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Engaging undergraduate researchers in macromolecular crystallography

Herbert Lawrence Axelrod¹, JuHe Lee, Ali H Saleh, Victoria Ngo, Michael J Collazo², Duilio Cascio, Christopher R Meyer³ and Madeline E Rasche¹ ¹California State University, USA

²UCLA-DOE Institute for Genomics and Proteomics, USA ³Fresno State University, USA

round-breaking work in bringing sophisticated X-ray diffraction methods within the reach of undergraduate researchers has Jbeen reported by established leaders in the field. The Department of Chemistry and Biochemistry at California State University is committed to providing undergraduate students opportunities to engage in independent, state of the art and cutting-edge research through its capstone CHEM 495 course. Since crystallographic structure determination is the mainstream technique and plays an ever-increasing role in pharmaceutical and biotechnology strategies, we sought to bring opportunities for undergraduate researchers to embrace X-ray diffraction methods and three-dimensional structure determination for improving an understanding of structure and function in for their projects. However, this method requires a significant investment in equipment and computational infrastructure which are inaccessible to most undergraduate programs. Fortunately, resources have been made generously available to us in Fullerton through the Stanford Synchrotron Radiation Lightsource and the UCLA-DOE Institute for Genomics and Proteomics. At these facilities, undergraduates have access to high-throughput crystallization robots and synchrotrons to collect X-ray diffraction data. Utilization of these resources has created unique opportunities for teams of undergraduate researchers to tackle novel research projects including the structure determination of ADP-Glucose Pyrophosphorylase (ADPG-PPase) a key enzyme involved in ratelimiting step of starch synthesis the from the thermophilic marine bacterium Thermotoga maritima and a key protein designated Orf19 that believed to catalyze one of the steps in the synthesis of tetrahydromethanopterin (THMPT). In several species of archaeal microbes that live in the digestive tract of ruminants including cattle, THMPT is a cofactor that is required for the production of methane. Methane is a potent greenhouse gas; therefore inhibition of the enzymes involved in THMPT biosynthesis is a promising strategy to help mitigate the emission of this gas from large-scale cattle and dairy farming. Knowledge of the structure of Orf19 is likely to lead to a better understanding of how effective inhibitors of the enzyme can be designed for diminishing the production of methane.

haxelrod@fullerton.edu

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