

Curriculum Vitae

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[1] Personal information

Yu Xue, Ph.D.,

Professor (from July, 2009),
Principle Investigator,
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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, Department of Systems Biology, 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. January 2013, “The Fourth SCOPUS Young Researcher Award”, China
2. July 2009, excellent oral presentation award for young scholars, CNHUPO 2009
3. May 2008, Fifty most excellent Ph.D. dissertations of Chinese Academy of Sciences (CAS).
4. June 2006, Travel Fellowship Award \$1000, 14th Annual International Conference on Intelligent Systems for Molecular Biology.
5. November 2006, Hong Kong “Qiu Shi” Scholarship for graduates.
6. October 2005, “Dong Gang” Scholarship for graduates.
7. 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 N ϵ -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*. doi: 10.1093/bib/bbs041.
- (*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”).