

Supplemental Figure S2.

GF14phi	1	MAAPPASSSAREEFVYLAKLAEQAERYEMVEFMEKVAEAVDKDELTVVEERNLLSVAYKN	60
Mp14-3-3a	1	MAAR---DEFREENVYMAKLAEQAERYDEMVEAMEKVAKTVDVVEELTVVEERNLLSVAYKN	57
GF14phi	61	VIGARRASWRIISSIEQKEESRGNDHVTTRDYRSKTESELKICDGIKLLDTRLVPA	120
Mp14-3-3a	58	VIGARRASWRIISSIEQKEESKGNDDHVAMIKDYRAKVESELSTICESILNLLDTHLIP	117
GF14phi	121	SANGDSKVFYLMKMGDYHRYLAEFKTCQERKDAEHTLTAYKAAQDIANAELAPTHPIRL	180
Mp14-3-3a	118	STTGESKVFYLMKMGDYHRYLAEFKTCGERKDAEHTLTAYKSAQDIALTELAPTHPIRL	177
GF14phi	181	GLALNFSVIFYEILNSPDRACNLAKQAFDEATAELDTLGEESYKDSTLIMQLLRDNLTLW	240
Mp14-3-3a	178	GLALNFSVIFYEILNSPDRACNLAKQAFDEATAELDTLGEESYKDSTLIMQLLRDNLTLW	237
GF14phi	241	TSDMQDESPEEIKKAAAPKPAEEQKEI	267
Mp14-3-3a	238	TSDMQEDAGDDTKEAKT-EDAEDS---	260

Supplemental Figure S2. Alignment of 14-3-3 proteins from *M. polymorpha* (Mp14-3-3a) and *A. thaliana* (GF14phi) with ClustalW (Thompson et al., 1994). Black blocks indicate identical amino acid residues; dashes indicate gaps introduced to allow for optimal alignment of sequences.