

## A . M A X B U R R O U G H S

### EDUCATION

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- PhD** Bioinformatics, Boston University, December 2007  
*Dissertation:* “Application of Computational Approaches to Decipher Function and Evolution of Selected Protein Folds”  
Committee: David L. Landsman (chair), L Aravind, Karen Allen, Dean Tolan, Temple Smith
- BS** Biochemistry, Brigham Young University-Hawaii, June 2003  
Minor, Mathematics  
Minor, Chemistry  
*Diploma of Recognition:* Summa Cum Laude (with Honors), Salutatorian

### RESEARCH EMPLOYMENT HISTORY

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- Research Scientist, 8/2012-current. Computational Biology Branch (CBB), National Center for Biotechnology Information (NCBI), National Library of Medicine (NLM), National Institutes of Health (NIH).
- Visiting Scientist, 4/2013-current. Division of Genomic Technologies (DGT), RIKEN Center for Life Science Technologies, RIKEN Yokohama Institute.
- Visiting Scientist, 8/2012-3/2013. Omics Science Center (OSC), RIKEN Yokohama Institute.
- Post-doctoral Researcher, 6/2008-7/2012. LSA Bioinformatics Team, OSC, RIKEN Yokohama Institute.
- Post-doctoral and Research Fellow, 01/08-06/08. NCBI, NLM, NIH. Dr. L Aravind, advisor
- Graduate student researcher, 9/2004-12/2007. NCBI, NLM, NIH. Dr. L Aravind, advisor.
- Research assistant, 01/02-06/03. Characterization of copper-ligand binding properties in Cox17 proteins. Dr. Daren Heaton, advisor.
- Summer internship, 2002. Stanford Linear Accelerator Center (SLAC), Stanford Synchrotron Radiation Laboratory (SSRL), Dr. Graham George, advisor.

### PUBLICATIONS, PRESENTATIONS, AND RESEARCH GRANTS

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#### Journal Publications (\* denotes joint first authorship, ^ denotes corresponding authorship)

- Zhang D, Burroughs AM, Vidal NM, Iyer LM, Aravind L. Unification of the Crinkler effector and RHSP transposon systems: identification and characterization of a novel, widespread pathogenic eukaryotic toxin-delivery system invoking DNA cleavage, in preparation.
- de Rie D, Vitting-Seerup K, Burroughs AM, Alam T, Medvedeva Y, Tarui H, Noma S, Lizio M, Severin J, Hasegawa A, Daub CO, Sætrom P, Fort A, Hashimoto K, Roudnicky F, Lassmann T, Mungall C, Summers K, Lee W, Goldowitz D, Detmar M, Kawaji H, Lecellier C, Mathelier A, Makeev V, Sandelin A, Rehli M, the FANTOM consortium, Hayashizaki Y, Carninici P, Forrest AR, de Hoon MJ. Transcriptional regulation of microRNA expression in human primary cells, in preparation.
- Burroughs AM^, Anand S, Iyer LM, Aravind L. Unification of the DNA binding domains of ArdC, XPC/Rad4, and Tc38: implications for bacterial conflict, eukaryotic mismatch repair, and kinetoplast replication, in preparation.
- Iyer LM\*, Anand S\*, Burroughs AM, Aravind L. Diverse polyvalent toxin delivery accompanies phage

infection, in preparation.

- [Burroughs AM](#)<sup>^</sup>, Glasner ME, Aravind L, Taylor EA. Natural history of the protocatechuate dioxygenase superfamily: emergence of a pervasive bacterial catabolic ring opening function from an ancestral RNA-modification function, in preparation.
- Yoshimoto R, Kaida D, Furuno M, Shohei N, [Burroughs AM](#), Suzuki H, Kawamura Y, Hayashizaki Y, Mayeda A, Nakagawa A, and Yoshida M. Global analysis of pre-mRNA subcellular localization following splicing inhibition by spliceostatin A. *RNA*, under review.
- [Burroughs AM](#), Zhang D, Schaeffer DE, Iyer LM, Aravind L. Comparative genomics, structural analysis, and function prediction of a vast, novel network of nucleotide-centric systems in biological conflicts and signaling. *Nucleic Acids Research*, 2015 Dec 15;43(22):10633-54.
- [Burroughs AM](#)<sup>^</sup>, Zhang D, Aravind L. The eukaryotic translation initiation regulator CDC123 defines a divergent clade of ATP-grasp enzymes with a predicted role in novel protein modifications. *Biology Direct*. 2015 May 15;10:21.
- Barry KP, Ngu A, Cohn EF, Cote JM, [Burroughs AM](#), Gerbino JP, Taylor EA. Exploring allosteric activation of LigAB from *Sphingobium* sp. strain SYK-6 through kinetics, mutagenesis and computational studies. *Archives of Biochemistry and Biophysics*. 2015 Feb 1;567:35-45.
- [Burroughs AM](#), Aravind L. Analysis of two domains with novel RNA-processing activities throws light on the complex evolution of ribosomal RNA biogenesis. *Frontiers in Genetics*. 2014 Dec 23;5:424.
- Boele J, Persson H, Shin JW, Ishizu Y, Newie IS, Søkilde R, Hawkins SM, Coarfa C, Ikeda K, Takayama K, Horie-Inoue K, Ando Y, [Burroughs AM](#), Sasaki C, Suzuki C, Sakai M, Aoki S, Ogawa A, Hasegawa A, Lizio M, Kaida K, Teusink B, Carninci P, Suzuki H, Inoue S, Gunaratne PH, Rovira C, Hayashizaki Y, de Hoon MJ. PAPD5-mediated 3' adenylation and subsequent degradation of miR-21 is disrupted in proliferative disease. *Proceedings of the National Academy of Sciences USA*. 2014 Aug 5;111(31):11467-72.
- Zhang D, Iyer LM, [Burroughs AM](#), Aravind L. Resilience of biochemical activity in protein domains in the face of structural divergence. *Current Opinions in Structural Biology*. 2014 Jun 18;26C:92-103.
- FANTOM Consortium and the RIKEN PMI and CLST (DGT). A promoter-level mammalian expression atlas. *Nature*. 2014 Mar 27;507(7493):462-70.
- Andersson R, Gebhard C, Miguel-Escalada I, Hoof I, Bornholdt J, Boyd M, Chen Y, Zhao X, Schmidl C, Suzuki T, Ntini E, Arner E, Valen E, Li K, Schwarzfischer L, Glatz D, Raithel J, Lilje B, Rapin N, Bagger FO, Jørgensen M, Andersen PR, Bertin N, Rackham O, [Burroughs AM](#), Baillie JK, Ishizu Y, Shimizu Y, Furuhashi E, Maeda S, Negishi Y, Mungall CJ, Meehan TF, Lassmann T, Itoh M, Kawaji H, Kondo N, Kawai J, Lennartsson A, Daub CO, Heutink P, Hume DA, Jensen TH, Suzuki H, Hayashizaki Y, Müller F; FANTOM Consortium, Forrest AR, Carninci P, Rehli M, Sandelin A. An atlas of active enhancers across human cell types and tissues. *Nature*. 2014 Mar 27;507(7493):455-61.
- [Burroughs AM](#)<sup>^</sup>, Aravind L. A highly conserved family of domains related to the DNA-glycosylase fold helps predict multiple novel pathways for RNA modifications. *RNA Biology*. 2014 Apr 1;11(4):360-72.
- Iyer LM, Zhang D, [Burroughs AM](#), Aravind L. Computational identification of novel biochemical systems involved in oxidation, glycosylation and other complex modifications of bases in DNA. *Nucleic Acids Research*. 2013 Sep;41(16):7635-55.

- Cernilogar FM, [Burroughs AM](#), Lanzuolo C, Breiling A, Imhof A, Orlando V. RNA-interference components are dispensable for transcriptional silencing of the drosophila bithorax-complex. *PLoS One*. 2013 Jun 13;8(6):e65740.
- Anantharaman V, Makarova KS, [Burroughs AM](#), Koonin EV, Aravind L. Comprehensive analysis of the HEPN superfamily: identification of novel roles in intra-genomic conflicts, defense, pathogenesis and RNA processing. *Biology Direct*. 2013 Jun 15;8:15.
- [Burroughs AM](#), Iyer LM, Aravind L. Two novel PIWI families: roles in inter-genomic conflicts in bacteria and Mediator-dependent modulation of transcription in eukaryotes. *Biology Direct*. 2013 Jun 8;8:13.
- [Burroughs AM](#), Sayyed BH, Voegtline TJ, Zabriskie TM, Silvaggi NR. Structural and Functional Characterization of MppR, a Protein of Unknown Function from *Streptomyces hygroscopicus*: Functional Diversity in the Acetoacetate Decarboxylase-Like Superfamily. *Biochemistry*. 2013 Jul 2;52(26):4492-506.
- Kato I, Begum NA, [Burroughs AM](#), Doi T, Kawai J, Daub CO, Kawaguchi T, Matsuda F, Hayashizaki Y, Honjo T. Nonimmunoglobulin target loci of activation-induced cytidine deaminase (AID) share unique features with immunoglobulin genes. *Proceedings of the National Academy of Sciences USA*. 2012 Feb 14;109(7):2479-84.
- [Burroughs AM](#)<sup>\*</sup>, Kawano M<sup>\*</sup>, Ando Y, Daub CO, Hayashizaki Y. pre-miRNA profiles obtained through application of locked nucleic acids reveals complex 5'/3' arm variation including concomitant cleavage and polyuridylation patterns. *Nucleic Acids Research* 2012 Feb;40(4):1424-37.
- Cernilogar FM<sup>\*</sup>, Onorati MC<sup>\*</sup>, Kothe GO, [Burroughs AM](#), Parsi KM, Breiling A, lo Sardo F, Saxena A, Miyoshi K, Siomi H, Siomi M, Carninci P, Gilmour DS, Corona DFV and Orlando V. Chromatin associated RNAi components control transcriptional regulation in *Drosophila*. *Nature*. 2011 Nov 6;480(7377):391-5.
- Ando Y<sup>\*</sup>, Tomaru Y<sup>\*</sup>, Morinaga A, [Burroughs AM](#), Kawaji H, Kubosaki A, Kimura R, Ino Y, Hirano H, Chiba J, Suzuki H, Carninci P, Hayashizaki Y. Nuclear pore complex proteins mediate nuclear localization of DICER protein in human cells. *PLoS One*. 2011;6(8):e23385.
- [Burroughs AM](#), Iyer LM, L Aravind. Functional diversification of the RING finger and other binuclear treble clef domains in prokaryotes and the early evolution of the ubiquitin system. *Molecular Biosystems* 2011 Jul;7(7):2261-77.
- Ando Y, Maida Y, Morinaga A, [Burroughs AM](#), Kimura R, Chiba J, Suzuki H, Masutomi K, Hayashizaki Y. Two-step cleavage of hairpin RNA with 5' overhangs by human DICER. *BMC Molecular Biology*. 2011 Feb 9;12(1):6.
- [Burroughs AM](#)<sup>\*</sup>, Ando Y<sup>\*</sup>, de Hoon M, Tomaru Y, Suzuki H, Hayashizaki Y, Daub CO. Deep-sequencing of human Argonaute-associated small RNAs provides insight into miRNA sorting and reveals Argonaute association with RNA fragments of diverse origin. *RNA Biology*. 2011 Jan 1;8(1).
- [Burroughs AM](#)<sup>\*</sup>, Ando Y<sup>\*</sup>, de Hoon M, Tomaru Y, Nishibu T, Ukekawa R, Funakoshi T, Kurokawa T, Suzuki H, Hayashizaki Y, Daub CO. A comprehensive survey of 3' animal miRNA modification events and a possible role for 3' adenylation in modulating miRNA targeting effectiveness. *Genome Res*. 2010 Oct;20(10):1398-410.
- Iyer LM, Abhiman S, [Burroughs AM](#), L Aravind. Biochemical systems with ATP-grasp, acetyltransferase-like and glutamine synthetase-like domains: synthesis of novel metabolites and peptide modifications of proteins. *Molecular Biosystems*. 2009 Dec; 5(12):1636-60.

- Burroughs AM, Iyer LM, L Aravind. Evolutionary history of the E1-like fold and architectural themes contributing to the catalytic roles of the E1-like protein. *Proteins*. 2009 Jun; 75(4):895-910.
- Iyer LM, Burroughs AM, L Aravind. Unraveling the biochemistry and provenance of pupylation: a prokaryotic analog of ubiquitination. *Biol Direct*. 2008 Nov 3; 3:45.
- Salzberg SL, Schatz M, Nagarajan N, Delcher AL, Burroughs AM [\*\*only members of University of Maryland group shown in published author order, see collaborations section]. Genome of the transgenic tropical fruit tree papaya (*Carica papaya* L.). *Nature*. 2008 Apr 24; 452(7190):991-6.
- Burroughs AM, Jaffee M, Iyer LM, L Aravind. Anatomy of the E2 ligase fold: implications for enzymology and evolution of ubiquitin/Ub-like protein conjugation. *Journal of Structural Biology*. 2008 May; 162(2):205-18.
- Peisach E, Wang L, Burroughs AM, L Aravind, Dunaway-Mariano D, Allen KN. The X-ray crystallographic structure and activity analysis of a Pseudomonas-specific subfamily of the HAD enzyme superfamily evidences a novel biochemical function. *Proteins*. 2008 Jan 1; 70(1):197-207.
- Burroughs AM, Balaji S, Iyer LM, L Aravind. Small but versatile: the extraordinary functional and structural diversity of the  $\beta$ -grasp fold. *Biology Direct*. 2007 Jul 2; 2(1):18.
- Burroughs AM, Balaji S, Iyer LM, L Aravind. A novel superfamily containing the  $\beta$ -grasp fold involved in binding diverse soluble ligands. *Biology Direct*. 2007 Jan 24; 2:4.
- Burroughs AM, Allen KN, Dunaway-Mariano D, and L Aravind. Evolutionary genomics of the HAD superfamily: understanding the structural adaptations and catalytic diversity in a superfamily of phosphoesterases and allied enzymes. *Journal of Molecular Biology*. 2006 Sep 1; 361(5):1003-34.
- Burroughs AM\*, Iyer LM\*, L Aravind. The prokaryotic antecedents of the ubiquitin-signaling system and the early evolution of ubiquitin-like  $\beta$ -grasp domains. *Genome Biology*. 2006 Jul 19;7(7):R60.
- Iyer LM, Burroughs AM, L Aravind. The ASCH superfamily: novel domains with a fold related to the PUA domain and a potential role in RNA metabolism. *Bioinformatics*. 2006 Feb 1; 22(3):257-63.
- Burroughs AM. The medical examination in United States immigration applications: the potential use of genetic testing leads to heightened privacy concerns. *Journal of Biolaw and Business*. 2005; 8(4):22-32.

#### Invited Publications

- Burroughs AM<sup>^</sup>, Aravind L<sup>^</sup>. Survey and Summary: RNA damage in biological conflicts and the diversity of responding RNA repair systems. *Nucleic Acids Research*. accepted, in press.
- Aravind L, Burroughs AM, Zhang D, Iyer LM. Protein and DNA modifications: evolutionary imprints of bacterial biochemical diversification and geochemistry on the provenance of eukaryotic epigenetics. Cold Spring Harbor Perspectives in Biology. 2014 Jul 1;6(7).
- Burroughs AM<sup>^</sup>, Ando Y, Aravind L. New perspectives on the diversification of the RNA interference system: insights from comparative genomics and small RNA sequencing. Wiley Interdisciplinary Reviews RNA. 2013 Dec 5.
- Ando Y, Burroughs AM<sup>^</sup>, Kawano M, de Hoon MJ, and Hayashizaki Y. Targeted methods to improve small RNA profiles generated by deep sequencing. Mallick B (editor): Experimental approaches to Regulatory RNAs,

Regulatory RNAs series. Springer-Verlag. 2012; 253-271.

- Burroughs AM, Iyer LM, L Aravind. Structure and evolution of ubiquitin and ubiquitin-related domains. Dohmen J and Scheffner M (editors): Ubiquitin family modifiers and the proteasome: Reviews and protocols, Methods in Molecular Biology series. Humana Press. 2012;832:15-63.
- Burroughs AM, Iyer LM, L Aravind. The natural history of ubiquitin and ubiquitin-related domains. Garcia M (editor): Frontiers in Bioscience: Ubiquitin-like proteins in the Encyclopedia of Bioscience, Frontiers in Bioscience. 2012 Jan 1;17:1433-60.
- Burroughs AM, Iyer LM, L Aravind. Comparative genomics and evolutionary trajectories of viral ATP dependent DNA-packaging systems. Volff J-N (editor): Gene and Protein Evolution, Genome Dynamics series. Basel, Karger, 2007, vol. 3, pp 48-65.

### Invited Talks

- Novel prokaryotic signaling systems centered on nucleotides and their derivatives: roles in biological conflicts and immunity. NIH Lambda Lunch Seminar Series hosted by Dr. Susan Gottesman, December 17, 2015.
- Ubiquitin modification and how it informs the evolution of protein modification systems. BYU-Hawaii campus-wide seminar, January 2014.
- The ubiquitin modification system: lessons for the evolution of protein modification systems. NCBI Computational Biology Branch Scientific Retreat, May 2013.
- Post-genome analysis of fundamental biological systems. Seminar at Shanghai Ocean University, January 2012.
- Surveying the pre-miRNA landscape with locked oligonucleotide acids (LNAs). Omics Science Center Annual Research Exchange Meeting, November 2011.
- Animal 3' miRNA addition: characterization and functional insights. Biochemistry and Molecular Biology (BMB) 2010 International Conference, Kobe, Japan.
- Animal 3' miRNA addition: characterization and functional insights. Omics Science Center annual retreat, 2010.
- Small promoter-derived RNA and the AGO proteins. Omics Science Center annual retreat, 2010.
- Application of computational approaches to decipher function and evolution in selected protein folds. Seminar given to the Genome Exploration Research Group at the Genomic Science Center, RIKEN-Yokohama Campus, Yokohama, Japan, February 2008.
- Comparative evolutionary genomics of the ubiquitin modification system. Seminar given at the National Institute for Genetics, Mishima, Japan, February 2008.
- Comparative evolutionary genomics of the ubiquitin modification system. Seminar given at the Computational Biology Research Center, Advanced Industrial Science and Technology Center, Tokyo, Japan, February 2008.
- Deciphering function and evolution of key protein folds. NIH Graduate Student Seminar Series, November 2007.
- Evolutionary adaptations and the discovery of a novel ligand-binding superfamily in the  $\beta$ -grasp fold.

Computational Biology Branch Seminar, NCBI/NLM/NIH, Oct. 2, 2007.

- The origin of ubiquitin signaling pathways: comparative genomics uncovers evidence of prokaryotic homologs. NIH Lambda Lunch Seminar Series hosted by Dr. Susan Gottesman, September 13, 2007.
- Genomic analysis uncovers novel prokaryotic ubiquitin-signaling systems. The Ubiquitin Family: Cold Spring Harbor Laboratory Meeting, April 2007.
- The evolutionary history of the ubiquitin signaling system and the discovery of a novel superfamily of  $\beta$ -grasp-like proteins. NIH Graduate Student Seminar Series, November 2006.
- Cloning mutant proteins. Annual Undergraduate Research Seminar, BYU-Hawaii campus, May 2003.

### Poster Presentations

- Ligation in response to RNA nuclease toxin attacks: discovery of novel pathways and mechanisms in RNA repair. RNA Society International Conference, Kyoto, Japan, June 2016.
- Functions and origins of vital yet poorly-understood ribosome assembly factors TSR3 and TSR4 and translation regulation factors NEMF and CDC123. EMBO Conference on Ribosome Biosynthesis, Brussels, Belgium, August 2015.
- Discovery of novel PIWI/AGO families in the Mediator complex and a mobile, three-gene operon: roles in eukaryotic transcription initiation and bacterial genome conflict. RNA Society International Conference, University of Wisconsin, USA, April, 2015.
- Novel PIWI/AGO families with roles in Mediator-dependent transcription in eukaryotes and bacterial inter-genome conflict throw light on the early evolution of RNAi systems. NIH Symposium: RNA Biology. March 2015.
- Analysis of small RNA associating with human Argonaute proteins. Molecular Biology Society of Japan International Conference, Yokohama, Japan, December 2011.
- Comparative profiling of the RNA content bound to human Argonaute proteins. RNA Society International Conference, Kyoto, Japan, June 2011.
- A comprehensive survey of 3' animal miRNA modification events and a possible role for 3' adenylation in modulating miRNA targeting effectiveness. Biochemistry and Molecular Biology (BMB) International Conference, Kobe, Japan, December 2010.
- A novel superfamily binding diverse soluble ligands. NIH Graduate Student Research Symposium, May 2007.
- Prokaryotic antecedents of the ubiquitin signaling system and the early evolution of ubiquitin-like  $\beta$ -grasp domains. NIH Research Festival, October 2006.
- Prokaryotic origins of the ubiquitin-signaling system. The Sixth International Workshop on Bioinformatics and Systems Biology, Boston, August 2006.

### Research Grants

- RIKEN OSC Research Project Grant, primary applicant. “AGO association with promoter-region derived small RNA”. 2011, \$20,000 USD.
- Internal Competitive RIKEN OSC Research Project Grant, primary applicant. “miRNA adenine/uridine addition.” 2009, \$25,000 USD.

## RESEARCH COLLABORATIONS

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### Ongoing Public Collaborative Efforts

- FANTOM International consortium member: 2008-present.  
Function characterization and promoter architecture of non-coding RNA.  
Current FANTOM director: Dr. Piero Carninci at RIKEN DGT, Center for Life Science Technologies  
Manuscripts in *Nature*, others in preparation.
- miRNA landscape analysis and targeting an increased understanding of miRNA maturation pathways and their clinical significance: 2011-present.  
With Dr. Michiel de Hoon, Genome Algorithms Development Unit, DGT, RIKEN.  
Manuscript in *PNAS*, others in preparation.
- Development of sequencing methods to isolate and characterize low-expression small noncoding RNA classes: 2010-present.  
With Dr. Mitsuoki Kawano, Niigata University of Pharmacy and Applied Life Sciences.  
Manuscript in *Nucleic Acids Research*, others in preparation.

### Completed Collaborative Efforts

- Genome landscape of AID-mediated changes to non-immunoglobulin genes: 2009-2012.  
With Dr. Tasuku Honjo, Kyoto University.  
Manuscript in *PNAS*.
- Small RNA and functional roles at heat shock and bithorax genome loci: 2010-2012.  
With Dr. Valerio Orlando, Telethon Institute and Dr. Filippo Cernilogar, Ludwig Maximilian University.  
Manuscripts in *Nature*, *PLoS One*.
- Member of the papaya (*Carica papaya*) genome sequencing consortium: 2006-2008.  
With Dr. Steven Salzberg, Johns Hopkins University and Dr. Ray Ming, University of Illinois.  
Manuscript in *Nature*.

## PROFESSIONAL SERVICES AND ACTIVITIES

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### Editorial Board

*Scientific Reports* (Nature Publishing Company journal), Chemical Biology Section.

### Peer review for funding agencies

National Science Foundation, Molecular and Cellular Bioscience Division  
European Research Council, Starting Grant Research Proposals

## Peer review for scholarly journals

*Nature Structural and Molecular Biology*  
*Nucleic Acids Research*  
*Journal of Molecular Biology*  
*RNA Biology*  
*Biochemistry*  
*Molecular Microbiology*  
*Proteins: Structure, Function, and Bioinformatics*  
*Genome Biology and Evolution*  
*BMC Genomics*  
*Evolutionary Biology*  
*BMC Evolutionary Biology*  
*PLoS One*  
*Biology Direct*  
*FEBS Letters*  
*Gene*  
*Frontiers in Plant Science*  
*Journal of Economic Entomology*  
*Microarrays*

## TEACHING EXPERIENCE

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### Courses

#### Organizer/Lecturer

- Understanding Development and Disease through Genomic Technologies. Joint course between RIKEN, Japan and the Karolinska Institute, Sweden. Winter, 2012.
- Functional Architecture of the Cell Nucleus. Joint course between RIKEN, Japan and the Karolinska Institute, Sweden. Fall, 2011.
- Medical and Developmental Genetics. Joint course between RIKEN, Japan and the Karolinska Institute, Sweden. Summer, 2010.
- Introduction to Laboratory Techniques. Foundation for Advanced Education in the Sciences (FAES), National Institutes of Health, Fall 2006.

### Teaching Seminars

- “Communicating your research effectively,” Omics Science Center Annual Retreat. August, 2011.

## HONORS AND AWARDS

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- National Library of Medicine, Length of Service Excellence Award, 2014.
- Manuscript selected as Featured Article in *Nucleic Acids Research*, November 2011.
- AAAS/Science Program for Excellence in Science, RIKEN Yokohama Nominee. 2011.
- Outstanding Oral Presentation Award, Omics Science Center Retreat, 2010.
- Postdoctoral Intramural Research Training Award (IRTA), NIH, 2008.
- Cecile M. Pickart Student Travel Award for outstanding research by a student in Ubiquitin-related research, The Ubiquitin Family: Cold Spring Harbor Laboratory Meeting, April 2007.
- Predoctoral Intramural Research Training Award (Pre-IRTA), NIH. 2003-2007.
- AAAS/Science Program for Excellence in Science, Boston University Bioinformatics Program Nominee. 2007, 2006.



- NIH/Boston University Graduate Partnerships Program Selectee, 2003.
- Salutatorian, Brigham Young University-Hawaii, Class of 2003.
- Phi Kappa Phi Outstanding Student in Biochemistry, Class of 2003.
- American Chemical Society Hawaii Chapter Most Outstanding Research Associate, 2003.
- David O. McKay Scholar, Brigham Young University-Hawaii, 1998, 2001-2003.

## **PROFESSIONAL AFFILIATIONS**

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- Molecular Biology Society of Japan (MBSJ), since 2010.
- American Association for the Advancement of Science (AAAS), 2006-2008 and since 2011.
- Φ K Φ: The Honor Society of Phi Kappa Phi, since 2001.

## **RESEARCH AND OTHER SKILLS**

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### **Computational Biology**

- Extensive experience with techniques in comparative sequence and structure analysis including identification of novel protein folds, reconstruction of the evolutionary history of protein domains, and various primary sequence and secondary structural comparisons for proteins as well as RNA and DNA.
- Implementation and working knowledge of theory behind various phylogenetic techniques including distance, maximum-likelihood, and Bayesian.
- Extensive experience in extraction, genome mapping, and analysis of data generated by high-throughput sequencer platforms including 454 Life Sciences, Illumina and MiSeq, Helicos (now defunct), SOLiD, and Pacific Biosciences.
- Extensive experience in design of RIP-seq, CAGE, small RNA-seq, RNA-seq, and ChIP-seq experiments and the detailed analysis of sequencing data derived from these experiments.
- Experience with analysis of sequencing data derived from genome sequencing experiments.
- Experience with gene microarray data analysis.

### **Computer Languages/Environments**

- Operating systems: UNIX, Linux, Windows
- Database management systems: Microsoft SQL, MySQL
- Languages: fluency with Perl and R, experience with C++

### **Molecular Biology**

- Recombinant DNA technology: DNA/RNA extraction, cloning, and expression techniques
- Protein isolation and characterization
- Microarray sample and chip preparation
- Working understanding of next-generation sequencing library preparation
- EXAFS experimental preparation and analysis

### **Languages**

- Fluent in the speaking, listening, reading, and writing of English
- Fluent in the speaking and listening of Japanese; working knowledge in the reading and writing of Japanese.