

Hua and Kao, Supplemental Figure 2

Pi SBP1	1	MA LP HHH LQ LHI QQ QP	--	QQS KS YRD IY NNM DG Q IS TP VAY FN GSN LP EQS OH PPY IP P
Ph SBP1	1	-- G T S H LQ LHI QQ QP	--	QQS KS YRD IY NNM DG Q IS TP VAY FN C SN LP EQS OH PPY IP P
Sc SBP1	1	MA LP HHH LQ LHI QQ QP	HQ	QQS KS YRD IY NNM DG Q I T TP V V Y FN GSN LP EQS OH PPY IP P
Pi SBP1	59	FQ VV GLA PG LVD DG GLD LQ WNY GL E PK RK RPK EQ D FL EN NNS QI SSI DF LQP RS VST GL G		
Ph SBP1	56	FQ VV GLA PG LVD DG GLD LQ WNY GL E PK RK RPK EQ D FL EN NNS QI SSI DF LQP RS VST GL G		
Sc SBP1	61	FQ VV GLA PG T A D DG GLD LQ WNY GL E PK K K RPK EQ D F M EN NNS QI S S V D L F Q R RS VST GL G		
Pi SBP1	119	LS LD NGR LA SSG DS AFL GL VGD DI ERE LQ RQD AE IDR YI KVQ GD RLR QA ILE KV QAN QL Q		
Ph SBP1	116	LS LD NGR LA SSG DS AFL GL VGD DI ERE LQ RQD AE IDR YI KVQ GD RLR QA ILE KV QAN QL Q		
Sc SBP1	121	LS LD NGR LA S S C DS AFL GL VGD DI ERE LQ RQD AE IDR YI KVQ GD RLR QA V L E KV QAN Q I Q		
Pi SBP1	179	TV TY VEE KV I QK LR EKE TE VED IN KKN ME LEL RT EQL AL EAN AW QQR AK YNE NL INT LK V		
Ph SBP1	176	TV TY VEE KV I QK LR EKE TE VED IN KKN ME LEL RT EQL AL EAN AW QQR AK YNE NL INT LK V		
Sc SBP1	181	A I TY VEE KV I QK LR ERD TE V D D IN KKN ME LEL R M E Q L D L EAN AW QQR AK YNE NL INT LK V		
Pi SBP1	239	NL QH VYA QS RDS KE GCG DS EVD DT ASC CN GRA TD LHL LC RDS NE MKE LM TCK VC RVN EV S		
Ph SBP1	236	NL E H VYA QS RDS KE GCG DS EVD DT ASC CN GRA TD LHL LC RDS NE MKE LM TCK VC RVN EV S		
Sc SBP1	241	NL QH VYA QS RDS KE GCG DS EVD DT ASC CN GRA TD LHL LC RDS K E MKE LM T C R V C R T N EV C		
Pi SBP1	299	ML LL PCK HL CLC KE CES KL SLC PL CQS TK YI GME I YM		
Ph SBP1	296	ML LL PCK HL CLC KE CES KL SLC PL CQS TK YI GME I YM		
Sc SBP1	301	ML LL PCK HL CLC KE CES KL SLC PL CQS TK YI GME V YM		
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Supplemental Figure 2. Alignment of the Deduced Amino Acid Sequences of Pi SBP1 of *P. inflata*, Ph SBP1 of *P. hybrida* and Sc SBP1 of *S. chacoense*. At a given site, the amino acid that is present in at least two of the three sequences is highlighted in dark shading, and the amino acid that is similar to the residue in dark shading is highlighted in gray shading. The RING-HC finger motif is enclosed in the box region, with the asterisks indicating the cysteine-histidine signature of the motif. The predicted coiled-coil region is overlined.