

Supplemental Materials

Molecular Biology of the Cell

Chase et al.

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hs_TorA      --nnknsqfwhsslldrnlid
hs_TorB      --nnkhsqlwhsglidknlid
hs_Tor2A     --dnphhgfsnsgimeerlld
hs_Tor3A     --etidngfghsrlvkenlld
mm_torsinA   --nnknsqfwhsslldrnlid
mm_torsinB   --nnkhsqlwhsglidknlid
mm_torsin2A  --dnpqhgfwrsgimeehlld
mm_torsin3A  --eaadsfgssgllkkhlld
dr_torsin    --kneksqfwhssllehhlld
dr_torsin-1B --nnknsqfwhtsllidknllvd
dr_torsin-3A --ea-eggfaqselmsghlld
dr_prosalusin --nnknsqfyhsriitekllit
dr_LOC100170794 ---ngnsgflhsslidhhlld
ce_OOC-5     ---nekglqmselisnhlld
ce_Tor-1     ---nekglrntelisnqlld
ce_Tor-2     ---neegglrntdmisnqlld
dm_torsin    ---nmdgmkkttmieshlvid
hv_tor1a_like ---kesggfyskliqllkellin
hv_tor1b_like ---nsqggfkdsniikrlalin
ta_33759     ddtsrtgfassefvkhcllvs

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Figure S1 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.

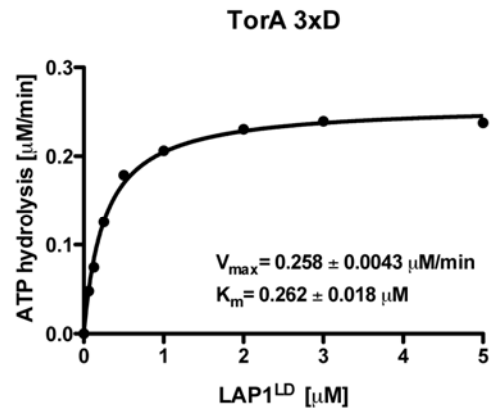
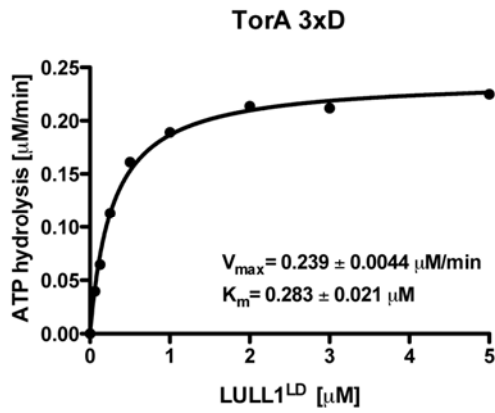
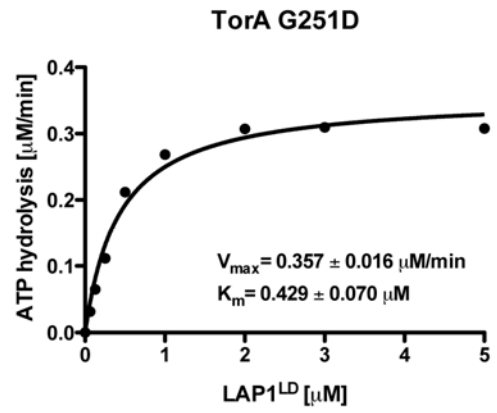
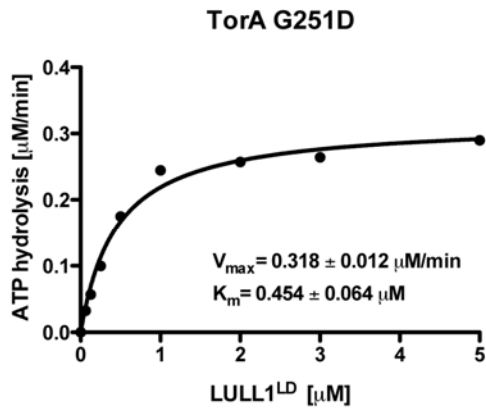
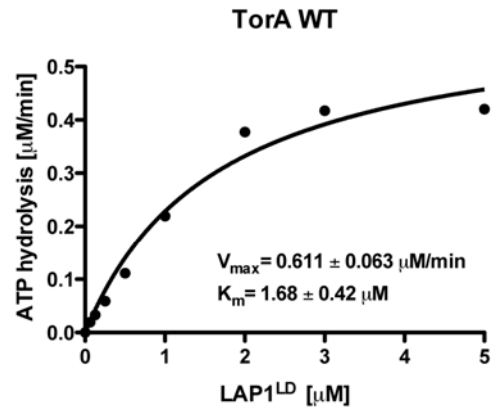
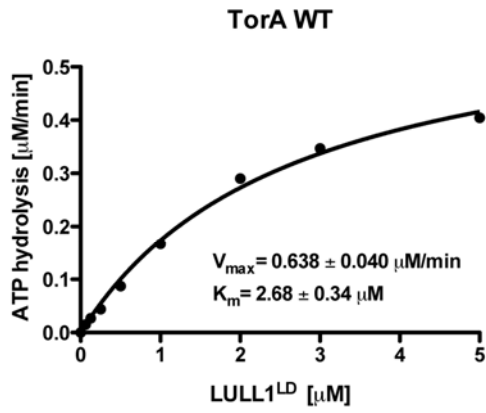


Figure S2 Chase et al.

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.#