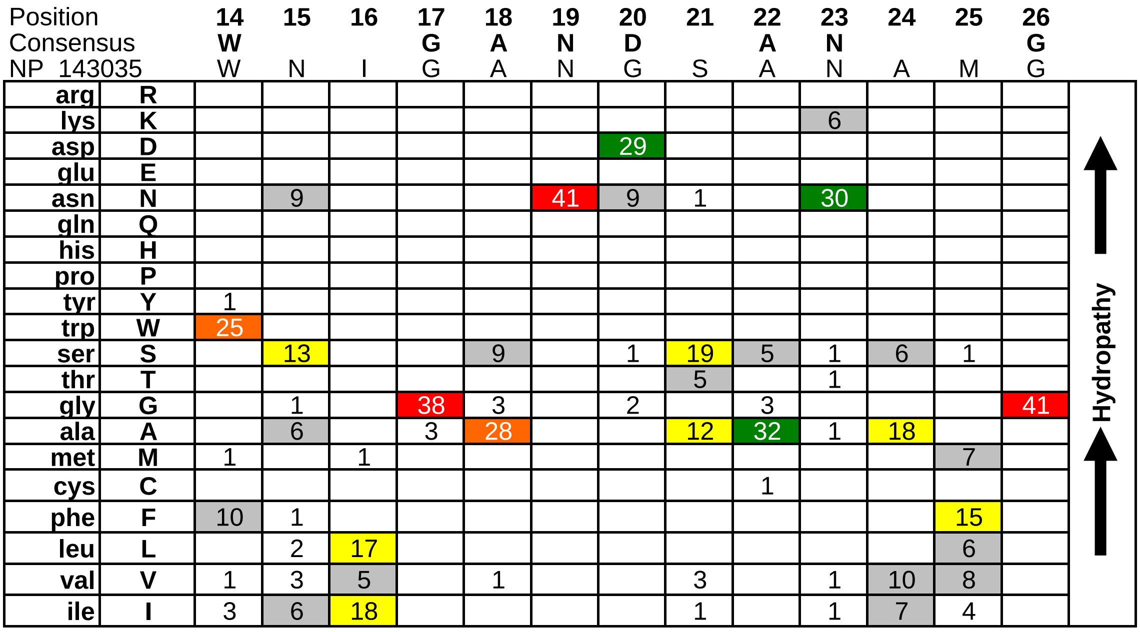
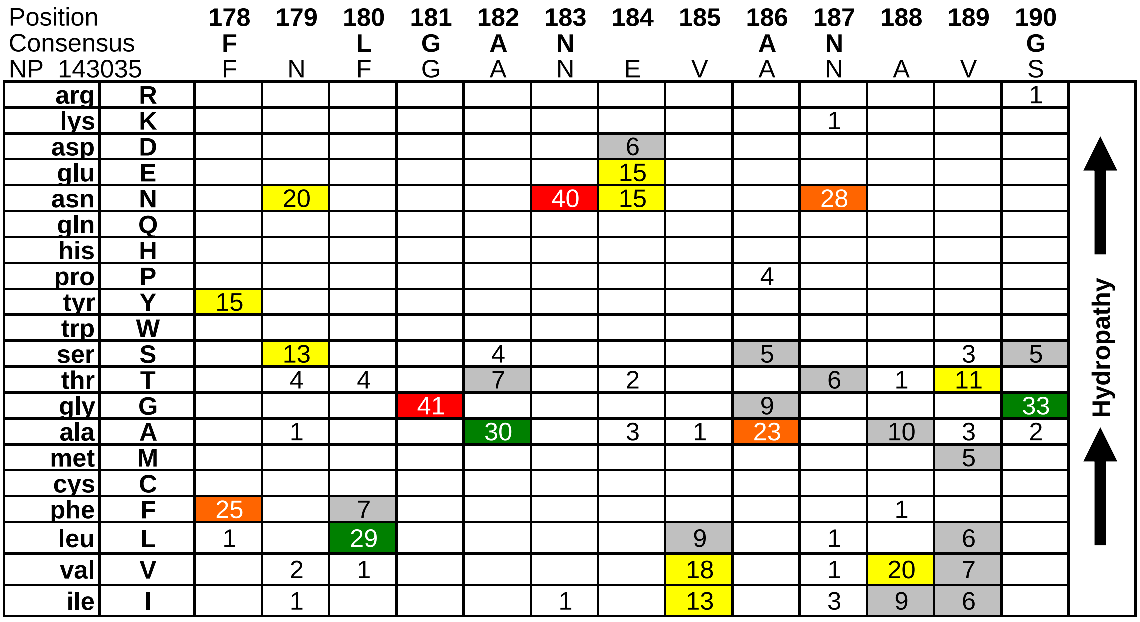
Figure 3S. ProfileGrid showing the N- and C-terminal motifs of cluster III-B from PiT family members. The first 3 rows of the Profile Grid are a position ruler, a majority consensus, and a template sequence from Pyrococcus horikoshi (accesion NP_143035). The remainning rows tabulate the frequency of 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 41. 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-B



Position		**14**	**15**	**16**	**17**	**18**	**19**	**20**	**21**	**22**	**23**	**24**	**25**	**26**
Consensus		**W**			**G**	**A**	**N**	**D**		**A**	**N**			**G**
NP_143035		W	N	I	G	A	N	G	S	A	N	A	M	G
arg	**R**													
lys	**K**										6			
asp	**D**							29						
glu	**E**													
asn	**N**		9				41	9	1		30			
gln	**Q**													
his	**H**													
pro	**P**													
tyr	**Y**	1												
trp	**W**	25												
ser	**S**		13			9		1	19	5	1	6	1	
thr	**T**								5		1			
gly	**G**		1		38	3		2		3				41
ala	**A**		6		3	28			12	32	1	18		
met	**M**	1		1									7	
cys	**C**									1				
phe	**F**	10	1										15	
leu	**L**		2	17									6	
val	**V**	1	3	5		1			3		1	10	8	
ile	**I**	3	6	18					1		1	7	4	

C-terminal motif
Cluster III-B



Position		**178**	**179**	**180**	**181**	**182**	**183**	**184**	**185**	**186**	**187**	**188**	**189**	**190**
Consensus		**F**		**L**	**G**	**A**	**N**			**A**	**N**			**G**
NP_143035		F	N	F	G	A	N	E	V	A	N	A	V	S
arg	**R**													1
lys	**K**										1			
asp	**D**							6						
glu	**E**							15						
asn	**N**		20				40	15			28			
gln	**Q**													
his	**H**													
pro	**P**									4				
tyr	**Y**	15												
trp	**W**													
ser	**S**		13			4				5			3	5
thr	**T**		4	4		7		2			6	1	11	
gly	**G**				41					9				33
ala	**A**		1			30		3	1	23		10	3	2
met	**M**												5	
cys	**C**													
phe	**F**	25		7								1		
leu	**L**	1		29					9		1		6	
val	**V**		2	1					18		1	20	7	
ile	**I**		1				1		13		3	9	6	