

# Dapeng Zhang

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## 1. EMPLOYMENT

- 7/2022-Present      **Associate Professor in Bioinformatics**  
Department of Biology, Program of Bioinformatics and Computational Biology, College of Arts and Sciences, Saint Louis University, USA
- 8/2016-6/2022      **Assistant Professor in Bioinformatics**  
Department of Biology, Program of Bioinformatics and Computational Biology, College of Arts and Sciences, Saint Louis University, USA
- 3/2014-8/2016      **Research Fellow in Computational Genomics**  
National Center for Biotechnology Information (NCBI), National Library of Medicine (NLM), National Institutes of Health (NIH), USA

## 2. EDUCATION AND TRAINING

- 8/2009-2/2014      **Intramural Research Program (IRP) Postdoctoral Fellow in Computational Genomics**, Advisor:  
Dr. L. Aravind,  
NCBI, NLM, NIH, USA
- 9/2004-6/2009      **Ph.D. in Fish Genomics**, Advisor: Dr. Vance L. Trudeau  
Centre for Advanced Research in Environmental Genomics, Department of Biology,  
University of Ottawa, Canada
- 9/2001-6/2004      **M.Sc. in Biochemistry**  
Department of Biochemistry, School of Life Sciences, Nanjing University, China
- 9/1997-7/2001      **B.Sc. in Bioengineering**  
School of Biological Sciences, Northeast Normal University, China

## 3. RESEARCH INTERESTS

Comparative and evolutionary genomics  
Genome and protein evolution  
Bioinformatics  
Toxin/effecter systems  
Biological conflicts  
Pathogen-host interactions

## 4. PROFESSIONAL SERVICES

### **Editorial board:**

*Microbiology Spectrum* (2022-2025)  
*Scientific Reports* (2023-)  
*Cancer Innovation* (2022-)  
*Frontiers in Genetics* (2020-)  
*PeerJ* (2019-)

### **Conference organization:**

Chair for a symposium of "Discovering molecular systems and mechanisms in biological conflicts" in ASM Microbe 2018  
- American Society for Microbiology. Atlanta, June 2018

### **Peer-reviewer for funding agencies:**

National Science Foundation  
Marsden Fund of the Royal Society of New Zealand  
French National Research Agency  
Israel Science Foundation

### **Peer-reviewer for scholarly journals: (>100 times)**

*Nature Microbiology*  
*Nature Communications*

*Nucleic Acids Research*  
*Molecular Phylogenetics and Evolution*  
*Current Opinion in Structural Biology*  
*Bioinformatics*  
*Journal of Molecular Biology*  
*BMC Genomics*  
*Database*  
*Applied and Environmental Microbiology*  
*Microbiology Spectrum*  
*Plos One*  
*Scientific Reports*  
*Frontiers in Endocrinology*  
*Frontiers in Genetics*  
*Frontiers in Plant Science*  
*Frontiers in Neuroscience*  
*General and Comparative Endocrinology*  
*Gene*  
*Infection, Genetics and Evolution*

## 5. PROFESSIONAL & COMMUNITY MEMBERSHIP

American Society for Microbiology (ASM)  
 International Society for Computational Biology (ISCB)  
 Society for Molecular Biology and Evolution (SMBE)  
 The American Phytopathological Society (APS)  
 The International Society for Molecular Plant-Microbe Interactions (IS-MPMI)  
 The Protein Society  
 North American Society for Comparative Endocrinology (NASCE)

## 6. JOURNAL PUBLICATIONS AND BOOK CHAPTERS

H-index: 32, Total citations>4100 (<https://scholar.google.com/citations?user=C6GQAYAAAAJ&hl=en>)

<sup>1</sup> Equally contributed authors

\* Corresponding author

+ Featured article, cover article, highly accessed or news highlight

# Representative publications

### **Manuscripts under Review:**

73. Tan Y, Scornet AL, Yap YF, **Zhang D**. Machine learning classification reveals distinct clusters of non-coding genomic allelic variations associated with antibiotic resistance. submitted.
72. Peng D, Lu C, Mitcheli K, Tan Y, **Zhang D**, Levavi-Sivan B, Hu W, Trudeau VL. Secretoneurin is an evolutionarily conserved neuropeptide that stimulates ovulation in zebrafish. submitted.
71. # Li H, **Zhang D**. Unveiling the Multifaceted Polymorphism of the Menshen Antiphage System. *Nucleic Acids Research*, under review.
70. Zhao Q, Bertolli S, Park Y, Tan Y, Cutler KJ, Srinivas P, Asfahl KL, Garcia CF, Gallagher L, Li Y, Wang Y, Coleman-Derr D, DiMaio F, **Zhang D**, Peterson B, Veasler D, Mougous JD. Umbrella toxin particles produced by *Streptomyces* block growth of vegetative hyphae in competing species. *Nature*, under review.
69. Gu Y, Li H, Deep A, Enustun E, **Zhang D**, Corbett K. Bacterial Shedu immune nucleases share a common enzymatic core regulated by diverse sensor domains. *Cell*, under review.
68. Tan Y, Aravind L, **Zhang D**. Genomic underpinnings of Cytoplasmic Incompatibility: CIF gene neighborhood diversification through lateral transfers and recombination in *Wolbachia*. *Genome Biology and Evolution*, under review.

### **Published Journal Articles:**

67. Shields K, Ranava D, Tan Y, **Zhang D**, Yap MF. Epitranscriptional m6A modification of rRNA negatively impacts translation and host colonization in *Staphylococcus aureus*. *PLoS Pathogens*, 2024, 20 (1), e1011968.
66. Hashemi B, Huntsman RJ, Li H, **Zhang D**, Xi Y. New presentation of CLIFAHHD syndrome with a novel variant in *NALCN* gene. *Clinical Case Reports*, 2023, 11(7): e7647.

65. Li H, Schneider T, Tan Y, **Zhang D\***. Ribonuclease T2 represents a distinct circularly permuted version of the BECR RNases. *Protein Science*, 2023, 32(1): e4531.
64. Li H, Tan Y, **Zhang D\***. Genomic discovery and structural dissection of a novel polymorphic toxin system in gram-positive bacteria. *Computational and Structural Biotechnology Journal*, 2022, 20:4517-4531.
63. Schneider T, Tan Y, Li H, Fisher J, **Zhang D\***. Photogloblin, a distinct family of non-heme binding globins, defines a potential photosensor in prokaryotic signal transduction systems. *Computational and Structural Biotechnology Journal*, 2022, 20: 261-273.
62. # Tan Y, Wang C, Schneider T, Li H, de Souza RF, Tang X, Hsieh TF, Wang X, Li X, **Zhang D\***. Comparative phylogenomic analysis reveals evolutionary genomic changes and novel toxin families in endophytic *Liberibacter* pathogens. *Microbiology Spectrum*, 2021, 9 (2), e00509-21.
61. Zhao Y, He W, Li W, Zhao Z, Wang Q, Hou Y, Tan Y, **Zhang D**. Acidic pH irreversibly activates the signaling enzyme *SARM1*. *FEBS Journal*, 2021, doi: 10.1111/febs.16104.
60. # Tan Y, Schneider T, Shukla P, Chandrasekharan M, Aravind L, **Zhang D\***. Unification and extensive diversification of M/ORF3-related ion channel proteins in coronaviruses and other nidoviruses. *Virus Evolution*, 2021, 7(1): veab014.
59. Hicks K, Tan Y, Cao W, Hathcock T, Boothe D, Kennis R, **Zhang D**, Wang X, White A. Genomic and in vitro pharmacodynamic analysis of rifampicin resistance at clinically relevant concentrations in multidrug-resistant canine *Staphylococcus pseudintermedius* isolates. *Veterinary Dermatology*, 2021, 32 (3), 219-e67.
58. Lin Z, Wang X, Wang J, Tan Y, Tang X, Werren J, **Zhang D**, Wang X. Comparative analysis reveals the expansion of mitochondrial DNA control region containing unusually high G-C tandem repeat arrays in *Nasonia vitripennis*. *International Journal of Biological Macromolecules*, 2020, S0141-8130(20)34933-3
57. Sur S, Nakanishi H, Steele R, **Zhang D**, Varvares M, Ray R. Long non-coding RNA ELDR enhances oral cancer growth by promoting ILF3-cyclin E1 signaling. *EMBO Reports*, 2020, 21(12):e51042.
56. # Tan Y, Schneider T, Leong M, Aravind L, **Zhang D\***. Novel Immunoglobulin Domain Proteins Provide Insights into Evolution and Pathogenesis of SARS-CoV-2-Related Viruses. *mBio* 2020, 11(3):e00760-20
55. Cao W, Hicks K, White A, Hathcock T, Kennis R, Boothe D, **Zhang D**, Wang X. Draft Genome Assemblies of Two *Staphylococcus pseudintermedius* Strains Isolated from Canine Skin Biopsy Specimens. *Microbiology Resource Announcements* 2020, 9(22):e00369-20.
54. Zhang C, Hung YH, Rim HJ, **Zhang D**, Frost JM, Shin H, Jang H, Liu F, Xiao W, Iyer LM, Aravind L, Zhang XQ, Fischer RL, Huh JH, Hsieh TF. The catalytic core of DEMETER guides active DNA demethylation in Arabidopsis. *Proceedings of the National Academy of Sciences of the United States of America* 2019, 116(35) 17563-17571.
53. Kostyniuk DJ, Marandel L, Jubouri M, Dias K, de Souza RF, **Zhang D**, Martyniuk CJ, Panseerat S, Mennigen JA. Profiling the rainbow trout hepatic miRNAome under diet-induced hyperglycemia. *Physiological Genomics* 2019, 51: 411–431.
52. Kostyniuk DJ, **Zhang D**, Martyniuk CJ, Marandel L, Gilmour KM, Mennigen J. Social status regulates the hepatic miRNAome in rainbow trout: Implications for posttranscriptional regulation of metabolic pathways. *Plos ONE*, 2019, 14 (6), e0217978.
51. Makarova K, Wolf YI, Karamycheva S, **Zhang D**, Aravind L, Koonin EV. Antimicrobial peptides, polymorphic toxins and self-nonself recognition systems in archaea: an untapped armory deployed in microbial conflicts. *mBio*, 2019, 10 (3), e00715-19.
50. Zeng Li<sup>1</sup>, **Zhang D<sup>1</sup>**, McLoughlin HS, Zalon AJ, Basappa J, Aravind L, Paulson HL. Loss of the Spinocerebellar Ataxia type 3 disease protein ATXN3 alters transcription of multiple signal transduction pathways. *Plos ONE*. 2018, 13(9): e0204438.
49. Wang Y<sup>1</sup>, Liu J<sup>1</sup>, Jin X<sup>1</sup>, **Zhang D**, Li D, Hao F, Feng Y, Gu S, Meng F, Tian M, Zheng Y, Xin L, Zhang X, Han X, Aravind L, Wei M. O-GlcNAcylation destabilizes the active tetrameric PKM2 to promote the Warburg effect. *Proceedings of the National Academy of Sciences of the United States of America* 2017, 114(52):13732-13737.

>80 citations

48. Burroughs AM, Kaur G, **Zhang D**, Aravind L. Novel clades of the HU/IHF superfamily point to unexpected roles in the eukaryotic centrosome, chromosome partitioning, and biologic conflicts. *Cell Cycle* 2017, 16 (11), 1093-1103.
47. + Li J, Bonkowski MS, Moniot S, **Zhang D**, Hubbard BP, Rajman LA, Ling AJ, Rajman LA, Qin B, Lou Z, Gorbunova V, Aravind L, Steegborn C, Sinclair DA. A conserved NAD<sup>+</sup> binding pocket that regulates protein-protein interactions during aging. *Science* 2017, 355 (6331), 1312-1317.  
>160 citations  
>150 news highlights (Altmetric)
46. Mennigen JA, **Zhang D**. MicroTrout: A comprehensive, genome-wide miRNA target prediction framework for rainbow trout, *Onchorynchus mykiss*. *Comparative Biochemistry and Physiology - Part D: Genomics & Proteomics* 2016, 20: 19–26.
45. He F, Jones JM, Figueroa-Romero C, **Zhang D**, Feldman EF, Meisler MH, Callaghan BC, Todd PK. Screening for novel hexanucleotide repeat expansions at ALS- and FTD-associated loci. *Neurology: Genetics* 2016, 2(3): e71.
44. Venables MJ, Navarro-Martín L, Basak A, Baum BR, **Zhang D**, Trudeau VL. Characterization of multiple nestin isoforms in the goldfish brain. *Comparative Biochemistry and Physiology - Part D: Genomics and Proteomics* 2016, 19:8-17.
43. # **Zhang D**, Burroughs AM, Vidal ND, Iyer LM, Aravind L. Transposons to toxins: the provenance, architecture and diversification of a widespread class of eukaryotic effectors. *Nucleic Acids Research* 2016, 44(8): 3513-3533.
42. Iyer LM, **Zhang D**, Aravind L. Adenine methylation in eukaryotic DNA: apprehending the complex evolutionary history and functional potential of an epigenetic modification. *BioEssays* 2016, 38(1):27-40.  
>120 citations
41. Burroughs AM, **Zhang D**, Iyer LM, Schaeffer D, Aravind L. Comparative genomic analyses reveal a vast, novel network of nucleotide-centric systems in biological conflicts, immunity and signaling. *Nucleic Acids Research* 2015, 43(22):10633-10654.  
>140 citations
40. Burroughs AM, **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, 10(1):21.
39. Xi Y, Honeywell C, **Zhang D**, Schwartzentruber J, Beaulieu CL, Tetreault M, Hartley T, Majewski J, Aravind L, Care4Rare Canada Consortium, Gollob M, Boycott KM, Gow RM. Whole exome sequencing identifies the TNNI3K gene as a cause of familial conduction system disease and congenital junctional ectopic tachycardia. *International Journal of Cardiology* 2015, 185:114-116.
38. Aravind L, **Zhang D**, de Souza RF, Anand S, Iyer LM. The natural history of ADP-ribosyltransferases. *Current Topics in Microbiology and Immunology* 2015, 384: 3-32.  
>90 citations
37. + 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, 6(7):a016063.  
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36. # **Zhang D**, Iyer LM, Burroughs AM, Aravind L. Resilience of biochemical activity in protein domains in the face of structural divergence. *Current Opinion in Structural Biology* 2014, 26C:92-103.
35. Pusapati G<sup>1</sup>, Hughes CE<sup>1</sup>, Dorn KV<sup>1</sup>, **Zhang D**<sup>1</sup>, Sugianto P, Aravind L, Rohatgi R. EFCAB7 and IQCE regulate Hedgehog signaling by tethering the EVC-EVC2 complex to the base of primary cilia. *Developmental Cell* 2014, 28(5):483-496.  
>60 citations
34. # Iyer LM<sup>1</sup>, **Zhang D**<sup>1</sup>, de Souza RF, Pukkila PJ, Rao A, Aravind L. Lineage-specific expansions of TET/JBP genes and a new class of DNA transposons shape fungal genomic and epigenetic landscapes. *Proceedings of the National Academy of Sciences of the United States of America* 2014, 111(5):1676-1683.
33. + 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, 41(16):7635-7655.  
NAR featured article (represents the top 5% of papers in terms of originality, significance and scientific excellence)

>90 citations

32. Li S, Huang X, **Zhang D**, Huang Q, Pei G, Wang L, Jiang W, Hu Q, Tan R, Hua ZC. Requirement of PEA3 for transcriptional activation of FAK gene in tumor metastasis. *PLoS ONE* 2013, 8(11):e79336.
31. Lado WE, **Zhang D**, Mennigen JA, Zamora JM, Popescu JT, Lewis JE, Trudeau VL. Rapid modulation of gene expression profiles in the forebrain of male goldfish following exposure to waterborne sex pheromones. *General and Comparative Endocrinology* 2013, 192:204-213.
30. **#+** **Zhang D**, Iyer LM, He F, Aravind L. Discovery of novel DENN proteins: implications for dynamics and evolution of eukaryotic intracellular membrane structures and human disease. *Frontiers in Genetics: Bioinformatics and Computational Biology* 2012, 3:283.  
>270 citations  
News Highlights on Alzheimer Research Forum and Birt-Hogg-Dubé Syndrome Foundation
29. **Zhang D**<sup>1</sup>, Xi Y<sup>1</sup>, Coccimiglio ML, Mennigen JA, Jonz M, Ekker M, Trudeau VL. Functional prediction and physiological characterization of a novel short trans-membrane protein 1 as a subunit of mitochondrial respiratory complexes. *Physiological Genomics* 2012, 44(23):1133-1140.
28. **Zhang D**, Aravind L. Novel transglutaminase-like peptidase and C2 domains elucidate the structure, biogenesis and evolution of the ciliary compartment. *Cell Cycle* 2012, 3861-3875.
27. **Zhang D**, Iyer LM, Aravind L. Bacterial GRAS domain proteins throw new light on gibberellic acid response mechanisms. *Bioinformatics* 2012, 28(19): 2407-2411.  
>80 citations
26. Aravind L, Anantharaman V, **Zhang D**, de Souza RF, Iyer LM. Gene flow and biological conflict systems in the origin and evolution of eukaryotes. *Frontier in Cellular and Infection Microbiology* 2012, 2:89.
25. **#+** **Zhang D**, de Souza RF, Anantharaman V, Iyer LM, Aravind L. Polymorphic toxin systems: Comprehensive characterization of trafficking modes, processing, mechanisms of action, immunity and ecology using comparative genomics. *Biology Direct* 2012, 7:18.  
>400 citations  
Featured as the No. 28 most accessed article all the time in the journal;  
A monograph of 76 pages, reporting over 150 novel toxin domains and over 90 novel immunity protein families involved in species conflict and host-pathogen interactions
24. **+** Iyer LM, **Zhang D**, Rogozin IB, Aravind L. Evolution of the deaminase fold and multiple origins of eukaryotic editing and mutagenic nucleic acid deaminases from bacterial toxin systems. *Nucleic Acids Research* 2011, 39(22):9473-9497.  
>130 citations  
NAR featured article and top accessed article (represents the top 5% of papers in terms of originality, significance and scientific excellence)
23. **#+** **Zhang D**, Iyer LM, Aravind L. A novel immunity system for bacterial nucleic acid degrading toxins and its recruitment in various eukaryotic and DNA viral systems. *Nucleic Acids Research* 2011, 39(11):4532-4552.  
>160 citations  
NAR featured article and top accessed article (represents the top 5% of papers in terms of originality, significance and scientific excellence)
22. **+** **Zhang D**, Aravind L. Identification of novel families and classification of the C2 domain superfamily elucidate the origin and evolution of membrane targeting activities in eukaryotes. *Gene* 2010, 469(1-2):18-30.  
>120 citations  
Highly accessed
21. Anantharaman V, **Zhang D**, Aravind L. OST-HTH: a novel predicted RNA-binding domain. *Biology Direct* 2010, 5:13.
20. Zhao E, Grey CL, **Zhang D**, Mennigen JA, Basak A, Chang JP, Trudeau VL. Secretoneurin (SN) is a paracrine factor from lactotrophs stimulating gonadotropin release in the goldfish pituitary. *American Journal of Physiology - Regulatory, Integrative and Comparative Physiology* 2010, 299(5):R1290-1297.
19. **Zhang D**, Duarte-Guterman P, Langlois VS, Trudeau VL. Temporal expression and steroidal regulation of piRNA pathway genes (*mael*, *piwi*, *vasa*) during *Silurana (Xenopus) tropicalis* embryogenesis. *Comparative Biochemistry and Physiology - Part C: Toxicology & Pharmacology* 2010, 152(2): 202-206.

18. Langlois VS, **Zhang D**, Cooke G, Trudeau VL. Evolution of steroid 5-alpha-reductases and comparison of their function with 5-beta-reductase. *General and Comparative Endocrinology* 2010, 166(3): 489-497.
17. # **Zhang D**<sup>1</sup>, Xiong H<sup>1</sup>, Mennigen JA, Popescu JT, Marlatt VL, Martyniuk CJ, Crump K, Xia X, Cossins AR, Trudeau VL. Defining neuroendocrine gene expression patterns associated with reproductive seasonality in fish. *PLoS ONE* 2009, 4(6): e5816.
16. **Zhang D**<sup>\*</sup>. Homology between DUF784, DUF1278 domains and the plant prolamin superfamily typifies evolutionary changes of disulfide bonding patterns. *Cell Cycle* 2009, 8(20): 3428-3430.
15. **Zhang D**, Popescu JT, Martyniuk CJ, Xiong H, Duarte-Guterman P, Yao L, Xia X, Trudeau VL. Profiling neuroendocrine gene expression changes following fadrozole-induced estrogen decline in the female goldfish. *Physiological Genomics* 2009, 38: 351-361.
14. + Zhao E, **Zhang D**, Basak A, Trudeau VL. New insights into granin-derived peptides: evolution and endocrine roles. *General and Comparative Endocrinology* 2009, 164(2-3): 161-174.  
Featured as cover article
13. **Zhang D**, Xiong H, Shan J, Xia X, Trudeau VL. Functional insight into Maelstrom in the germline piRNA pathway: a unique domain homologous to the DnaQ-H 3'-5' exonuclease, its lineage-specific expansion/loss and evolutionarily active site switch. *Biology Direct* 2008, 3:48.
12. Popescu JT, Martyniuk CJ, Mennigen JA, Xiong H, **Zhang D**, Xia X, Cossins AR, Trudeau VL. The goldfish (*Carassius auratus*) as a model for neuroendocrine signaling. *Molecular and Cellular Endocrinology* 2008, 293(1-2):43-56.
11. + Xiong H, **Zhang D**, Martyniuk CJ, Trudeau VL, Xia X. Using generalized Procrustes analysis for normalization of cDNA microarray data. *BMC Bioinformatics* 2008, 9:25.  
Highly accessed
10. + **Zhang D**, Trudeau VL. The XS domain of a plant specific SGS3 protein adopts a unique RNA recognition motif (RRM) fold. *Cell Cycle* 2008, 7(14):2268-2270.  
Faculty of 1000 Biology
9. Marlatt VL, Martyniuk CJ, **Zhang D**, Xiong H, Watt J, Xia X, Moon T, Trudeau VL. Auto-regulation of estrogen receptor subtypes and gene expression profiling of 17beta-estradiol action in the neuroendocrine axis of male goldfish. *Molecular and Cellular Endocrinology* 2008, 283(1-2):38-48.  
>130 citations
8. Li S, Wang L, **Zhang D**, Hua Z. Cloning and characterization of 5'UTR and promoter region of chicken focal adhesion kinase gene. *Journal of Nanjing Agricultural University* 2007, 20 (4):102-107. (in Chinese)
7. **Zhang D**, Martyniuk CJ, Trudeau VL. SANTA domain: a novel conserved protein module in *Eukaryota* with potential involvement in chromatin regulation. *Bioinformatics* 2006, 22 (20):2459-2462.
6. + **Zhang D**, Trudeau VL. Integration of membrane and nuclear estrogen receptor signaling. *Comparative Biochemistry and Physiology - Part A: Molecular & Integrative Physiology* 2006,144 (3):306-315.  
>130 citations  
Top accessed for 5 years
5. **Zhang D**, Wang J, Hua Z. Conservation status of SARS proteins. *Journal of Southeast University (Medical Science Edition)* 2005, 24 (1):32-35. (in Chinese)
4. **Zhang D**, Wang J, Yang J, Hua Z. Conserved motifs mapping of the SARS-RdRp. *Chinese Journal of Virology* 2004, 20 (4):371-377. (in Chinese)
3. Zhang J, **Zhang D**, Huz Z. FADD and its phosphorylation. *IUBMB Life* 2004, 56:395-402.

#### **Book Chapters:**

2. Aravind L, **Zhang D**, Iyer LM. The TET/JBP family of nucleic base-modifying 2-oxoglutarate and iron-dependent dioxygenases. *2-Oxoglutarate-Dependent Oxygenases* 2015, 3 (12): 289-308.
1. **Zhang D**, Trudeau VL. Estrogen signaling mechanisms. *Signal Transduction: Pathways, Mechanisms and Diseases* 2009, 273-288.



## 7. ORAL, POSTER AND CONTRIBUTED PRESENTATIONS

### **Oral presentations:**

27. Unveiling the Complexity of Protein Toxin Systems: Insights from Genome Mining. The Sino-Micro23 conference (the 2023 Annual Meeting of the Overseas Chinese Society of Microbiology), Changchun, China, 2023
26. Decoding Biological Conflicts Using Comparative Genomics. University of Washington (UW) and Howard Hughes Medical Institute (HHMI), December 10, 2022
25. Decoding biological conflicts using comparative genomics. The State Key Laboratory of Bioreactor Engineering (SKLBE), East China University of Science and Technology (ECUST), July 2022
24. Decoding biological conflicts using comparative genomics. PAG Asia 2022 conference (virtual conference), June 2022
23. Comparative genomic analysis of citrus Huanglongbing-associated bacteria. Plant Biology 2020 conference, July 2020 (virtual conference)
24. Comparative genomic analysis of Citrus Huanglongbing-associated bacteria. American Phytopathological Society (APS) annual meeting - Plant Health 2020, August 2020 (virtual conference)
22. Natural Genetic Algorithm for Protein Evolution. SLU Biology Department 1st Annual Research Retreat, November 2019
21. Discovering Codes and Origin of Genomic DNA Modifications, SLU BCB Master Program New Student Orientation, August 2019
20. Discovering Molecular Foundations of Biological Conflicts. North Carolina State University/Gene-EG Seminar Series, October 2018
19. Unraveling the evolutionary and biological contexts of polymorphic toxin Systems. ASM Microbe 2018 - American Society for Microbiology. Atlanta, June 2018
18. A common molecular foundation underlying eukaryotic species conflicts. Bioinformatics & Beers 2018, Danforth Plant Science Center, February 2018
17. Computational identification of polymorphic toxin systems in bacteria. Mini Symposium on Systems Biology Analysis of Immunity and Infectious Diseases, School of Medicine, Saint Louis University, 2017
16. Discovering codes and evolution of DNA modifications. 6th Annual St. Louis Ecology, Evolution, and Conservation (SLEEC) Retreat, Principia College, Illinois, September 17, 2016
15. Computational identification of a novel class of polymorphic toxin systems in bacteria. Pittsburgh Supercomputing Center, University of Pittsburgh, June 2016
14. A common molecular foundation underlying eukaryotic species conflicts of pathogenesis, parasitism, and symbiosis. The 1st NIH-CSSA Research Symposium, NIH, June 2016
13. A new widespread class of eukaryotic effectors: understanding domain architectures, functional diversification and their evolutionary links to transposons. NCBI Computational Biology Branch Seminar Series, Bethesda, MD, April 12, 2016
12. Understanding complex biological systems using protein domain-centric strategies. Beijing Institute of Genomics, Chinese Academy of Sciences, Beijing, China, 2015
11. Understanding complex biological systems using protein domain-centric strategies: Application to organismal defense systems, DNA modification pathways, and human disease etiology. Department of Biological Sciences, University of Maryland, Baltimore County, 2015
10. Uncovering molecular foundations of diseases by using domain-centric strategies. NCBI Computational Biology Branch Seminar Series, June 24, 2014
9. Discovery and characterization of polymorphic toxin systems. College of Life Science, Jilin University, China, 2012
8. Bacterial toxin systems: a bioinformatic perspective. Institute of Genetics and Cytology, Northeast Normal University, China, 2012

7. Dissecting polymorphic toxin systems by domain analysis and comparative genomics. NCBI Computational Biology Branch Seminar Series, 2012
6. Comparative genomic analysis finds a new widespread bacterial polymorphic toxin system. Biocuration 2012- The Conference of the International Society for Biocuration, April 2-4, 2012 Washington DC, USA
5. Discovery of a novel immunity system for diverse bacterial nucleic acid degrading toxins. NCBI Computational Biology Branch Seminar Series, 2011
4. Identification of hormone-regulated gene expression changes in neuroendocrine system. Department of Biology Seminar Series, University of Ottawa, 2009
3. Maelstrom function in a new germline piRNA pathway: evolutionary and structural insights. Department of Biology Seminar Series, University of Ottawa, 2008
2. Functional insight into Maelstrom proteins in the germline small RNA pathway: a novel domain with a derived DnaQ exonuclease fold and its lineage-specific evolutionary expansion/loss. Robert Cedergren Bioinformatics Colloquium 2007. Nov. 8-9, University of Montreal
1. Understanding estrogen action in the goldfish brain. Department of Biology Seminar Series, University of Ottawa, 2006

**Poster and contributed presentations:**

39. Tan Y, Li H, Schneider T, Shaw E, Qian S, Iyer L, Aravind L, **Zhang D**. PTSdb, a comprehensive database for prokaryotic polymorphic toxins and related systems. Lakeside Conference on Protein Toxins and Effectors 2022, Fontana-on-Geneva Lake, Wisconsin. October 2022.
38. Schneider T, Tan Y, Li H, Fisher J, **Zhang D**. Photoglobins, a distinct family of tetrapyrrole binding globins, defines a potential photosensor in prokaryotic signal transduction systems. ASM2022 General Meeting, June 2022, Washington DC.
37. Tan Y, Li H, Schneider T, Aravind L, **Zhang D**. PTSdb, a comprehensive database for prokaryotic polymorphic toxins and related systems. ASM2022 General Meeting, June 2022, Washington DC.
36. Tan Y, Yap MF, **Zhang D**. Emergence and evolution of MLS resistance: a comparative genomic analysis of the diversity and dynamics of uORF-palindrome interactions in the erm gene neighborhood. ASM2022 General Meeting, June, 2022, Washington DC.
35. Tan Y, Schneider T, Leong M, Shukla P, Chandrasekharan M, Aravind L, **Zhang D**. Identification and evolutionary diversification of novel immunoglobulin and ion channel proteins in SARS-CoV-2 and related viruses. ISCB Rocky Mountain Bioinformatics Conference 2021. December 2021.
34. Tan Y, **Zhang D**. Comparative genomics of Liberibacter pathogens associated with citrus Huanglongbing and potato Zebra Chip. The 3rd Annual Biology Research Retreat, November 2021.
33. Tan Y, Schneider T, Leong M, Shukla P, Chandrasekharan M, Aravind L, **Zhang D**. Identification and evolutionary diversification of novel immunoglobulin and ion channel proteins in SARS-CoV-2 and related viruses. ISMB/ECCB 2021 conference, July 2021.
32. Tan Y, Wang C, Schneider T, Li H, Li X, **Zhang D**. Identification of novel toxin families in citrus Huanglongbing causative Liberibacter pathogens by comparative phylogenomics. ETOX 2021 conference, June 2021.
31. Tan Y, Schneider T, Leong M, Shukla P, Chandrasekharan M, Aravind L, **Zhang D**. Identification and evolutionary diversification of novel immunoglobulin and ion channel proteins in SARS-CoV-2 and related viruses. ASM/FEMS World Microbe Forum 2021, June 2021.
30. Strege K, **Zhang D**. New Programs for Alignment Visualization and Detection of Repeat Type Toxins. SLU BCB 2019 Colloquium, Fall 2019
29. Schneider T, Tan Y, **Zhang D**. Photoglobins, a novel globin family with a potential light-sensing activity. 9th Annual St. Louis Ecology, Evolution, and Conservation (SLEEC) Retreat, Lewis and Clark Community College, Illinois, September 21, 2019



28. Tan Y, **Zhang D**. A New CR-Effector Family Underlying Fungal Meiotic Drive. 9th Annual St. Louis Ecology, Evolution, and Conservation (SLEEC) Retreat, Lewis and Clark Community College, Illinois, September 21, 2019
27. Tan Y, **Zhang D**. A New CR-Effector Family Underlying Fungal Meiotic Drive. The annual GSA Research Symposium, St. Louis University, April 2019
26. Schneider T, **Zhang D**. Revising the Model of Globin Evolution. Biology Undergraduate Research Symposium. St. Louis University, 2019 (won the top prize, the Keath Undergraduate Research Award)
25. **Zhang D**, Burroughs AM, Iyer LM, Aravind L. Comparative Genomics of Crinkler-like Proteins: Understanding Structural and Catalytic Diversity in a Key Class of Plant Toxins. 2017 APS Annual Meeting - American Phytopathological Society, San Antonio, Texas, Aug 5-9, 2017.
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