

Guangchuang Yu

Post-doctoral Fellow

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EDUCATION

<i>The University of Hong Kong,</i>	Ph.D. Evolution Study of Influenza A virus	2017
<i>Anhui Medical University,</i>	M.S. Biochemistry and Molecular Biology	2009
<i>South China Agricultural University,</i>	B.S. Biotechnology	2005
<i>Institut Pasteur, Paris,</i>	Train the Trainers	2015

CERTIFICATE

Certificate of Teaching and Learning in Higher Education, Centre for Enhancement of Teaching and Learning, The University of Hong Kong 2015

EMPLOYMENT

State Key Laboratory of Infectious Diseases, School of Public Health, The University of Hong Kong:

Post-doctoral Fellow 2017

College of Life Science and Technology, Jinan University:

Bioinformatician 2009–2013

TEACHING

Student Helper, The University of Hong Kong 2013–2014

BIOL6001 Presentation Skills and Research Seminars in Biological Sciences

Lecturer, Jinan University 2011–2012

Functional Proteomics

AWARDS

2013–2017 *Postgraduate Studentships.* The University of Hong Kong.

2012 *Best paper of the year 2010.* Journal of Integrated OMICS.

GRANTS

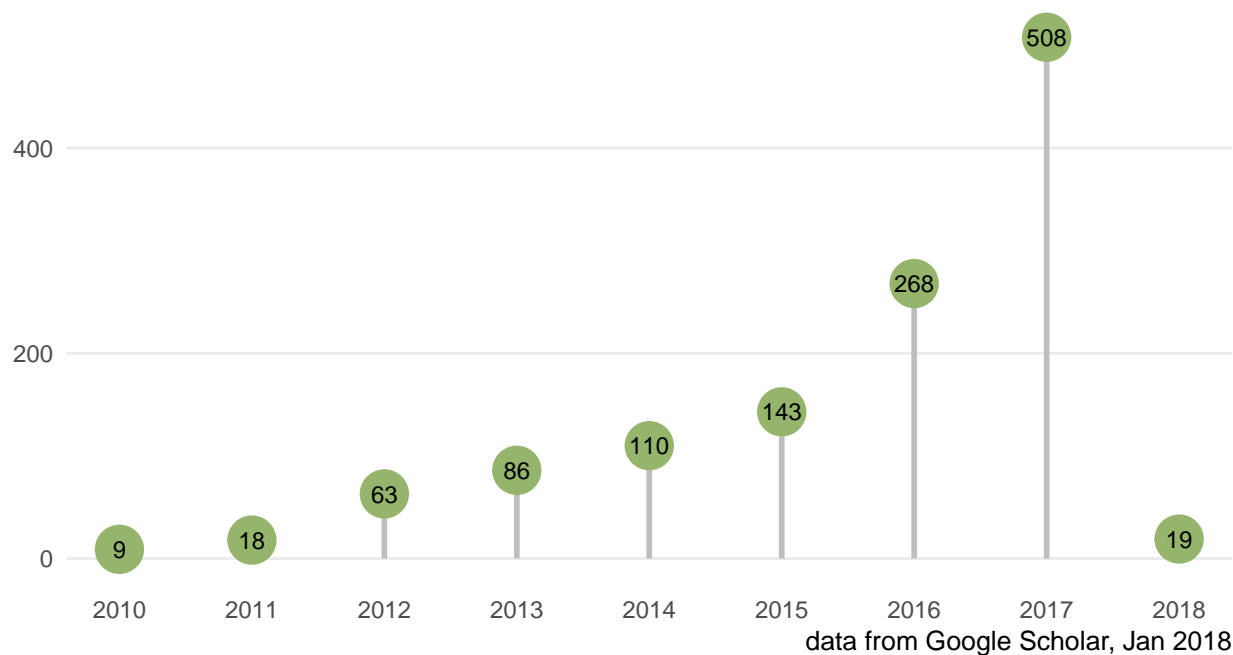
2013 (completed) *PI,* Investigate functions of hnRNPK in regulating cytokinesis of human lung cancer cell. Fundamental Research Funds for the Central Universities (21613414), CNY 100,000

2011 (completed) *PI,* Dynamic proteomic analysis of HeLA cell cycle, Fundamental Research Funds for the Central Universities (21611303), CNY 20,000

PUBLICATIONS

Journal Articles

Citation = 1255, H-index = 14, I10-index = 18



🔥 : ESI Hot Paper (X2)

🏆 : ESI Highly Cited Paper (X5)

Methods in Ecology and Evolution (X1, rank 11 in *Environment Ecology*, IF = 5.708)

Bioinformatics (X3, rank 4 in *Computer Science*, IF = 7.307)

([†] indicates equal contribution, * indicates corresponding)

1. G Yu, DK Smith, H Zhu, Y Guan, TTY Lam*. [ggtree: an R package for visualization and annotation of phylogenetic trees with their covariates and other associated data](#). *Methods in Ecology and Evolution*. 2017, 8(1):28-36. 🔥🏆 cited by 65
2. G Yu, QY He*. [ReactomePA: an R/Bioconductor package for reactome pathway analysis and visualization](#). *Molecular BioSystems*. 2016, 12(2):477-479. 🏆 cited by 50
3. G Yu*, LG Wang, QY He*. [ChIPseeker: an R/Bioconductor package for ChIP peak annotation, comparison and visualization](#). *Bioinformatics*. 2015, 31(14):2382-2383. 🔥🏆 cited by 98
4. G Yu*, LG Wang, GR Yan, QY He*. [DOSE: an R/Bioconductor package for Disease Ontology Semantic and Enrichment analysis](#). *Bioinformatics*. 2015, 31(4):608-609. cited by 55
5. G Yu[†], LG Wang[†], XH Meng, QY He*. [LXtoo: an integrated live Linux distribution for the bioinformatics community](#). *BMC Research Notes*. 2012, 5(1):360.
6. G Yu, LG Wang, Y Han, QY He*. [clusterProfiler: an R package for comparing biological themes among gene clusters](#). *OMICS: A Journal of Integrative Biology*. 2012, 16(5):284-287. 🏆 cited by 366
7. G Yu, QY He*. [Functional similarity analysis of human virus-encoded miRNAs](#). *Journal of Clinical Bioinformatics*. 2011, 1(1):15.
8. G Yu[†], CL Xiao[†], X Bo, CH Lu, Y Qin, S Zhan, QY He*. [A new method for measuring functional similarity of microRNAs](#). *Journal of Integrated OMICS*. 2011, 1(1):49-54.
9. G Yu[†], CL Xiao[†], CH Lu[†], HT Jia, F Ge, W Wang, XF Yin, HL Jia, JX He*, QY He*. [Phosphoproteome profile of human lung cancer cell line A549](#). *Molecular BioSystems*. 2011, 7(2):472-479.

10. G Yu[†], F Li[†], Y Qin, X Bo^{*}, Y Wu, S Wang^{*}. [GOSemSim: an R package for measuring semantic similarity among GO terms and gene products](#). *Bioinformatics*. 2010, 26(7):976-978. 🏆 cited by 313
11. X Sun[†], G Yu[†], Q Xu, N Li, C Xiao, X Yin, K Cao, J Han, QY He^{*}. [Putative cobalt- and nickel-binding proteins and motifs in *Streptococcus pneumoniae*](#). *Metallomics*. 2013, 5(7):928-935.
12. YY Zhu[†], G Yu[†], Y Zhang, Z Xu, YQ Huang, GR Yan^{*}, QY He^{*}. [A novel andrographolide derivative AL-1 exerts its cytotoxicity on K562 cells through a ROS-dependent mechanism](#). *Proteomics*, 2013, 13(1):169-178.
13. XY Yang, K He, G Du, X Wu, G Yu, Y Pan, G Zhang^{*}, X Sun^{*}, QY He^{*}. [Integrated Translatomics with Proteomics to Identify Novel Iron-Transporting Proteins in *Streptococcus pneumoniae*](#). *Frontiers in Microbiology*. 2016, 7:78.
14. PY Huang, CCD Lee, CH Yip, CL Cheung, G Yu, TTY Lam, DK Smith, H Zhu^{*}, Y Guan^{*}. [Genetic characterization of highly pathogenic H5 influenza viruses from poultry in Taiwan, 2015](#). *Infection, Genetics and Evolution*. 2016, 38:96-100.
15. SH Xu, JZ Huang, ML Xu, G Yu, XF Yin, D Chen^{*}, GR Yan^{*}. [ACK1 Promotes Gastric Cancer Epithelial-Mesenchymal Transition and Metastasis through AKT-POU2F1-ECD Signaling](#). *The Journal of Pathology*. 2015, 236(2):175-185.
16. Z Guo, J Han, XY Yang, K Cao, K He, G Du, G Zeng, L Zhang, G Yu, Z Sun, QY He^{*}, X Sun^{*}. [Proteomic analysis on the copper resistance of *Streptococcus pneumoniae*](#). *Metallomics*. 2015, 7(3):448-454.
17. XY Yang, L Zhang, J Liu, N Li, G Yu, K Cao, J Han, G Zeng, Y Pan, X Sun^{*}, QY He^{*}. [Proteomic analysis on the antibacterial activity of a Ru\(II\) complex against *Streptococcus pneumoniae*](#). *Journal of Proteomics*. 2015, 115:107-116.
18. N Wang[†], J Zhang[†], L Zhang, XY Yang, N Li, G Yu, J Han, K Cao, Z Guo, X Sun^{*}, QY He^{*}. [Proteomic analysis of putative heme-binding proteins in *Streptococcus pyogenes*](#). *Metallomics*. 2014, 6(8):1451-1459.
19. H Sun^{*}, J Weng, G Yu, RH Massawe. [A DNA-Based Semantic Fusion Model for Remote Sensing Data](#). *PLoS One*. 2013, 8(10):e77090.
20. GR Yan[†], Z Tan[†], Y Wang, ML Xu, G Yu, Y Li^{*}, QY He^{*}. [Quantitative Proteomics Characterization on the Anti-tumor Effects of Isodexyephantopin against Nasopharyngeal Carcinoma](#). *Proteomics*. 2013, 13(21):3222-3232.
21. J Li, X Lu, Q Wu, G Yu, Z Xu, L Qiu, Z Pei, Y Lin, J Pang^{*}. [Design, SAR, angiogenic activities evaluation and pro-angiogenic mechanism of new marine cyclopeptide analogs](#). *Current Medicinal Chemistry*. 2013, 20(9):1183-1194.
22. Y Han, G Yu, H Sarioglu, A Caballero-Martinez, F Schlott, M Ueffing, H Haase, C Peschel, AM Krackhardt^{*}. [Proteomic investigation of the interactome of FMNL1 in hematopoietic cells unveils a role in calcium-dependent membrane plasticity](#). *Journal of Proteomics*. 2013, 78:72-82.
23. Y Ma[†], J Yang[†], X Fan[†], H Zhao, W Hu, Z Li, G Yu, X Ding, J Wang, X Bo, X Zheng, Z Zhou^{*}, S Wang^{*}. [Cellular MicroRNA let-7c Inhibits M1 Protein Expression of the H1N1 Influenza A Virus in Infected Human Lung Epithelial Cells](#). *Journal of Cellular and Molecular Medicine*. 2012, 16(10):2539-2546.
24. GR Yan[†], FY Zhou[†], BL Dang, Y Zhang, G Yu, X Liu, QY He^{*}. [Genistein-induced mitotic arrest of gastric cancer cells by downregulating KIF20A, a proteomics study](#). *Proteomics*. 2012, 12(14):2391-2399.
25. X Sun[†], XY Yang[†], XF Yin, G Yu, CL Xiao, X He, QY He^{*}. [Proteomic Analysis of Membrane Proteins from *Streptococcus pneumoniae* with Multiple Separation Methods plus High Accuracy Mass Spectrometry](#). *OMICS: A Journal of Integrative Biology*. 2011, 15(10):683-694.

Books

G Yu, "Bioinformatics II", in "Functional Protein Research", 385-425, Qing-Yu He (Eds), *Science Press*, 2012. (China's Twelfth Five-Year National Important Books Project, in Chinese)

CONFERENCE PROCEEDINGS

Presentations

1. **ggtree for tree visualization & annotation** (invited), Phylogenetic tree visualization workshop/hackathon, The Field Museum of Natural History, Chicago, May. 2017
2. **Computational Methods in Ecology and Evolution**, The Second International Workshop on Environmental Microbiomes, Sun Yat-sen University, Guangzhou, April. 2017
3. **ggtree for visualization and annotation of phylogenetic trees** (invited), The 9th China-R Conference, Renmin University of China, Beijing, May. 2016

Posters

1. **ggtree: a programming package for complex data integration and analysis in phylogeny to identify potential genetic markers of influenza a virus that determine interspecies transmission**, Scientific Advisory Board (SAB) Meeting for the Theme-based Research Scheme on Viral, Host and Environmental Determinants of Influenza Virus Transmission and Pathogenesis, The University of Hong Kong, Hong Kong, Jun. 2017
2. **Phylogeny-guided genome assembly method for short read nucleotide sequences from co-infecting influenza A viruses**, Options IX for the control of influenza, International Society for Influenza and other Respiratory Virus Disease, Chicago, Aug. 2016
3. **ggtree: an R package for visualization and annotation of phylogenetic tree with different types of meta-data**, The 20th Research Postgraduate Symposium, The University of Hong Kong, Hong Kong, Dec. 2015

PUBLIC MEDIA

“Plotting trees + data” lecture by Guangchuang Yu. <https://youtu.be/tqspAXMoUQE>

PROFESSIONAL AFFILIATIONS

- **Member**, International Society for influenza and other Respiratory Virus Disease 2016
- **Steering Committee**, International Network for Data Analysis, Institut Pasteur 2015
- **Visiting student**, Beijing Institute of Radiation Medicine 2005-2009

PROFESSIONAL SERVICES

Associate Editor

- Journal of Integrated OMICS, 2011-present

Reviewer

- Bioinformatics
- BMC Bioinformatics
- Computational Biology and Chemistry
- Current Bioinformatics
- Gastroenterology Research and Practice
- Molecular BioSystems
- R Journal

SOFTWARE DEVELOPMENT

R ranking: ranked 51/68825 worldwide by [Git Awards](#)

- [badger](#): Badge for R Package
- [dlstats](#): Download Stats of R Packages
- [emojifont](#): Emoji and Font Awesome in Graphics
- [ggimage](#): Use Image in 'ggplot2'
- [meme](#): Create Meme
- [rvcheck](#): R/Package Version Check
- [scatterpie](#): Scatter Pie Plot
- [shadowtext](#): Shadow Text Grob and Layer
- [ChIPseeker](#): ChIPseeker for ChIP peak Annotation, Comparison, and Visualization
- [clusterProfiler](#): statistical analysis and visualization of functional profiles for genes and gene clusters
- [DOSE](#): Disease Ontology Semantic and Enrichment analysis
- [ggtree](#): an R package for visualization and annotation of phylogenetic trees with their covariates and other associated data
- [GOSemSim](#): GO-terms Semantic Similarity Measures
- [meshes](#): MeSH Enrichment and Semantic analyses
- [ReactomePA](#): Reactome Pathway Analysis
- [seqcombo](#): Visualization Tool for Sequence Recombination and Reassortment
- [tidytrees](#): A Tidy Tool for Phylogenetic Tree Data Manipulation
- [TIPars](#): Taxa Insertion by Parsimony
- [treeio](#): Base Classes and Functions for Phylogenetic Tree Input and Output

Contributions to open source libraries

- [cowsay](#): Messages, Warnings, Strings with Ascii Animals
- [fitting](#): Fit Different Regression Lines and Show Equation Parameters
- [kableExtra](#): Construct Complex Table with 'kable' and Pipe Syntax
- [MSnbase](#): Base Functions and Classes for Mass Spectrometry and Proteomics
- [scholar](#): Analyse Citation Data from Google Scholar