# Shengwei Li

## PERSONAL INFORMATION

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|---|---|
| Gender: | Male |
| Date of Birth: | 25/02/1998 |
| Address: | No. 639 Longmian Avenue, Jiangning District, Nanjing 211198, Jiangsu, China |
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| Mobile: | +86-15195979383 |
| Citizenship: | People's Republic of china |

## EDUCATIONAL BACKGROUND

*2020.09 – 2023.06*     M.Sc. Biomedicine, China Pharmaceutical University     ***Grade: 87.43***

Core Courses: Pharmaceutical bioinformatics, Pharmacogenomics, Pharmaceutical information mining, Frontiers and applications of genomics, Computer-aided drug design, Academic English Writing and Translation, Professional literature study and writing

*2016.09 – 2020.06*     B.Sc Pharmacy, Jiangxi University of Traditional Chinese Medicine     ***Grade: 80.8***

Core Courses: Advanced Mathematics, Mathematical statistics, Physics, Computer Basics, Anatomy and Physiology, Microbiology and Immunology, Biochemistry, Organic Chemistry, Analytical Chemistry, Natural Pharmaceutical Chemistry, Pharmacology, Industrial Pharmacy, Biopharmaceuticals

## AWARDS

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|---|---|
| *2022.05* | National Scholarship, China Pharmaceutical University |
| *2022.04* | Special Scholarship for Graduate Students, China Pharmaceutical University |
| *2021.09-2022.06* | Postgraduate Second Class Scholarship, China Pharmaceutical University |
| *2019.09-2020.06* | Special Scholarships, Jiangxi University of Traditional Chinese Medicine |
| *2017.09-2018.06* | Academic Third Class Scholarship, Jiangxi University of Traditional Chinese Medicine |
| *2016.09-2017.06* | Academic Second Class Scholarship, Jiangxi University of Traditional Chinese Medicine |

## RECORDS OF STANDARD TESTS

IELTS:     6.0

CET-6:     513

## SKILLS

➢ Familiar with Linux operating environment

➢ Ability to program in shell,R and Python

➢ Experience in high-throughput sequencing data analysis, including RNA-seq, scRNA-seq, Chip-seq, ATAC-seq and WES-seq

➢ Familiar with Adobe Acrobat DC, Photoshop

**PUBLICATIONS**

1.  **Li SW**, Liu Q, Zhou H, Lu H, Wang X. Subtyping of sarcomas based on pathway enrichment scores in bulk and single cell transcriptomes. *J Transl Med*. 2022; 20(1):48. Published 2022 Jan 29. doi:10.1186/s12967-022-03248-3

2.  Zhu X[#], **Li SW**[#], Luo J, et al. Subtyping of Human Papillomavirus-Positive Cervical Cancers Based on the Expression Profiles of 50 Genes. *Front Immunol*. 2022; 13:801639. Published 2022 Jan 21. doi:10.3389/fimmu.2022.801639

3.  Yao J[#], **Li SW**[#], Wang X. Identification of Breast Cancer Immune Subtypes by Analyzing Bulk Tumor and Single Cell Transcriptomes. *Front Cell Dev Biol*. 2022; 9:781848. Published 2022 Jan 3. doi:10.3389/fcell.2021.781848

4.  **Li SW**, Han LF, He Y, Wang XS. Immunological classification of hepatitis B virus-positive hepatocellular carcinoma by transcriptome analysis. World J Hepatol. 2022;14(12):1997-2011. doi:10.4254/wjh.v14.i12.1997