			-		
Α			B		
	YETJ_BACSU/1-214	60	RRRKAV	150	S A AMMA Y S V I G T I V F S L Y I L Y D L N Q I K
	YBHL_ECOLI/1-234	79	K L S A <mark>G V</mark>	164	E A LMWA VT Y I <mark>G</mark> V I VF V <mark>G</mark> L T A YD T Q K L K
	A0A2G9LPJ1_9ARCH/1-275	123	RRK <mark>G</mark> GF	212	G L F G I I I D A A V L L I F L G F V MY D MS M I L
	A8DJZ0_9BACT/1-239	88	R R V K <mark>G V</mark>	176	S VF S LA I S <mark>S G A</mark> V L L F A <mark>G Y</mark> V L Y D T S N I V
	A0A1S5WLC9_COWPX/1-237	90	RHKH <mark>P</mark> L	175	ETVELALS AFGALVF CGF I I YDTHS L I
	BI1_ARATH/1-247	85	E HQK	173	A <mark>S</mark> I F K F E L Y F <mark>G</mark> L L I F V <mark>G Y</mark> M V V D T Q E I I
	BXI1_YEAST/1-297	130	Q E Q R R L P WY V	234	S KFN L L YG WLG A I L F T A Y L F I D T Q L I F
	P91373_CAEEL/1-342	166	ARS IDY	261	AS LAS I VVYGG LILF S AF LLYD TQ R LV
	LFG1_HUMAN/1-371	221	R R K H <mark>P</mark> W	306	R I LE I VYA <mark>S</mark> L <mark>G</mark> A L L F T C F L A VD T Q L L L
	LFG2_HUMAN/1-316	162	R R H F <mark>P W</mark>	251	PWLHAVYAALGAGVFTLFLALDTQLLM
	LFG3_HUMAN/1-311	158	R R R F <mark>P W</mark>	247	YWLHMLYAAL <mark>G</mark> AICFTLFLAYDTQLVL
	LFG4_HUMAN/1-238	91	RHKY <mark>P</mark> L	176	E I ME L V L A A A G A L L F C G F I I Y D T H S L M
	GHITM_HUMAN/1-345	177	VRS I PY	273	ATLYS VAMYGG LVLF SMFLLYDTQ KVI
	BI1_HUMAN/1-237	78	HETEQK	167	IWLFQ AN LYV <mark>G</mark> LVVMC <mark>G</mark> FVLFDTQLII
	BI1_MOUSE/1-237	78	HETEQK	167	IWLFQANLYLGLLVMCGFVLFDTQLII
~					*
С					
С	YETJ_BACSU/1-214	193		Contraction of the second s	3 I LS SDD
С	YBHL_ECOLI/1-234	216	YLDFINLFLMLLI	R I F <mark>(</mark>	G I LS S D D
С	YBHL_ECOLI/1-234 A0A2G9LPJ1_9ARCH/1-275	216 254	Y L <mark>D</mark> FI <mark>NLFLMLLI Y LD</mark> FL <mark>NIFIRILO</mark>	R I F <mark>(</mark> Q L L V	G I LS SDD
С	YBHL_ECOLI/1-234 A0A2G9LPJ1_9ARCH/1-275 A8DJZ0_9BACT/1-239	216 254 218	YLDFINLFLMLLI YLDFLNIFIRILO FLDFF <mark>G</mark> LFIHLLI	R I F <mark>(</mark> Q L L V N I L N	G I LS S DD
С	YBHL_ECOLI/1-234 A0A2G9LPJ1_9ARCH/1-275 A8DJZ0_9BACT/1-239 A0A1S5WLC9_COWPX/1-237	216 254 218 217	YLDFINLFLMLLI YLDFLNIFIRILO FLDFFGLFIHLLI YLDIINLFLHLLO	R I F C Q L L V N I L N Q L L I	I LS S DD
С	YBHL_ECOLI/1-234 A0A2G9LPJ1_9ARCH/1-275 A8DJZ0_9BACT/1-239 A0A1S5WLC9_COWPX/1-237 B11_ARATH/1-247	216 254 218 217 217	YLDFINLFLMLLI YLDFLNIFIRIL FLDFFGLFIHLL YLDIINLFLHLL FTDFVAVFVRIL	RIF <mark>C</mark> QLLV NILN QLLE IIMI	I LSSDD
С	YBHL_ECOLI/1-234 A0A2G9LPJ1_9ARCH/1-275 A8DJZ0_9BACT/1-239 A0A1S5WLC9_COWPX/1-237 B11_ARATH/1-247 BXI1_YEAST/1-297	216 254 218 217 217 276	YLDFINLFLMLL YLDFLNIFIRIL FLDFFGLFIHLL YLDIINLFLHLL FTDFVAVFVRIL YLDIVNLFLSIL	RIF QLLV NILN QLLF IIMI RIL/	I LS S DD
С	YBHL_ECOLI/1-234 A0A2G9LPJ1_9ARCH/1-275 A8DJZ0_9BACT/1-239 A0A1S5WLC9_COWPX/1-237 B11_ARATH/1-247 BXI1_YEAST/1-297 P91373_CAEEL/1-342	216 254 218 217 217 276 319	YLD F IN LF LMLL YLD F LN IF I R I LC F LD F F G LF IH LL YLD I IN LF LH LL F TD F VA VF VR I L YLD I VN LF LS I L YMD VLN IFMR LV	RIF QLLV NILN QLLF IIMI RIL MIM	G I LS S DD
С	YBHL_ECOLI/1-234 A0A2G9LPJ1_9ARCH/1-275 A8DJZ0_9BACT/1-239 A0A1S5WLC9_COWPX/1-237 B11_ARATH/1-247 BX11_YEAST/1-297 P91373_CAEEL/1-342 LFG1_HUMAN/1-371	216 254 218 217 217 276 319 352	YLDFINLFLMLL YLDFLNIFIRIL FLDFFGLFIHLL YLDIINLFLHLL FTDFVAVFVRIL YLDIVNLFLSIL YMDVLNIFMRLV YTDIINIFLYL	RIFC QLLV QLLF QLLF IIMI RILA MIMC TIIC	G I LS S DD
С	YBHL_ECOLI/1-234 A0A2G9LPJ1_9ARCH/1-275 A8DJZ0_9BACT/1-239 A0A1S5WLC9_COWPX/1-237 B11_ARATH/1-247 BX11_YEAST/1-297 P91373_CAEEL/1-342 LFG1_HUMAN/1-371 LFG2_HUMAN/1-316	216 254 218 217 217 276 319 352 297	YLDFINLFLMLLI YLDFLNIFIRIL FLDFFGLFIHLLM YLDIINLFLHLL YLDIVNLFLSIL YMDVLNIFMRLV YTDIINIFLYIL YLDIIYIFTFFL	RIFC QLLV NILN QLLE IIMI RILA MIMC TIIC QLFC	G I LS S DD
С	YBHL_ECOLI/1-234 A0A2G9LPJ1_9ARCH/1-275 A8DJZ0_9BACT/1-239 A0A1S5WLC9_COWPX/1-237 B11_ARATH/1-247 BXI1_YEAST/1-297 P91373_CAEEL/1-342 LFG1_HUMAN/1-371 LFG2_HUMAN/1-316 LFG3_HUMAN/1-311	216 254 218 217 217 276 319 352 297 293	YLD F IN LF LMLL YLD F LN IF IR ILC FLD F F G LF IH LL YLD I IN LF LH LLC F TD F VA VF VR IL YLD I VN LF LS ILL YMD VLN IF MR LV YTD I IN IF LY IL YLD I IN IF TF FLC YTD I I Y IF TF VLC	RIFC QLLV NILN QLLE IIMI RILA MIMC TILC QLFC QLMC	G I LS S DD
С	YBHL_ECOLI/1-234 A0A2G9LPJ1_9ARCH/1-275 A8DJZ0_9BACT/1-239 A0A1S5WLC9_COWPX/1-237 B11_ARATH/1-247 BXI1_YEAST/1-297 P91373_CAEEL/1-342 LFG1_HUMAN/1-371 LFG2_HUMAN/1-316 LFG3_HUMAN/1-311 LFG4_HUMAN/1-238	216 254 218 217 217 276 319 352 297 293 218	YLD F IN LF LML LI YLD F LN IF I R I LC F LD F F G LF I H LL YLD I IN LF LH LLC YLD I VN LF LS I LL YMD VLN I FMR LV YTD I IN IF LYI L YLD I Y IF TF F LC YTD I IY IF TF VLC YLD I N LF LH LL	RIFC QLLV VILN QLLE IIMI RILA MIMC TIIC QLFC QLMC RFLE	G I LS S DD
С	YBHL_ECOLI/1-234 A0A2G9LPJ1_9ARCH/1-275 A8DJZ0_9BACT/1-239 A0A1S5WLC9_COWPX/1-237 B11_ARATH/1-247 BX11_YEAST/1-297 P91373_CAEEL/1-342 LFG1_HUMAN/1-371 LFG2_HUMAN/1-316 LFG3_HUMAN/1-311 LFG4_HUMAN/1-238 GHITM_HUMAN/1-345	216 254 218 217 217 276 319 352 297 293 218 323	YLD F IN LF LMLL YLD F LN IF IR ILC FLD F F G LF IH LLN YLD I IN LF LH LLC FTD F VAVF VR IL YMD VLN IFMR LVY YTD I IN IF LYIL YLD I YIF F LC YLD I IN IF LH LL YMD T LN IFMR VA	R I F C Q L L V N I L N Q L L F I I MI R I L A M I MC T I I C Q L F C Q L MC R F L F T M L A	G I LS S DD
С	YBHL_ECOLI/1-234 A0A2G9LPJ1_9ARCH/1-275 A8DJZ0_9BACT/1-239 A0A1S5WLC9_COWPX/1-237 B11_ARATH/1-247 BXI1_YEAST/1-297 P91373_CAEEL/1-342 LFG1_HUMAN/1-371 LFG2_HUMAN/1-316 LFG3_HUMAN/1-311 LFG4_HUMAN/1-238	216 254 218 217 217 276 319 352 297 293 218	YLD F IN LF LML L YLD F LN IF IR I L F LD F F G LF IH LL YLD I IN LF LH LL F TD F VA VF VR I L YMD VLN IF MR LV YTD I IN IF LY I L YLD I YIF T F L YLD I IY IF T F L YLD I IN LF LH LL YMD T LN IF MR VA F LD F I T VF RK LM	R I F C Q L L V Q L L E I I MI R I L A MIMC T I I C Q L F C Q L MC R F L E T ML A MI L A	G I LS S DD

Figure S1. Partial sequence alignments of TMBIM family members selected from different organism species relative to BsYetJ residues Arg60, Asp171, and Asp195. Related to Figure 2. TMBIM-conserved residues are indicated by stars. Residues equivalent to RRRK in BsYetJ were indicated by a red box. TMBIM family members of different organism species were extracted from UNIPROT database (www.uniprot.org). Their sequences were aligned by using MAFFT (mafft.cbrc.jp) with the option of L-INS-i recommended for <200 sequences with one conserved domain and long gaps. Partial alignments were shown for BsYetJ Arg60 (A), Asp171 (B), and Asp195 (C). The sequence coloring scheme follows the Clustal X standard in JalView (www.jalview.org) at a conservation level of 15%. Organism species and their entry names are: Bacillus subtilis: YETJ\_BACSU; Escherichia coli: YBHL\_ECOLI; Candidatus Woesearchaeota archaeon: A0A2G9LPJ1\_9ARCH; Chloracidobacterium thermophilum: A8DJZ0\_9BACT; Cowpox virus: A0A1S5WLC9\_COWPX; Saccharomyces cerevisiae: BXI1\_YEAST; Caenorhabditis elegans: P91373\_CAEEL; Arabidopsis thaliana: BI1\_ARATH; Homo sapiens: LFG2\_HUMAN/TMBIM2, LFG3\_HUMAN/TMBIM1, LFG1\_HUMAN/TMBIM3, LFG4 HUMAN/TMBIM4, GHITM HUMAN/TMBIM5, BI1 HUMAN/TMBIM6; Mus musculus: BI1\_MOUSE.