acad Sci U S A*. 2005 Feb 8;102(6):2232-7. PMID: 15677315



News and Views:

1. **Plaisier CL**, Baliga NS: [Harnessing the power of human tumor-derived cell lines for the rational design of cancer therapies](#). *Pigment Cell Melanoma Res*. 2012 Jul;25(4):406-8. doi: 10.1111/j.1755-148X.2012.01020.x. PMID: 22781216



Presentations in International Scientific Meetings:

1. **Plaisier CL**, TCGA: [Genomic drivers differ across 33 tumor types, but factors regulating hallmarks of cancer are similar](#). American Association for Cancer Research, Apr. 14th 2018. **(Poster)**
2. **Plaisier CL**, Sissons JR, Shafiani S, Min D, Mai D, Gilchrist M, Peschon JJ, Larson RP, Bergthaler A, Baliga NS, Urdahl KB, Aderem A: [miRNA Regulatory Network of the Macrophage Response to Mycobacterium tuberculosis](#). Systems Biology of Infectious Diseases: Pathogenesis to Personalized Medicine, Aug. 17-20th 2014. **(Poster)**
3. **Plaisier CL**, Baliga NS: [Identifying miRNAs that Bind Co-Regulated Transcripts](#). MicroRNAs and Non-Coding RNAs and Cancer (J5), Keystone Symposium, Feb. 2011. **(Poster)**
4. **Plaisier CL**, Reiss DJ, Baliga NS: [Gene Expression Regulatory Networks of Human Disease: High Grade Glioma](#). Institute for Systems Biology 9th Annual International Symposium: Systems Biology and Global Health, April 18-19, 2010. **(Poster)**
5. **Plaisier CL**, Haas B, Laakso M, Pajukanta P: [Cross-species Comparisons of GWAS Data as a Screening Tool to Identify Novel Loci for LDL-C](#). XV International Symposium on Atherosclerosis, June 14-18, 2009. **(Oral Presentation)**

6. **Plaisier CL**, van der Kallen CJ, de Bruin TW, Schadt EE, Pajukanta P: Identification of Downstream Targets of USF1. European Atherosclerosis Society 76th Congress, June 10-13, 2007. (**Oral Presentation**)
7. Kyttälä M, **Plaisier CL**, Aouizerat B, de Bruin TW, van der Kallen CJ, Pajukanta P: Identification of a Gene on Chromosome 11p Regulating Plasma Triglyceride Levels. European Atherosclerosis Society 76th Congress, June 10-13, 2007. (**Oral Presentation**)
8. **Plaisier CL**, van der Kallen CJ, de Bruin TW, Pajukanta P: Constriction of the Region for Familial Combined Hyperlipidemia on 11p. American Society of Human Genetics Annual Meeting, Oct 9-13, 2006. (**Poster**)
9. **Plaisier CL**, Lusi AJ, Naoumova RP, Shoulders CC, de Bruin TW, Pajukanta P: Fine mapping a Region on Chromosome 11p for Familial Combined Hyperlipidemia. International Symposium on Atherosclerosis, International Atherosclerosis Society, Jun 18-22, 2006. (**Poster**)
10. **Plaisier CL**, Lusi AJ, Cantor RM, Naoumova RP, Shoulders CC, de Bruin TW, Pajukanta P: Fine mapping a Locus for Familial Combined Hyperlipidemia on 11p. Genome Sequence Variation and the Inherited Basis of Common Disease and Complex Traits, Keystone Symposium, Jan. 2006. (**Poster**)



Service Activities:

Peer Review Referee

Biomedicine & Pharmacotherapy, BMC Systems Biology, Cell Systems, Journal of Theoretical Biology, Nucleic Acids Research and Scientific Reports

Working Groups

Co-Chair of NIAID Systems Biology Modeling Working Group



Teaching Experience:

1. Systems Biology of Disease (598/494), Professor – *Arizona State University* (Spring 2018): Designed, developed curriculum, instructed and managed a two day a week graduate level course for the ASU Spring Semester 2018 on Systems Biology of Disease.
2. Systems Biology of Disease, Course Developer and Instructor – *Institute for Systems Biology* (July 2012 - Present): Designed, developed curriculum, instructed and managed the week long Systems Biology of Disease course (<https://www.systemsbiology.org/course/>).
3. Systems Biology of Disease, Masterclass Instructor – *University of Cape Town* (August 2015): Taught three day masterclass on patient stratification and biomarker discovery to 16 researchers from the University of Cape Town.
4. Introduction to Systems Biology using a Cancer Model, Fraser Lecture Series – *Western Washington University* (April 2016): Taught a day long course on biomarker discovery in cancer for the Fraser Lecture Series at Western Washington University.



Volunteer Education Experience:

1. STEM Fellow, Industry Expert – *Washington Alliance for Better Schools* (Sept 2013-June 2014): Advised 10th grade teachers on developing new curriculum around antibiotic resistance that met Next Generation Science Standards (NGSS) for STEM (science, technology, engineering and math) learning in Washington classrooms.
2. Science Communication Fellow – *Pacific Science Center* (October 2014 – Present): Developed a lesson and activity that teaches young children to adults that come for Meet a Scientist Day how to create gene expression networks using an LED circuit board that I built representing a system of cell differentiation events.
3. Big Data Mentor – *Washington State Board for Community and Technical Colleges* (October 2014 – Present): Developed a curriculum and instructed community college faculty on how to incorporate quantitative reasoning and big data into their classes by giving them access to environmental or patient cancer data they could use.