# Sheng Wang

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## Education

**POSTDOCTORAL SCHOLAR| 2019.07 – PRESENT| UNIVERSITY OF CALIFORNIA, SAN FRANCISCO**

- Institute for Neurodegenerative Diseases

**VISITOR GRADUATOR SCHOLAR | 2016.11 – 2019.06 | UNIVERSITY OF CALIFORNIA, SAN FRANCISCO**

- Institute for Neurodegenerative Diseases

**PHD | 2013.09 – 2019.01 | CHINA AGRICULTURAL UNIVERISTY & NATIONAL INSTITUTE OF BIOLOGICAL SCIENCES, BEIJING, CHINA**

- Major: Molecular biology and biochemistry

**BACHELOR | 2009.09 – 2013.06 | CHINA AGRICULTURAL UNIVERISTY, CHINA**

- Major: Biological science

## Research Experience

**VISITOR GRADUATE SCHOLAR, UCSF, SAN FRANCISCO, CA 2016-2019**

Genetic study on Tourette syndrome (TD) and autistic spectrum disorder (ASD). Researches mainly focused on *de novo* variants detection, including *de novo* SNVs/INDELs and *de novo* CNVs, from whole-exome sequencing data and genotyping data. Following with systematic biological analysis to investigate the functional contribution of the *de novo* events. By integrating suitable bioinformatics tools to study the genetic risks underlying ASD and TD. Routine work also contained the confirmation of variants by wet-lab work.

**PHD CANDIDATE, NATIONAL INSTITUTE OF BIOLOGICAL SCIENCES, BEIJING 2014-2016**

Research focused on mosaicism in multiple tissues from heathy individual donors. By unitizing single-cell whole-genome sequencing and bulk-tissue whole-genome sequencing, we expected to detect mosaic mutations in different tissues which could occur at different developmental stages. We were looking forward to explaining the origin of different somatic mutations and also offer a clue to the establishment of varies somatic mutation signatures in distinct non-cancer samples.

**PHD CANDIDATE ROTATION, NATIONAL INSTITUTE OF BIOLOGICAL SCIENCES, BEIJING 2013-2014**

Epigenetic markers, including DNA methylation and histone modification etc., function together to regulate the genes expression. To study the interaction of DNA methylation and histone modification, a stable cell line carrying a hypermethylated EGFP marker was established and followed with high-throughput screening which involved more than one hundred thousand of small chemicals. Through the screening, we sought to find chemicals that could affect gene expression without changing the state of DNA methylation, which could be a candidate drug in the treatment of DNA methylation related disease.

**RESEARCH ASSISTANT 2010-2012**

- Learn protein related skills and protein design
- Collage funded program to study the function of flap structure-specific endonuclease1(fen1) in *Neurospora crassa*.

## Research Experience

**VOLUNTEER IN STAR & RAIN INSTITUTE, BEIJING** **2014-2016**

- Help collect samples as well as questionnaires from ASD (autism spectrum disorder) families

## Skills

**DRY-LAB WORK**

- DNA sequencing related analysis, such as BWA, GATK, Picard, samtools, etc.
- Programming languages: Python, R, Perl, bash, SQLite/MySQL

**WET-LAB WORK**

- Next-generation sequencing related methods, such as whole genome/exome/targeted re-sequencing
- Molecular biological skills

**COMMUNICATION**

- Native speaker of Mandarin
- Oral and written of English

## Publication

**Wang S**, Mandell JD, et al. (2018). De Novo Sequence and Copy Number Variants Are Strongly Associated with Tourette Disorder and Implicate Cell Polarity in Pathogenesis. Cell Rep. 24, 3441-3454.e12.

Zhou WZ, Zhang J, Li Z, Lin X, Li J, **Wang S**, et al. (2019). Targeted resequencing of 358 candidate genes for autism spectrum disorder in a Chinese cohort reveals diagnostic potential and genotype–phenotype correlations. Hum. Mutat. 40, 801–815.

Yang X, Yang X, Chen J, Li S, Zeng Q, Huang AY, Ye AY, Yu Z, **Wang S**, et al. (2019). ATP1A3 mosaicism in families with alternating hemiplegia of childhood. Clinical Genetics 96, 43–52.

Willsey AJ, Morris MT, **Wang S**, et al. (2018). The Psychiatric Cell Map Initiative: A Convergent Systems Biological Approach to Illuminating Key Molecular Pathways in Neuropsychiatric Disorders. Cell 174, 505–520.

Huang AY, Yang X, **Wang S**, et al. (2018). Distinctive types of postzygotic single-nucleotide mosaicisms in healthy individuals revealed by genome-wide profiling of multiple organs. PLOS Genet. 14, e1007395.

Ye AY, Dou Y, Yang X, **Wang S**, et al. (2018). A model for postzygotic mosaicisms quantifies the allele fraction drift, mutation rate, and contribution to de novo mutations. Genome Res. 28, 943–951.

Dou Y, Yang X, Li Z, **Wang S**, et al. (2017). Postzygotic single-nucleotide mosaicisms contribute to the etiology of autism spectrum disorder and autistic traits and the origin of mutations. Hum. Mutat. 38, 1002–1013.

Yang X, Liu A, Xu X, Yang X, Zeng Q, Ye AY, Yu Z, **Wang S**, et al. (2017). Genomic mosaicism in paternal sperm and multiple parental tissues in a Dravet syndrome cohort. Sci. Rep. 7, 15677.

Xu X, Yang X, Wu Q, Liu A, Yang X, Ye AY, Huang AY, Li J, Wang M, Yu Z, **Wang S**, et al. (2015). Amplicon Resequencing Identified Parental Mosaicism for Approximately 10% of “de novo” SCN1A Mutations in Children with Dravet Syndrome. Hum. Mutat. 36, 861–872.

Huang AY, Xu X, Ye AY, Wu Q, Yan L, Zhao B, Yang X, He Y, **Wang S**, et al. (2014). Postzygotic single-nucleotide mosaicism in whole-genome sequences of clinically unremarkable individuals. Cell Res, 24:1311-1327.