

Satyanarayan Rao

Indian Institute of Technology, Roorkee,
India

Department of Biological Sciences and
Bioengineering

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EDUCATION

Assistant Professor, BSBE

Postdoctoral Fellow, Ramachandran Lab
Nov. 2018-Jul. 2023

Ph.D., Computational Biology
2012-2018

Integrated Post Graduation
2005-2010

Intermediate (12th)
2001-2003

Secondary (10th)
2001

Indian Institute of Technology, Roorkee,
Uttarakhand, India

University of Colorado, Denver | Anschutz
Medical Campus, Aurora, Colorado, USA

University of Southern California, Los
Angeles, California, USA

ABV-Indian Institute of Information
Technology & Management (IIITM),
Gwalior, Madhya Pradesh, India

Gaya College Gaya, Bihar Intermediate
Education Council

Sarvoday Vidhya Mandir, Bihar Secondary
Education Board

FELLOWSHIPS/SCHOLARSHIP

1. Cancer League of Colorado (2022)
2. Viterbi Fellowship (2012-2014)

3. JRF (2011-2012)

4. GATE (2008-2010)

For monitoring cancers using blood test
For studying role of DNA methylation in
protein-DNA interactions

Contributing to the development of scoring
function ([pcSM](#)) for decoy selection in
protein-structure prediction

As a GATE qualified fellow

AWARDS

1. Professional Development Award

For American Association Cancer
Research (AACR) Annual Meeting 2021

PATENTS

1. Signatures in Cell-free DNA to Detect Disease, Track Treatment Response, and Inform Treatment Decisions United States Patent: [WO2022061080A1](#)

PUBLICATIONS

(https://scholar.google.com/citations?user=N_dl42AAAAAJ&hl=en)

*Equal Contribution, #Corresponding Author

Preprints

1. Han AL, Paul KV, **Rao S**, Brechbuhl HM, Sartorius CA, Ramachandran S, Kabos P. Estradiol (E2) concentration shapes the chromatin binding landscape of the estrogen receptor. bioRxiv, 2022
<https://doi.org/10.1101/2022.09.23.509212>

Peer-reviewed Journal Publications

2. Chiu TP, **Rao S**, Rohs R. Physicochemical models of protein–DNA binding with standard and modified base pairs. Proceedings of the National Academy of Sciences, 2023; 120(4), e2205796120
<https://doi.org/10.1073/pnas.2205796120>
3. **Rao S***, Han A*, Zukowski A, Kopin E, Sartorius CA, Kabos P, Ramachandran S. Transcription Factor-Nucleosome Dynamics from Plasma cfDNA identifies ER-driven states in Breast Cancer. Science Advances, 2022; 8(34):eabm4358
<https://doi.org/10.1126/sciadv.abm4358>
4. **Rao S***, Ramachandran S. A computational pipeline to visualize DNA-protein binding states using dSMF data. STAR Protocols 2022; s 3, 101299
<https://doi.org/10.1016/j.xpro.2022.101299>
5. **Rao S**, Ahmad K, Ramachandran S. Cooperative Binding between distant transcription factors is a hallmark of active enhancers. Molecular Cell 2021; 81:8:1651-1665
<https://doi.org/10.1016/j.molcel.2021.02.014>
6. Zukowski A*, **Rao S***, Ramachandran S. Phenotypes from cell-free DNA. Open Biology 2020; 10:200119
<http://dx.doi.org/10.1098/rsob.200119>
7. Lara-Gonzalez S, Dantas Machado AC, **Rao S**, Napoli AA, Birktoft Jens, Di Felice R, Rohs R, Lawson CL. The RNA polymerase α subunit recognizes the

DNA shape of the upstream promoter element. *Biochemistry* 2020; 59:48: 4523-4532

<https://doi.org/10.1021/acs.biochem.0c00571>

8. **Rao S**, Chiu TP, Kribelbauer JF, Mann RS, Bussemaker HJ, & Rohs R. Systematic prediction of DNA shape changes due to CpG methylation explains epigenetic effects on protein-DNA binding. *Epigenetics and Chromatin* 2018;11(6).
<https://doi.org/10.1186/s13072-018-0174-4>
9. Chiu TP, **Rao S**, Mann RS, Honig B, & Rohs R. Genome-wide prediction of minor-groove electrostatic potential enables biophysical modeling of protein-DNA binding. *Nucleic Acids Res.* 2017
<https://doi.org/10.1093/nar/gkx915>
10. Dantas Machado AC, Zhou T, **Rao S***, Goel P, Rastogi C, Lazarovici A, Bussemaker HJ & Rohs R. Evolving insights on how cytosine methylation affects protein-DNA binding. *Brief. Funct. Genomics.* Oxford University Press; 2015;14:61–73.
<https://doi.org/10.1093/bfpg/elu040>
11. Mishra A, **Rao S**, Mittal A, & Jayaram B. Capturing native/native like structures with a physico-chemical metric (pcSM) in protein folding. *Biochim. Biophys. Acta - Proteins Proteomics.* 2013;1834:1520–31
<https://doi.org/10.1016/j.bbapap.2013.04.023>

Peer-reviewed Conference Publications

1. **Rao S**, Pattanaik KK, & Bhattacharya M. Toolkit for grid-enabled high resolution image processing. *Signal Process. Syst. (ICSPS)*, 2010 2nd Int. Conf. 2010;3:V3-724-V3-728.
<https://doi.org/10.1109/ICSPS.2010.5555764>
2. Goel S, Garg V, Ranjan P, **Rao S***, & Bhattacharya M. ASR system integration with asterisk for SIP or IAX softphone clients. 2009 Int. Assoc. Comput. Sci. Inf. Technol. - Spring Conf. IACSIT-SC 2009. 2009. p. 100–4
<https://doi.org/10.1109/IACSIT-SC.2009.87>

NEWS AND VIEWS ---

1. Molecular Cell Cover: The submitted cover image relating to Rao et al., *Mol Cell*, 2021 for Molecular Cell April 15, 2021 issue was selected to be the cover for that issue.
[https://www.cell.com/molecular-cell/issue?pii=S1097-2765\(20\)X0009-8#fullCover](https://www.cell.com/molecular-cell/issue?pii=S1097-2765(20)X0009-8#fullCover)

2. Commentary by Abdulhay NJ, and Ramani V: Rao et al., Mol Cell, 2021 was selected for featured review for Molecular Cell April 15, 2021 issue.
<https://pubmed.ncbi.nlm.nih.gov/33861946/>
3. News coverage by University of Colorado Cancer Center: Findings from Rao et al., Mol Cell, 2021 was covered by the Cancer Center at CU Anschutz.
<https://news.cuanschutz.edu/cancer-center/how-transcription-factors-work-together-in-cancer-formation>
4. News coverage by University of Colorado Cancer Center: Findings from Rao et al., Sci Adv, 2022 was covered by the Cancer Center at CU Anschutz.
<https://news.cuanschutz.edu/cancer-center/researchers-find-less-risky-way-to-monitor-breast-cancer-progression>

TALKS

1. Competing for DNA: Presented at IIT Roorkee, April 27, 2022
2. Competing for DNA: Presented at IIIT Delhi, April 06, 2022
3. Competing for DNA: Presented at NCBS Bangalore, April 01, 2022
4. Competing for DNA: Presented at IMSc Chennai March 31, 2022
5. Competing for DNA: Presented at IIT Bombay, March 30, 2022
6. Tracking Cancers Using Transcription Factors: Presented at IIT Delhi, November 17, 2021
7. Lightning Talk at Annual Event (virtual) Sci-ROI, September 25 – October 3, 2021
8. Transcription Factor-Nucleosome Dynamics Inferred from Plasma cfDNA Delineates Tumor Phenotype: Presented in the Department (BMG) Talk January 29, 2021
9. How do Proteins Bind Enhancers? Presented in the Department (BMG) Talk May 22, 2020
10. In vivo Mapping of Transcription Factor Cooperativity Genome-wide: presented in Postdoctoral Association Seminar Series May 21, 2020
11. In vivo Mapping of Transcription Factor Cooperativity Genome-wide: presented in Cold Spring Harbor Laboratory Meeting March 11–13, 2020 — Systems Biology: Global Regulation of Gene Expression
12. Non-Invasive Inference of Transcription Factor-Nucleosome Dynamics in Humans: presented in the Department (BMG) Talk October 04, 2019

POSTER PRESENTATIONS

***Equal contribution, #Presented**

1. **Rao S**, Zukowski A, Weirich A, Kabos P, Stensland EM, Eide IJZ, Brustugun OT, Ramachandran S. Using cell-free DNA to predict response to immunotherapy in non-small cell lung cancer pre- and post-treatment. Selected for e-poster, June 2-6, 2023 at **ASCO Annual Meeting, 2023**
2. **Rao S**^{#*}, Han A*, Zukowski A, Kopin E, Kabos P, & Ramachandran S. Transcription Factor-Nucleosome Dynamics inferred from plasma cfDNA delineates tumor and tumor-microenvironment phenotype: Selected for e-poster April 10-15, 2021 at **AACR Annual Meeting, 2021 (virtual)**.
3. **Rao S**[#], Chiu TP, Kribelbauer JF, Mann RS, Bussemaker HJ, & Rohs R. Systematic prediction of DNA shape changes due to CpG methylation explains epigenetic effects on protein-DNA binding. Presented in "System Biology: Global Regulation of Gene Expression", March 20-23, 2018 at **CSHL, New York**.
4. Chiu TP*, **Rao S**^{#*}, Xin B*, & Rohs R. Transcription factor family-specific DNA readout by multiscale specificity models. Presented in "System Biology: Global Regulation of Gene Expression", February 26-March 2, 2017 at **CSHL, New York**.
5. **Rao S**, Bussemaker HJ, & Rohs R. High-throughput prediction of DNA shape features for methylated DNA. Presented in "ISCB/RECOMB 2016 Regulatory and Systems Genomics", November 6-9, 2016 at **Phoenix, Arizona**.
6. **Rao S**^{#*}, Dantas Machado AC*, Goel P*, Zhou T*, Rastogi C*, Bussemaker HJ, & Rohs R. Evolving insights on how cytosine methylation affects protein-DNA binding. Presented at "19th Conversation on Biomolecular Structure & Dynamics", June 9-13, 2015 at **Albany, New York**.

COMPUTATIONAL SKILLS

Programming/Scripting language

Tools

Simulations/Modeling

Operating Systems

Computational Biology related skillsets
(selected)

Visualization

Python, R, C++/Advance Bash

Bioconductor, Anaconda

GROMACS, AMBER

*nix, Windows

Big Data Science, Machine Learning,
Snakemake, NGS data analysis
ggplot2, seaborn, gnuplot

TEACHING/WORK EXPERIENCE

Project-Level Mentoring at University of Colorado, Anschutz medical Campus

Mentored three undergraduates, and three graduate students in computational biology aspects of the project. Particularly, training them in programming language and project design. Programming languages include Python, R and Bash Scripting, design included Snakemake.

Teaching Assistant at University of Colorado Denver | Anschutz Medical Campus, Aurora

Durations: Spring 2019, Spring 2020

Course: MOLB 7900, Practical Computational Biology for Biologists using Python

Teaching Assistant at USC, Los Angeles

Duration: Spring, 2018

Course: BISC 312: Molecular Biochemistry

Duration: Spring, 2016

Course: BISC 120: General Biology, Organismal Biology and Evolution

Duration: Spring, 2015

Course: BISC 150: Nature of Human Health and Disease

Duration: Fall, 2014

Course: BISC 481: Structural Bioinformatics, from Atoms to Cells

Responsibilities included:

- Holding office hours, grading exams
- Taking lab sessions (BISC 120 & 150)

Junior Research Fellow at SCFBio, IIT Delhi

Duration: January, 2011-July, 2012

Mentor: Professor B. Jayaram

Responsibilities included:

- Developing scoring function to discriminate native or near-native like protein structures from set of decoys; [Mishra et al., 2013](#)
- Developing code for spatial distribution of C-alpha atoms of native structures in terms of n, k space distribution; [Mittal et al., 2012](#)

ACHIEVEMENTS/ACCOLADES

- Procured All India Rank **142** in Graduate Aptitude Test for Engineers (**GATE, conducted by IIT**) 2008 in Information Technology stream.
- Won **1st Prize** in **Akraman-The Hacking Contest** in National Level Technical Fest **Infotsav'07** at ABV-IIITM, Gwalior; shared with Vikash Garg
- Stood among top 1% students who appeared for All India Engineering Entrance Examination (AIEEE), 2005, with **AIR – 3222**.
- Active member of table tennis and cricket team represented institute in **Twaran'08-'09** (National sport festival of ABV-IIITM).

EXTRACURRICULAR ACTIVITIES

I am an active student of Kalaripayattu, an Indian Martial Arts form, and being mentored by Guru Anil Natyaveda. I take good interest in doing Improvisation (past member of Vidushak at USC) and I am enthusiastic about sports particularly for Table Tennis.

Languages: Hindi, English

I want to acknowledge all the efforts put in toward open-source software/tools which help bring science to the next level!

REFERENCES

on request.