

Table S2. ADK proteins from diverse eukaryotes contain conserved potential SNF1/AMPK/SnRK1 phosphorylation sites

Species	% Identity, entire protein	T68	T105	S175	S196
<i>Arabidopsis thaliana</i> (ADK2)	100	IAGGAT <u>Q</u> NSI	MKKDA <u>T</u> AAGV	FFLTV <u>S</u> PESI	FTMNL <u>S</u> APFI
<i>Arabidopsis thaliana</i> (ADK1)	92	IAGGAT <u>Q</u> NSI	MKKDA <u>T</u> AAGV	FFLTV <u>S</u> PESI	FTMNL <u>S</u> APFI
<i>Vitis vinifera</i>	86	IAGGAT <u>Q</u> NSI	-	FFLTV <u>S</u> PESI	FMMNL <u>S</u> APFI
<i>Populus trichocarpa</i>	86	IAGGAT <u>Q</u> NSI	MKKNS <u>T</u> EAGV	FFLTV <u>S</u> PESI	FTMNL <u>S</u> APFI
<i>Solanum tuberosum</i>	85	IAGGAT <u>Q</u> NSI	-	FFLTV <u>S</u> PESI	FMMNL <u>S</u> APFI
<i>Nicotiana tabacum</i>	86	IAGGAT <u>Q</u> NSI	-	FFLTV <u>S</u> PESI	FMMNL <u>S</u> APFI
<i>Gossypium hirsutum</i>	85	IAGGAT <u>Q</u> NSI	-	FFLTV <u>S</u> PESI	FMMNL <u>S</u> APFI
<i>Sorghum bicolor</i>	82	IAGGAT <u>Q</u> NSI	-	FFLTV <u>S</u> PDSI	FMMNL <u>S</u> APFI
<i>Oryza sativa</i>	82	IAGGAT <u>Q</u> NSI	-	FFLTV <u>S</u> PDSI	FLMNL <u>S</u> APFI
<i>Glycine max</i>	81	IAGGAT <u>Q</u> NSI	-	FFLTV <u>S</u> PDSI	FMMNL <u>S</u> APFI
<i>Zea mays</i>	82	IAGGAT <u>Q</u> NSI	-	FFLTV <u>S</u> PDSI	FLMNL <u>S</u> APFI
<i>Physcomitrella patens</i>	67	IAGGAT <u>Q</u> NTI	MFKLA <u>S</u> EGGV	FFLTV <u>S</u> PESM	FMMNL <u>S</u> ASFV
<i>Chlamydomonas reinhardtii</i>	53	-	MTEVA <u>T</u> AEGV	FFITV <u>S</u> PASI	-
<i>Mus musculus</i>	57	-	-	FFLTV <u>S</u> PESV	FTLNL <u>S</u> APFI
<i>Danio rerio</i>	59	-	-	FFLTV <u>S</u> LESI	FCLNL <u>S</u> APFI
<i>Rattus norvegicus</i>	57	-	-	FTMNL <u>S</u> APFV	FTLNL <u>S</u> APFI
<i>Macaca mulatta</i>	56	-	-	FFLTV <u>S</u> PESV	FTLNL <u>S</u> APFI
<i>Homo sapiens</i>	56	-	-	FFLTV <u>S</u> PESV	FTLNL <u>S</u> APFI
<i>Saccharomyces cerevisiae</i>	40	-	-	FHLT <u>V</u> SPDAI	FVLNF <u>S</u> APFI

ADK proteins from diverse eukaryotes contain conserved potential SnRK1 phosphorylation sites. ADK protein sequences were compared to determine the extent of conservation at sites corresponding to T68, T105, S175, and S196 in *Arabidopsis* ADK1 and ADK2. Amino acids shown in red are critical for SnRK1 recognition, and serine/threonine residues underlined are predicted to be phosphorylated by SnRK1. A hyphen (-) indicates the site is not conserved.