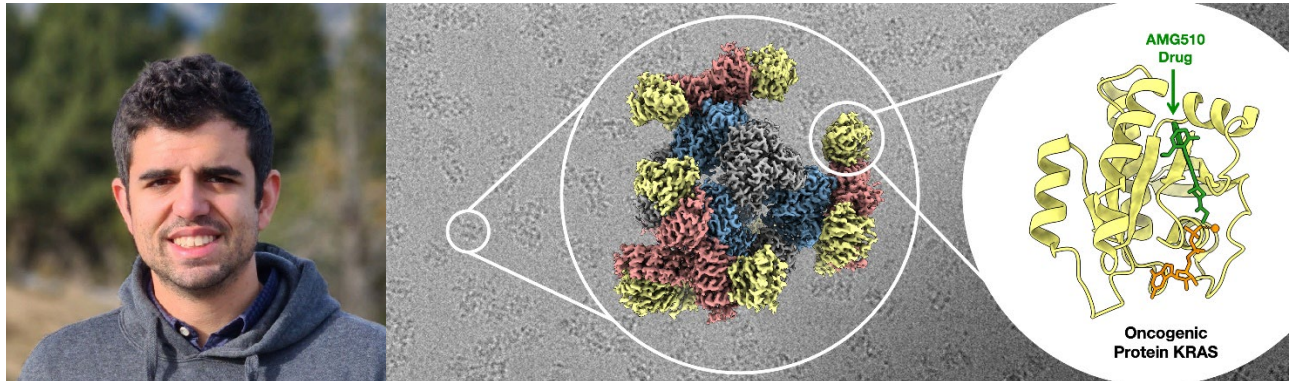




CryoEM Current Practices Webinar

Engineered Protein Cages for Imaging of Small Proteins by Cryo-EM



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Recent technical advances have made cryo-electron microscopy (cryo-EM) an attractive method for atomic structure determination, but problems of low signal-to-noise prevent routine structure determination of proteins smaller than about 50 kDa. We have developed symmetric protein imaging scaffolds to display and solve the structure of small proteins. In earlier work, we demonstrated the design of a novel protein cage scaffold with sufficient rigidity and modularity to reach an imaging resolution of 3.8 Å for a 26 kDa protein. In the present work, we use molecular engineering techniques to further rigidify a new cryo-EM imaging scaffold, enabling 3 Å or better resolution imaging to be achieved, even for very small proteins. We apply this system to the key cancer signaling protein KRAS (19 kDa in size), obtaining four structures of oncogenic mutational variants by cryo-EM. Importantly, a structure for the key G12C mutant bound to an inhibitor drug (AMG510) reveals significant conformational differences compared to prior data in the crystalline state. The findings highlight the promise of cryo-EM scaffolds for advancing the design of drug molecules against small therapeutic protein targets in cancer and other human diseases.

All are welcome to attend. Registration is at no-cost, but sign-up is required:
https://us02web.zoom.us/webinar/register/WN_6Vc1PwERRL6z7S_AtPqDQ