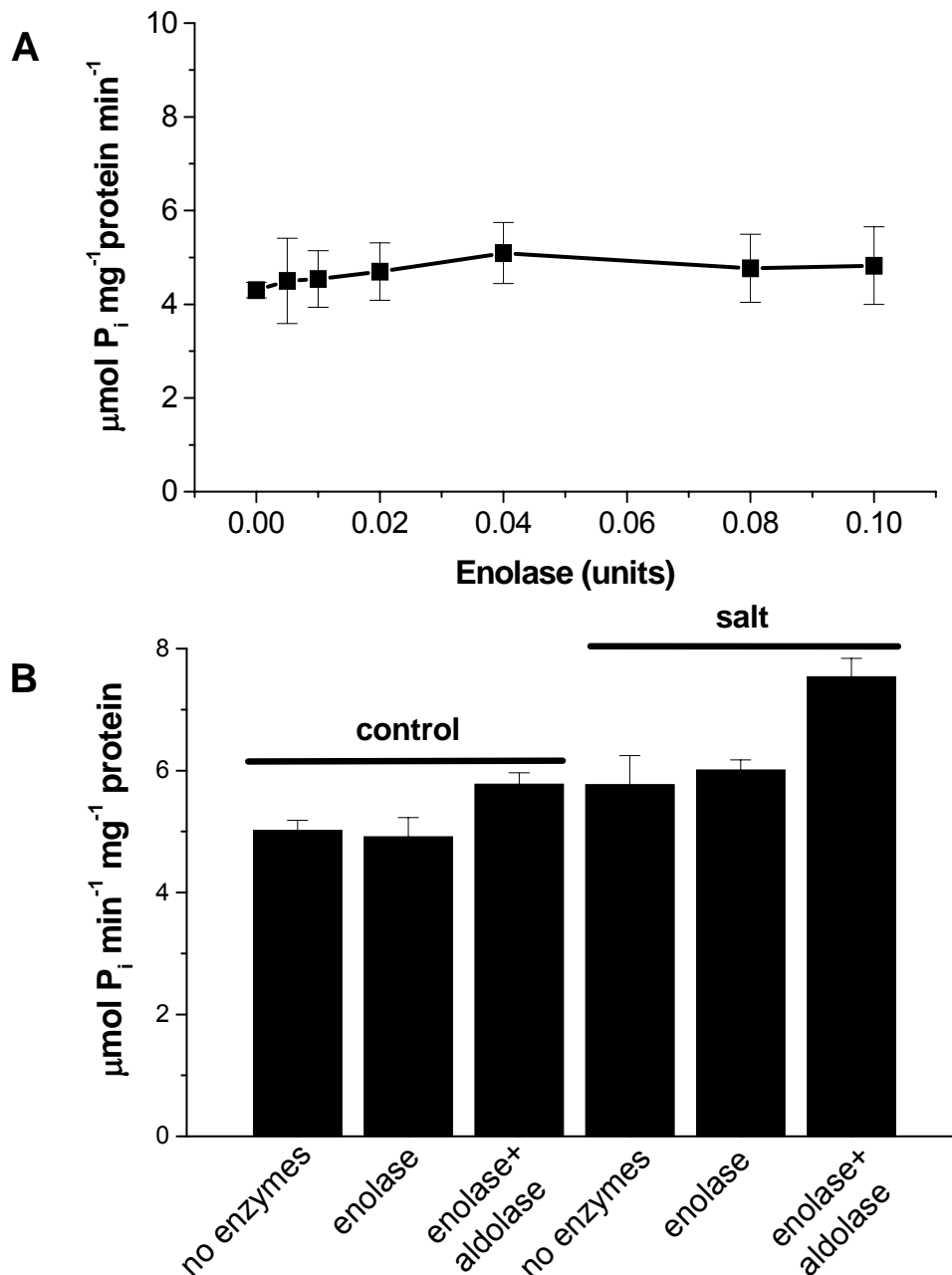


**Supplemental Figure 1.** Aldolase stimulates V-ATPase hydrolytic activity in *Ananas comosus*

V-ATPase hydrolytic activity (bafilomycin insensitive, azide and vanadate sensitive) was estimated by spectrophotometric measurement of inorganic phosphate release as described in Methods. Activity was measured in tonoplast vesicles (15 ug protein) isolated from *Ananas comosus* (pineapple) over a range of aldolase concentrations. Data represent means  $\pm$  SE of three replicate experiments. Each replicate experiment was performed using independent membrane preparations. The solid lines show the fit of the kinetic data with the Michaelis-Menten equation. The  $\chi^2$  value indicates the goodness-of-fit and confirmed that the data fitted the equation at a probability level of at least  $P < 0.01$ ,



**Supplemental Figure 2:** Yeast enolase does not stimulate V-ATPase hydrolytic activity *in vitro*.

(A) V-ATPase hydrolytic activity (bafilomycin sensitive, azide and vanadate insensitive) was estimated by spectrophotometric measurement of inorganic phosphate release as described in Methods. Activity was measured in tonoplast vesicles (15  $\mu\text{g}$  protein) isolated from salt-treated *M. crystallinum* over a range of enolase concentrations.

(B) V-ATPase activity was measured in the absence or presence of 0.03 units aldolase and 0.04 units enolase in tonoplast isolated from *M. crystallinum* plants grown under control conditions or in the presence of 200 mM NaCl. Data represent means  $\pm$  SE of three replicate experiments. Each replicate experiment was performed using independent membrane preparations.

**Supplemental Table 1.** Peptide precursor mass and mass accuracy of identified peptides.

Spot #	# Identified Peptides <sup>a</sup>	MH <sup>+</sup> <sup>b</sup>	DeltaM <sup>c</sup>
131	3	1573.84318	-0.12645
		1323.76308	0.03572
		1790.92830	-0.20357
132	2	1573.84318	-0.05894
		1510.84753	-0.14954
225	2	973.52005	-0.05180
		1076.50474	0.00088
241	5	1259.73580	0.04950
		1448.71283	-0.02892
		1346.73144	-0.13037
		2216.11533	0.06802
		1766.89594	-0.10919
318	2	1596.91080	-0.03954
		1715.93266	-0.02662
414	3	1563.80131	-0.14270
		1088.57686	0.03899
		2501.18982	0.00376

<sup>a</sup>Number of matched peptides from MS/MS. Proteins were identified by 2 or more unique peptides.

<sup>b</sup>Peptide precursor mass

<sup>c</sup>Mass accuracy

**Supplemental Table 2.** Gel Scanning Parameters used for the Typhoon scanner.

<b>CyDye</b>	<b>Emission filter (nm) /Band Pass</b>	<b>Laser (nm)</b>	<b>Resolution (<math>\mu\text{m}</math>)</b>	<b>PMT<sup>a</sup> (V)</b>
Cy2	520/40	Blue 488	100	600
Cy 3	580/30	Green 532	100	600
Cy 5	670/30	Red 633	100	600

<sup>a</sup>Photomultiplier tube voltage