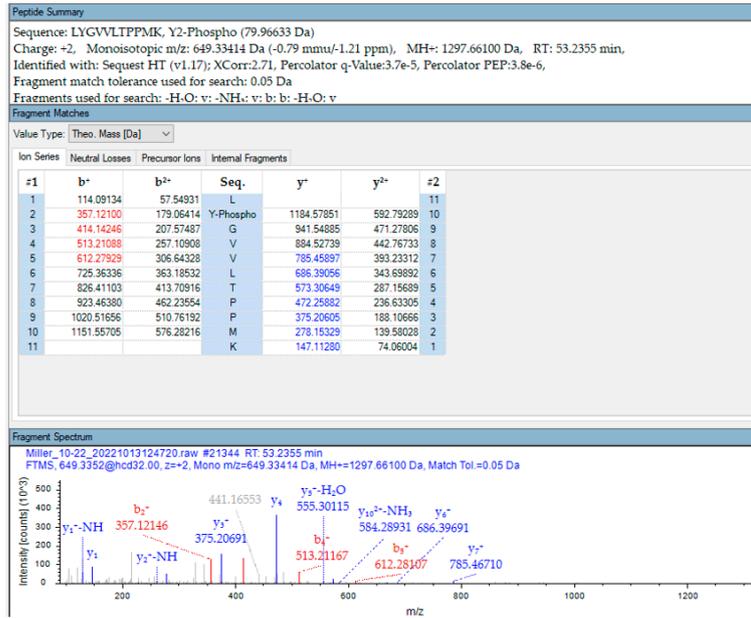


A.



B.

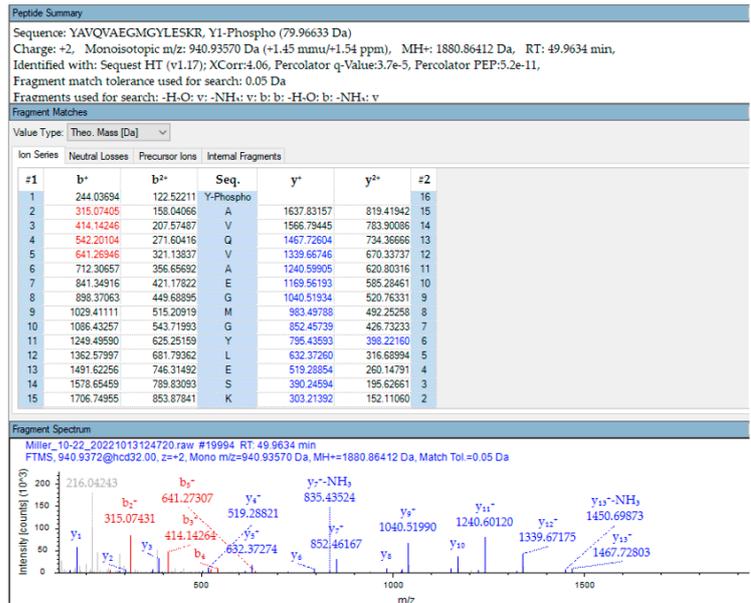


Figure S1. Mass spectrometry analysis of Ack1 peptides phosphorylated by Mer. These peptides were tyrosine phosphorylated in the reaction with Mer, but not in the Ack1 autophosphorylation reaction. (A) LC/MS/MS analysis of peptide containing Y193. Fragment matches are at the top, and a sample fragmentation spectrum is shown below. (B) LC/MS/MS analysis of peptide containing Y232.

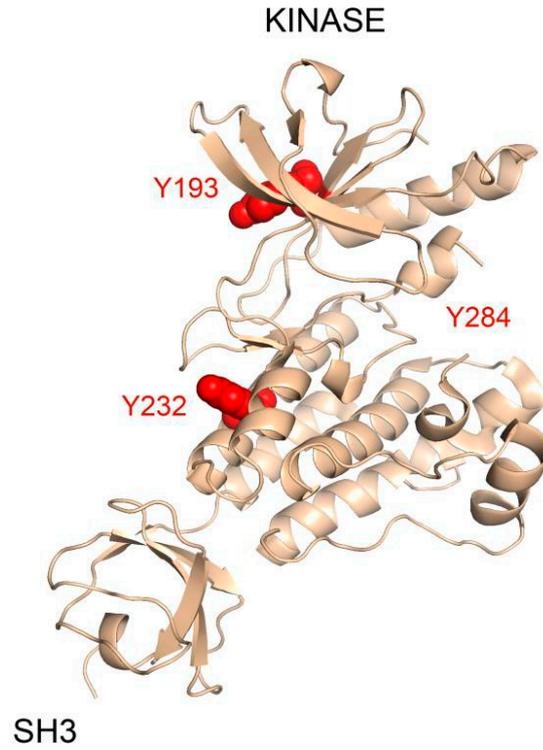


Figure S2. Structure of Ack1 kinase and SH3 domains. Y193 and Y232 are shown as red spheres on the structure of Ack1 (pdb code = 4HZS). Y284 in the activation loop is not resolved in this structure.

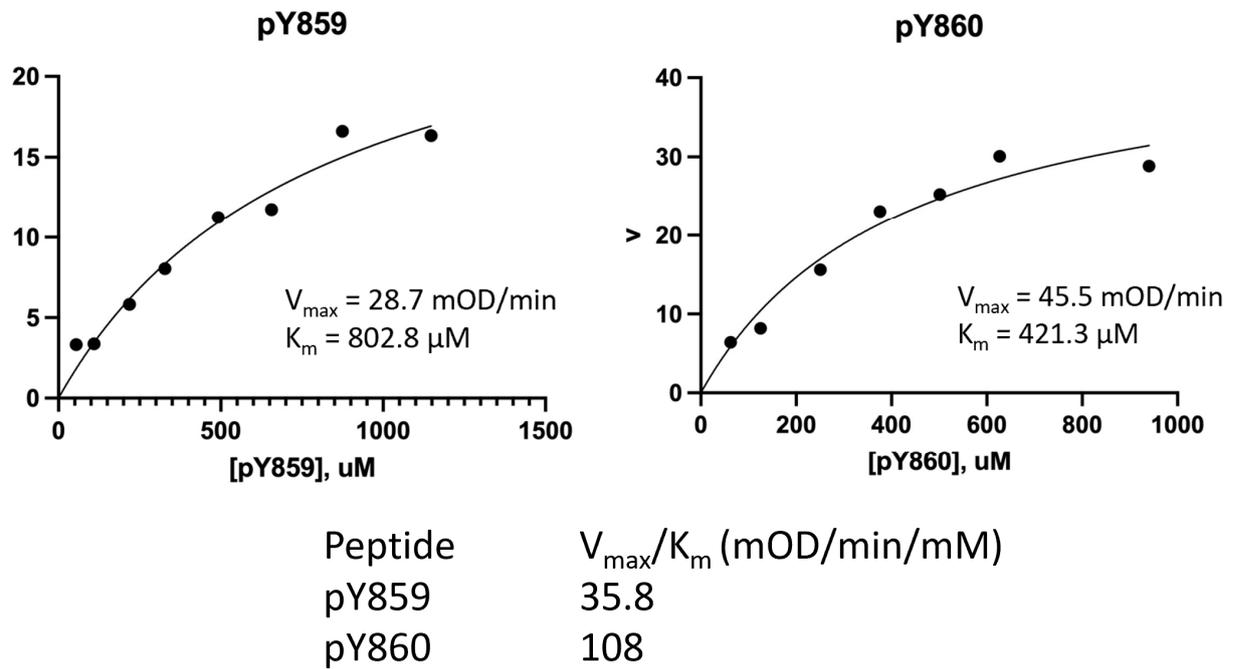


Figure S3. Mer phosphorylation of Ack1 MHR phosphopeptides. Steady state kinetic measurements were performed with the continuous spectrophotometric assay. Curve fitting was performed with GraphPad Prism (v.9), and the kinetic constants are shown.