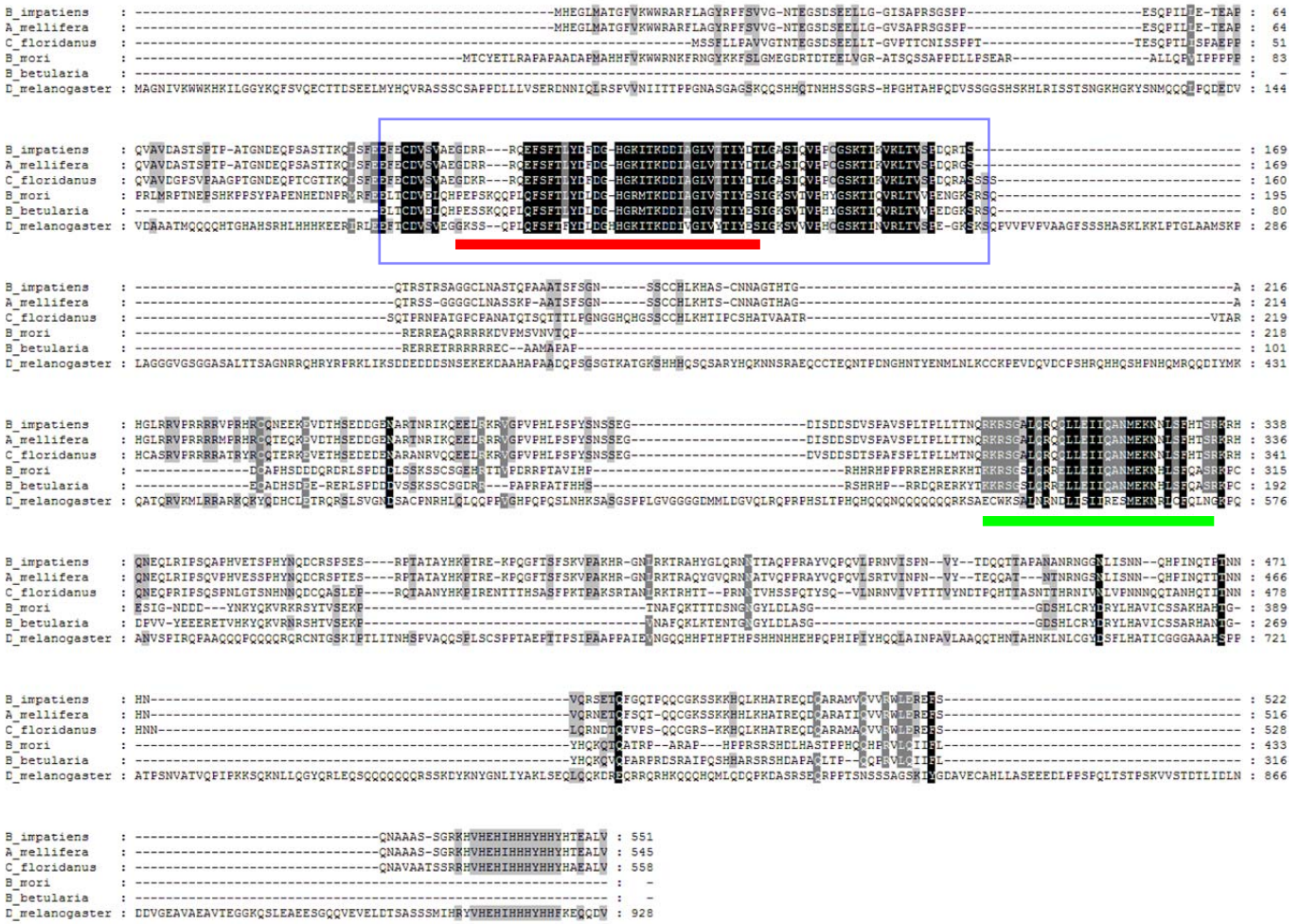


A



B

	<i>B. impatiens</i>	<i>A. mellifera</i>	<i>C. floridanus</i>	<i>B. mori</i>	<i>B. betularia</i>	<i>D. melanog...</i>
<i>B. impatiens</i>		92.9%	67.0%	18.2%	18.9%	13.0%
<i>A. mellifera</i>	92.9%		66.4%	18.3%	18.7%	12.7%
<i>C. floridanus</i>	67.0%	66.4%		17.9%	19.0%	13.7%
<i>B. mori</i>	18.2%	18.3%	17.9%		74.5%	16.1%
<i>B. betularia</i>	18.9%	18.7%	19.0%	74.5%		18.5%
<i>D. melanogaster</i>	13.0%	12.7%	13.7%	16.1%	18.5%	

FIG S1 Multiple alignment of insect nkd protein sequences. (A) multiple alignment of *A. mellifera* (XP_001120899), *Bombus impatiens* (XP_012249347), *Drosophila melanogaster* (NP_524788), *Bombyx mori* (XP_004930158), *Biston betularia* (AFP57440), and *Camponotus floridanus* (EFN66676) nkd protein sequences. Black and grey shadings indicate identity and high conservation of amino acids, respectively. The region responsible for interaction with dsh is indicated with the blue box. The nuclear localization motif is underlined by the green bar. The red bar highlights the EF-hand domain. (B) Identity matrix between different nkd protein sequences. Black and grey shadings indicate degree of identity from high to low.