

# Savar D Sinha

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## EDUCATION

### California Institute of Technology

*Bachelor of Science in Computer Science*

Pasadena, CA

*Sept 2022 – June 2026*

### Hamilton High School

*High School Diploma*

Chandler, AZ

*July 2018 – May 2022*

## STANDARDIZED TEST SCORES

### SAT: 1580

*Reading: 780; Math: 800*

### ACT: 35

## RELATED COURSES

### 2023-2024:

**CS 024 — Introduction to Computing Systems**

**Ma 002 — Differential Equations**

**Ph 012A — Waves, Quantum Physics, and Statistical Mechanics**

### 2022-2023:

CS 001X — Intermediate Computer Programming

CS 002 — Introduction to Programming Methods

CS 003 — Introduction to Software Design

Ma/CS 006A — Introduction to Discrete Mathematics

CS 021 — Decidability and Tractability

Ph 001BC — Classical Mechanics and Electromagnetism (Analytical)

Ph 021 — Computational Physics Lab II

## HONORS AND AWARDS

**SURF Award** 2023

**Summa Cum Laude, Hamilton High School** 2022

**National Merit Finalist** 2022

**Top 300 Regeneron STS Scholars** 2022

**3rd Place Arizona Science and Engineering Fair** 2021

**AP Scholar with Distinction** 2020-2022

## PUBLICATIONS AND MANUSCRIPTS

**Sinha SD**, Wideman JG (2023) The persistent homology of mitochondrial ATP synthases. *IScience*, 26(5), 106700. doi: [10.1016/j.isci.2023.106700](https://doi.org/10.1016/j.isci.2023.106700).

Macher JN, Coots NL, Girard EB, Langerak A, Muñoz-Gómez SA, **Sinha SD**, Vos R, Wissels R, Gile G, Renema W, Wideman JG. (2023) Single-Cell Genomics Reveals the Divergent Mitochondrial Genomes of Retaria (Foraminifera and Radiolaria). *MBio*, 0(0), e00302-23. doi: [10.1128/mbio.00302-23](https://doi.org/10.1128/mbio.00302-23)

Singh RP, Poh Y-P, **Sinha SD**, Wideman JG. (2023) Evolutionary history of oxysterol binding proteins (OSBPs) reveals complex history of duplication and loss in animals and fungi. *Contact*. 2023;6. doi: [10.1177/25152564221150428](https://doi.org/10.1177/25152564221150428).

Záhonová K, Lax G, **Sinha SD**, Leonard G, Richards TA, Lukeš J, Wideman JG. (2021) Single-cell genomics unveils a canonical origin of the diverse mitochondrial genomes of euglenozoans. *BMC Biology*. 19: 103. doi: [10.1186/s12915-021-01035-y](https://doi.org/10.1186/s12915-021-01035-y).

## ORAL/POSTER RESEARCH PRESENTATIONS

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**Sinha SD** et. al (2023) Combination genomic and epigenomic analysis of plasma cell-free DNA identifies stemness features associated with worse prognosis in high-risk metastatic castration-resistant prostate cancer. 2023 Radiation Oncology Research Retreat, WashU School of Medicine.

**Sinha SD**, Wideman JG (2021) The persistence of homology: Diversity and evolution of eukaryotic ATP synthases. ASU CME Lab Meeting Presentation.

Záhonová K, Lax G, **Sinha SD** et al. (2021) Single-cell genomics unveils a canonical origin of the diverse mitochondrial genomes of euglenozoans. International Society of Protistologists 2021 Online Poster (page 62).

**Sinha SD**, Muñoz-Gómez SA, Wideman JG (2021) The persistence of homology: Diversity and evolution of eukaryotic ATP synthases. International Society of Protistologists 2021 Online Poster (page 83).

**Sinha SD**, Wideman JG (2020) Evolution of Eukaryotic ATP Synthase. ASU Evolutionary Biology Symposium 2020.

## RESEARCH IN THE MEDIA

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Accelerate your Research with AlphaFold, a Powerful Protein Prediction Application. 2021 Marisa Brazil. Highlighting our use of AlphaFold - figure by **Savar Sinha**. [ASU RTO website](#).

## RESEARCH EXPERIENCE

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**Dr. Aadel Chaudhuri, Washington University School of Medicine in St. Louis, Department of Radiation Oncology** June 2023 – August 2023

- Used Griffin pipeline to analyze nucleosome protection of the promoter regions of prostate cancer marker genes
- Compared methylation at transcription factor binding sites of high-risk and low-risk patients to demonstrate higher accessibility of some transcription factors in one group relative to the other
- Developed Bash, AWK, R, and Python scripts to parse and analyze large datasets.
- Created Kaplan-Meier plots to compare progression-free and total survival for risk-stratified patients

**Dr. Jeremy G. Wideman, Arizona State University, Center for Mechanisms of Evolution, Biodesign Institute, School of Life Sciences** Feb 2020 – May 2023

- Identified orthologues of animal and fungal ATP synthase subunits across over 200 eukaryotes spanning the tree of life.
- Utilized bioinformatic tools such as BLAST, MUSCLE, and HMMER on ASU's AGAVE cluster computing server to identify extremely divergent ATP synthase subunits in various lineages.
- Developed Bash, AWK, and Python scripts to perform such analyses on large datasets.
- Predicted the structures of divergent ATP synthase subunits via machine-learning based software such as AlphaFold2.
- Visualized structures using PyMOL.

**Science Fair** 2019-2022

- The Persistence of Homology: Unity and Diversity in Eukaryotic ATP Synthases (2022)
- Evolution of Eukaryotic ATP Synthase (2021)
- Monte Carlo Simulation of Tertiary Protein Folding in a 3D Lattice Model (2020)
- Ising Spin Model: from Ferromagnets to Financial Markets (2019)

## TECHNICAL SKILLS

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**Languages:** Java, Python, C, C++, Bash, AWK, R, Matlab

**Developer Tools:** VS Code, PyCharm, IntelliJ, Jupyter Notebook, RStudio, Git

**Python Libraries:** pandas, NumPy, SciPy, Matplotlib, TensorFlow, sklearn

## MISCELLANEOUS

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### **Indian Classical Music**

2012 – Present

- Won 1st Place in Bharathotsav International 2021 competition
- Sangeetshri School of Music (2018 – 2020)
- Phoenix Gharana (2012 – 2017)

### **Cello**

2014 – Present

- Caltech Symphony Orchestra (2022 – present)
- Chandler Symphony Orchestra (2019 – 2022)
- Metropolitan Youth Symphony (2018 – 2019)
- Phoenix Youth Symphony (2017 – 2018)