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ACG34981          RLLAEGKVPIGVGENTKISNCIIDMNARVGRNVSITNKEG-VQEADRPDE
P55234 (Embryo)  RLLAEGKVPIGVGENTKISNCIIDMNCQGWKERLHNKQGRGRSKSPDRPGR
P55241 (SH2)     KLLLAGKVPVGIGRNTKIRNCIIDMNARIGKNVVINSKG--IQEADHPEE
ABD66656         ELLAEGKVPIGIGENTTIQKCIIDKNARIGKKVVISNSEG-VDEADRTSE
                .**  *****:*.***.* :***** *.:  ::  ...  ...*:. .

ACG34981          GYYIRSGIVVVLKNATIKDGTVI
P55234 (Embryo)  RILIRSGIVVVLKNATIKDGTVI
P55241 (SH2)     GYYIRSGIVVILKNATINDGSVI
ABD66656         GFYIRSGITVVLKNATIADGLVI
                *****.*:***** * ** **

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Supplemental Figure S6. Alignment of maize AGPase large subunit isoforms and location of recovered peptides. Maize AGPase large subunit isoforms identified by Genbank accession number were aligned using the program CLUSTALW. Characterized isoforms are the product of the *sh2* gene (P55241)^{1,2} and the embryo-expressed isoform (P55234)³. Two additional putative AGPase large subunit homologs have been identified by genomic or cDNA sequence but are not yet characterized (ACG34981, ABD66656). Yellow highlighted residues indicate peptide sequences from proteins that associate with starch biosynthetic enzymes (see Supplemental Table S1 for details). All the recovered peptides are specific to the SH2 isoform. Green highlighted residues indicate predicted plastid targeting peptides according to ChloroP.

References

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