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❖ *Research Interests*

· Design, evaluation and optimization of Bioinformatics Algorithms

· Data integration and transOmics in biomedical fields

· Probing the molecular events underlying the diseases via computational approaches

❖ *Education Background*

· Sep. 2013 - Jun. 2017, Ph.D. candidate, Chongqing University▲, China.

· Sep. 2010 - Jun. 2013, MSc. Degree, Chongqing University▲, China.

· Sep. 1999 - Jun. 2003, Bachelor's degree, Northwest A & F University▲, China.

❖ *Work Experience*

· Dec. 2020-, associate Professor, graduate advisor in Bioinformatics, Chongqing Normal University.

· Jun. 2017 – Nov. 2020, assistant professor, Chongqing Normal University,

· Jun. 2004 - Jul. 2010, lecturer, Wuhan Bioengineering Institute, Wuhan.

· Sep. 2003 - Jun. 2004, technician, Academy of Military Medical Sciences, Beijing.

❖ *Honors and Awards*

· First Prize of "Teaching Skill Competition for Young Teachers, College of Life Science, CNU", 2019.

· Professional Award of "Teaching Skill Competition for New Teachers", CNU, 2017.

· Excellent graduate with Master's degree, Chongqing University, 2013.

· The first-grade scholarship of CQU, Chongqing University, 2010 - 2013.

· Prize on the supervisor of Excellent Bachelor Thesis, Department of education, Hubei Province, 2009.

· Prize of "Teaching Skill Competition for Young Teachers-G2", Wuhan Bioengineering Institute, 2008.

· Second Prize of the "Scientific Research Achievements", Wuhan Bioengineering Institute, Jan. 2008.

· Prominent teacher of WBI, Wuhan Bioengineering Institute, Sep. 2005, 2006.

· Outstanding graduate with Bachelor's degree, Northwest A & F University, Jul. 2003.

· Excellent Student and Second-class scholarship, Northwest A&F University, Sep. 2002.

· Outstanding leader of Student, Education Department of Shaanxi Province, May. 1999.

❖ *Membership & Certificate*

· Teaching qualification certificate of China, 2005

· Membership of Chinese Society of Cell Biology (ID: S235000376M), 2007

· Council member of Chongqing Society of Bioinformatics, 2016

· The member of Association for Computing Machinery (ACM) (ID: 9152152)

· The member of China Computer Federation (CCF) (ID: 72981M)

▲ A national key University, and one of the 985 project universities which were supported by Central Government of China.

❖ *Books and Chapters*

- Peng Yinxiang, <u>Li Bo</u> and Chen Hongxing. (2007). ***Gene engineering***, 1st ed. Wuhan: HUST press. (*As co-editor-in-chief, I presided over the entire book, which consists of 317 pages*).
- Deng Zhengdong, <u>Li Bo</u>, Wang Yafen. (2007). ***Handbook of cell biology experiments***, 2nd. Wuhan Bioengineering Institute: internal release.
- <u>Li Bo</u>, Fu Guangming. (2006). ***Environmental biotechnology***. In Li Rongqian, editor: Introduction of Bioengineering, 2nd. Wuhan: Central China Normal University press, pp. 159-171. (*Be invited to write a book chapter*).
- <u>Li Bo</u>. (2006). ***Bioreactor***. In Huang Fangyi and Ye Bin, editors: ***Fermentation Engineering***, 2nd ed. Wuhan: Central China Normal University press, pp. 37-55. (*Be invited to write a book chapter*).

❖ *Publications* (including first author, corresponding author and others[1-43]. including ones in teaching & scientific research, and papers to be submitted; Authorship includes first author, corresponding author and others).

1 李勃, 何昊, 张晓曦, 李映红 & 杨丹. 立足方法学基点 培育生物信息学素养. *生物学杂志*: 1-5 (2021) [CSCD, 第一作者].

2 李勃 & 朵泓睿. 单细胞 RNA 测序数据分析方法研究进展. *重庆师范大学学报(自然科学版)* 38(05): 129-135+142 (2021) [CSCD, 第一作者].

3 Yin, H., Zheng, X., Tang, X., Zang, Z., Li, B., He, S., Shen, R., Yang, H. & Li, S. Potential biomarkers and lncRNA-mRNA regulatory networks in invasive growth hormone-secreting pituitary adenomas. *Journal of endocrinological investigation* 44(9): 1947-1959 (2021) [IF=4.256].

4 Yang, Q., Li, B., Chen, S., Tang, J., Li, Y., Li, Y., Zhang, S., Shi, C., Zhang, Y., Mou, M., Xue, W. & Zhu, F. MMEASE: Online meta-analysis of metabolomic data by enhanced metabolite annotation, marker selection and enrichment analysis. *J Proteomics* 232: 104023 (2021) [IF=4.044, Co-first author].

5 Wang, X., Chai, Z., Pan, G., Hao, Y., Li, B., Ye, T., Li, Y., Long, F., Xia, L. & Liu, M. ExoBCD: a comprehensive database for exosomal biomarker discovery in breast cancer. *Briefings in bioinformatics* 22(3): bbaa088 (2021) [IF=11.622].

6 Bo, W., Chen, L., Qin, D., Geng, S., Li, J., Mei, H., Li, B. & Liang, G. Application of quantitative structure-activity relationship to food-derived peptides: Methods, situations, challenges and prospects. *Trends in Food Science & Technology* 114: 176-188 (2021) [IF=12.563, Corresponding author].

7 刘杰, 李勃, 陈晓洁 & 陈斌. 埃及伊蚊不同组织的基因共表达模式分析. *昆虫学报* 63(10): 1171-1182 (2020).

8 刘杰, 李勃 & 陈斌. 中华按蚊雌、雄蚊转录组比较分析. *重庆师范大学学报(自然科学版)* 37(03): 54-59 (2020).

9 李勃, 陶靖心 & 魏晋艺. 短学时情况下生物信息学课程教学改革——以重庆师范大学为例. *西部素质教育* 6(05): 183-184 (2020) [第一作者].

10 李勃, 方斌, 陶靖心 & 刘明伟. 秀丽隐杆线虫基因组编码区的碱基分布特征参数研究. *重庆师范大学学报(自然科学版)* 37(03): 14-20 (2020) [CSCD, 第一作者].

11 Yang, Q., Li, B., Tang, J., Cui, X., Wang, Y., Li, X., Hu, J., Chen, Y., Xue, W., Lou, Y., Qiu, Y. & Zhu, F. Consistent gene signature of schizophrenia identified by a novel feature selection strategy from comprehensive sets of transcriptomic data. *Briefings in bioinformatics* 21(3): 1058-1068 (2020) [IF=11.622].

12 Wei, J., Lu, H., Tao, J., Hao, Y., Huang, D. & Li, B. The complete mitogenome of Lasioglossum affine

(Hymenoptera: Halictidae) and phylogenetic analysis. *Mitochondrial DNA. Part B, Resources* 5(3): 3784-3785 (2020) [IF=0.658].

13 Wang, X., Chai, Z., Li, Y., Long, F., Hao, Y., Pan, G., Liu, M. & Li, B. Identification of Potential Biomarkers for Anti-PD-1 Therapy in Melanoma by Weighted Correlation Network Analysis. *Genes* 11(4) (2020) [IF=4.096, Corresponding author].

14 Tao, J., Hao, Y., Li, X., Yin, H., Nie, X., Zhang, J., Xu, B., Chen, Q. & Li, B. Systematic Identification of Housekeeping Genes Possibly Used as References in Caenorhabditis elegans by Large-Scale Data Integration. *Cells* 9(3) (2020) [IF=6.600, Corresponding author].

15 Tang, J., Wang, Y., Fu, J., Zhou, Y., Luo, Y., Zhang, Y., Li, B., Yang, Q., Xue, W., Lou, Y., Qiu, Y. & Zhu, F. A critical assessment of the feature selection methods used for biomarker discovery in current metaproteomics studies. *Briefings in bioinformatics* 21(4): 1378-1390 (2020) [IF=11.622].

16 Tang, J., Fu, J., Wang, Y., Li, B., Li, Y., Yang, Q., Cui, X., Hong, J., Li, X., Chen, Y., Xue, W. & Zhu, F. ANPELA: analysis and performance assessment of the label-free quantification workflow for metaproteomic studies. *Briefings in bioinformatics* 21(2): 621-636 (2020) [IF=11.622].

17 张莉娟, 尹华春, 李勃 & 陈斌. 10 种昆虫过氧化氢酶基因的全基因组鉴定与特征预测. *重庆师范大学学报(自然科学版)* 36(03): 36-43+32 (2019).

18 李勃, 倪雅诗 & 陶靖心. "生物信息学"课程在线教学资源库的设计与构建——以重庆师范大学为例. *无线互联科技* 16(22): 95-96 (2019) [第一作者].

19 Zuo, X., Li, B., Zhu, C., Yan, Z. W., Li, M., Wang, X. & Zhang, Y. J. Stoichiogenomics reveal oxygen usage bias, key proteins and pathways associated with stomach cancer. *Scientific reports* 9(1): 11344 (2019) [IF=4.379].

20 Yin, Y., Li, B., Mou, K., Khan, M. T., Kaushik, A. C., Wei, D. & Zhang, Y. J. Stoichioproteomics reveal oxygen usage bias, key proteins and pathways in glioma. *BMC medical genomics* 12(1): 125 (2019) [IF=3.063, Co-first author].

21 Yang, Q. X., Wang, Y. X., Li, F. C., Zhang, S., Luo, Y. C., Li, Y., Tang, J., Li, B., Chen, Y. Z., Xue, W. W. & Zhu, F. Identification of the gene signature reflecting schizophrenia's etiology by constructing artificial intelligence-based method of enhanced reproducibility. *CNS neuroscience & therapeutics* 25(9): 1054-1063 (2019) [IF=5.243].

22 Yang, Q., Wang, Y., Zhang, S., Tang, J., Li, F., Yin, J., Li, Y., Fu, J., Li, B., Luo, Y., Xue, W. & Zhu, F. Biomarker Discovery for Immunotherapy of Pituitary Adenomas: Enhanced Robustness and Prediction Ability by Modern Computational Tools. *International journal of molecular sciences* 20(1) (2019) [IF=5.923].

23 Tang, J., Fu, J., Wang, Y., Luo, Y., Yang, Q., Li, B., Tu, G., Hong, J., Cui, X., Chen, Y., Yao, L., Xue, W. & Zhu, F. Simultaneous Improvement in the Precision, Accuracy, and Robustness of Label-free Proteome Quantification by Optimizing Data Manipulation Chains. *Molecular & cellular proteomics : MCP* 18(8): 1683-1699 (2019) [IF=5.911].

24 Nie, X., Wei, J., Hao, Y., Tao, J., Li, Y., Liu, M., Xu, B. & Li, B. Consistent Biomarkers and Related Pathogenesis Underlying Asthma Revealed by Systems Biology Approach. *International journal of molecular sciences* 20(16) (2019) [IF=5.923, Corresponding author].

25 Li, X., Li, X., Li, Y., Yu, C., Xue, W., Hu, J., Li, B., Wang, P. & Zhu, F. What Makes Species Productive of Anti-Cancer Drugs? Clues from Drugs' Species Origin, Druglikeness, Target and Pathway. *Anti-cancer agents in medicinal chemistry* 19(2): 194-203 (2019) [IF=2.505].

26 Hu, J., Yin, H., Li, B. & Yang, H. Identification of Transcriptional Metabolic Dysregulation in Subtypes of Pituitary Adenoma by Integrated Bioinformatics Analysis. *Diabetes, metabolic syndrome*

and obesity : targets and therapy 12: 2441-2451 (2019) [IF=3.168, Corresponding author].

27 Cui, X., Yang, Q., Li, B., Tang, J., Zhang, X., Li, S., Li, F., Hu, J., Lou, Y., Qiu, Y., Xue, W. & Zhu, F. Assessing the Effectiveness of Direct Data Merging Strategy in Long-Term and Large-Scale Pharmacometabonomics. *Frontiers in pharmacology* 10: 127 (2019) [IF=5.810, Co-first author].

28 Mei, T., Fu, W. B., Li, B., He, Z. B. & Chen, B. Comparative genomics of chemosensory protein genes (CSPs) in twenty-two mosquito species (Diptera: Culicidae): Identification, characterization, and evolution. *PloS one* 13(1): e0190412 (2018) [IF=3.240].

29 Ding, Y. R., Li, B., Zhang, Y. J., Mao, Q. M. & Chen, B. Complete mitogenome of Anopheles sinensis and mitochondrial insertion segments in the nuclear genomes of 19 mosquito species. *PloS one* 13(9): e0204667 (2018) [IF=3.240].

30 Yang, Q., Li, B. & Zhu, F. in *Proceedings of the 5th International Conference on Bioinformatics and Computational Biology.* 17-20.

31 Yang, F., Fu, T., Zhang, X., Hu, J., Xue, W., Zheng, G., Li, B., Li, Y., Yao, X. & Zhu, F. Comparison of computational model and X-ray crystal structure of human serotonin transporter: potential application for the pharmacology of human monoamine transporters. *Molecular Simulation* 43(13-16): 1089-1098 (2017) [IF=2.178].

32 Wang, P., Zhang, X., Fu, T., Li, S., Li, B., Xue, W., Yao, X., Chen, Y. & Zhu, F. Differentiating Physicochemical Properties between Addictive and Nonaddictive ADHD Drugs Revealed by Molecular Dynamics Simulation Studies. *ACS chemical neuroscience* 8(6): 1416-1428 (2017) [IF=4.418].

33 Li, B., Tang, J., Yang, Q., Li, S., Cui, X., Li, Y., Chen, Y., Xue, W., Li, X. & Zhu, F. NOREVA: normalization and evaluation of MS-based metabolomics data. *Nucleic Acids Res* 45(W1): W162-w170 (2017) [IF=16.971, First author].

34 郑国勋, 薛伟伟, 王盼盼, 杨凤园, 李勃, 李晓凤, 李映红 & 朱峰. in *中国化学会第30届学术年会-第二十五分会：化学信息学与化学计量学.* 1.

35 Zheng, G., Xue, W., Wang, P., Yang, F., Li, B., Li, X., Li, Y., Yao, X. & Zhu, F. Exploring the Inhibitory Mechanism of Approved Selective Norepinephrine Reuptake Inhibitors and Reboxetine Enantiomers by Molecular Dynamics Study. *Scientific reports* 6: 26883 (2016) [IF=4.379].

36 Xue, W., Wang, P., Li, B., Li, Y., Xu, X., Yang, F., Yao, X., Chen, Y. Z., Xu, F. & Zhu, F. Identification of the inhibitory mechanism of FDA approved selective serotonin reuptake inhibitors: an insight from molecular dynamics simulation study. *Physical chemistry chemical physics : PCCP* 18(4): 3260-3271 (2016) [IF=3.676].

37 Li, B., Tang, J., Yang, Q., Cui, X., Li, S., Chen, S., Cao, Q., Xue, W., Chen, N. & Zhu, F. Performance Evaluation and Online Realization of Data-driven Normalization Methods Used in LC/MS based Untargeted Metabolomics Analysis. *Scientific reports* 6: 38881 (2016) [IF=4.379, First author].

38 Jing, Y., Li, B., Chen, N., Li, X., Hu, J. & Zhu, F. The discrimination of learning styles by Bayes-based statistics: An extended study on ILS system. *Control and Intelligent Systems* 43(2): 68-75 (2015) [EI, Co-first author].

39 Jia, X., Liu, S., Zheng, H., Li, B., Qi, Q., Wei, L., Zhao, T., He, J. & Sun, J. Non-uniqueness of factors constraint on the codon usage in Bombyx mori. *BMC genomics* 16(1): 356 (2015) [IF=3.969].

40 高山, 张宁, 李勃, 徐硕, 叶彦波 & 阮吉寿. 下一代测序中 ChIP-seq 数据的处理与分析. *遗传* 34(06): 773-783 (2012).

41 陈园园, 李勃 & 邓林红. 基于强迫振荡技术的呼吸道阻力及其可变性测量. *医用生物力学* 27(04): 460-463 (2012).

42 Long, J., Li, M., Ren, Q., Zhang, C., Fan, J., Duan, Y., Chen, J., Li, B. & Deng, L. Phylogenetic and molecular evolution of the ADAM (A Disintegrin And Metalloprotease) gene family from Xenopus tropicalis, to Mus musculus, Rattus norvegicus, and Homo sapiens. *Gene* 507(1): 36-43 (2012) [IF=3.688].

43 李勃, 熊海燕, 陈红星 & 邓继先. 猪血清白蛋白基因 5′端调控区的克隆与分析. *广西师范大学学报(自然科学版)* 27(03): 58-61 (2009) [中文核心, 第一作者].

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