Curriculum Vitae

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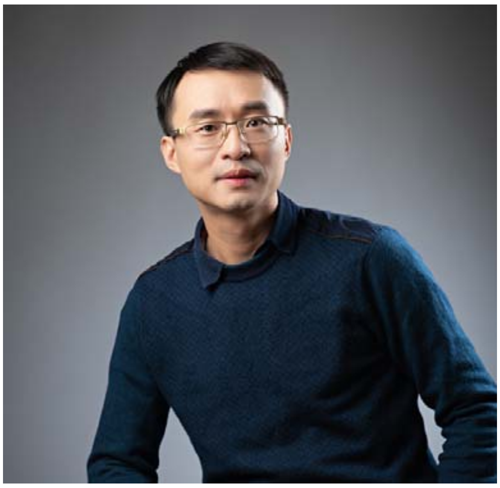

[1] Personal information

Yu Xue（薛宇）, Ph.D.,

Professor (from July, 2009),
Principle Investigator,
Department of Bioinformatics & Systems Biology（生物信息与系统生物学系）,
College of Life Science and Technology（生命科学与技术学院）,
Huazhong University of Science and Technology（华中科技大学）,
Room 618, Eastern Campus of HUST,
No. 1037, Luoyu Road,
Wuhan, 430074, Hubei, P.R.China

Phone: +86-27-87793903
Fax: +86-27-87793172
Email: xueyu@hust.edu.cn; xueyuhust@gmail.com
Personal Website: http://www.biocuckoo.org/
ResearcherID: http://www.researcherid.com/rid/G-5929-2011
Google Scholar: http://scholar.google.co.uk/citations?user=ToryLMcAAAAJ&hl=en
Sciencenet's Blog: http://blog.sciencenet.cn/u/DaCaiNiao

[2] Keywords

Post-translational modification, bioinformatics, phosphorylation, sumoylation, methylation, acetylation, phosphoproteomics, Group-based prediction system

[3] Education

1998.09 – 2002.07 University of Science and Technology of China, undergraduate
2002.09 – 2007.01 University of Science and Technology of China, postgraduate, Ph.D. program

[4] Research experience

2007.01 – 2007.07 Research Assistant, Life Science School, University of Science and Technology of China

2007.07 – 2009.06 Associate Professor, Department of Systems Biology, Life Science School, University of Science and Technology of China

2009.07 – present Professor, Biomedical Engineering, College of Life Science and Technology, Huazhong University of Science and Technology

[5] Scientific titles and degrees

The 1st International Conference on Translational Biomedical Informatics (ICTBI), Dec. 8-10, 2012, co-chair

Reviewer for: Nucleic Acids Research; Journal of Proteome Research; Briefings in Bioinformatics; BMC Bioinformatics; PLoS ONE, Proteins: Structure, Function, and Bioinformatics; Journal of Molecular Modeling; Database; Transactions on Computational Biology and Bioinformatics; Cell Research; BMC Genomics; Scientific Reports; BBA - Proteins and Proteomics; Cellular & Molecular Immunology; Genomics, Proteomics & Bioinformatics; Protein & Cell

Ph.D., 2007.01, Life Science School, University of Science and Technology of China

B.E., 2003.07, Computer Science and Technology department, University of Science and Technology of China

B.E., 2002.07, Polymer Science and Technology department, University of Science and Technology of China

[6] Scientific Disciplines

- Computational studies of Post-translational modifications (PTMs)
- Bioinformatics & Systems Biology
- Comparative Proteomics

- Network analysis of PTMs

[7] Honors and Awards

1. May 2016, excellent oral presentation award for young scholars, CNHUPO, China
2. October 2015, “Grand Challenges 2015 – Young Scientists”, Bill & Melinda Gates Foundation & MOST of China
3. 2014, supported by the National Program for Support of Top-Notch Young Professionals, China
4. January 2013, “The Fouth SCOPUS Young Researcher Award”, China
5. July 2009, excellent oral presentation award for young scholars, CNHUPO, China
6. May 2008, Fifty most excellent Ph.D. dissertations of Chinese Academy of Sciences (CAS).
7. June 2006, Travel Fellowship Award $1000, 14th Annual International Conference on Intelligent Systems for Molecular Biology.
8. November 2006, Hong Kong “Qiu Shi” Scholarship for graduates.
9. October 2005, “Dong Gang” Scholarship for graduates.
10. June 2005, excellent article of graduates in USTC (Second class).

[8] Publications – journals (2004-)

1. Fengfeng Zhou*, **Yu Xue***, Guoliang Chen, Xuebiao Yao. (2004) GPS: a novel group-based phosphorylation predicting and scoring method. Biochem. *Biophys. Res. Commun.*, 325, 1443-1448.
2. Fengfeng Zhou*, **Yu Xue***, Hualei Lu, Guoliang Chen, Xuebiao Yao. (2005) A genome-wide analysis of sumoylation-related biological processes and functions in human nucleus. *FEBS Lett.*, 579, 3369-3375.
3. **Yu Xue***, Fengfeng Zhou*, Minjie Zhu, Kashif Ahmed, Guoliang Chen, Xuebiao Yao. (2005) GPS: a comprehensive www server for phosphorylation sites prediction. *Nucleic. Acids Res.*, 33, W184-W187.
4. Fengfeng Zhou*, **Yu Xue***, Xuebiao Yao, and Ying Xu. (2006) CSS-Palm: palmitoylation site prediction with a clustering and scoring strategy (CSS). *Bioinformatics*, 22, 894 – 896.
5. **Yu Xue***, Ao Li*, Lirong Wang, Huanqing Feng and Xuebiao Yao. (2006) PPSP: Prediction of PK-Specific Phosphorylation Site with Bayesian Decision Theory. *BMC Bioinformatics*, 7, 163.
6. **Yu Xue***, Fengfeng Zhou*, Chuanhai Fu, Ying Xu and Xuebiao Yao. (2006) SUMOsp: a web server for sumoylation site prediction. *Nucleic. Acids Res.*,

34, W254-W257.

7. Hu Chen*, **Yu Xue***, Ni Huang, Xuebiao Yao and Zhirong Sun. MeMo: (2006) A web tool for prediction of protein methylation modifications. *Nucleic. Acids Res.*, 34, W249-W253.
8. **Yu Xue***, Dan Liu*, Chuanhai Fu, Zhen Dou, Qing Zhou, Xiaowei Tang, and Xuebiao Yao. (2006) A novel genome-wide full-length kinesin prediction analysis reveals additional mammalian kinesins. *Chinese Science Bulletin*, 51(15), 1836- 1847.
9. Fengfeng Zhou*, **Yu Xue***, Xuebiao Yao, and Ying Xu. (2006) A general user interface for prediction servers of proteins' post-translational modification sites. *Nature Protocols*, 1(3), 1318-1321.
10. Ao Li*, **Yu Xue***, Changjiang Jin, Minghui Wang, and Xuebiao Yao. (2006) Prediction of Nε-acetylation on internal lysines implemented in Bayesian Discriminant Method. *Biochem. Biophys. Res. Commun.*, 350(4), 818-824.
11. **Yu Xue***, Hu Chen*, Changjiang Jin, Zhirong Sun and Xuebiao Yao. (2006) NBA-Palm: prediction of palmitoylation site implemented in Naive Bayes algorithm. *BMC Bioinformatics*, 7, 458.
12. Changjiang Jin, Xin Cai, Hui Ma, **Yu Xue**, Jianhui Yao and Xuebiao Yao. (2007) An efficient site-directed mutagenesis method for ColE1-type ori plasmid. *Analytical Biochemistry*, 363 (1), 151-153.
13. Yu J, Lan J, Zhu Y, Li X, Lai X, **Xue Y**, Jin C, Huang H. (2008) The E3 ubiquitin ligase HECTD3 regulates ubiquitination and degradation of Tara. *Biochem Biophys Res Commun*. 367(4):805-12.
14. Cheng Z, Ke Y, Ding X, Wang F, Wang H, Ahmed K, Liu Z, Xu Y, Aikhionbare F, Yan H, Liu J, **Xue Y**, Powell M, Liang S, Reddy SE, Hu R, Huang H, Jin C, Yao X. (2008) Functional characterization of TIP60 sumoylation in UV-irradiated DNA damage response. *Oncogene*. 27(7):931-41.
15. Yu J, Lan J, Zhu Y, Li X, Lai X, **Xue Y**, Jin C, Huang H. (2008) The E3 ubiquitin ligase HECTD3 regulates ubiquitination and degradation of Tara. *Biochem Biophys Res Commun*. 367(4):805-12.
16. Gao X, Jin C, **Xue Y¶**, Yao X¶. (2008) Computational analyses of TBC protein family in eukaryotes. *Protein Pept Lett*. 15:505-9.
17. **Xue Y***, Ren J*, Gao X, Jin C, Wen L, Yao X. (2008) GPS 2.0, a tool to predict kinase-specific phosphorylation sites in hierarchy. *Mol Cell Proteomics*. 7(9):1598-608.
18. Ren J, Wen L, Gao X, Jin C, **Xue Y¶**, Yao X¶. (2008) CSS-Palm 2.0: an updated software for palmitoylation sites prediction. *Protein Eng Des Sel*. 21(11):639-44.
19. Gao X, Jin C, Ren J, Yao X, **Xue Y†**. (2008) Proteome-wide prediction of PKA phosphorylation sites in eukaryotic kingdom. *Genomics*. 92(6):457-63.
20. Ren J, Wen L, Gao X, Jin C, **Xue Y¶**, Yao X¶. (2009) DOG 1.0: Illustrator of Protein Domain Structures. *Cell Research*. 19:271-3.
21. Xu Y, Wang Z, Zhao Y, **Xue Y¶**. (2008) A New Alignment Algorithm to

Identify Definitions Corresponding to Abbreviations in Biomedical Text. WKDD 2008, 118-124.

22. Zhao Y, Xu Y, Wang Z, Jin C, Gao X, **Xue Y¶**, Yao X¶. (2008) Proteome-Wide Analysis of Amino Acid Absence in Composition and Plasticity. ICIC 2008, *LNCS* 5226, 167-178.
23. Xu Y¶, Wang Z, Lei Y, Zhao Y, **Xue Y¶**. (2008) MBA: a literature Mining system for extracting Biomedical abbreviations. *BMC Bioinformatics*. 10:14.
24. Han G, Ye M, Jiang X, Chen R, Ren J, **Xue Y**, Wang F, Song C, Yao X, Zou H. (2009) Comprehensive and reliable phosphorylation site mapping of individual phosphoproteins by combination of multiple stage mass spectrometric analysis with a target-decoy database search. *Analytical Chemistry*, 81:5794-805.
25. Ren J, Gao X, Jin C, Zhu M, Wang X, Shaw A, Wen L, Yao X¶, **Xue Y¶**. (2009) Systematic study of protein sumoylation: Development of a site-specific predictor of SUMOsp 2.0. *Proteomics*, 9:3409-3412.
26. Ren J, Liu Z, Gao X, Jin C, Ye M, Zou H, Wen L, Zhang Z, **Xue Y¶**, Yao X¶. (2010) MiCroKit 3.0: an integrated database of midbody, centrosome and kinetochore. *Nucleic Acids Research*, 38:D155-160.
27. Ren J, Jiang C, Gao X, Liu Z, Yuan Z, Jin C, Wen L, Zhang Z¶, **Xue Y¶**, Yao X¶. (2010) PhosSNP for systematic analysis of genetic polymorphisms that influence protein phosphorylation. *Molecular & Cellular Proteomics*, 9:623-34.
28. **Xue Y¶**, Liu Z, Gao X, Jin C, Wen L, Yao X, Jian Ren¶. (2010) GPS-SNO: Computational prediction of protein S-nitrosylation sites with a modified GPS algorithm. *PLoS ONE*, 5:e11290.
29. **Xue Y¶**, Gao X, Cao J, Liu Z, Jin C, Wen L, Yao X, Ren J¶. (2010) A summary of computational resources for protein phosphorylation. *Current Protein and Peptide Science*, 11:485-96. (Review)
30. Liu Z, Cao J, Gao X, Zhou Y, Wen L, Yang X, Yao X, Ren J¶, **Xue Y¶**. (2011) CPLA 1.0: an integrated database of protein lysine acetylation. *Nucleic Acids Research*, 39:D1029-34.
31. **Xue Y¶**, Liu Z, Cao J, Ma Q, Gao X, Wang Q, Jin C, Zhou Y, Wen L, Ren J¶. (2011) GPS 2.1: enhanced prediction of kinase-specific phosphorylation sites with an algorithm of motif length selection. *Protein Eng Des Sel*. 24:255-60.
32. Zhang Y, Yang Y, Zhang H, Jiang X, Xu B, **Xue Y**, Cao Y, Zhai Q, Zhai Y, Xu M, Cooke HJ, Shi Q. (2011) Prediction of novel pre-microRNAs with high accuracy through boosting and SVM. *Bioinformatics*. 27:1436-7.
33. Liu Z, Cao J, Gao X, Ma Q, Ren J¶, **Xue Y¶**. (2011) GPS-CCD: a novel computational program for the prediction of calpain cleavage sites. *PLoS One*. 6:e19001.
34. Liu Z, Cao J, Ma Q, Gao X, Ren J¶, **Xue Y¶**. (2011) GPS-YNO2: computational prediction of tyrosine nitration sites in proteins. *Mol Biosyst*. 7:1197-204.

35. Ren J, Gao X, Liu Z, Cao J, Ma Q, **Xue Y†**. (2011) Computational analysis of phosphoproteomics: progresses and perspectives. *Curr Protein Pept Sci*. 12:591-601.
36. Liu Z, Ma Q, Cao J, Gao X, Ren J¶, **Xue Y¶**. (2011) GPS-PUP: computational prediction of pupylation sites in prokaryotic proteins. *Mol Biosyst*. 7:2737-40.
37. Liu Z, Yuan F, Ren J, Cao J, Zhou Y, Yang Q¶, **Xue Y¶**. (2012) GPS-ARM: computational analysis of the APC/C recognition motif by predicting D-boxes and KEN-boxes. *PLoS One*. 7:e34370.
38. Cai R, Liu Z, Ren J, Ma C, Gao T, Zhou Y, Yang Q¶, **Xue Y¶**. (2012) GPS-MBA: computational analysis of MHC class II epitopes in type 1 diabetes. *PLoS One*. 7:e33884.
39. Zhang Y, Xu B, Yang Y, Ban R, Zhang H, Jiang X, Cooke HJ, **Xue Y¶**, Shi Q¶. (2012) CPSS: a computational platform for the analysis of small RNA deep sequencing data. *Bioinformatics*. 2012, 28:1925-7.
40. Song C, Ye M, Liu Z, Cheng H, Jiang X, Han G, Songyang Z, Tan Y, Wang H, Ren J¶, **Xue Y¶**, Zou H¶. (2012) Systematic analysis of protein phosphorylation networks from phosphoproteomic data. *Mol Cell Proteomics*. 11(10):1070-83.
41. Gao T, Liu Z, Wang Y, Cheng H, Yang Q, Guo A, Ren J, **Xue Y†**. (2013) UUCD: a family-based database of ubiquitin and ubiquitin-like conjugation. *Nucleic Acids Res*. 41:D445-51.
42. Liu Z, Ren J, Cao J, He J, Yao X, Jin C¶, **Xue Y¶**. (2013) Systematic analysis of the Plk-mediated phosphoregulation in eukaryotes. *Brief Bioinform*. 14(3):344-60.
43. Wang Y, Dai Z, Cheng H, Liu Z, Pan Z, Deng W, Gao T, Li X, Yao Y, Ren J, **Xue Y†**. (2013) Towards a better understanding of the novel avian-origin H7N9 influenza A virus in China. *Sci Rep*. 2013;3:2318.
44. Liu Z, Wang Y, **Xue Y†**. (2013) Phosphoproteomics-based network medicine. *FEBS J*, 280(22):5696-704.
45. Yang Z, Guo G, Zhang M, Liu CY, Hu Q, Lam H, Cheng H, **Xue Y**, Li J, Li N. (2013) Stable isotope metabolic labeling-based quantitative phosphoproteomic analysis of Arabidopsis mutants reveals ethylene-regulated time-dependent phosphoproteins and putative substrates of constitutive triple response 1 kinase. *Mol Cell Proteomics*. 12(12):3559-82.
46. Liu Z, Wang Y, Gao T, Pan Z, Cheng H, Yang Q, Cheng Z, Guo A, Ren J, **Xue Y†**. (2014) CPLM: a database of protein lysine modifications. *Nucleic Acids Res*. 42(1): D531-6.
47. Wang Y, Liu Z, Cheng H, Gao T, Pan Z, Yang Q, Guo A, **Xue Y†**. (2014) EKPD: a hierarchical database of eukaryotic protein kinases and protein phosphatases. *Nucleic Acids Res*. 42(1):D496-502.
48. Liu Z, Wang Y, Zhou C, **Xue Y**, Zhao W, Liu H. (2014) Computationally characterizing and comprehensive analysis of zinc-binding sites in proteins.

Biochim Biophys Acta. 1844(1 Pt B):171-80.

49. Yao Y, Ma L, Jia Q, Deng W, Liu Z, Zhang Y, Ren J, **Xue Y**, Jia H, Yang Q. (2014) Systematic characterization of small RNAome during zebrafish early developmental stages. *BMC Genomics*. 2014, 15:117.
50. Zhao Q, Xie Y, Zheng Y, Jiang S, Liu W, Mu W, Liu Z, Zhao Y, **Xue Y¶**, Ren J¶. (2014) GPS-SUMO: a tool for the prediction of sumoylation sites and SUMO-interaction motifs. *Nucleic Acids Res*. 42:W325-30.
51. Qi L, Liu Z, Wang J, Cui Y, Guo Y, Zhou T, Zhou Z, Guo X¶, **Xue Y¶**, Sha J. (2014) Systematic Analysis of the Phosphoproteome and Kinase-substrate Networks in the Mouse Testis. *Mol Cell Proteomics*. 13(12):3626-38.
52. Deng W, Wang Y, Liu Z, Cheng H, **Xue Y†**. (2014) HemI: A Toolkit for Illustrating Heatmaps. PLoS One. 9(11):e111988.
53. Pan Z, Liu Z, Cheng H, Wang Y, Gao T, Ullah S, Ren J, **Xue Y†**. (2014) Systematic analysis of the in situ crosstalk of tyrosine modifications reveals no additional natural selection on multiply modified residues. Sci Rep. 4:7331.
54. Cheng H, Deng W, Wang Y, Ren J, Liu Z¶, **Xue Y¶**. (2014) dbPPT: a comprehensive database of protein phosphorylation in plants. Database (Oxford). 2014:bau121.
55. Huang Z, Ma L, Wang Y, Pan Z, Ren J, Liu Z¶, **Xue Y¶**. (2015) MiCroKiTS 4.0: a database of midbody, centrosome, kinetochore, telomere and spindle. Nucleic Acids Res. 43:D328-34.
56. Zhang HM, Liu T, Liu CJ, Song S, Zhang X, Liu W, Jia H, **Xue Y**, Guo AY. (2015) AnimalTFDB 2.0: a resource for expression, prediction and functional study of animal transcription factors. Nucleic Acids Res. 43:D76-81.
57. Tian M, Cheng H, Wang Z, Su N, Liu Z, Sun C, Zhen B, Hong X, **Xue Y**, Xu P. (2015) Phosphoproteomic analysis of the highly-metastatic hepatocellular carcinoma cell line, MHCC97-H. Int J Mol Sci. 16(2):4209-25.
58. Pan Z, Wang B, Zhang Y, Wang Y, Ullah S, Jian R, Liu Z¶, **Xue Y¶**. (2015) dbPSP: a curated database for protein phosphorylation sites in prokaryotes. Database (Oxford). 2015:bav031.
59. Liu Z, Cai Y, Guo X, Li A, Li T, Qiu J, Ren J, Shi S, Song J, Wang M, Xie L, **Xue Y†**, Zhang Z, Zhao X. (2015) Post-translational modification (PTM) bioinformatics in China: progresses and perspectives. DHEREDITAS (Beijing), 2015, 37(7): 621-634.
60. Liu W, Xie Y, Ma J, Luo X, Nie P, Zuo Z, Lahrmann U, Zhao Q, Zheng Y, Zhao Y, **Xue Y¶**, Ren J¶. (2015) IBS: an illustrator for the presentation and visualization of biological sequences. Bioinformatics. 2015, 31(20):3359-61.
61. Wang Y, Cheng H, Pan Z, Ren J, Liu Z¶, **Xue Y¶**. (2015) Reconfiguring phosphorylation signaling by genetic polymorphisms affects cancer susceptibility. J Mol Cell Biol. 7(3):187-202.

62. Feng W, Zhang W, Wang H, Ma L, Miao D, Liu Z, **Xue Y**, Deng H, Yu L. (2015) Analysis of phosphorylation sites on autophagy proteins. Protein Cell. 6(9):698-701.
63. IC4R Project Consortium, Hao L, Zhang H, Zhang Z, Hu S, **Xue Y**. (2016) Information Commons for Rice (IC4R). Nucleic Acids Res. 44(D1):D1172-80.
64. Gao Y, Li Y, Zhang C, Zhao M, Deng C, Lan Q, Liu Z, Su N, Wang J, Xu F, Xu Y, Ping L, Chang L, Gao H, Wu J, **Xue Y**, Deng Z, Peng J, Xu P. (2016) Enhanced Purification of Ubiquitinated Proteins by Engineered Tandem Hybrid Ubiquitin-binding Domains (ThUBDs). Mol Cell Proteomics. 2016 Apr;15(4):1381-96.
65. Zhong Z, Yang L, Zhang YE, **Xue Y**, He S. (2016) Correlated expression of retrocopies and parental genes in zebrafish. Mol Genet Genomics. 291(2):723-37.
66. Klionsky DJ, ..., **Xue Y**, ..., Zughaier SM. (2016) Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy. 12(1):1-222.
67. He CL, Bian YY, **Xue Y**, Liu ZX, Zhou KQ, Yao CF, Lin Y, Zou HF, Luo FX, Qu YY, Zhao JY, Ye ML, Zhao SM, Xu W. (2016) Pyruvate Kinase M2 Activates mTORC1 by Phosphorylating AKT1S1. Sci Rep. 6:21524.
68. Ullah S, Lin S, Xu Y, Deng W, Ma L, Zhang Y, Liu Z¶, **Xue Y¶**. (2016) dbPAF: an integrative database of protein phosphorylation in animals and fungi. Sci Rep. 6:23534.
69. Guo X, Lv X, Fang C, Lv X, Wang F, Wang D, Zhao J, Ma Y, **Xue Y**, Bai Q, Yao X, Chen Y. (2016) Dysbindin as a novel biomarker for pancreatic ductal adenocarcinoma identified by proteomic profiling. Int J Cancer. 2016 Oct 15;139(8):1821-9.
70. Zhang J, Tian Y, Yan L, Zhang G, Wang X, Zeng Y, Zhang J, Ma X, Tan Y, Long N, Wang Y, Ma Y, He Y, **Xue Y**, Hao S, Yang S, Wang W, Zhang L, Dong Y, Chen W, Sheng J. (2016) Genome of Plant Maca (Lepidium meyenii) Illuminates Genomic Basis for High-Altitude Adaptation in the Central Andes. Mol Plant. 9(7):1066-77.
71. **Xue Y†**, Wang Y, Shen H. (2016) Ray Wu, fifth business or father of DNA sequencing? Protein Cell. 7(7):467-70.
72. Xie Y, Zheng Y, Li H, Luo X, He Z, Cao S, Shi Y, Zhao Q, **Xue Y**, Zuo Z, Ren J. (2016) GPS-Lipid: a robust tool for the prediction of multiple lipid modification sites. Sci Rep. 6:28249.
73. **Xue Y**, Lameijer EW, Ye K, Zhang K, Chang S, Wang X, Wu J, Gao G, Zhao F, Li J, Han C, Xu S, Xiao J, Yang X, Ying X, Zhang X, Chen WH, Liu Y, Zhang Z, Huang K, Yu J. (2016) Precision Medicine: What Challenges Are We Facing? Genomics Proteomics Bioinformatics. 14(5):253-261.
74. Xu Y, Ding YX, Ding J, Wu LY, **Xue Y†**. (2016) Mal-Lys: prediction of lysine malonylation sites in proteins integrated sequence-based features with mRMR feature selection. Sci Rep. 6:38318.

75. Deng W, Wang C, Zhang Y, Xu Y, Zhang S, Liu Z¶, **Xue Y¶**. (2016) GPS-PAIL: prediction of lysine acetyltransferase-specific modification sites from protein sequences. Sci Rep. 6:39787.
76. Xu Y, Zhang S, Lin S, Guo Y, Deng W, Zhang Y, **Xue Y†**. (2017) WERAM: a database of writers, erasers and readers of histone acetylation and methylation in eukaryotes. Nucleic Acids Res. 45(D1):D264-D270.
77. Li S, Shui K, Zhang Y, Lv Y, Deng W, Ullah S, Zhang L¶, **Xue Y¶**. (2017) CGDB: a database of circadian genes in eukaryotes. Nucleic Acids Res. 45(D1):D397-D403.
78. Deng W, Wang Y, Ma L, Zhang Y, Ullah S, **Xue Y†**. (2017) Computational prediction of methylation types of covalently modified lysine and arginine residues in proteins. Brief Bioinform. 18(4):647-658.
79. Bezabih G, Cheng H, Han B, Feng M, **Xue Y**, Hu H, Li J. (2017) Phosphoproteome Analysis Reveals Phosphorylation Underpinnings in the Brains of Nurse and Forager Honeybees (Apis mellifera). Sci Rep. 7(1):1973.
80. **Xue Y¶**, Wang XJ¶. (2017) Bioinformaticians wrestling with the big biomedical data. J Genet Genomics. 44(5):223-225.
81. Xu H, Zhou J, Lin S, Deng W, Zhang Y, **Xue Y†**. (2017) PLMD: an updated data resource of protein lysine modifications. J Genet Genomics. 44(5):243-250.
82. Chen LL, Wang YB, Song JX, Deng WK, Lu JH, Ma LL, Yang CB, Li M¶, **Xue Y¶**. (2017) Phosphoproteome-based kinase activity profiling reveals the critical role of MAP2K2 and PLK1 in neuronal autophagy. Autophagy. 2017;13(11):1969-1980.
83. BIG Data Center Members. (2018) Database Resources of the BIG Data Center in 2018. Nucleic Acids Res.46(D1):D14-20.
84. Zhou J, Xu Y, Lin S, Guo Y, Deng W, Zhang Y, Guo A, **Xue Y†**. (2018) iUUCD 2.0: an integrated database of regulators for ubiquitin and ubiquitin-like conjugation. Nucleic Acids Res. 46(D1):D477-453.
85. Deng W, Ma L, Zhang Y, Zhou J, Wang Y, Liu Z, **Xue Y†**. (2018) THANATOS: an integrative data resource of proteins and post-translational modifications in the regulation of autophagy. Autophagy. 2018, 14(2): 296-310.

(*Co-first author, ¶Co-corresponding author, †Corresponding author)

[9] Publications – book chapters (2004-)

1. **Xue Y**, Liu Z, Cao J, Jian Ren. (2011) Computational Prediction of Post-Translational Modification Sites in Proteins. *Systems and Computational Biology - Molecular and Cellular Experimental Systems*, InTech - Open Access Publisher, ISBN: 978-953-307-280-7. (Book Chapter 6, has been accessed 2,000 times on Jan. 19, 2013, the 2nd of “most downloaded chapters”).
2. Gao T, Liu Z, Wang Y, **Xue Y†**. (2013) Ubiquitin and Ubiquitin-Like

Conjugations in Complex Diseases: A Computational Perspective. Translational Bioinformatics, Volume 4 2013, "Bioinformatics for Diagnosis, Prognosis and Treatment of Complex Diseases", Editors: Bairong Shen. ISBN: 978-94-007-7974-7 (Print), 978-94-007-7975-4 (Online) (Book Chapter 9) http://link.springer.com/book/10.1007%2F978-94-007-7975-4.

3. Cheng H, Wang Y, Liu Z, **Xue Y†**. (2015) Computational identification of protein kinases and kinase-specific substrates in plants. Methods Mol Biol. 2015;1306:195-205.

[10] Graduated Ph.D. students

1. 2013/06, Dr. Zexian Liu, “Bioinformatics of Covalent Modification Proteomics and Zinc-Metallomics”.
2. 2014/05, Dr. Tianshun Gao, “Bioinformatic studies of the ubiquitin conjugation system”.
3. 2014/05, Dr. Yuangen Yao, “Prediction and analysis of small RNA during zebrafish early developmental stages”.
4. 2015/05, Dr. Han Cheng, “Bioinformatic studies of plant phosphoproteomes”.
5. 2016/05, Dr. Shahid Ullah, “Computational analyses of the protein phosphorylation in eukaryotes and the application in circadian regulation”.
6. 2016/05, Dr. Lili Ma, “Bioinformatic studies of protein post-translational modifications in the regulation of mitosis and autophagy”.
7. 2017/05, Dr. Yongbo Wang, “Phosphoproteome-based modeling and analysis of kinase-substrate phosphorylation networks”.
8. 2017/05, Dr. Wankun Deng, “Post translational modifications of proteins: Bioinformatic prediction and data resource integration”.