

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

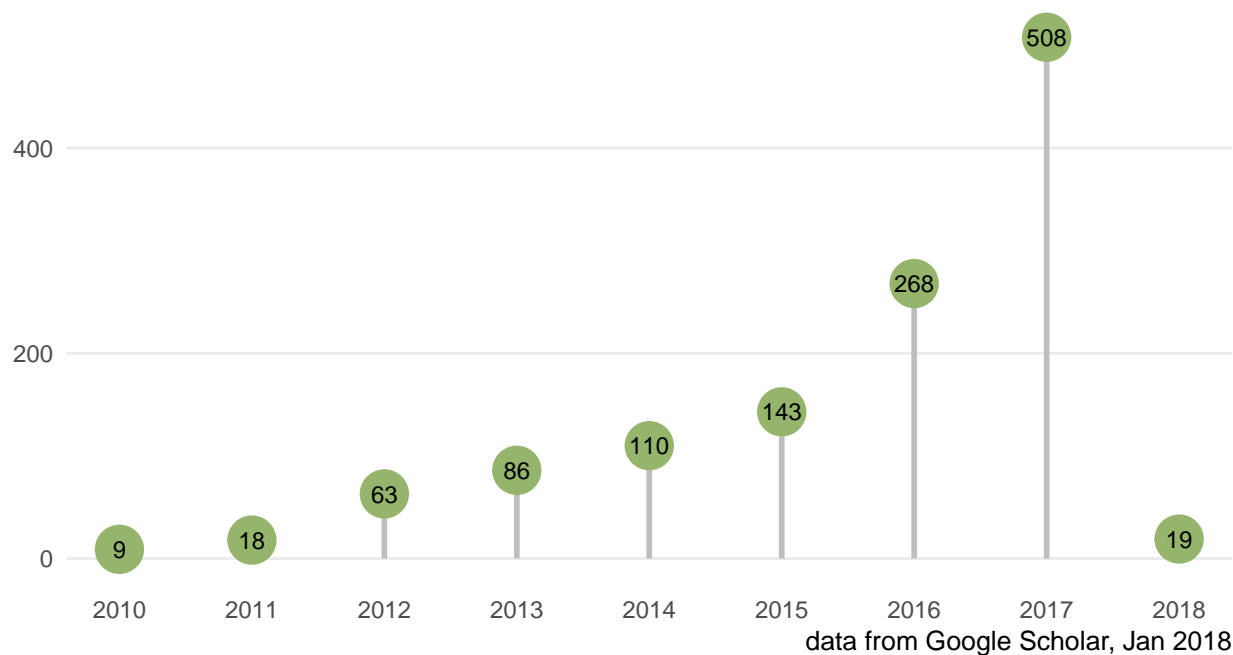
2013 (completed) *PI*, Investigate functions of hnRNPK in regulating cytokinesis of human lung cancer cell. Fundamental Research Funds for the Central Universities (21613414), CNY 100,000

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