

Zhenglin Du

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RESEARCH INTERESTS

I am interested in developing algorithms and using computational skills for multi-omics and phenotypic data to understand the intrinsic nature of the genomics and biological processes, especially in the field of multi-omics data integration and curation on precision medicine and comparative genomics studies. My recent research focuses on the study of genetic variations of the Chinese populations and *de novo* assembly of genomes.

EDUCATION

PhD in Biochemistry & Molecular Biology, China Agricultural University, China, 2002-2007

BS in Biology, China Agricultural University, China, 1998-2002

WORKING EXPERIENCE

Senior Engineer, Beijing Institute of Genomics, CAS, Beijing, December 2011 –Present

Engineer, Beijing Institute of Genomics, CAS, Beijing, June 2008 –November 2011

Bioinformatician, Beijing Genomics Institute, Shenzhen, July 2007 –May 2008

MAIN PUBLICATIONS * denotes co-first author; ^ denotes corresponding author

1. **Zhenglin Du** as co-first author in BIG Data Center Members (#), Data Center Members, Database Resources of the BIG Data Center in 2018, **Nucleic Acids Res**, 2018, 46(D1): D14-D20.
2. Yan, H., Xie, JB., ... & **^Du, Z.**, **^Wang, ET.**, **^Chen, WF.** (2017). Evolutionarily Conserved nodE, nodO, TISS, and Hydrogenase System in Rhizobia of Astragalus membranaceus and Caragana intermedia. **Frontiers in Microbiology**.
3. *Li, Y., *Zhang, Q., ***Du, Z.**, Lu, Z., Liu, S., Zhang, L., ... & Fang, X. (2016). MicroRNA 200a inhibits erythroid differentiation by targeting PDCD4 and THRB. **British Journal of Haematology**.
4. *Yu, L., *Wang, G. D., *Ruan, J., *Chen, Y. B., *Yang, C. P., *Cao, X., *Wu, H., ***Du, Z.**, ... & Yang, J. (2016). Genomic analysis of snub-nosed monkeys (*Rhinopithecus*) identifies genes and processes related to high-altitude adaptation. **Nature Genetics**.
5. Xie J, Shi H, **Du Z**, Wang T, Liu X, Chen S: Comparative genomic and functional analysis reveal conservation of plant growth promoting traits in *Paenibacillus polymyxa* and its closely related species. **Scientific reports** 2016, 6:21329.
6. Li BQ, Zong YY, **Du Z**, Chen, Y., Zhang, Z., Qin, G., ... & Tian, S. (2015). Genomic characterization reveals insights into patulin biosynthesis and pathogenicity in *Penicillium* species. **Molecular Plant-Microbe Interactions**, (ja).
7. Huang Y, Li Y, Burt DW, Chen H, Zhang Y, Qian W, Kim H, Gan S, Zhao Y, Li J, Yi K, Feng H, Zhu P, Li B, Liu Q, Fairley S, Magor KE, **Du Z**, et al. (2013). The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. **Nature genetics**, 45(7), 776-783.
8. Wang J, Wang W, Li R, Li Y, Tian G, Goodman L, Fan W, Zhang J, Li J, Zhang J, Guo Y, Feng B, Li H, Lu Y, Fang X, Liang H, **Du Z**, et al. (2008). The diploid genome sequence of an Asian individual. **Nature**, 456(7218), 60-65.