

Figure 1S. ProfileGrid showing the N- and C-terminal motifs of cluster I and II from PiT family members. The first 3 rows of the Profile Grid are a position ruler, a majority consensus, and a template sequence PitA from *E. coli* (accession P0AFJ9). The remaining 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 I and II

Position		14	15	16	17	18	19	20	21	22	23	24	25	26	
Consensus		F	I	N	G	F	H	D	T	A	N	A	V	A	
P0AFJ9		A	I	N	G	F	H	D	T	A	N	A	V	A	
arg	R											1			Hydropathy ↑
lys	K						1				11				
asp	D							712							
glu	E								1						
asn	N		148	379			355		11		693	70			
gln	Q										2				
his	H						354								
pro	P									3					
tyr	Y	75											6		
trp	W	102				1							5		
ser	S		56			3			27	24		230		20	
thr	T		104	2		1	4		234	4	5	4		1	
gly	G		115		714	38				24		13		282	
ala	A	34	25			317		2	109	648	3	390		408	
met	M	22	29	2		3							206		
cys	C	3							4	1					
phe	F	398	2			330				10			127		
leu	L	38	19	12		21			9			1	3		
val	V	11	61	72					313			2	182	3	
ile	I	31	155	247					6			3	185		

C-terminal motif Cluster I and II

Position		178	179	180	181	182	183	184	185	186	187	188	189	190	
Consensus		F	A	H	G	A	N	D	G	Q	K	G	I	G	
P0AFJ9		F	S	H	G	A	N	D	G	Q	K	G	I	G	
arg	R			11		3									Hydropathy ↑
lys	K										368				
asp	D							711						1	
glu	E														
asn	N		10			5	655				341				
gln	Q			8			34			357					
his	H			694		2					4				
pro	P									10		1			
tyr	Y	40										1			
trp	W														
ser	S		159		5	223	6		13	101		45	1	11	
thr	T	7	29			101			16			170	8		
gly	G		90		708	137	8		117	8		107	1	669	
ala	A	1	400		1	181	8	3	236	236		356	10	33	
met	M		5			7				1	1	2	277		
cys	C					1						2			
phe	F	479	4			1						4			
leu	L	155		1		50			1	1			4		
val	V	10	17			1	3		289			17	113		
ile	I	22				2			42			9	300		