

Supplementary Table S1. Percent identity of *EcRACK1* amino acid sequences compared with other species predicted by Clustal2.1 program.

Species		Similarity (%)											
<i>Scylla paramamosain</i>	100.00												
<i>Exopalaemon</i>	94.65												
<i>carinicauda</i>		100.00											
<i>Penaeus japonicus</i>	95.60	96.86	100.00										
<i>Eriocheir sinensis</i>	96.86	96.54	98.11	100.00									
<i>Pacifastacus leniusculus</i>	95.91	96.86	97.80	98.43	100.00								
<i>Drosophila melanogaster</i>	79.50	79.50	80.13	79.50	79.18	100.00							
<i>Bombyx mori</i>	82.65	81.70	82.97	82.65	82.33	87.07	100.00						
<i>Branchiostoma belcheri</i>	72.15	72.78	73.10	73.10	72.78	72.47	73.42	100.00					
<i>Gallus gallus</i>	77.92	77.60	78.86	78.55	77.92	76.66	78.23	81.33	100.00				
<i>Homo sapiens</i>	77.92	77.60	78.86	78.55	77.92	76.66	78.23	81.33	100.00	100.00			
<i>Ruditapes philippinarum</i>	77.92	77.60	78.86	78.55	77.92	76.66	78.23	81.33	100.00	100.00	100.00		
<i>Pocillopora damicornis</i>	74.60	75.24	76.19	75.56	74.92	73.33	74.29	74.92	81.90	81.90	81.90	100.00	