

Shiyang He

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RESEARCH/WORKING EXPERIENCE

Postdoctoral Scholar in Dr. Yi Yin lab, UCLA, CA, USA	08/2025 – present
Postdoctoral researcher in Dr. Jernej Murn lab, UC Riverside, CA, USA.	07/2024 – 07/2025
PhD candidate in Dr. Jernej Murn lab, UC Riverside, CA, USA.	09/2019 – 06/2024
Bioinformatician, Bainuo Gene, Shenzhen, China.	09/2018 – 09/2019
Research assistant, Shenzhen Second People's Hospital, Shenzhen, China.	07/2015 – 04/2018
Internship, Beijing Genomics Institute, Shenzhen, China.	03/2013 – 07/2015

EDUCATION

PhD in Genetics, Genomics & Bioinformatics	06/2024
University of California, Riverside, USA	
Master of Genetics	07/2015
University of Chinese Academy of sciences, Beijing, China	
Bachelor of Biology Sciences	07/2012
Sun Yat-sen University, Guangzhou, China	
Selected Courses: Genetics, Molecular Biology, Tumor biology, Bioinformatics, Virus Molecular Biology, Genome Science, Signal Transduction, and Bioinformatics.	

HONORS & AWARDS

CIRM TRANSCEND trainee award	02/2025
Dissertation Completion Fellowship Award	02/2024
Dissertation Year Program Award	04/2023
The best oral presentation in the program annual symposium	10/2022
The Dean's Distinguished Fellowship	09/2019
The best of three good students	05/2015
Distinguished undergraduate dissertation in the college	07/2012
The distinguished student assistant in the Zhuhai campus library of Sun Yat-sen University	07/2009
The distinguished English class presentation in Sun Yat-sen University	12/2008

SKILLS

Molecular biology: NGS library preparation (CLIP-seq, RNA-seq, TTchem-seq, BID-seq, Pseudo-seq), Gene cloning, Western Blot, cell culture, lenti-virus making and cell transfection, siRNA knocking down.

Computation Language: Perl, R, C++, and Python programming, Linux/unix

Data analysis: RNA-seq, CLIP-seq, Ribosome profiling, TTchem-seq, BID-seq, Pseudo-seq, Poly (A) tail sequencing, End-seq, Genome assembly and annotation, whole exome analysis, tumor somatic mutation analysis, MHC binding prediction, HLA typing with NGS data.

PATENTS

A method and device for constructing genomic target region sequencing library. Co-author.	06/2016
The tumor neo-antigen prediction and tandem minigene design software (V1.0). Co-author.	02/2021

PUBLICATIONS

1. **S He**, P Chovanec, Y Yin. Protocol for mapping sister chromatid exchanges and structural variations using sci-L3-strand-seq, STAR protocols 7 (4) (2026)
2. P Chovanec, **S He**, Y Yin. Genome-wide mapping of Cas9-induced sister chromatid exchange across single and over 200 genomic sites in human cells. *eLife* 15, RP112073 (2026)
3. Y Liu*, **S He**, K Pyo, S Zheng, M Chen, B Braschi, S Cheloufi, N Slavov, ... Composition and RNA binding specificity of metazoan RNase MRP. *Nucleic Acids Research* 53 (16), gkaf829(2025)
4. Y Liu*, **S He***, K Pyo, R Franklin, IB Maaz, C Cai, K Shah, S Cheloufi, ... Reversible proliferative arrest induced by rapid depletion of RNase MRP. *Nature Communications* 16 (1), 5342 (2025)
5. S Wei, X Dai, J Yuan, **S He**, K Shah, S Guo, Z Duan, J Murn, Y Wang. Quantitative Proteomics Identifies Profilin-1 as a Pseudouridine-Binding Protein. *Journal of the American Chemical Society* 147 (2), 1458-1462 (2025)
6. Larsen PB, **He S**, Meyer TJ, Szurman-Zubrzycka M, Alfs C, Kwasniewska J, Pervis A, Gajecka M, Veerabahu A, Beaulieu TR, Bolaris SC, Eekhout T, De Veylder L, Abel S, Szarejko I, Murn J. The stem cell niche transcription factor ETHYLENE RESPONSE FACTOR 115 participates in aluminum-induced terminal differentiation in Arabidopsis roots. *Plant Cell Environ.* doi: 10.1111/pce.15032. (2024)
7. Shah K*, **He S***, Turner DJ*, Corbo J, Rebbani K, Dominguez D, Bateman JM, Cheloufi S, Igreja C, Valkov E, Murn J. Regulation by the RNA-binding protein Unkempt at its effector interface. *Nat Commun.* doi: 10.1038/s41467-024-47449-4. (2024)
8. **He, S.**, Valkov, E., Cheloufi, S. & Murn, J. The nexus between RNA-binding proteins and their effectors. *Nat Rev Genet*, doi:10.1038/s41576-022-00550-0. (2022)
9. Franklin, R., Guo, Y., **He, S.** et al. Regulation of chromatin accessibility by the histone chaperone CAF-1 sustains lineage fidelity. *Nat Commun* 13, 2350. (2022)
10. Lin, Z.R.*, Wang, M.Y., **He, S.Y.**, Cai, Z.M., and Huang, W.R. TACC3 transcriptionally upregulates E2F1 to promote cell growth and confer sensitivity to cisplatin in bladder cancer. *Cell death & disease* 9, 72. (2018)
11. Chen, W.*, Luo, K.*, Ke, Z., Kuai, B., **He, S.**, Jiang, W., Huang, W., and Cai, Z. TBK1 Promote Bladder Cancer Cell Proliferation and Migration via Akt Signaling. *Journal of Cancer* 8, 1892-1899. (2017)
12. Qiao, X.*, Su, R.*, Wang, Y.*, Wang, R.*, Yang, T., Li, X., Chen, W., **He, S.**, Jiang, Y., Xu, Q., et al. Genome-wide Target Enrichment-aided Chip Design: a 66 K SNP Chip for Cashmere Goat. *Scientific reports* 7, 8621. (2017)
13. Zhang, L.*, Zhang, M., and **He, S.** The complete mitochondrial genome of great cormorant, *Phalacrocorax carbo* (*Phalacrocorax*, *Phalacrocoracidae*). *Mitochondrial DNA Part A, DNA mapping, sequencing, and analysis* 28, 1-2(2017).
14. Yang, J.*, Chen, X.*, Bai, J.*, Fang, D.*, Qiu, Y.*, Jiang, W.*, Yuan, H., Bian, C., Lu, J., **He, S.**, et al. The *Sinocyclocheilus* cavefish genome provides insights into cave adaptation. *BMC biology* 14, 1. (2016)
15. Chang, L.*, **He, S.***, Mao, D.*, Liu, Y., Xiong, Z., Fu, D., Li, B., Wei, S., Xu, X., Li, S., et al. Signatures of Crested Ibis MHC Revealed by Recombination Screening and Short-Reads Assembly Strategy. *PloS one* 11, e0168744. (2016)
16. **He, S.***, Lu, J., Jiang, W., Yang, S., Yang, J., and Shi, Q. The complete mitochondrial genome sequence of a cavefish *Sinocyclocheilus anshuiensis* (Cypriniformes: Cyprinidae). *Mitochondrial DNA Part A, DNA mapping, sequencing, and analysis* 27, 4256-4258. (2016)
17. Chang, L.*, **He, S.**, Zhang, J., Zhang, Q., and Li, S. The complete mitochondrial genome sequence of *Eudocimus ruber* (Pelecaniformes:Threskiornithidae). *Mitochondrial DNA Part A, DNA mapping, sequencing, and analysis* 27, 2941-2942. (2016)
18. Hu XX, Lu J, **He SY**, Li XF, Liu HJ, Han LJ. The complete mitochondrial genome of *Astatotilapia burtoni*. *Mitochondrial DNA A DNA Mapp Seq Anal.* 27(4):2379-80. doi: 10.3109/19401736.2015.1028039. (2016)
19. Fan, Q., Chen, S., Li, M., **He, S.**, Zhou, R., and Liao, W. Development and characterization of microsatellite markers from the transcriptome of *Firmiana danxiaensis* (Malvaceae s.l.). *Applications in plant sciences* 1. (2013)