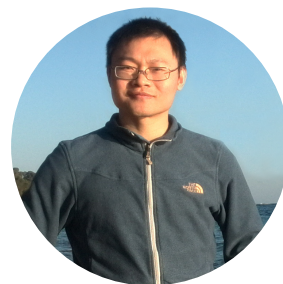


Shengwei Hou

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Education

FuhrmanLab, Department of Biological Sciences, University of Southern California

Los Angeles, United States

POSTDOC - RESEARCH ASSOCIATE IN BIOINFORMATICS

Api. 2018 - now

- “Metagenomic and Metatranscriptomic Data Analyses of Marine Microbial Communities” supervised by **Prof. Jed A. Fuhrman**

Freiburg Institute for Advanced Studies (FRIAS), Freiburg University

Freiburg, Germany

POSTDOCTORAL RESEARCHER IN BIOINFORMATICS

Oct. 2017 - Feb. 2018

- “Genome-Wide Map Pairwise sRNA-RNA Interactions in *Staphylococcaceae aureus*” supervised by **Prof. Wolfgang R. Hess**

Cyanolab, Freiburg University

Freiburg, Germany

PH.D. IN BIOINFORMATICS

Sep. 2013 - Apr. 2018

- “Genomic and transcriptomic Analyses of Marine Microorganisms” supervised by **Prof. Wolfgang R. Hess**
- *Ph.D. Defense Grading*: Dissertation: 1.0, Examination: 1.0, Overall: 1.0 (scale 5.0-1.0).

XuLab, Institute of Hydrobiology, Chinese Academy of Sciences

Wuhan, China

MASTER OF MOLECULAR GENETICS

2009.09-2013.06

- “*HetR Binding Site Upstream of patA Is Required for Heterocyst Patterning*” supervised by **Prof. Xudong Xu**
- *Master Defense Grading*: 93.4 (scale 0.0-100.0).
- *GPA*: 3.38/4.0

Southwest University, China

Chongqing, China

BACHLOR OF BIOLOGY, MAJORING IN BIOLOGY AND BIOTECHNOLOGY

2005.09-2009.07

- “*Cloning of IFN- γ from Newcastle Disease Virus (NDV) Stimulated Swine Lymphocytes*” supervised by **Prof. Huamao Du**
- *GPA (overall)*: 3.55/4.0
- *GPA (major)*: 3.74/4.0

Conferences & Workshops

2017 ELIXIR-IIB Training Programme on Machine Learning

San Michele all'Adige, Italy

PARTICIPANT: “MACHINE LEARNING FOR BIOLOGISTS”

4th - 7th Sept. 2017

- Adopted basic machine learning skills for genomic and transcriptomic data analyses

2016 MaCuMBA “Marine Microbiome: Discovery & Innovation” International Conference

Berlin, Germany

POSTER: TAXONOMIC AND TRANSCRIPTIONAL DYNAMICS OF THE MICROBIAL COMMUNITY DURING A TRICHODESMIUM BLOOM

27th - 30th Jun. 2016

- Presented the primary analysis results of metagenomic and metatranscriptomic data sets

2015 Black Forest Summer School on “NGS data for phylogenetics”

Feldberg, Germany

POSTER: DIFFERENTIAL RNA-SEQ ANALYSIS OF MICROBIAL POPULATIONS (META-DRNA-SEQ)

14th - 17th Sept. 2015

- Presented the mdRNA-Seq results

2014 EU MaCuMBA Project General Assembly

Cadiz, Spain

PRESENTATION: METATRANSCRIPTOME ANALYSIS OF MARINE MICROBIAL POPULATIONS USING dRNA-SEQ APPROACH

21st - 27th Sept. 2014

- Introduced the dRNA-Seq method and its potential application in marine microbial communities

2013 Training Course of Bernstein Center Freiburg, Department of Neurobiology and Neurotechnology

Freiburg, Germany

PARTICIPANT: “SCIENTIFIC PROGRAMMING IN PYTHON”

14th Oct. - 1st Nov. 2013

- Learned basic Python syntax and scientific libraries

2013 International PHOTO.COMM Training Workshop

Freiburg, Germany

PARTICIPANT: “BIOINFORMATIC ANALYSIS OF TRANSCRIPTOMIC AND GENOMIC DATASETS IN METABOLIC CONTEXT”

8th - 12th Sept. 2013

- Adopted basic bioinformatics data analysis skills

Teaching Assistantships

“Genetics” and “Microbiology” given by Prof. Wolfgang R. Hess at Freiburg University

Freiburg, Germany

TEACHING ASSISTANT

2016 - 2017 semester

- Assisted students in finding homolog search using BLAST Suite during the hands on session

“Bioinformatics” for Bachelor Students given by Dr. Wolfgang Maier at Freiburg University

Freiburg, Germany

TEACHING ASSISTANT

Jun. 20th - Jul. 15th 2016

- Prepared course materials for image processing module
- Gave one-day lecture on image processing using CellProfiler
- Answered questions and solved problems during the hands on session

“Python Crash Course” for Biologists given by Dr. Björn Grüning at Freiburg University

Freiburg, Germany

TEACHING ASSISTANT

15th - 18th Dec. 2015

- Prepared the Jupyter notebooks for this course
- Answered questions and solved problems during the hands on session

Publications

Note: [§]Co-First Author, * Corresponding Author

Xiaoming Tan[§], **Shengwei Hou**[§], Kuo Song, Jens Georg, Stephan Klähn, Xuefeng Lu*, Wolfgang R. Hess*. The Primary Transcriptome of the Fast-Growing Cyanobacterium *Synechococcus elongatus* UTEX 2973. (**submitted**)

Shengwei Hou, Manuel Brenes, Alicia M. Muro-Pastor, Wolfgang R. Hess*. Lost in recombination ? CRISPR-Cas systems in complex cyanobacteria. (**submitted**)

Weichao Huang*, Ilka Haferkamp, Bernard Lepetit, Carolina Río Bártulos, **Shengwei Hou**, Wolfgang Jeblick, Peter G. Kroth. Reduced vacuolar β -1,3-glucan synthesis affects carbohydrate metabolism, plastid homeostasis and structure in *Phaeodactylum tricornutum*. **Proc. Natl. Acad. Sci.** April 18, 2018, ahead of print

Jonna E. Teikari, David P. Fewer, Rashmi Shrestha, **Shengwei Hou**, Niina Leikoski, Minna Hämäläinen, Asko Simojoki, Wolfgang R. Hess, and Kaarina Sivonen*. Strains of the toxic and bloom-forming *Nodularia spumigena* (cyanobacteria) can degrade methylphosphonate and release methane. **The ISME J** 2018 Feb 14:1.

Shengwei Hou[§], Mario López-Pérez[§], Ulrike Pfreundt, Natalia Belkin, Kurt Stüber, Bruno Huettel, Richard Reinhardt, Ilana Berman-Frank, Francisco Rodriguez-Valera and Wolfgang R. Hess*. Benefit from decline: The primary transcriptome of *Alteromonas macleodii* str. Te101 during *Trichodesmium* demise. **The ISME J** 2018 Jan 15:1

Dan Miller, Ulrike Pfreundt, **Shengwei Hou**, Steffen Lott, Wolfgang R Hess and Ilana Berman-Frank*. Winter Mixing Induces Reshuffling and Impacts Gene Expression of Marine Microbial Populations in the Gulf of Aqaba. **Aquat Microb Ecol** 80:223-242.

Jonna E. Teikari[§], **Shengwei Hou**[§], Matti Wahlsten, Wolfgang R. Hess* and Kaarina Sivonen*. Comparative genomics of the Baltic Sea toxic cyanobacteria *Nodularia spumigena* UHCC 0039 and its response on varying salinity. **Frontiers in microbiology** 2018 Mar 8;9:356

Tao Zhu[§], **Shengwei Hou**[§], Xuefeng Lu*, Wolfgang R. Hess*. Draft Genome Sequences of Nine Cyanobacterial Strains from Diverse Habitats. **Genome Announc.** 2017 Mar 2;5(9). pii: e01676-16.

Ulrike Pfreundt[§], Dina Spungin[§], **Shengwei Hou**, Björn Voß, Ilana Berman-Frank, Wolfgang R. Hess*. Genome of a giant bacteriophage from a decaying *Trichodesmium* bloom. **Marine Genomics** 2017 Feb 22. pii: S1874-7787(17)30033-8.

Shengwei Hou, Ulrike Pfreundt, Dan Miller, Ilana Berman-Frank, Wolfgang R Hess*. mdRNA-Seq analysis of microbial communities. **Sci. Rep.** 2016 Oct 19;6:35470.

Shengwei Hou, Fang Zhou, Shan Peng, Hong Gao and Xudong Xu*. The HetR-binding site that activates expression of *patA* in vegetative cells is required for normal heterocyst patterning in *Anabaena* sp. PCC 7120. **Sci. Bull.** 2015 Jan;60(2):192-201.

Yun Wang, **Shengwei Hou**, Fei Ke and Hong Gao*. Bibliometric analysis of research on microcystins in China and worldwide from 1991 to 2011. **Desalination and water treatment** 53(1):1-12

Zhiwei Hou, Yun Wang, Hong Gao* and **Shengwei Hou***. The principle of dRNA-seq and its applications in prokaryotic transcriptome analyses. **Yi Chuan** 2013 Aug;35(8):983-91 (**in Chinese**).

Ye Du, Yan Cai, **Shengwei Hou** and Xudong Xu*. Identification of the HetR-recognition sequence upstream of *hetZ* in *Anabaena* sp. Strain PCC 7120. **J. Bacteriol.** 2012 May;194(9):2297-306.