Center for Genomics
and Systems Biology
New York University

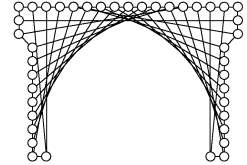Center for Genomics & Systems Biology
NYU Department of Biology

NEW YORK UNIVERSITY
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Department of Biology
Center for Genomics & Systems Biology
12 Waverly Place, 8th Floor
New York, NY 10003

CENTER FOR GENOMICS
AND SYSTEMS BIOLOGY
NEW YORK UNIVERSITY

NYU Center for Genomics and Systems Biology
Meeting with Simons Foundation

May 17th 2013

I.   Overview of NYU Center for Genomics and Systems Biology

II.   Presentations by Principal Investigators (CVs attached)

        Dr. Fabio Piano – Director

        Dr. Jane Carlton – Microbiome

        Dr. Gloria Coruzzi – Plant Systems Biology

        Dr. Kristin Gunsalus – Systems Biology of Animal Development

        Dr. Richard Bonneau (Aviv Madar, presenting) – Network Inference in Humans

        Dr. Dennis Shasha (NYU Courant) – Computational Provenance

III.   Summary and Discussion

Meeting Participants

| New York University	Simons Foundation
Richard Bonneau (Aviv Madar)	Jim Simons
Jane Carlton	Gerry Fischbach
Gloria Coruzzi	Marian Carlson
Kristin Gunsalus	Yuri Tschinkel
Fabio Piano	Any Millis
Dennis Shasha	

NYU Center for Genomics and Systems Biology

Our mission:

How do regulatory networks operate?
How they have evolved to generate diversity across the six kingdoms of life?

FUNGI
ANIMALIA
PLANTAE

Center for Genomics
and Systems Biology
New York University

ARCHAEA
PROTISTA
BACTERIA
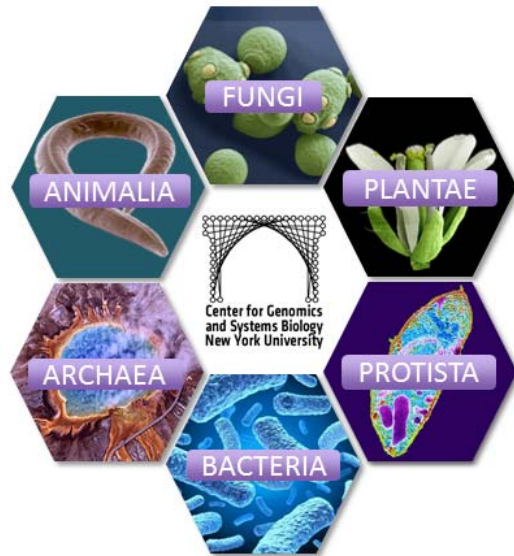
Approaches: Systems Biology & Networks, Comparative Functional Genomics, & Bioinformatic Pipelines

Focus: Model organisms and phylogenetically related species

Center for Genomics & Systems Biology
NYU Department of Biology

The mission of the Center for Genomics & Systems Biology is to define how regulatory networks operate and how they have evolved to generate diversity across species. For this work, we use approaches that span systems biology, comparative functional genomics & bioinformatic analysis focusing on model organisms and phylogenetically related species. The research involves the combined skills of genomicists, bioinformaticians, systematists, and evolutionary biologists all working together. The genomics and bioinformatics faculty in our center are engaged in collaborative projects with scientists at NYU's Courant Institute of Mathematical Sciences, other scientific institutions in the greater New York City area, including The American Museum of Natural History (AMNH), The New York Botanical Garden (NYBG), and the Cold Spring Harbor Laboratories (CSHL), as well as collaborators from around the world. The unique intellectual synergisms brought about by this collaborative genomic consortium group, enables us to develop unique approaches to address questions of comparative functional genomics.

NYU Center for Genomics and Systems Biology Faculty List

Kenneth D. Birnbaum
Research Interests: Developmental and evolutionary genomics of plants. The origin and genetic programming of cell types

Richard A. Bonneau
Research Interests: Systems Biology and Protein Modeling

Jane Carlton
Research Interests: Comparative genomics of eukaryotic microbes (protists); genomics and global public health

Gloria M. Coruzzi
Research Interests: Plant Systems Biology and Evolutionary Genomics

Patrick Eichenberger
Research Interests: Comparative and functional genomics of endospore-forming bacteria

Sevinc Ercan
Research Interests: Developmental Genomics, Epigenetics, Chromatin

David J. J. Gresham
Research Interests: Genomics of adaptive evolution, growth-rate regulation and post-transcriptional gene regulation

Kristin Gunsalus
Research Interests: Developmental systems biology

Edo Kussell
Research Interests: Computational biology, evolution, and biological physics

Fabio Piano (Director)
Research Interests: Genomics, genetics and evolution of early *C. elegans* development

Michael Purugganan
Research Interests: Plant Evolutionary Genomics

Matthew Rockman
Research Interests: Evolutionary and molecular causes of heritable variation in animals

Mark L. Siegal
Research Interests: evolutionary systems biology; robustness and evolution of complex trait

Christine Vogel
Research Interests: mass spectrometry, quantitative proteomics, dynamical systems, translation regulation, stress response, protein evolution

Presentations by:

Dr. Fabio Piano (Director)
We study the genetic and evolutionary mechanisms underlying early embryonic development using a combination of molecular genetic and functional genomics approaches in the animal model C. elegans and related nematodes.

Dr. Jane Carlton
The Carlton lab uses the tools of comparative genomics (bioinformatics, genomics, molecular evolution, and population genetics) to compare the genomes of related species of protist, including the malaria parasite Plasmodium, and species of trichomonad such as the sexually-transmitted pathogen Trichomonas vaginalis. Our ultimate goal is to reveal the biological mechanisms that parasites use to interact with their hosts, and identify characteristics that can be exploited to develop better methods of control, e.g. drugs, vaccines, diagnostics and surveillance tools.

Dr. Gloria Coruzzi
Our research in Plant Systems Biology aims to predictively model and manipulate gene regulatory networks affecting nitrogen-regulation of metabolism and root development exploiting the genomes of Arabidopsis and its natural variants. We have also developed phylogenomic approaches to identify genes associated with the evolution of key plant traits such as seeds.

Dr. Kristin Gunsalus
Our laboratory is interested in the integrative analysis of diverse functional genomics data to identify groups of genes that work in specific cellular and developmental processes. We use integrative approaches to analyze and interpret large-scale datasets and to generate testable hypotheses on gene function in different biological systems, including C. elegans and mouse early embryogenesis.

Dr. Richard Bonneau (Aviv Madar, presenting)
Our goal is to develop and apply state-of-the art methods to infer genomic networks, integrating computational approaches with multiple integrated data types (RNA expression, proteomics, metabolomics and genome structure). My group is also working on protein folding prediction, to assist functional studies through examining protein structure/function relationships.

Dr. Dennis Shasha (NYU Courant)
My research focuses on biological computing (including experimental design), pattern recognition and querying in trees and graphs, pattern discovery in time series, cryptographic file systems, database tuning, and wireless.

Principal Investigator CVs

In order of presentation:

Dr. Fabio Piano – Director

Dr. Jane Carlton – Microbiome

Dr. Gloria Coruzzi – Plant Systems Biology

Dr. Kristin Gunsalus – Systems Biology of Animal Development

Dr. Richard Bonneau (Aviv Madar, presenting) – Network Inference in Humans

Dr. Dennis Shasha (NYU Courant) – Computational Provenance

BIOGRAPHICAL SKETCH			
NAME **Fabio Piano, Ph.D**	POSITION TITLE **Director of CGSB, Professor**		
EDUCATION/TRAINING			
INSTITUTION AND LOCATION	DEGREE	YEAR	FIELD OF STUDY
New York University, New York, NY	BA	1985-1988	Biology
New York University, New York, NY	MS	1988-1990	Biology
New York University, New York, NY	M.Phil	1990-193	Biology
New York University, New York, NY	PhD	1993-1995	Biology
Cornell University, Ithaca, NY	Postdoc	1996-2001	Functional Genomics

B. Positions and Honors
Professional Positions
Summer 1988   Research Fellow, New York University.
1992-1993   James Arthur Fellow, New York University.
1996-1999   Post-Doctoral Fellow of the Damon Runyon-Walter Winchell Foundation for Cancer Research
1999-2001   Research Associate II, Cornell University
2002-2007   Assistant Professor, New York University
2009-Present Director, Center for Genomics and Systems Biology, New York University
2007-2013   Associate Professor, New York University
2010-Present Provost, New York University Abu Dhabi
2013-Present Professor, New York University

Honors, Awards, and Professional Memberships
1988 (Summer)   Research Fellowship, New York University
1992-1993   James Arthur Fellowship, New York University
1995   Gladys Mateyko Award for Excellence in Biology, New York University
1996-1999   Post-Doctoral Fellowship, Damon Runyon-Walter Winchell Foundation for Cancer Research
2002   Whitehead Fellowship, New York University
2003-Present   Faculty of 1000, member Genomics

C. Selected Peer-reviewed Publications (from 48 total)

1. **Piano F**, Schetter AJ, Morton DG, Gunsalus KC, Reinke V, Kim SK, and Kemphues KJ. Gene clustering based on RNAi phenotypes of ovary-enriched genes in *C. elegans. Curr Biol* (2002) 12:1959-64.

2. Gunsalus KC, Yueh WC, MacMenamin P, and **Piano F**. RNAiDB and PhenoBlast: web tools for genome-wide phenotypic mapping projects. *Nucleic Acids Res* (2004) 32:D406-10.

3. Li S, Armstrong CM, Bertin N, Ge H, Milstein S, Boxem M, Vidalain PO, Han JD, Chesneau A, Hao T, Goldberg DS, Li N, Martinez M, Rual JF, Lamesch P, Xu L, Tewari M, Wong SL, Zhang LV, Berriz GF, Jacotot L, Vaglio P, Reboul J, Hirozane-Kishikawa T, Li Q, Gabel HW, Elewa A, Baumgartner B, Rose DJ, Yu H, Bosak S, Sequerra R, Fraser A, Mango SE, Saxton WM, Strome S, Van Den Heuvel S, **Piano F**, Vandenhaute J, Sardet C, Gerstein M, Doucette-Stamm L, Gunsalus KC, Harper JW, Cusick ME, Roth FP, Hill DE, and Vidal M. A map of the interactome network of the metazoan *C. elegans. Science* (2004) 303:540-3.

4. Gunsalus KC*, Ge H*, Schetter AJ*, Goldberg DS*, Han JD, Hao T, Berriz GF, Bertin N, Huang J, Chuang LS, Li N, Mani R, Hyman AA, Sonnichsen B, Echeverri CJ, Roth FP[§], Vidal M[§], and **Piano F**[§]. Predictive models of molecular machines involved in *Caenorhabditis elegans* early embryogenesis. Nature (2005) 436:861-5. [*Co-first author; [§]Corresponding author]

5. Sönnichsen B, Koski LB, Walsh A, Marschall P, Neumann B, Brehm M, Alleaume AM, Artelt J, Bettencourt P, Cassin E, Hewitson M, Holz C, Khan M, Lazik S, Martin C, Nitzsche B, Ruer M, Stamford J, Winzi M, Heinkel R, Roder M, Finell J, Hantsch H, Jones SJ, Jones M, **Piano F**, Gunsalus KC, Oegema K, Gonczy P, Coulson A, Hyman AA, and Echeverri CJ. Full-genome RNAi profiling of early embryogenesis in *Caenorhabditis elegans. Nature* (2005) 434:462-9.

6. Motegi F, Velarde NV, **Piano F**, and Sugimoto A. Two phases of astral microtubule activity during cytokinesis in *C. elegans* embryos. *Dev Cell* (2006) 10:509-20.

7. Schetter A, Askjaer P, **Piano F**, Mattaj I, and Kemphues K. Nucleoporins NPP-1, NPP-3, NPP-4, NPP-11 and NPP-13 are required for proper spindle orientation in *C. elegans. Dev Biol* (2006) 289:360-71.

8. Utku Y, Dehan E, Ouerfelli O, **Piano F**, Zuckermann RN, Pagano M, and Kirshenbaum K. A peptidomimetic siRNA transfection reagent for highly effective gene silencing. *Mol Biosyst* (2006) 2:312-7.

9. Lall S, Grun D, Krek A, Chen K, Wang YL, Dewey CN, Sood P, Colombo T, Bray N, Macmenamin P, Kao HL, Gunsalus KC, Pachter L, **Piano F***, and Rajewsky N*. A genome-wide map of conserved microRNA targets in *C. elegans. Curr Biol* (2006) 16:460-71. [*Corresponding author]

10. Maruyama R, Velarde NV, Klancer R, Gordon S, Kadandale P, Parry JM, Hang JS, Rubin J, Stewart-Michaelis A, Schweinsberg P, Grant BD, **Piano F**, Sugimoto A, and Singson A. EGG-3 regulates cell-Surface and cortex rearrangements during egg activation in *Caenorhabditis elegans. Curr Biol* (2007) 17:1555-60.

11. Boxem M, Maliga Z, Klitgord N, Li N, Lemmens I, Mana M, de Lichtervelde L, Mul JD, van de Peut D, Devos M, Simonis N, Yildirim MA, Cokol M, Kao HL, de Smet AS, Wang H, Schlaitz AL, Hao T, Milstein S, Fan C, Tipsword M, Drew K, Galli M, Rhrissorrakrai K, Drechsel D, Koller D, Roth FP, Iakoucheva LM, Dunker AK, Bonneau R, Gunsalus KC, Hill DE, **Piano F**, Tavernier J, van den Heuvel S, Hyman AA, Vidal M. A protein domain-based interactome network for *C.elegans* early embryogenesis. *Cell* (2008) 134:534-45.

12. Brauchle M, Kiontke K, MacMenamin P, Fitch DH, **Piano F**. Evolution of early embryogenesis in rhabditid nematodes. *Dev Biol* (2009) 335:253-62.

13. Parry JM, Velarde NV, Lefkovith AJ, Zegarek MH, Hang JS, Ohm J, Klancer R, Maruyama R, Druzhinina MK, Grant BD, **Piano F**, Singson A. EGG-4 and EGG-5 link events of the Oocyte-to-embryo transition with meiotic progression in *C. elegans. Curr Biol* (2009) 19:1752-7.

14. Celniker SE, Dillon LA, Gerstein MB, Gunsalus KC, Henikoff S, Karpen GH, Kellis M, Lai EC, Lieb JD, MacAlpine DM, Micklem G, **Piano F**, Snyder M, Stein L, White KP, Waterston RH; modENCODE Consortium. Unlocking the secrets of the genome. *Nature* (2009) 459:927-30.

15. Mangone M, Manoharan AP, Thierry-Mieg D, Thierry-Mieg J, Han T, Mackowiak S, Mis E, Zegar C, Gutwein MR, Khivansara V, Attie O, Chen K, Salehi-Ashtiani K, Vidal M, Harkins TT, Bouffard P, Suzuki Y, Sugano S, Kohara Y, Rajewsky N, **Piano F***, Gunsalus KC*, Kim JK*. The landscape of *C. elegans* 3'UTRs. *Science* (2010) 329:432-5. [*Corresponding author]

16. Fernandez AG, Mis EK, Bargmann BO, Birnbaum KD, **Piano F**. Automated sorting of *C. elegans* using laFACS. *Nat Methods* (2010) 7:417-8.

17. White AG, Cipriani PG, Kao H-L, Lees B, Geiger D, Sontag E, **Gunsalus KC**, Piano F. Rapid and accurate developmental stage recognition of *C. elegans* from high-throughput image data. 2010 *IEEE Conference on Computer Vision and Pattern Recognition* (*CVPR*). DOI: http://dx.doi.org/10.1109/CVPR.2010.5540065

18. Gerstein M…(115 other authors)… Strome S*, Gunsalus KC*, Micklem G*, Liu XS*, Reinke V*, Kim SK*, Hillier LW*, Henikoff S*, **Piano F***, Snyder M*, Stein L*, Lieb JD*, Waterston RH*. Integrative Analysis of Functional Elements in the *Caenorhabditis elegans* Genome by the modENCODE Project. *Science* (2010) 330:1775-87. [*Corresponding author]

19. Green R, Kao H-L, Audhya A, Arur S, Schulman M, Schloissnig S, Niessen S, Laband K, Wang S, Hyman A, Desai A, Schedl T, **Piano F**, Gunsalus KC*, Oegema K*. High-Resolution Phenotypic Profiling Based on the Complex Architecture of the *C. elegans* Gonad Syncytium. *Cell* (2011) 145:470-482. [*Corresponding author] (*selected for video abstract*)

20. Fernandez AG, Bargmann BOR, Mis EK, Edgley ML, Birnbaum KD, and Piano F. High-throughput fluorescence-based isolation of live C. elegans larvae. <u>Nat Protoc</u>. 2012 Jul 19;7(8):1502-10. doi: 10.1038/nprot.2012.084.

21. Shinar T, Mana M, **Piano F**, Shelley MJ. A model of cytoplasmically driven microtubule-based motion in the single-celled Caenorhabditis elegans embryo. *Proc Natl Acad Sci USA* (2011) 108(26):10508-13.

D. Other Support

NAME **Carlton, Jane**	POSITION TITLE **Faculty Director of Genomic Sequencing, NYU Center for Genomics & Systems Biology, and Professor, NYU Biology**
eRA COMMONS USER NAME Carlton	

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	YEAR	FIELD OF STUDY
U Edinburgh, Edinburgh, Scotland, UK	B.Sc.	1990	Genetics
U Edinburgh, Edinburgh, Scotland, UK	Ph.D.	1995	Parasite genetics
U Edinburgh, Edinburgh, Scotland, UK	Postdoc	1995-1997	Molecular parasitology
U Florida, Gainesville, FL, USA	Postdoc	1997-1999	Genomics/bioinformatics

A. Personal Statement

My area of expertise is whole genome sequencing, bioinformatics and comparative evolutionary genomics of **eukaryotic microbes**. My lab members are involved in the sequencing and analysis of several important parasite genomes, and we also scan the genomes for genetic variation to understand their evolution and impact on human health and disease. More recently our project to characterize the female microbiome associated with an STD parasite was published, and we have ongoing studies to characterize the microbial diversity present on the surface of paper currency circulating in New York City.

B. Positions and Honors
Professional Positions
1999-2000   Assistant Scientist (non-tenured track faculty), University of Florida, Gainesville, FL
2000-2001   Research Fellow (VP), National Center for Biotechnology Information, NIH, Bethesda, MD
2001-2006   Associate Investigator (faculty), The Institute for Genomic Research, Rockville, MD
2006-2011   Associate Professor, Dept Medical Parasitology, NYU School of Medicine, New York, NY
2009-2011   Director of Genomics, NYU School of Medicine, New York, NY
2006-present Adjunct Research Associate, American Museum of Natural History, New York, NY
2011-present Affiliate, Division of Medical Parasitology/Dept of Microbiology, NYU School of Medicine
2011-present Professor and Faculty Director of Genomic Sequencing, Center for Genomics and
                Systems Biology, Dept of Biology, New York University, New York, NY

Other Experience and Professional Memberships
1995-present Member, American Society of Tropical Medicine and Hygiene
2006-present Member American Society Microbiology
2001-present *Ad hoc* member various study sections including: NIAID Genomics, Computational Biology and
                Technology 2008; NHGRI Special Emphasis Panel ZRG1 GGG-J (52) Human Microbiome
                Project 2008; NIH Genomics, Computational Biology and Technology (GCAT) study section
                2008 & 2009; NIH Pathogenic Eukaryotes (PTHE) study section 2009; Development of New
                tools for Computational Analysis of Human Microbiome Project Data (ZRG1 GGG-N) 2010.
2007-2012   Co-chair NHGRI/NIAID Eukaryotic Pathogens and Disease Vectors Sequencing Target
                Selection working group
1996-present Reviewer various journals including: Nature, Nature Genetics, Science, Gene, Genomics, BMC
                Genomics, PLoS Pathogens, PloS Biology, PloS Computational Biology, Heredity, PNAS
2003-present Editorial Board member of: BMC Genomics, Database, Trends in Parasitology, PLoS NTD
2010-present Scientific Advisor, BBC/Public Radio International radio program 'The World'

Awards and Nominations
1993   Young Investigator Award, Scottish Universities Molecular Parasitology Group
2004   Martin J. Rodbell Award, The Institute for Genomic Research, Rockville, MD
2006/10 NYU School of Medicine Dean's Honors
2009   Nominated for 2009 Blavatnik Awards for Young Scientists
2010   Stoll-Stunkard Award, American Society of Parasitologists
2011   Nominated for 2011 Dan David Prize in Genome Research
2012   Elected Fellow of the American Association for the Advancement of Science

Scientific Meetings Organized and Coordinated
Co-organizer with George Weinstock, Julian Parkhill, Matt Berriman, joint bi-annual Cold Spring Harbor/Wellcome Trust Sanger Institute conference 'Infectious Disease Genomics and Global Health', Hinxton Campus, Cambridge, UK: September 2008, September 2010, October 2012, October 2013.

C. Selected peer-reviewed publications (selected from >90 publications)
1. *Plasmodium* genomics and the art of sequencing malaria parasite genomes' **Jane M. Carlton**, Steven A. Sullivan and Karine G. Le Roch. In *Malaria Parasites: Comparative Genomics, Evolution and Molecular Biology* Editors **J. Carlton**, S. Perkins and K. Deitsch, Caister Academic Press, February 2013.

2. Brotman RM, Bradford LL, Conrad M, Gajer P, Ault K, Peralta L, Forney LJ, **Carlton JM**, Abdo Z, Ravel J. Association Between Trichomonas vaginalis and Vaginal Bacterial Community Composition Among Reproductive-Age Women. Sex Transm Dis. 2012 Oct;39(10):807-812.

3. Neafsey DE, Galinsky K, Jiang RH, Young L, Sykes SM, Saif S, Gujja S, Goldberg JM, Young S, Zeng Q, Chapman SB, Dash AP, Anvikar AR, Sutton PL, Birren BW, Escalante AA, Barnwell JW, **Carlton JM**. The malaria parasite Plasmodium vivax exhibits greater genetic diversity than Plasmodium falciparum. Nat Genet. 2012 Sep;44(9):1046-50. **Front cover article.**

4. Conrad MD, Gorman AW, Schillinger JA, Fiori PL, Arroyo R, Malla N, Dubey ML, Gonzalez J, Blank S, Secor WE, **Carlton JM**. Extensive Genetic Diversity, Unique Population Structure and Evidence of Genetic Exchange in the Sexually Transmitted Parasite Trichomonas vaginalis. PLoS Negl Trop Dis. 2012 Mar;6(3).

5. Reed DL, Currier RW, Walton SF, Conrad M, Sullivan SA, **Carlton JM**, et al. The evolution of infectious agents in relation to sex in animals and humans: brief discussions of some individual organisms. Ann N Y Acad Sci. 2011 Aug;1230(1):74-107.

6. Malik SB, Brochu CD, Bilic I, Yuan J, Hess M, Logsdon JM Jr, **Carlton JM**. Phylogeny of parasitic parabasalia and free-living relatives inferred from conventional markers vs. Rpb1, a single-copy gene. PLoS One. 2011;6(6):e20774

7. **Carlton JM**, Adams JH, Silva JC, Bidwell SL, Lorenzi H, et al. Comparative genomics of the neglected human malaria parasite Plasmodium vivax. *Nature*. 2008 Oct 9;455(7214):757-63. **Front cover article.**

8. **Carlton JM**, Hirt RP, Silva JC, Delcher AL, Schatz M, et al. Draft genome sequence of the sexually transmitted pathogen Trichomonas vaginalis. *Science*. 2007 Jan 12;315(5809):207-12. **Front cover article.**

9. **Carlton JM.** Toward a malaria haplotype map. *Nat Genet.* 2007 Jan;39(1):5-6.

10. 'The nuts and bolts of sequencing protist genomes.' Daniella Bartholomeu, Neil Hall, **Jane Carlton**. In *Genomics and Evolution of Microbial Eukaryotes*, Oxford University Press, September 2006, edited by Laura A. Katz and Debashish Bhattacharya.

D. Other Support
ACTIVE
1 R01 AI097080-01 P. Kissinger (PI)   07/01/12-06/30/17
NIH/NIAID "*Trichomonas vaginalis* repeat infections among HIV negative women"

1U19AI089676-01 J. Carlton (PI)   07/01/10-06/30/17
NIH/NIAID "Center for the Study of Complex Malaria in India"

COMPLETED (relevant awards completed during last 3 years only)
S10 RR026950-01 J. Carlton (PI)   04/01/10-03/31/11
NIH/NCRR "Roche 454 Next Generation Sequencer for Human Microbiome and Infectious Disease Research"

BIOGRAPHICAL SKETCH				
NAME **Coruzzi, Gloria M.**	POSITION TITLE Carroll & Milton Petrie Professor of Biology			
EDUCATION/TRAINING				
INSTITUTION AND LOCATION	DEGREE	YEAR(s)	FIELD OF STUDY	
Fordham University, New York, NY	B.S.	1976	Biology, *cum Laude*	
NIH Predoctoral Fellow, New York University School of Medicine, New York, NY		1976-1979	Yeast mitochondrial Genetics	
New York University School of Medicine, Department of Cell Biology	Ph.D.	1979	Cell & Molecular Biology	
Postdoctoral Research Associate, Columbia University, New York, NY		1979-1980	Yeast Molecular Genetics	
NIH Postdoctoral Fellow Rockefeller University, New York, NY		1980-1983	Plant Molecular Biology	

A. Personal Statement

My lab has developed systems biology approaches to study gene regulatory networks involved in nitrogen-use efficiency, an important trait in agriculture. To enable network construction in plants, we developed the Arabidopsis multinetwork a resource that includes all known edges based on DNA, RNA and protein interactions. This and other tools used to integrate, analyze and visualize genomic data in a systems biology context, are embodied in a software platform called VirtualPlantv1.3 (www.virtualplant.org) developed in collaboration with colleagues at NYU Courant Institute for Math & Computer Science. I am also engaged in an NSF-funded Plant Genome Project on the Comparative Genomics of Seed Evolution with co-PIs at NYC institutions specializing in evolution. This includes the New York Botanical Garden, the American Museum of Natural History, and Cold Spring Harbor labs. A community resource developed in this project is the BigPlantv1.0 matrix http://nypg.bio.nyu.edu/bp/, the largest genome-scale phylogeny including 150 seed plants. This resource is now available as an interactive browser called PhyloBrowse, which enables researchers to explore the genomic underpinnings of plant diversification across a wide range of species.

B. Positions and Honors
Professional Positions
1983-1989   Assistant Professor, Rockefeller University, Laboratory of Plant Molecular Biology
1990-1991   Associate Professor, Rockefeller University, Laboratory of Plant Molecular Biology
2003-2011   Chair, New York University, Department of Biology
1991-present Carroll & Milton Petrie Professor, New York University, Department of Biology

Other Experience and Professional Memberships
1995-present New York Botanical Garden, Botanical Science Committee
1996-2000   International Society of Plant Molecular Biology, Board Member
1998-present Editorial Board, Current Opinions in Plant Biology
2001-2005   Associate Editor, Plant Physiology
2004-present Editorial Board, Trends in Plant Science
2011-present Editor, G3: Genes, Genomes, Genetics (Genetics Society of America)
2002   National Academy of Sciences: Workshop on National Plant Genomic Initiative
2008-present Member of the Corporation of the New York Botanical Garden
2012-present Scientific Advisory Board, Donald Danforth Plant Science Center in St. Louis, MO
2012-present International Arabidopsis Informatics Consortium (IAIC) Scientific Board

Awards and Nominations
1996   Herbert and Margaret Sokol Award in the Sciences, NYU
1996-2011   Carroll and Milton Petrie Chair in Biology, NYU
2005   Fellow of the American Association for the Advancement of Science (AAAS)
2010   Fellow of the American Society of Plant Biologists (ASPB)
2012   CNRS/EDIGE Fellow, Biochem., Physiol. & Mol. Biol. of Plants, Montpellier, France

Patents

The technology below is licensed by several major Ag-biotech companies for commercial evaluation.

Patent No. 60/919,818: Methods of affecting nitrogen assimilation in plants

Inventors: G. Coruzzi, D. Nero, and R. A. Gutierrez (Altered expression of TFs: CCA1, GLK1, BZIP1)

Patent No. 5,955,651: Transgenic plants that exhibit enhanced nitrogen assimilation

Inventors: G. Coruzzi and T. Brears. (Altered expression of N-assimilation pathway target genes, GLN1 and ASN1)

C. Selected peer-reviewed publications (selected from 118 total)

1. Bargmann B, Marshall-Colon A, Efroni I, Ruffel S, Birnbaum KD, **Coruzzi GM**, Krouk G. (2013) "TARGET: A transient transformation systems for genome-wide transcription factor target assessment." ***Mol. Plant***.

2. Ristova D, Rosas U, Krouk G, Ruffel S, Birnbaum KD, **Coruzzi GM**. (2013) "RootScape: a landmark-based system for rapid screening of root architecture in Arabidopsis." Plant Physiol. 161(3):1086-96.

3. Ruffel S, Krouk G, Shasha D, Birnbaum KD, and **Coruzzi GM**. (2011) "Nitrogen-economics of root foraging: Transitive closure of the nitrate-cytokinin relay and new systemic signals for N-supply vs. demand." ***Proc. Natl. Acad. Sci.*** 108(45):18524-9.

4. Katari MS, Nowicki SD, Aceituno FF, Nero D, Kelfer J, Thompson LP, Cabello JM, Davidson RS, Goldberg AP, Shasha DE, **Coruzzi GM**, Gutierrez RA. (2010) "VirtualPlant: a software platform to support systems biology research." ***Plant Physiol.*** 152(2): 500-515.

5. Krouk G, Tranchina D, Lejay L, Cruikshank A, Shasha D, **Coruzzi G**, Gutierrez R. (2009) "A systems approach uncovers restrictions for signal interactions regulating genome-wide responses to nutritional cues in Arabidopsis." ***PloS Comp. Biol.*** Mar 5(3):e1000326. (**Highly Accessed**).

6. Gutiérrez RA, Stokes TL, Thum*, Xu X, Obertello M, Katari MS, Tanurdzic M, Dean A, Nero D, McClung CR, **Coruzzi GM**. (2008) "Systems approach identifies an organic nitrogen-responsive gene network that is regulated by the master clock control gene *CCA1.*" ***Proc. Natl. Acad. Sci. USA*** vol 105, 4939-4944. **Faculty of 1000 (Recommended: Factor 3)**.

7. Gifford M, Dean A, Gutierrez R, **Coruzzi G**, Birnbaum K (2008) "Cell-Specific Nitrogen Responses Mediate Developmental Plasticity." ***Proc. Natl. Acad. Sci.*** 105, 803-808. **Faculty of 1000 (Must read: Factor 6)**

8. Gutiérrez RA, Lejay L, Chiaromonte F, Shasha DE, **Coruzzi GM**. (2007) "Qualitative network models and genome-wide expression data define carbon/nitrogen-responsive biomodules in Arabidopsis." ***Genome Biol.*** 8: R7. **Faculty 1000** (**Must Read: Factor 6).**

D. Other Support

Active

5R01 GM032877-28   Coruzzi (PI)   05/01/2009 – 04/30/2014
NIH "A Systems Approach to Regulatory Networks Controlling N-assimilation"

MCB-1158273   Coruzzi (PI)   04/01/2012 – 03/31/2015
NSF "A Systems Approach to the NPK Nutriome and its Effect on Biomass"

MCB-0929338   Coruzzi (PI)   07/15/2009 – 06/30/2014
NSF "Arabidopsis 2010: Nitrogen Networks in Plants"

DE-FG02-92ER20071   Coruzzi (PI)   06/01/2011 – 05/31/2014
DOE "Asparagine Synthetase Regulatory Network and Plant Nitrogen Metabolism"

IOS-0922738   Coruzzi (PI)   08/01/2010 – 07/31/2014
NSF "GEPR Genomics of Comparative Seed Evolution"

Completed Support

DBI-0445666   Coruzzi (PI)   06/01/2005 – 11/30/2011
NSF "Conceptual Data Integration for the Virtual Plant"

BIOGRAPHICAL SKETCH				
NAME **Gunsalus, Kristin C.**		POSITION TITLE **Associate Professor**		
EDUCATION/TRAINING				
INSTITUTION AND LOCATION	DEGREE	YEAR	FIELD OF STUDY	
Cornell University, Ithaca, NY	BA	1980-1984	Chemistry, Biology	
MIT, Cambridge, MA	n/a	1985-1988	Biochem, Neurobiology	
Cornell University, Ithaca, NY	PhD	1990-1997	Genetics & Development	
Rutgers University, Piscataway, NJ	Postdoc	1997-2000	Structural Genomics	
Cold Spring Harbor Labs, Cold Spring Harbor, NY	n/a	2000	Bioinformatics	

A. Personal Statement

I have over 25 years experience in molecular genetics and 12 years in bioinformatics and systems biology. A long-standing theme of my work is the study of developmental networks, focusing on the generation and analysis of integrative genetic and phenotypic networks in early embryogenesis in *C. elegans*.

B. Positions and Honors
Professional Positions
1984 (Summer)   Research Assistant to Dr. Katsuko Suhara, University of Illinois, Urbana, IL
1985   Research Assistant, Laboratory of Dr. George Hess, Department of Biochemistry, Cell, & Molecular Biology, Cornell University, Ithaca, NY
1990   Research Assistant, laboratory of Dr. Michael L. Goldberg, Section of Genetics & Development, Cornell University, Ithaca, NY
2002 – 2006   Research Assistant Professor, Department of Biology, NNY
2005 – 2006   Project Director of Bioinformatics, Center for Computation in Science and Society, NYU, NY
2006 – 2012   Assistant Professor, Dept. of Biology, Center for Genomics & Systems Biology, NYU, NY
2006 – present   Faculty Member, Computational Biology Program, NYU, NY
2010 – present   Director of Bioinformatics, Center for Genomics & Systems Biology, NYU, NY
2012 – present   Associate Professor, Department of Biology and CGSB, NYU, NY

Awards and Nominations
1986 – 1988   W. M. Keck Foundation Fellowship in Biology, Dept. of Biology, MIT, Cambridge, MA
1993 – 1996   NIH Training Grant Fellowship, Section of Genetics & Development, Cornell U, Ithaca, NY
1996   Research Travel Grant, Cornell University, Ithaca, NY
1998 – 2001   NIH (NHGRI) Postdoctoral Fellowship, Rutgers, Cornell University
2002 – 2005   NSF ADVANCE Fellows Award, New York University, New York, NY
2004 – 2005   NYU Challenge Fund Award
2006   National Academies Education Fellow in the Life Sciences
2007   NYU Whitehead Fellowship for Junior Faculty in Biomedical and Biological Sciences

Other Experience and Professional Memberships
2000 – present   Online database resource provider: *C. elegans* RNAi database (www.rnai.org)
2003, 2007   NSF Study Section panelist
2004 – present   Peer review for *Adv Bioinf, Bioinformatics, BMC Bioinformatics, Genome Biol, Genome Res, ISMB, Nat Biotech, Nat Meth, Nucl Acids Res, PLoS, PLoS Comp Biol, Plant Physiol*
2004   Co-organizer, 3rd Annual Symposium of NYU Center for Comparative Functional Genomics
2005   Lecturer, Faculty Research Network, "BIO 2010: Integrative Approaches to Teaching Life Sciences", NYU, June 2005
2005 – present   Developer and curator of web-based interactive network browser (www.gnetbrowse.org)
2005 – 2007   Co-organizer and lecturer, Howard Hughes Summer Institute at NYU: workshop for high school teachers to help integrate genomics and bioinformatics into their curriculum
2005 – 2007   Co-organizer, Annual ORFeome Meeting, DFCI-Harvard Medical School
2006 – present   Design, instruction of advanced undergrad course: Genome Biology
2007 – present   Database resource: *C. elegans* 3'UTRs and their functional elements (www.utrome.org)
2009 – present   Design, instruction of introductory graduate course: Programming for Biologists
2010   Co-organizer, 3rd Annual Berlin Summer Meeting, BIMSB, MDC, Germany
2011 – present   Associate Editor, *Genes|Genomes|Genetics (G3)*, a Genetics Society of America journal
2012, 2013   NIH Study Section panelist (Developmental Systems Biology, Biodata Mgmt. and Analysis)
2012   Co-organizer, 11th Annual Symposium of the NYU Center for Genomics & Systems Biology

2012 – present   Scientific Advisory Board, EURATRANS Consortium (European large-scale functional genomics in the rat for translational research)

2013   Judge, Blavatnik Young Investigator Award, New York Academy of Sciences

C. Selected peer-reviewed publications (10 selected from 35 total)

1. Li S…(36 other authors)… Piano F, Vandenhaute J, Sardet C, Gerstein M, Doucette-Stamm L, **Gunsalus KC**, Harper JW, Cusick ME, Roth FP, Hill DE, Vidal M. A map of the interactome network of the metazoan *C. elegans*. *Science* 2004; 303:540-3.

2. Sönnichsen B, Koski L, Walsh A, Marshall P, Neumann F, Brehm M, Alleaume A-M, Artelt J, Bettencourt P, Cassin E, Hewitson M, Holz C, Khan M, Lazik S, Martin C, Nitzsche B, Ruer M, Stamford J, Winzi M, Heinkel R, Röder M, Finell J, Häntsch H, Jones S, Jones M, Piano F, **Gunsalus KC**, Oegema K, Gönczy P, Coulson A, Hyman AA, and Echeverri CJ. Full-genome RNAi profiling of early embryogenesis in *Caenorhabditis elegans*. *Nature* 2005; 434:462-69.

3. **Gunsalus KC***, Ge H*, Schetter A*, Goldberg DS*, Han JD, Hao T, Berriz GF, Bertin N, Huang J, Chuang LS, Li N, Mani R, Hyman AA, Sönnichsen B, Echeverri CJ, Roth FP, Vidal M, and Piano F. Predictive models of molecular machines involved in early C. elegans embryogenesis. *Nature* 2005;436:861-65. [*Co-first author]

4. Lall S, Grun D, Krek A, Chen K, Wang YL, Dewey CN, Sood P, Colombo T, Bray N, MacMenamin P, Kao HL, **Gunsalus KC**, Pachter L, Piano F, and Rajewsky N. A Genome-Wide Map of Conserved MicroRNA Targets in *C. elegans*. *Curr Biol* 2006; 16:460-71.

5. Boxem M, Maliga Z, Klitgord N, Li N, Lemmens I, Mana M, de Lichtervelde L, Mul JD, van de Peut D, Devos M, Simonis N, Yildirim MA, Cokol M, Kao HL, de Smet AS, Wang H, Schlaitz AL, Hao T, Milstein S, Fan C, Tipsword M, Drew K, Galli M, Rhrissorrakrai K, Drechsel D, Koller D, Roth FP, Iakoucheva LM, Dunker AK, Bonneau R, **Gunsalus KC**, Hill DE, Piano F, Tavernier J, van den Heuvel S, Hyman AA, Vidal M. A protein domain-based interactome network for *C.elegans* early embryogenesis. *Cell* 2008;134:534-45.

6. Kao H-L and **Gunsalus KC**. Browsing Multidimensional Networks with the Generic Network Browser (NBrowse). *Curr Protoc Bioinformatics* 2008; Chapter 9:Unit 9.11

7. Mangone M, Manoharan AP, Thierry-Mieg D, Thierry-Mieg J, Han T, Mackowiak S, Mis E, Zegar C, Gutwein MR, Khivansara V, Attie O, Chen K, Salehi-Ashtiani K, Vidal M, Harkins TT, Bouffard P, Suzuki Y, Sugano S, Kohara Y, Rajewsky N, Piano F*, **Gunsalus KC***, Kim JK*. The landscape of *C. elegans* 3'UTRs. *Science* 2010; 329:432-5. [*Corresponding author]

8. Gerstein M…(115 other authors)… Strome S*, **Gunsalus KC***, Micklem G*, Liu XS*, Reinke V*, Kim SK*, Hillier LW*, Henikoff S*, Piano F*, Snyder M*, Stein L*, Lieb JD*, Waterston RH*. Integrative Analysis of Functional Elements in the *Caenorhabditis elegans* Genome by the modENCODE Project. *Science* 2010; 330:1775-87. [*Corresponding authors]

9. Rhrissorrakrai K and **Gunsalus KC**. MINE: Module Identification in Networks. *BMC Bioinformatics* 2011; 12:192.

10. Green R, Kao H-L, Audhya A, Arur S, Schulman M, Schloissnig S, Niessen S, Laband K, Wang S, Hyman A, Desai A, Schedl T, Piano F, **Gunsalus KC***, Oegema K*. High-Resolution Phenotypic Profiling Based on the Complex Architecture of the *C. elegans* Gonad Syncytium. *Cell* 2011;145:470-482.(*selected for video abstract*)

D. Active Research Support

5 R01 HD046236-06 K. Gunsalus (PI)   12/01/08 – 11/30/13
NIH-NICHD "A systematic RNAi-based map of *C. elegans* embryogenesis"

1 U01 HG004276-01 F. Piano (PI)   05/04/07 – 03/31/13
NIH-NHGRI "Encyclopedia of *C. elegans* 3'UTRs and their regulatory elements"

1 R01 GM085503-01 K. Gunsalus (PI)   09/01/08 – 08/31/13
NIH-NIGMS "A systems biology approach to mammalian early embryogenesis"

1 RC2 HG005839-01 Manolis Kellis (PI)   09/30/09 – 08/31/2013
NIH-NHGRI "A Data Analysis Center (DAC) for integration of fly and worm modENCODE datasets"

BIOGRAPHICAL SKETCH				
NAME **Bonneau, Richard**	POSITION TITLE **Associate Professor and Co-Director of Informatics**			
EDUCATION/TRAINING				
INSTITUTION AND LOCATION	DEGREE	YEAR	FIELD OF STUDY	
Florida State University, Florida	B.A.	1997	Biochemistry	
University of Washington, Washington	Ph.D.	2001	Ab Initio Structure Prediction	

A. Personal Statement
I focus on two main categories of computational biology: learning networks from functional genomics data and predicting and designing protein and peptoid structure. In both areas I have played key roles in achieving critical field-wide milestones. In the area of structure prediction I was one of the early authors on the Rosetta code, which was one of the first codes to demonstrate accurate and comprehensive ability to predict protein structure in the absence of sequence homology. My lab has also made key contributions to the areas of genomics data analysis. We have also started a new project with political scientists and experimental psychologists to apply methods for learning network structure from time series to social media time series data using Twitter, online blogs about politics, and Facebook as our initial data sources (recently funded by NSF INSPIRE).

B. Positions and Honors
Professional Positions
1994-1996	Board Member, FSU Center for Participant Education.
1994-1996	Undergraduate Research. Florida State University, w/ Tim Logan.
1997	Research Assistant. National High Magnetic Field Laboratory, Tallahasse.
1997-1998	High School Teacher. NOVA High, Seattle.
1997-2001	University of Washington. Graduate Student David Baker lab.
2001	Structural GenomiX, Inc. San Diego. Sr. Scientist.
2001-2006	Institute for Systems Biology, Seattle, WA. Sr. Research Scientist.
2007-2010	Senior Advisor. Tacitus, LLC, Philadelphia, PA, USA.
2005-Present	Associate Professor, New York University Center for Comparative Functional Genomics and New York University, Courant Institute, Dept. of Computer Science

Awards and Fellowships
1993	Florida Academic Scholars Award & International Baccalaureate Diploma
1996	American Cancer Society – James Jay Fisher Fellowship
1998	Howard Hughes Medical Institute pre-doctoral Fellowship in the Biological Sciences
2008	One of top 20 scientists under 40, Discover magazine

C. Selected Peer-reviewed publications
For a current list see: http://scholar.google.com/citations?user=Wq8XTykAAAAJ&hl

1. Youngs N, Penfold-Brown D, Drew K, Shasha D, **Bonneau R**. Parametric Bayesian priors and better choice of negative examples improve protein function prediction. Bioinformatics. 2013 May 1;29(9):1190-8. PubMed PMID: 23511543.

2. Greenfield A, Hafemeister C, **Bonneau R**. Robust data-driven incorporation of prior knowledge into the inference of dynamic regulatory networks. Bioinformatics. 2013 Apr 15;29(8):1060-7.PubMed PMID: 23525069.

3. Ciofani M, Madar A, Galan C, Sellars M, Mace K, Kirigin FK, Birchmeier C, Wagner EF, Murphy KM, Myers RM, **Bonneau R***, Littman DR* (2012) . A validated regulatory network for Th17 cell specification Cell. 2012 Oct 12;151(2):289-303. PMID: 23021777; PubMed Central PMCID: PMC3503487. * denotes co-corresponding authors.

4. Baltz AG, Munschauer M, Schwanhäusser B, Vasile A, Murakawa Y, Schueler M, Youngs N, Penfold-Brown D, Drew K, Milek M, Wyler E, **Bonneau R**, Selbach M, Dieterich C, Landthaler M. The mRNA-Bound Proteome and Its Global Occupancy Profile on Protein-Coding Transcripts. (2012) Mol Cell. 46(5):674-90. PMID: 22681889.

5. Renfrew PD, Choi EJ, **Bonneau R**, Kuhlman B (2012) Incorporation of Noncanonical Amino Acids into Rosetta and Use in Computational Protein-Peptide Interface Design. PLoS ONE 7(3): e32637. doi:10.1371/journal.pone.0032637.

6. Drew K, Winters P, Butterfoss GL, Berstis V, Uplinger K, Armstrong J, Riffle M, Schweighofer E, Bovermann B, Goodlett DR, Davis TN, Shasha D, Malmström L, **Bonneau R**. (2011) The proteome folding project: proteome-scale prediction of structure and function. Genome Res. 21(11):1981-94.

7. Waltman P, Kacmarczyk T, Bate AR, Kearns DB, Reiss DJ, Eichenberger P, **Bonneau R**. Multi-species integrative biclustering. Genome Biol. 2010;11(9):R96. Epub 2010, Sep 29. PubMed PMID: 20920250.

8. Greenfield A, Madar A, **Bonneau R**. DREAM4: Combining Genetic and Dynamic Information to Identify Biological Networks and Dynamical Models. DREAM4 top performers special collection. PLoS ONE 2010, 5(10): e13397. doi:10.1371/journal.pone.0013397.

9. **Bonneau R***, Facciotti MT, Reiss DJ, Madar A, Baliga NS*, et al. A predictive model for transcriptional control of physiology in a free living cell. (2007) Cell. Dec 131:1354-1365.

10. **Bonneau R**, Tsai J, Ruczinski I, Chivian D, Rohl C, Strauss CEM, Baker D. (2001) Rosetta in CASP4: Progress in ab initio protein structure prediction. Proteins. 45(S5)119-126.

D. Other Support

BIOGRAPHICAL SKETCH			
NAME **Shasha, Dennis**	POSITION TITLE **Professor of Computer Science**		
EDUCATION/TRAINING			
INSTITUTION AND LOCATION	DEGREE	YEAR	FIELD OF STUDY
Yale University	B.S.	1977	Engineering and Applied Science
Syracuse University	M.S.	1980	Computer Science
Harvard University	Ph.D.	1984	Applied Mathematics

A. Personal Statement

I am a professor of computer science at the Courant Institute of New York University where I work with biologists on pattern discovery for network inference; with computational chemists on algorithms for protein design; and on computational reproducibility. Other areas of interest include database tuning as well as tree and graph matching. Because I like to type, I have written six books of puzzles about a mathematical detective named Dr. Ecco, a biography about great computer scientists, and a book about the future of computing. I have also written four technical books about database tuning, network inference, time series, DNA computing, and statistics. I have co-authored over sixty journal papers, seventy conference papers, and fifteen patents. I have also written the puzzle column for various publications including Scientific American.

B. Positions and Honors
Professional Positions
1984 - 1990   Assistant Professor, Courant Institute of Mathematical Sciences, New York University.
1990 - 1995   Associate Professor, Courant Institute of Mathematical Sciences, New York University.
1995 - Present   Full Professor, Courant Institute of Mathematical Sciences, New York University.
1998 - 1999   Invited Professor, INRIA, Roquencourt, France.

Other Experience and Professional Memberships
1993 - Present   Co-Editor-in-Chief (with Gottfried Vossen) of Information Systems. Publisher: Elsevier North Holland
2003-Present: Distinguished Science Advisor, New York Hall of Science

C. Selected Peer-reviewed Publications
1. Lingeman JM, **Shasha DE** (2012) *Network inference in molecular biology a hands-on framework.* Springer, New York, NY. ISBN 978-1461431121.

2. Ruffel S, Krouk G, **Shasha D**, Birnbaum KD, Coruzzi GM (2011) "Nitrogen economics of root foraging: Transitive closure of the nitrate-cytokinin relay and distinct systemic signaling for N supply vs. demand." ***Proc. Natl. Acad. Sci.*** 108(45):18524-9.

3. Katari MS, Nowicki SD, Aceituno FF, Nero D, Kelfer J, Thompson LP, Cabello JM, Davidson RS, Goldberg AP, **Shasha DE**, *Coruzzi* GM Gutierrez, RA. (2010) "VirtualPlant: a software platform to support systems biology research." ***Plant Physiol.*** 152 (2), 500-515.

4. Chen H, Bandyopadhyay S, **Shasha DE**, Birnbaum KD (2010) "Estimation of genome-wide redundancy in Arabidopsis thaliana." ***BMC Evol. Biol.*** 10:357; doi:10.1186/1471-2148-10-357.

5. Krouk G, Mirowski P, LeCun Y, Shasha D, Coruzzi G. (2010) "Predictive network modeling of the high-resolution dynamic plant transcriptome in response to nitrate." ***Genome Biol.*** 11 (12) R123.

6. Lagana A, Forte S, Giudice A, Arena MR, Puglisi PL, Giugno R, Pulvirenti A, Shasha D, Ferro A (2009) "miRo: a miRNA knowledge base." **Database: The Journal of Biological Databases and Curation** Oxford University Press; doi: 10.1093/database/bap008.

7. Krouk G, Tranchina D, Lejay L, Cruikshank AA, **Shasha D**, Coruzzi GM, Guitierrez RA (2009) "A Systems Approach Uncovers Restrictions for Signal Interactions Regulating Genome-wide Responses to Nutritional Cues in Arabidopsis.: *PLOS Comp. Biol.* 5(3):e1000326.

8. Thum KE, Shin MJ, Gutierrez R, Katari M, Nero D, **Shasha D**, Coruzzi GM (2007) "An integrated genetic, genomic and systems approach defines gene networks regulated by the interaction of light and carbon signaling pathways." *BMC Syst. Biol.* 2:31.

9. Gutierrez RA, Lejay L, Dean A, Chiaromonte F, **Shasha DE**, Coruzzi GM (2007) "Qualitative network models and genome-wide expression data define carbon/nitrogen-responsive molecular machines in Arabidopsis." *Genome Biol.* 8:R7, 11.

10. Gutiérrez RA, Gifford ML, Poultney C, Wang R, **Shasha DE**, Coruzzi GM, and Crawford NM (2007) "Insights into the genomic nitrate response using genetics and the Sungear software system." *J. Exp. Bot.* 58(9):2359-67; doi:10.1093/jxb/erm079.

11. Ferro A, Giugno R, Pigola G, Pulvirenti A, Skripin D, Bader GD, **Shasha D** (2007) "NetMatch: a Cytoscape Plugin for Searching Biological Networks." *Bioinformatics* 23(7):910-912; doi:10.1093/bioinformatics/btm032.

12. Cui X, Vinar T, Brejova B, **Shasha D**, Li M (2007) "Homology search for genes." *Bioinformatics* 23(13):i97-i103 17646351 (P,S,E,B,D).

13. Poultney CS, Gutirrez RA, Katari MS, Gifford ML, Paley WB, Coruzzi GM, **Shasha DE** (2006) "Sungear: Interactive visualization and functional analysis of genomic datasets." *Bioinformatics* 23(2):259-61; doi:10.1093/bioinformatics/btl496.

14. Lejay L, **Shasha DE**, Palenchar PM, Kouranov AY, Cruikshank AA, Chou MF, Coruzzi GM (2004) "Adaptive Combinatorial Design to explore Large Experimental Spaces: approach and validation." *Syst. Biol.* 1(2):206-212.

15. Birnbaum K, **Shasha DE**, Wang JY, Jung JW, Lambert GM, Galbraith DW, Benfey PN (2003) "A gene expression map of the Arabidopsis root." *Science* 302(5652):1956-60.

D. Other Support
ACTIVE

5R01 GM032877-28	Coruzzi (PI)	05/01/09 - 04/30/14
NIH "A Systems Approach to Regulatory Networks Controlling N-assimilation"		Role: Co-Investigator

MCB-0929338	Coruzzi (PI)	07/15/09 - 06/30/13
NSF "Arabidopsis 2010: Nitrogen Networks in Plants"		Role: Co-Investigator

IOS-0922738	Coruzzi (PI)	08/01/10 - 07/31/14
NSF "Genomics of Comparative Seed Evolution"		Role: Co-Investigator

MCB-1158273	Coruzzi (PI)	04/01/12 - 05/31/15
NSF "A Systems Approach to the NPK Nutriome and its Effect on Biomass"		Role: Co-Investigator

COMPLETED

IIS – 1050388	Shasha (PI)	09/01/10 - 08/31/12
NSF "Collaborative Research: A Community Experiment Platform for Reproducibility and Generalizability"		

DBI-0445666	Coruzzi (PI)	06/01/05 - 11/30/11
NSF "Conceptual Data Integration for the Virtual Plant"		Role: Co-Investigator