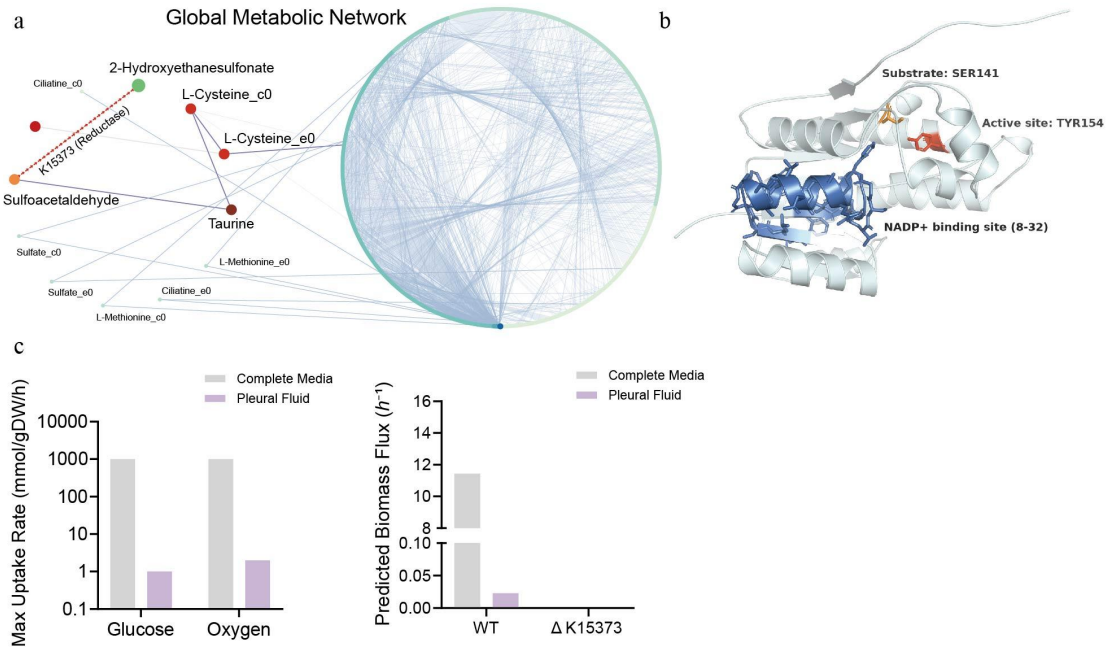


Supplementary Figure S1. Genome-scale metabolic modeling (GSMM) confirms the pathogenic essentiality of K15373 reductase in Klebsiella pneumoniae.

(a) Topological network visualization highlighting K15373 as a central detoxification hub; (b) Three-dimensional protein structure model of K15373 sulfoacetaldehyde reductase; (c) Flux Balance Analysis comparing wild-type vs. ΔK15373 knockout under complete media (left) and pleural fluid-mimicking hypoxic conditions (right).