

**Ankur Garg, Ph.D.**  
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### **Summary**

- Broadly-trained scientist with 14+ years' experience in structural biology, biochemistry, and biophysics
- Accomplished structural biologist with demonstrated expertise in cryo-EM and X-ray crystallography for multiple target classes (multi-protein, protein-nucleic acid, and protein-inhibitor complexes, etc.)
- Highly-skilled in the design and execution of gene-to-structure workflows
- Proven ability to manage multiple programs simultaneously while leading cross-functional collaborations on accelerated timelines
- Experienced trainer and supervisor of technicians, Ph.D. students, and postdocs

### **Experience**

**Aug 2025 – present                      Research Investigator, HHMI / Cold Spring Harbor Laboratory**

Primary project: Structural dynamics between human Argonaute-2 and Ck1 $\alpha$  kinase in miRNA-mediated gene silencing

Collaborative projects: Structure-based drug design against DYRK1A kinase; Biochemical characterization of Dis3L2 ribonuclease

Current responsibilities:

- Design, execution, and troubleshooting of **gene-to-structure** workflows for 5-6 concurrent projects
- Determination of multi-component macromolecular structures by **cryo-EM** (sample preparation and optimization, grid preparation, negative stain EM, data collection, data processing, validation)
- Determination of macromolecular structures by **X-ray crystallography** (crystallization screening and optimization, crystal harvesting, synchrotron data collection, data processing, model building, refinement, validation)
- Construct design, cloning, and protein production in *E. coli*, insect, and mammalian systems
- Protein purification, biochemical analysis, and biophysical characterization
- Coordination of collaborations with multiple research labs around the world
- Training and supervision of technicians, graduate students, and junior postdocs
- User training, maintenance, and basic repairs of different biophysical and biochemical apparatus

**May 2019 – Jul 2025                      Postdoctoral scientist, HHMI / Cold Spring Harbor Laboratory**

Advisor: Leemor Joshua-Tor, Ph.D.

Primary project: Structural mechanisms of human Microprocessor mediated pri-miRNA processing

Collaborative projects: Structural basis of 1) FN3K kinase-mediated phosphorylation of protein glycation; 2) heterodimeric assembly of bZIP transcription factors; 3) RNA pol-II pause release

**Sep 2013 – Apr 2018                      Ph.D. scholar, Max Delbrück Center for Molecular Medicine, Berlin**

Advisor: Udo Heinemann, Ph.D.

Primary project: Structure-functional analysis of ZC3H12C RNase-mediated regulation of immune responses, via a novel RNA element

## Skills

<b>Structural biology</b>	<b>Electron Microscopy</b> (sample screening and optimization, grid preparation, negative stain EM, single particle cryo-EM, data collection, processing, model building, refinement, and structure validation) <b>X-ray crystallography</b> (protein and protein-nucleic acid complex crystallization, crystal optimization, X-ray diffraction data collection, processing, model building, refinement, and structure validation)
<b>Biophysics</b>	Protein thermal melting, microscale thermophoresis (MST), surface plasmon resonance (SPR), mass-photometry (MP), circular dichroism (CD), light scattering (RALS/MALS), differential scanning calorimetry (DSC), analytical ultracentrifugation (AUC)
<b>Molecular biology</b>	Construct design (protein & nucleic acids), cloning, recombinant protein expression and purification, process optimization, <i>in vitro</i> RNA transcription and purification
<b>Biochemistry</b>	Nucleic acid labelling and detection, enzymatic activity assays, nucleic acid binding assays, pull-down assays

## Academic Credentials

2013–2018 – Dr. rer. nat. / Ph.D. (Structural Biology), Freie University-Berlin, Germany

2009–2011 – Master of Technology (Industrial Biotechnology), National Institute of Technology–Karnataka, India

2004–2008 – Bachelor of Engineering (Biotechnology), Dr. B.R. Ambedkar University, Agra, India

## Publications (most recent first; \* denotes equal contribution)

1. Matos GR\*, **Garg A\***, Costa SM, Pereira P, Arraiano CM, Joshua-Tor L, Viegas SC. Structural and mechanistic insights into Dis3L2-mediated degradation of structured RNA. 2025. *RNA* (accepted)
2. Javad-zada MM, Zou X, Okamura K, Shang R, **Garg A**, Lee E, Joshua-Tor L, Fromm B, Lai EC. Repeated emergence of giant microRNA hairpins across invertebrates. 2025. *Cell Reports*. 44(9):116243
3. **Garg A**, On KF, Xiao Y, Elkayam E, David Y, Joshua-Tor L. The molecular basis of human FN3K mediated phosphorylation of glycosylated substrates. 2025. *Nat Commun*. 16(1):941
4. **Garg A**, Sheng R, Lai EC, Joshua-Tor L. The structural landscape of Microprocessor mediated processing of pri-let-7 miRNAs. 2024. *Mol Cell*. 84(21):4175-4190
5. **Garg A**, Roske Y, Yamada S, Uehata T, Takeuchi O, Heinemann U. PIN and CCCH Zn-Finger domains coordinate RNA targeting in ZC3H12 family endoribonucleases. 2021. *Nucleic Acids Res*. 49(9):5369-5381
6. Wang P, Liu L, Nair MS, Yin MT, Luo Y, Wang Q, Yuan T, Mori K, Solis AG, Yamashita M, **Garg A**, Purpura LJ, Laracy JC, Yu J, Joshua-Tor L, Sodroski J, Huang Y, Ho DD. SARS-CoV-2 neutralizing antibody responses are more robust in patients with severe disease. 2020. *Emerg Microbes Infect*. 9(1):2091-2093
7. Meyers K, Liu L, Lin WH, Luo Y, Yin M, Wu Y, Wontakal S, Rai A, Carpio FL, Fernando S, Dowlatshahi M, Elkayam E, **Garg A**, Joshua-Tor L, Wolk J, Alpert B, Romney ML, Costabile B, Gelardi E, Vallese F, Clarke O, Mancina F, Uhlemann AC, Sobieszczyk M, Perelson A, Huang Y, Hod E, Ho DD. Antibody testing documents the silent spread of SARS-CoV-2 in New York prior to the first reported case. 2020. *preprint doi: 10.21203/rs.3.rs-39880/v1*
8. **Garg A**, Liu L, Ho DD, Joshua-Tor L. Heterologous expression and purification of SARS-CoV2 nucleocapsid protein. 2020. *Bio-101*: e5005. doi: 10.21769/BioProtoc.5005
9. **Garg A**, Heinemann U. A novel form of RNA double helix based on G·U and C·A+ wobble base pairing. 2018. *RNA*. 24(2):209-218

10. Khan S, **Garg A**, Camacho N, Van Rooyen J, Kumar Pole A, Belrhali H, Ribas de Pouplana L, Sharma V, Sharma A. Structural analysis of Plasmodium falciparum Lysyl-tRNA Synthetase provides platform for drug development. 2013. *Acta Crystallogr D Biol Crystallogr*. 69:785-95
11. Khan S, **Garg A**, Sharma A, Camacho N, Picchioni D, Saint-Léger A, Ribas de Pouplana L, Yogavel M, Sharma A. An appended domain results in an unusual architecture for the malaria parasite Tryptophanyl-tRNA Synthetase. 2013. *PLoS One*. 8(6):e66224