

Figure S1. Mrh1 transmembrane topology prediction. Results obtained from the DeepTMHMM application (dtu.biolib.com/DeepTMHMM, accessed September 28, 2022) for the Mrh1 protein. Top panel: protein domain orientation relative to the inner and outer part of the cytoplasmic membrane. Bottom panel: probability associated with the inner and outer orientation for each protein domain.

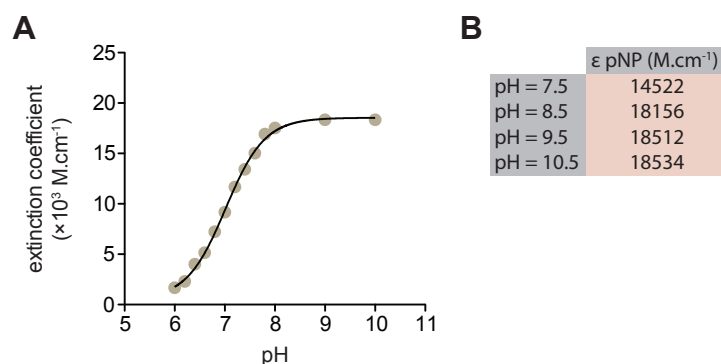


Figure S2. para-nitrophenol extinction coefficient modeling. **A.** Extinction coefficient curve fitting. Discreet extinction coefficient data from Biggs 1954 [50] was used to model para-nitrophenol extinction coefficients between pH 6 and 10. **B.** Extinction coefficients for para-nitrophenol at the indicated pH used in this study based on modelling shown in A.

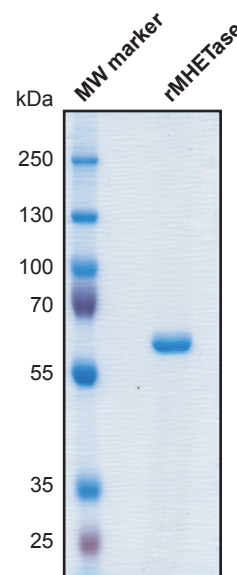


Figure S3. Purified recombinant MHETase. Molecular weights of reference markers in kDa are indicated