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AAK69628 (Leaf)           KGGIVTVIKDALLPSGTVI
AAZ82467 (BT2 Plastidial) KGGIVTVIKDALLPSGTVI
AAK69627 (BT2 Cytoplasmic) KGGIVTVIKDALLPSGTVI
AAK39640 (Embryo)        KSGIVTVIKDALIPSGTII
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Supplemental Figure S7. Alignment of maize AGPase small subunit isoforms and location of recovered peptides. Sequences identified by Genbank accession number were aligned using the program CLUSTALW. Two distinct products from the *bt2* gene, the cytoplasmic and plastidial forms, are included¹. Highlighted residues indicate peptide sequences from proteins that associate with starch biosynthetic enzymes (see Supplemental Table S1 for details). Grey highlighted residues indicate peptide sequences that are identical in all four predicted polypeptides. Green highlighted residues indicate peptide sequences that are identical in the *bt2* products and the leaf form of the AGPase small subunit. Yellow highlighted residues indicate peptide sequences that are unique to the products of the *bt2* gene. The data indicate that a product of *bt2* associates with the starch biosynthetic enzymes.

References

1. Rosti, S, Denyer, K. (2007) Two paralogous genes encoding small subunits of ADP-glucose pyrophosphorylase in maize, Bt2 and L2, replace the single alternatively spliced gene found in other cereal species. *J Mol Evol* **65**, 316-327.