

Supporting Information

Jackson et al. 10.1073/pnas.1304097110

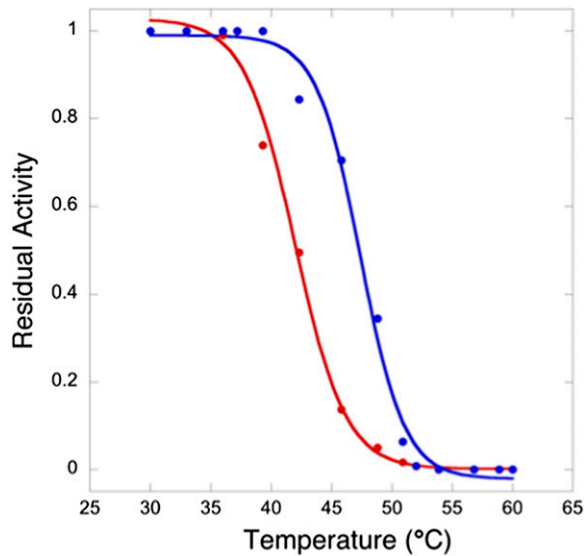


Fig. S1. Plot of residual activity of *Lucilia cuprina* (LcαE7; red) and LcαE7-4 (blue). Points are averages of three measurements; protein was incubated at the temperatures indicated for 15 min before being placed on ice. Activity was measured with 4-nitrophenyl butyrate and converted to a percentage of maximum activity.

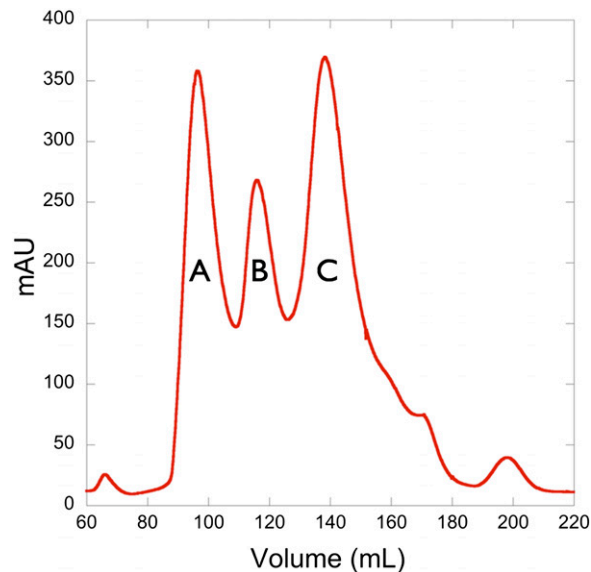


Fig. S2. Size exclusion chromatography of LcαE7-4. Pure LcαE7-4 protein (postaffinity chromatography) was loaded onto a Sephacryl S300 column. Protein eluted in three peaks. Peak A corresponds to a high-molecular weight aggregate and did not crystallize in any condition tested. Peak B crystallized as dimeric LcαE7-4. Peak C crystallized as monomeric LcαE7-4.

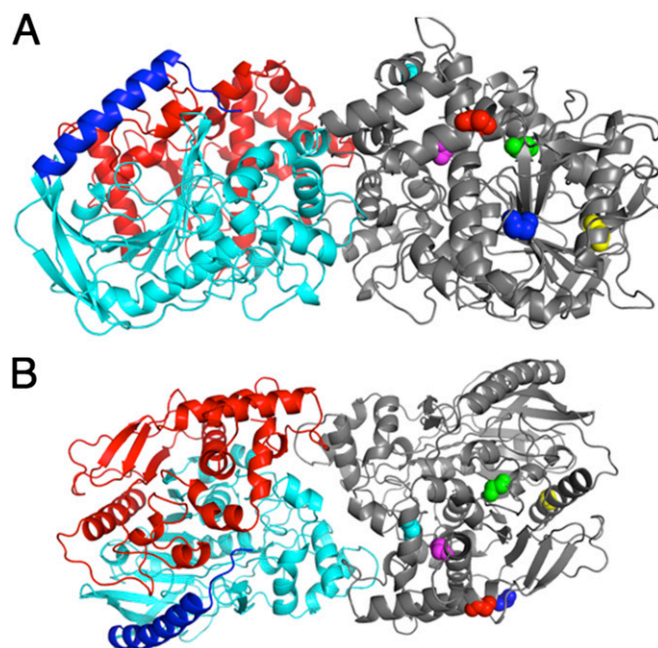


Fig. 53. Cartoon of the *LcαE7* dimer from (A) the side and (B) above the active site. The N-terminal membrane association helix is colored blue, the N-terminal one-half of the protein is colored cyan, and the C-terminal one-half is colored red. The locations of stabilizing mutations are shown as spheres (cyan, M364L; magenta, I419F; green, A472T; yellow, I505T; blue, K530E; red, D554G). The biological dimer is pictured, and the dimerization interface is highlighted.

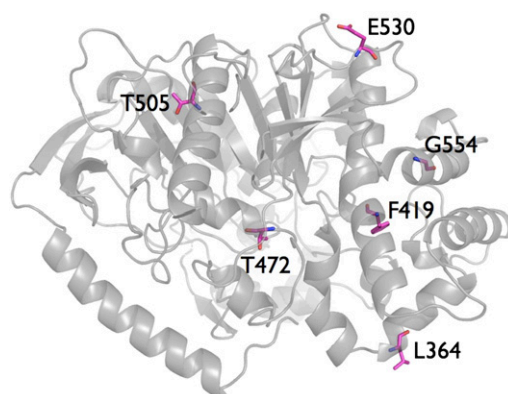


Fig. 54. Stabilizing mutations accumulated through directed evolution. The mutations that accumulated are represented as sticks. All mutations were located in the C-terminal one-half of the protein, with M364L, K530E, and D554G being surface-exposed. I419F, I505T, and A472T are located in the interior of the protein.

