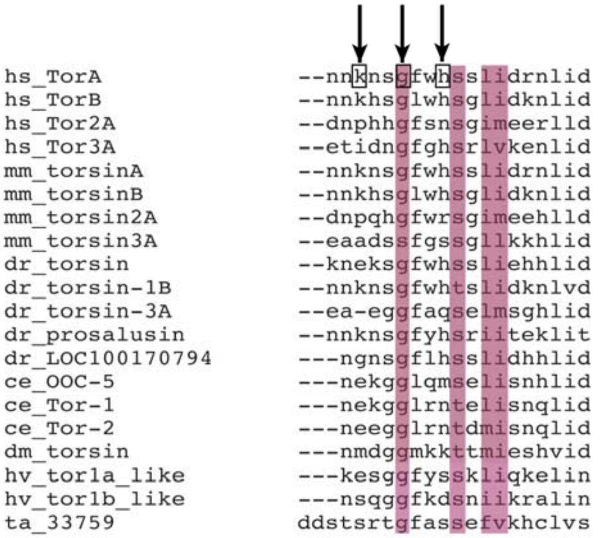
Supplemental Materials

Molecular Biology of the Cell

Chase et al.



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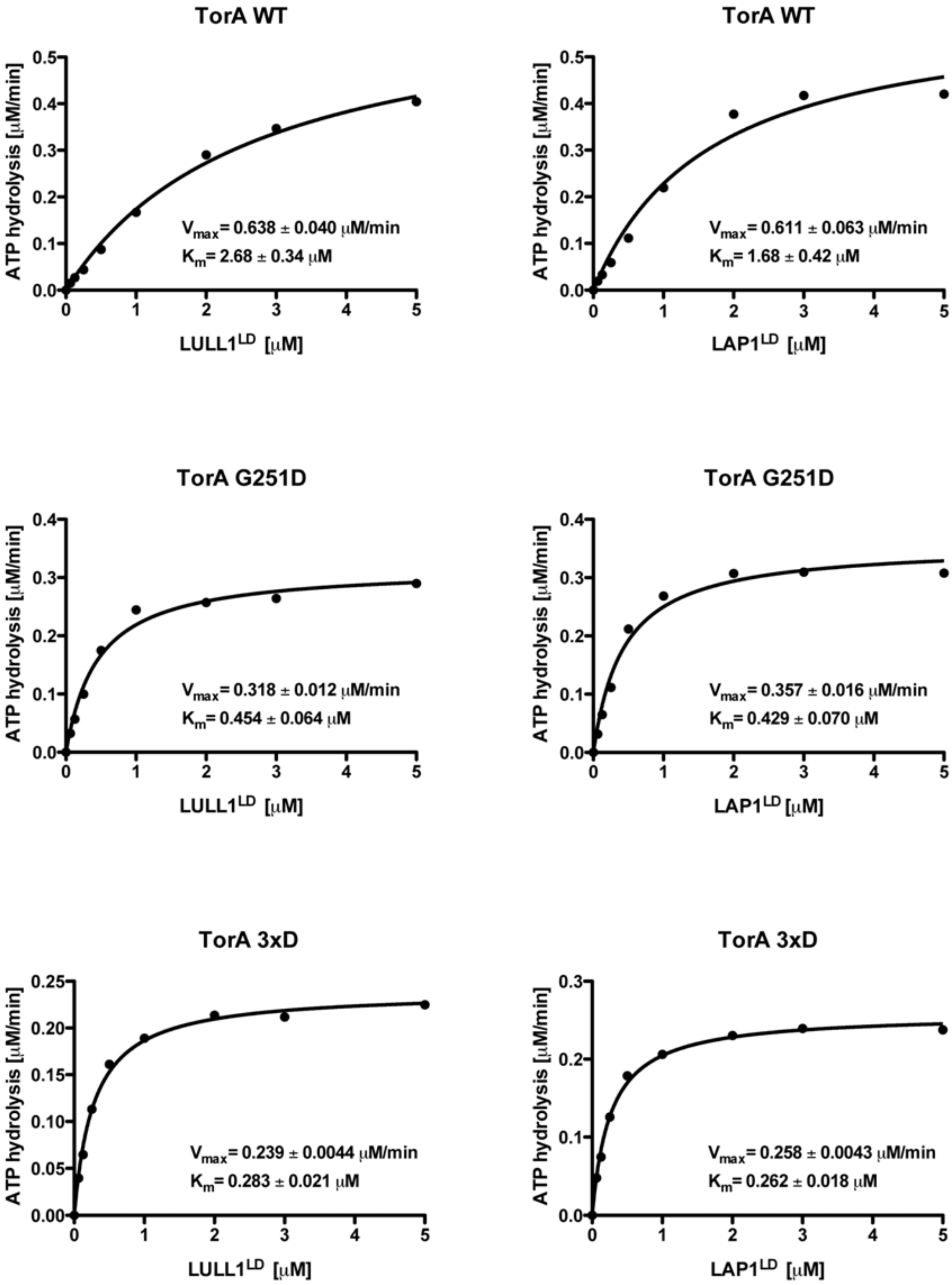
Supplementary Figure 1: Sequence alignment of TorA and B in organisms with known Torsin homologs. The residue G251 is strictly conserved (pink) in TorA from human to *Trichoplax adhaerens*,one of the most basic metazoan organisms. Predicted intra-protomer Torsin-Torsin contact sites at residues 248, 251, and 254 mutated in this study are boxed and indicated with arrows. Other conserved residues are shaded in pink.



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Supplementary Figure 2: Cofactor-dependent ATPase activation of TorA ‘back’ interface mutants relative to wild-type TorsinA. Initial velocities of ATP hydrolysis were determined by quantifying the Pi released in the presence of 3 uM Torsin and the indicated concentrations of LAP1^{LD} or LULL1^{LD}. Data were fit to Michaelis-Menten kinetics, which yielded the apparent K$_{m}$ and V$_{max}$ values shown, with the error representing the standard deviation of three independent sets of reactions. Each point on the graph is the average of a triplicate measurement of the initial velocity with the respective LAP1^{LD} or LULL1^{LD} concentration.#