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XP_006857404.1_Amborella trichopoda_D     ------TVGTKAKTNL
RWR97591.1_Cinnamomum micranthum_D        ------TAGIKAKTNL
XP_008789436.1_Phoenix dactylifera_M      ------AAGGQAKTNL
GAV66157.1_Cephalotus follicularis_D      ------AAKNKPKTNL
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XP_002285672.1_Vitis vinifera_D           ------AAGNKPKTNL
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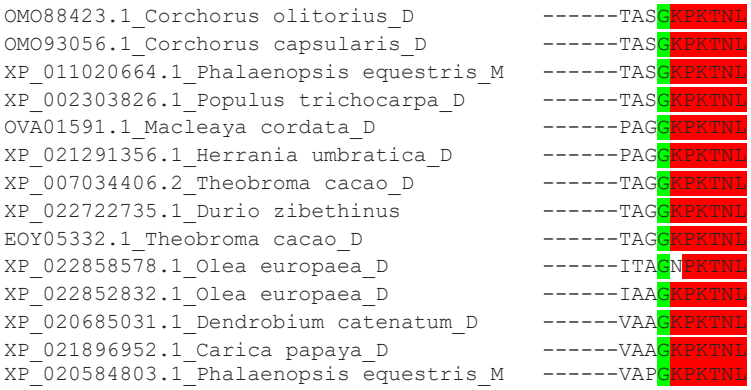

Supplementary Figure 1: Multiple sequence alignment of the last ten amino acids of the putative peroxisomal glutathione reductases.

The rice peroxisomal glutathione reductase was used as a query sequence in NCBI-BLASTp and orthologs were obtained. The last ten amino acids were used for multiple sequence alignment using the Clustal omega program. The digits at the top of the amino acid residue denote the positions of residues. The symbol “>” denotes the end of the amino acid sequence. All the consensus amino acid residues till -6 have been highlighted in red colour. At -7 the consensus amino acids serine and glycine have been highlighted with yellow and green, respectively. The numbers at the extreme left denote the accession number, followed by the name of the plant species, D - dicot, and M- monocot.