

## NSF BIOGRAPHICAL SKETCH

NAME: Zhang, Ying

POSITION TITLE & INSTITUTION: Associate Professor, University of Rhode Island

### (a) PROFESSIONAL PREPARATION

INSTITUTION	LOCATION	MAJOR / AREA OF STUDY	DEGREE (if applicable)	YEAR YYYY
Beijing Normal University	Beijing, Beijing	Computer Science	BS	2004
Sanford Burnham Prebys Medical Discovery Institute	San Diego, CA	Computational Biology	PHD	2011
Marine Biological Laboratory	Woods Hole, MA	Microbial Diversity Course	Other training	2012 - 2012
Woods Hole Oceanographic Institution	Woods Hole, MA	Microbial Ecology	Postdoctoral Fellow	2011 - 2013

### (b) APPOINTMENTS

2019 - present Associate Professor, University of Rhode Island, Kingston, RI  
2013 - 2019 Assistant Professor, University of Rhode Island, Kingston, RI  
2011 - 2013 Postdoctoral Scholar, Woods Hole Oceanographic Institution, Woods Hole, MA

### (c) PRODUCTS

#### Products Most Closely Related to the Proposed Project

1. Dufault-Thompson K, Jian H, Cheng R, Li J, Wang F, Zhang Y. A Genome-Scale Model of *Shewanella piezotolerans* Simulates Mechanisms of Metabolic Diversity and Energy Conservation. *mSystems*. 2017 March 28; 2(2):- . Available from: <https://msystems.asm.org/content/2/2/e00165-16> DOI: 10.1128/mSystems.00165-16
2. Steffensen J, Dufault-Thompson K, Zhang Y. PSAMM: A Portable System for the Analysis of Metabolic Models. *PLOS Computational Biology*. 2016; 12(2):e1004732-. Available from: <https://dx.plos.org/10.1371/journal.pcbi.1004732> DOI: 10.1371/journal.pcbi.1004732
3. Zhang Y, Sievert S. Pan-genome analyses identify lineage- and niche-specific markers of evolution and adaptation in Epsilonproteobacteria. *Frontiers in Microbiology*. 2014 March 19; 5:-. Available from: <http://journal.frontiersin.org/article/10.3389/fmicb.2014.00110/abstract> DOI: 10.3389/fmicb.2014.00110
4. Waite D, Vanwonterghem I, Rinke C, Parks D, Zhang Y, Takai K, Sievert S, Simon J, Campbell B, Hanson T, Woyke T, Klotz M, Hugenholtz P. Comparative Genomic Analysis of the Class Epsilonproteobacteria and Proposed Reclassification to Epsilonbacteraeota (phyl. nov.). *Frontiers in Microbiology*. 2017 April 24; 8:-. Available from: <http://journal.frontiersin.org/article/10.3389/fmicb.2017.00682/full> DOI: 10.3389/fmicb.2017.00682
5. Pimentel Z, Zhang Y. Evolution of the Natural Transformation Protein, ComEC, in Bacteria. *Frontiers in Microbiology*. 2018 December 12; 9:-. Available from: <https://www.frontiersin.org/article/10.3389/fmicb.2018.02980/full> DOI: 10.3389/fmicb.2018.02980

## Other Significant Products, Whether or Not Related to the Proposed Project

1. Zhang Y, Thiele I, Weekes D, Li Z, Jaroszewski L, Ginalski K, Deacon A, Wooley J, Lesley S, Wilson I, Palsson B, Osterman A, Godzik A. Three-Dimensional Structural View of the Central Metabolic Network of *Thermotoga maritima*. *Science*. 2009 September 17; 325(5947):1544-1549. Available from: <https://www.sciencemag.org/lookup/doi/10.1126/science.1174671> DOI: 10.1126/science.1174671
2. Mokszycki M, Leatham-Jensen M, Steffensen J, Zhang Y, Krogfelt K, Caldwell M, Conway T, Cohen P. A Simple In Vitro Gut Model for Studying the Interaction between *Escherichia coli* and the Intestinal Commensal Microbiota in Cecal Mucus. *Applied and Environmental Microbiology*. 2018 November 30; 84(24):- . Available from: <http://aem.asm.org/lookup/doi/10.1128/AEM.02166-18> DOI: 10.1128/AEM.02166-18
3. Steffensen J, Dufault-Thompson K, Zhang Y. FindPrimaryPairs: An efficient algorithm for predicting element-transferring reactant/product pairs in metabolic networks. *PLOS ONE*. 2018; 13(2):e0192891-. Available from: <https://dx.plos.org/10.1371/journal.pone.0192891> DOI: 10.1371/journal.pone.0192891
4. Fernández Robledo JA, Yadavalli R, Allam B, Pales Espinosa E, Gerdol M, Greco S, Stevick RJ, Gómez-Chiarri M, Zhang Y, Heil CA, Tracy AN, Bishop-Bailey D, Metzger MJ. From the raw bar to the bench: Bivalves as models for human health. *Dev Comp Immunol*. 2019 Mar;92:260-282. PubMed PMID: [30503358](https://pubmed.ncbi.nlm.nih.gov/30503358/); PubMed Central PMCID: [PMC6511260](https://pubmed.ncbi.nlm.nih.gov/PMC6511260/).
5. Williams L, Cullen N, DeGiorgis J, Martinez K, Mellone J, Oser M, Wang J, Zhang Y. Variation in genome content and predatory phenotypes between *Bdellovibrio* sp. NC01 isolated from soil and *B. bacteriovorus* type strain HD100. *Microbiology*. 2019 December 01; 165(12):1315-1330. Available from: <https://qa.microbiologyresearch.org/content/journal/micro/10.1099/mic.0.000861> DOI: 10.1099/mic.0.000861

### (d) SYNERGISTIC ACTIVITIES

1. Constructed open-source software for the annotation and analysis of genome-scale metabolic models (<https://zhanglab.github.io/psamm/>) and a model repositories for the community sharing of manually curated models (<https://github.com/zhanglab/psamm-model-collection>). All the model edits are tracked using the Git version tracking functions, which is enabled through applying the YAML-based model format.
2. Software development for the rapid metagenomic binning and read analysis using deep learning. The computational pipeline under development is accessible via the open source GitHub repository, <https://github.com/zhanglab/ReadsClassification>.
3. Faculty mentor to undergraduate research fellows of underrepresented backgrounds from the NIH-funded Maximizing Access to Research Careers (MARC) Undergraduate Student Training in Academic Research (U-STAR) program.
4. NMDC Champion of the National Microbiome Data Collaborative. Promote sustainable data discovery using the FAIR (findable, accessible, interoperable, and reusable) principles.