

ScPHO89	-----MALHQFDYIFAIALMFLAFLDAFNIGANDVANSFASSISSRSLKYWQA	47
TgPiT	MEAVAELSAPSLAGAPGEYTWIVAVAGVTCFLTAFAIGANDVANTFSSSVGSRAIPLWAA	60
PfPiT	-----MVTGPDMLLWLVIITSGIACFFMAFVTGANDIANTFSTSIGSKAISIKKA	48
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ScPHO89	MVLAGLCEFLGAVLAGARVSGTIKNNIIDSSIFTNDPAVLMMLTMTSALIGSSCWLTFATA	107
TgPiT	IGMSAVLETVGATLLGGAVTDSIRSKIIDFEVFRETGPSILMTGMLCALVGAGLWLFNLH	120
PfPiT	LIVAFFFEALGASLLGGTVDTSIRSKIIINFQVFYDTPFLMLGMCCALMGATVWLAVATR	108
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ScPHO89	IGMPVSTTHSIVGGTIGAGIAAGGANGVVGWWSGVSQIIASWFIAPILAGAIAAIVFSIS	167
TgPiT	LGLPVSTTHSIIGALLGFGLASGNVRAVK--WTQVAFIVGSWVAAPLAASAAGATIFVCM	178
PfPiT	AGLPVSTTHSIIGALLGFGLATGNMKSII--WEKINNIVISWLAAPILAGTCSAIAFTVL	166
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ScPHO89	RFSVLEVKSLERSIKNALLLVGVLVFATFSILTM---LIVWK-----GSPNLHL---	213
TgPiT	RRLILRSRQPLRRAKRFLWIFIYLLITLTFVFLVFKNFFELNVSCDQMVAGGRVEHFEP	238
PfPiT	RMLILRKKNSFEI IKMYWFLIFLITLPFSVFLIFHNPIVINTQCKM-KKDGKVIIVSSPC	225
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ScPHO89	--DDLSE----TET----AVSIVLTGAASIVYFIFFFYPFYRRKVLVDQDWT----LKLIDI	259
TgPiT	RISRWADAHSGTALGIAVALSVALTFVISC--LVYRFAFYRVESYRRRQKRSSRTEPRDA	296

ScPHO89	IHAQVNDRDMLSGDLKGM-YERSKFYDNRVEYIYSVLQAITAATMSFAHGANDVANATGP	428
TgPiT	-----HAEGSTEDDLVARLQTGAEVFDTELEFFSACQVVSACMGCIAHSANDTANAIGP	701
PfPiT	-----NGKGG---DPKNMENVIIENFDPQTEIVFSSLQIISAILGVVAQSANDTANAIGP	485
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ScPHO89	LSAVYVIWKTNTIGAKSEVPVWVLAYGGVALVIGCWTYGYNIIKNLGNKMILQSPSRGFS	488
TgPiT	FAAILTVYQSGSADSEIGSPWYILLFGGLSMSLGLLALLGYRVIKTVGVKLVKITPARGFS	761
PfPiT	FAAVFNTYNNGIR-GKIKVQWYILLFGGLSMSLGLSIMGYRVIKTVGMKLIKITPARGFT	544
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ScPHO89	IELAVAITTVMATQLGIPTSTTQIAVGGIVAVGLCNKD-----	526
TgPiT	MELGAAWTVLIFSAIGIPLSTTHCAVGSTVGVGLMEPKHPRRETGDGP-----VAEGEE	815
PfPiT	IELISGLVVLFFSICGIPLSSTHCAVSSVIGLGLVEAKMNADNKRHARKSMDKDIIQVDK	604
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ScPHO89	-----LKSVNWRMVAWCYSGWFLTLPIAGLIAGIINGIILNAPRFGV	568
TgPiT	-----PKKRAVQCPVINTASVNWKLFGGVFVSWIITIAFSALVTAALFSFAAYSP----	865
PfPiT	DKSFTLLEKIKYPFSFLNTSCVNLRLFRVFLSWILTUVFSATVTAGIYSFAAYSPSYIM	664
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ScPHO89	EYQMT 573	
TgPiT	VS--- 865	
PfPiT	KMQTV 669	

S1 Fig. Alignments of N-terminal and C-terminal sequences of TgPiT with ScPHO89 and PfPiT, showing the conserved glutamic residues (in green) in TgPiT for P_i import.