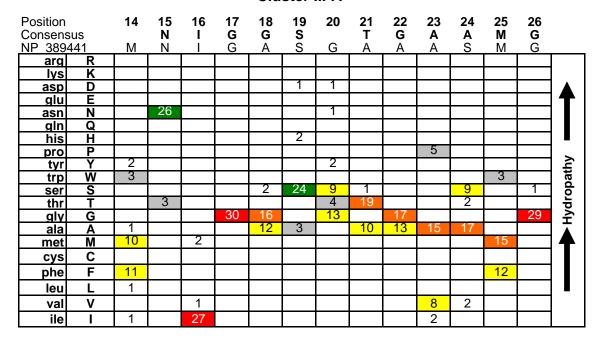
Figure 2S. ProfileGrid showing the N- and C-terminal motifs of cluster III-A from PiT family members. The first 3 rows of the Profile Grid are a position ruler, a majority consensus, and a template sequence CysP from Bacillus subtilis (accesion NP_389441). The remainning rows tabulate the frequency of the amino acids (sorted by hydropathy) at each position of the alignment (no gaps are present on the motifs). Cells are color shaded according to the next frequency value: <10% (white), >10% (gray), >25% (yellow), >50% (orange), >70% (green), >90% (red). The number of sequences included in the alignment is 714. Position ruler numbering is the same used in Figure 4C. This figure was edited from the JProfileGrid program (Roca et al., BMC Bioinformatics 2008, 9:554

N-terminal motif Cluster III-A



C-terminal motif Cluster III-A

Position Consensus NP 389441		178 F F	179 S S	180 A A	181 G G	182 M	183 N N	184 N N	185 V V	186 A A	187 N N	188 A A	189 ∨ ∨	190 A G	
arg	R														
lys	K														
asp	D							1							
glu	Е														T
asn	N						15	29			28				
gln	Q														
his	Н						1								
pro	P									2					>
tyr	Υ	3													Hydropathy
trp	W														ba
ser	S		24	4		2	14		1	1	1	1		2	2
thr	T		3			4							1		yd
gly	G				30					1				13	Ĭ
ala	Α		3	22		12			5	26		29	2	15	lack
met	М					12									T
cys	С														
phe	F	27													
leu	L			2							1				
val	٧								19				22		
ile			·	2		·			5	·		·	5	·	

Threshold	Color
0	White
0.1	Grey 25%
0.25	Yellow
0.5	Orange
0.7	Green
0.9	Red
Sequences:	714