

DETERMINING THE MECHANISM OF THE UBIQUITIN CONJUGATING ENZYME UBC13 WITH QM/MM AND METADYNAMICS

Aaron Davis, Walker Jones & Serban Zamfir

Dr. Isaiah Sumner

Department of Chemistry and Biochemistry, James Madison University, 800 South Main Street, Harrisonburg, Virginia, 22807

Ubc13 is an E2 enzyme that catalyzes a post translational modification of proteins called lysine ubiquitination, i.e. the addition of ubiquitin to the lysine of a target protein via a thioester aminolysis reaction. Lysine ubiquitination is important because one of its functions is to signal for the degradation of damaged proteins, and defects in this process are linked to different disorders. The accepted mechanism for Ubc13-catalyzed ubiquitination is a stepwise mechanism that creates an oxyanion intermediate. This intermediate is hypothesized to be stabilized by a nearby asparagine residue, which is known as the “oxyanion hole.” However, the validity of the accepted mechanism has come into question because (1) there has never been a comprehensive study of the ubiquitination mechanism, (2) the accepted mechanism was inferred from the reverse reaction, and (3) recent studies suggest a different role for the oxyanion hole. In our study, we use QM/MM and metadynamics, a rare-events sampling method, to determine the mechanism.

Research for this project was funded by the National Science Foundation, grant numbers CHE-1062629 in 2013 and CHE-1461175 in 2015, The Extreme Science and Engineering Discovery Environment (XSEDE), which is supported by National Science Foundation grant number ACI-1053575, and The Thomas F. and Kate Miller Jeffress Memorial Trust, Bank of America, N.A., Trustee.