



Figure S4. Multiple sequence alignment of PeAPY1 and PeAPY2 (apyrase from *Populus euphratica*) with other apyrases from different species. The APY sequences are from *P. euphratica* (PeAPY1, PeAPY2), *Populus trichocarpa* (PtAPY1, PtAPY2), *Arabidopsis thaliana* (AtAPY1, AtAPY2) and *Nicotiana tabacum* (NtAPY1, NtAPY2). Full length amino sequences of APYs were obtained by similarity searching on NCBI website (<http://www.ncbi.nlm.nih.gov/>). The accession numbers of these sequences are provided in Supplemental Table S1. The multiple sequence alignment of amino sequence was performed by ClustalW. Shadings in black, red, blue, indicate identical and conserved amino acid residues.