

# SIDDHARTH S. TOMAR

## PERSONAL INFORMATION

*Born in India*, 08 May 1994

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## EDUCATION

*Master of Science*

2016-2018 KTH Royal Institute of Technology

Master's programme in Molecular Techniques in Life Science, a joint program with Karolinska Institutet and Stockholm University

Duration: 2 years (full time)

Date of graduation: 31-May-2018

Country: *Sweden*

*Bachelor of Technology*

2012-2016 Jaypee University of Information Technology

GPA: 8.6 out of 10 · *Specialization in Bioinformatics*

Duration: 4 years (full time)

Date of graduation: 09-July-2016

Country: *India*

## BIOINFORMATICS SKILLS

*Workflows*

Genome/Transcriptome assembly, Quantification, Differential expression, Novel gene discovery, Time series analysis, Weighted correlation network analysis

*Programming*

C++/C (INCLUDING CUDA AND MPI), JAVA, PYTHON, PERL, R

*Databases*

MySQL

*Machine learning*

SCIKIT-LEARN, TENSORFLOW

*Documentation*

L<sup>A</sup>T<sub>E</sub>X, MARKDOWN

*Version control*

GIT

*Model organisms*

HUMAN, MICE, *P. ABIES*

## LAB SKILLS

*Genetic Engineering*

Gene cloning using bacteria, Gene disruption and gene replacement in bacteria

*General*

DNA isolation, RNA isolation, Plasmid and genomic DNA isolation, PCR, Sanger and Illumina sequencing

## COURSEWORK - KEYWORDS

*Molecular biology*

Systems biology, Genetics, translational research in cardiology, neurodegenerative disorders, homology search, multiple sequence alignment, phylogeny reconstruction, protein topology prediction, biophysical chemistry, molecular dynamics, comparative genomics, proteomics, mass spectrometry, antibody assays, short and long read sequencing, microarrays, bead based assays, droplet barcoding, single cell sequencing, ChIP sequencing

## RESEARCH EXPERIENCE

*Jun'18–present*      KAROLINSKA INSTITUTET - Sweden

*SciLifeLab -  
Stockholm*

I'm currently working as a research assistant in Dr Claudia Kutter's group in Science For Life laboratory, Stockholm. My current work builds upon my experience in my master's thesis and is more focused on the developmental dynamics of PIWI-interacting RNA (piRNA) in mice and their interplay with transposons. This project also involves an in-depth characterization of piRNA genes with respect to their function in regulating genomic integrity and as an individual class of genes.

Reference: Claudia KUTTER · +46-704933896 · [claudia.kutter@ki.se](mailto:claudia.kutter@ki.se)

*Jun–Aug '17*      KAROLINSKA INSTITUTET - Sweden

*SciLifeLab -  
Stockholm*

After being awarded SciLifeLab Summer Fellowship, I joined Dr. Claudia Kutters group at the Karolinska Institute/SciLifeLab. My work was focused on annotating various RNA classes from mice liver at various developmental stages by using of total RNA sequencing data. This project involved methods for discovering novel developmental stage-specific noncoding RNAs and correlation with other meta resources to mark functionality.

Reference: Claudia KUTTER

*Jun–Aug '15*      INSTITUTE OF ONCOLOGY RESEARCH - Switzerland

*IOSI-IOR*

Worked under Dr. Francesco Bertoni's group at Institute of Oncology Research, Bellinzona, Switzerland on performance profiling of short read aligners (using Nvidia CUDA framework) for testing scalability in GPGPU environment. I studied impact of GPU based tools on NGS analysis pipeline and included cost versus performance analysis.

Reference: Ivo KWEE +41-794283375 · [ivo.kwee@ior.iosl.ch](mailto:ivo.kwee@ior.iosl.ch)

*Master's thesis*

*Micro-evolution of regulatory RNAs*

In this master thesis project, I am currently investigating the functional contribution of regulatory RNA in speciation in closely related mice species. This involves studying dynamics of their species-specific gene expression by utilizing ChIP sequencing to define active promoters along with short and total RNA sequencing.

Supervisor: Claudia KUTTER

*Bachelor's thesis*

*Improving the computation of positive selection using codon models*

In my bachelor project, I successfully modified software algorithms to reduce the redundancy and increase the sensitivity by employing Branch-Site Model on GPU architecture. By running simulations, I tested the gains in efficiency and performance to validate that my algorithm modifications were appropriate.

## PROJECTS

*2017*      KTH ROYAL INSTITUTE OF TECHNOLOGY

*Course Project*

Assembling reference transcriptome for *P. abies* using massively parallel and PacBio real time sequencing data. This project involved utilization of large amount of data (>700 million reads) and optimization techniques for transcriptome assembly.

Reference: Lars ARVESTAD · +4687906436 · [lars.arvestad@scilifelab.se](mailto:lars.arvestad@scilifelab.se)

*2017*      STOCKHOLM UNIVERSITY

*Course Project*

Constructing a SVM based predictor for classifying topological features of  $\beta$  barrels based on their sequence.

*2014*      Jaypee University of Information Technology

*Course Project*

Identification of novel leads against dimeric interface(DBP) in *P. vivax* using computer-aided drug design. For this project, I investigated the structural dynamics of Duffy binding proteins with respect to the phylum Apicomplexa.

	2013	Jaypee University of Information Technology
<i>Course Project</i>	Created an application written in Java for searching repeat content in a given genome. Simple machine learning technique was used, applying the Hidden Markov Model. Lempel–Ziv–Welch algorithm was also used and modified according to requirements. Perl was used as a wrapper and as text acquisition/annotation search engine.	

#### POSTER PRESENTATION AND CONFERENCES

	2018	2 <sup>nd</sup> Uppsala Transposon Symposium
<i>Poster</i>	Micro-evolution of regulatory RNA in <i>M. domesticus</i> and <i>M. castaneus</i>	

#### OTHER INFORMATION

<i>Scholarships</i>	2017 · Science for Life Laboratory summer fellowship
	2017 · Karolinska Institutet Foundation scholarship

<i>Languages</i>	ENGLISH · Fluent
	HINDI · Native

Last updated on January 14, 2019