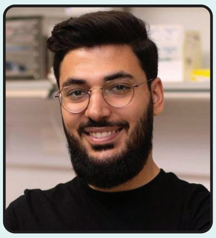

SAMI CHAABAN

sami.chaaban@gmail.com

Cambridge, UK

Google Scholar GitHub LinkedIn

Experienced structural biologist integrating experimental and computational approaches to decode complex biological systems and drive discovery

Employment

Investigator Scientist
MRC Laboratory of Molecular Biology
Cambridge, UK
Aug. 2024 — Present

- Addressing long-standing questions in cytoskeleton biology using cryo-electron microscopy (cryo-EM) and single-molecule biophysics in the lab of Andrew Carter
- Developing novel computational methods to analyze both electron and light microscopy datasets
- Applying machine learning based approaches to analyze cryo-EM image data
- Completed formal EMBO training in laboratory leadership, covering leadership styles, communication, feedback, motivation, and conflict management.

Postdoctoral Fellow
MRC Laboratory of Molecular Biology
Cambridge, UK
Sept. 2019 — Aug. 2024

- Solved the structure of the massive 4 MDa dynein protein complex, revealing how its architecture and conformational changes enable regulated motor activity
- Guided students through advanced research techniques, which includes supervision of a Master's thesis
- Published peer-reviewed articles in Nature and other leading scientific journals
- Earned prestigious awards and fellowships, including:
  - EMBO Postdoctoral Fellowship (2020–2022)
  - Joan A. Steitz Postdoc Prize (2022) *read about it here*
- Spearheaded institute-wide software deployments for structure prediction (e.g., AlphaFold) and protein binder design (e.g., BindCraft) to communicate with the computer cluster (SLURM)

Education

Ph.D., Biology
McGill University
Montréal, Canada
Sept. 2013 — Aug. 2019

- Used biophysical and structural techniques to investigate the protein tubulin from *Caenorhabditis elegans*, revealing broader insights into tubulin dynamics
- Graduated with distinction
- Awarded the Alexander Graham Bell Graduate Scholarship (2014-2017) and Cellular Dynamics of Macromolecular Complexes Scholarship (2012)
- GPA: 4.00/4.00
- Transferred from the M.Sc. program (2011-2013) directly into the Ph.D. program

B.Sc., Biology
McGill University
Montréal, Canada
Sept. 2007 — May 2011

- Dean's Honour List: Science (2008-2009), Engineering (2007-2008)
- Elected President of the Biology Undergraduate Student Union
- GPA: 3.87/4.00

Software development

github.com/sami-chaaban

Starparser

- Command-line interface to manipulate and mine data from cryo-electron microscopy data files (Relion STAR files)
- Provides 40+ functions
- Built with pandas, matplotlib, numpy, scipy

Alphascreen

- Command-line interface for AlphaFold prediction screens
- Retrieves sequences from UniProt and generates optimized inputs for pairwise predictions
- Assesses and ranks interactions
- Built with pandas, matplotlib, numpy, pymol, unipressed, biopython

Subflow

- Graphical user interface for processing cryo-EM images into structures, including filament subtraction
- Enables real-time, on-the-fly data analysis
- Built with tkinter, starparser, subprocess, threading, pandas, cryosparc-tools, scipy, mrcfile

Tracy

- Graphical user interface for processing single molecule imaging data
- Uses kymographs for robust particle tracking
- Analyses and organises track behaviour
- Built with PyQt, matplotlib, numpy, scipy

Seminars

AlphaFold: Use and Applications
Cambridge, UK
2023 — Present

- Giving annual lectures at the biophysics seminar series hosted by the MRC Laboratory of Molecular Biology
- Providing an introduction to protein structure prediction, focusing on AlphaFold
- Describing how to interpret AlphaFold results and use it in hypothesis-driven and curiosity-driven research
- Example lecture: youtube.com/embed/z7vyZD3ICkA?si=_jEYzP-3N5yYwZTq

Invited/competitive talks (selected)

- **JIP1/JIP3 enable a dynein-kinesin supercomplex**
  Dynein meeting 2025
  July 2025, Ann Arbor, MI, USA (conference, competitive)
- **Cryo-EM studies of cooperation between dynein/dynactin and kinesin-1**
  European Molecular Biology Laboratory
  June 2024, Heidelberg, Germany (conference, competitive)
- **Structure of the dynein motor complex bound to microtubules by cryo-EM**
  Human Technopole
  Januray 2023, Milan, Italy (virtual) (seminar series, invited)
- **Structure of the dynein motor complex bound to microtubules by cryo-EM**
  Centre de Recherce en Biologie Structurale, McGill University
  July 2022, Montréal, Canada (seminar series, invited)

Selected Publications Google Scholar

Structure of dynein-dynactin on microtubules shows tandem adaptor binding
Chaaban & Carter, 2022
Nature

Developed a method to solve the structure of the dynein-dynactin complex sparsely decorating microtubules by cryo-EM, revealing the molecular logic of the protein interactions therein.

Navigating protein structure prediction in the era of machine learning
Chaaban*, Ratkevičiūtė*, Lau*, 2024 **equal contribution*
The Biochemist

Presented a user-focused review of the latest protein structure prediction algorithms, showcasing their popular applications in biological research while highlighting key limitations and pitfalls.

A microtubule bestiary: structural diversity in tubulin polymers
Chaaban & Brouhard, 2017
Molecular Biology of the Cell

Explored the fascinating diversity of microtubule biology across the tree of life.

A force-sensitive mutation reveals a non-canonical role for dynein in anaphase progression
Salvador-Garcia et al., 2024
Journal of Cell Biology

Used AlphaFold2 to rationalize how mutations in dynein might impact its interaction with tubulin.

Asgard archaea reveal the conserved principles of ESCRT-III membrane remodeling
Souza*, Espadas*, Chaaban* et al., 2025 **equal contribution*
Science Advances

Adapted a filament-analysis method that I developed for a different biological problem to solve a structure of proteins decorating membranes.

The structure and dynamics of *C. elegans* tubulin reveals the mechanistic basis of microtubule growth
Chaaban et al., 2018
Developmental Cell

Used single-molecule biophysics and cryo-EM to understand the behaviour of highly dynamic filaments.

The synthetic diazonamide DZ-2384 has distinct effects on microtubule curvature and dynamics without neurotoxicity
Wieczorek, Bechstedt, Chaaban, Brouhard, 2016
Science Translational Medicine

Analysed the conformations of tubulin polymers and how they are affected by a chemotherapy drug candidate.

Macromolecular Crowding Pushes Catalyzed Microtubule Growth to Near the Theoretical Limit
Wieczorek*, **Chaaban*,** Brouhard, 2013 **equal contribution*
Cellular and Molecular Bioengineering

Described the biophysical properties of tubulin polymerization in the presence of crowding agents.

Programming Languages

Python
Shell scripting *Bash, Csh*

Language Proficiency

English *native*
French *professional*
Arabic *intermediate*

Hobbies

Music
  Piano: *jazz, improvisation*
  Acoustic guitar: *busking*
Bouldering