

Supplementary information

Figure S1. Nucleotide sequence, deduced amino acid sequence and phylogenetic analysis of *Artemia* Plk1.

(A) Nucleotide and deduced amino acid sequences of the cDNA encoding Plk1. The nucleotide and amino acid residue numbers are indicated on the left. The start (ATG) and stop codons (TAA) are underlined. The asterisk denotes termination of amino acids. (B) Amino acid sequence alignment of the *Artemia* Plk1 kinase domain with that from other species. The GenBank numbers of the sequences used are parthenogenetic: *Artemia* Plk1-K (this work), *Daphnia pulex* Plk1-K (EFX84439.1), *Drosophila virilis* Plk1-K (XP_002048022.1), *Caenorhabditis elegans* Plk-K (NP001021173.1), *Mus musculus* Plk1-K (EDL17273.1), *Homo sapiens* Plk1-K (NP_005021.2). The Thr residue, the most important phosphorylation site within Plk1, is denoted by an asterisk (*). (C) Phylogenetic analysis of the amino acid sequences of *Artemia* Plk1 and Plk1 molecules from other species using the neighbor-joining method. The sequences used and their GenBank numbers are: *Artemia parthenogenetica* (this work), *Ailuropoda melanoleuca* (XP_002926608.1), *Bos taurus* (DAA15528.1), *Pongo abelii* (XP_002826287.1), *Homo sapiens* (AAA56634.1), *Oryctolagus cuniculus* (XP_002711895.1), *Mus musculus* (NP_035251.3), *Rattus norvegicus* (AAH83926.1), *Monodelphis domestica* (XP_001377703.2), *Gallus gallus* (NP_001025810.1), *Xenopus (Silurana) tropicalis* (NP_998844.1), *Xenopus laevis* (NP_001080788.1), *Danio rerio* (NP_001003890.3), *Ciona intestinalis* (XP_002126066.1), *Halocynthia roretzi* (ADI78955.1), *Saccoglossus kowalevskii* (XP_002730953.1), *Hemicentrotus pulcherrimus* (BAB18588.1), *Patiria pectinifera* (BAC22692.1), *Daphnia pulex* (EFX84439.1), *Acromyrmex echinator* (EGI58003.1), *Camponotus floridanus* (EFN69812.1), *Drosophila melanogaster* (NP_524179.2), *Culex quinquefasciatus* (XP_001847637.1), *Aedes aegypti* (XP_001663586.1), *Trichinella spiralis* (XP_003378887.1), *Ascaris suum* (ADY43234.1), *Brugia malayi* (XP_001894280.1), *Oikopleura dioica* (CBY08321.1), *Monosiga brevicollis* MX1 (XP_001750918.1), *Nematostella vectensis* (XP_001625752.1). The Plk1 sequence from *Nematostella vectensis* was used as an out-group sequence. Bootstrap percentage values for 1000 replicate analyses are shown at the branch points. The bar at the bottom indicates the branch length corresponding to the mean number of differences (0.1) per residue along each branch.

Figure S2. Nucleotide sequence, deduced amino acid sequence, and phylogenetic analysis of *Artemia* Aurora A.

(A) Nucleotide and deduced amino acid sequences of the cDNA encoding Aurora A. The nucleotide and amino acid residue numbers are indicated on the left. The start (ATG) and stop codons (TAA) are underlined. The asterisk denotes termination of amino acids. (B) Amino acid sequence alignment of *Artemia* Aurora A with that of Aurora A molecules from other species. The GenBank numbers of the sequences used here are: parthenogenetic *Artemia* AUR (this work), *Caenorhabditis elegans* AIR-1 (NP_505119.1), *Drosophila melanogaster* AUR (NP_476749.1), *Xenopus tropicalis* AUR (NP_001016570.1), *Homo sapiens* AUR (BC001280.1), and *Mus musculus* AUR (AAH14711.1). (C) Phylogenetic analysis of the amino acid sequences of *Artemia* Aurora A and those from other species. The sequences used here and their GenBank numbers are parthenogenetic: *Artemia* (this work), *Sus scrofa*

