

**Table 1S.** Histidine kinases with domain organization similar to BceS and YvqE of *Bacillus subtilis*

Organism	Histidine Kinase	ACC-Nr.	length [aa]	TM spacing (1)	ABC transporter (2)	function	remark	Reference
<b>Bacillus</b>								
<i>B. anthracis</i>	BA1956	AAP25850	351	8	no	unknown		genome
<i>B. cereus</i>	BC1801 or VanS	AAP08775	358	12	no	unknown		genome
	BC1957	AAP08928	348	10	yes	unknown	multidrug res.	genome
<i>B. halodurans</i>	BH3912	BAB07631	334	9	yes	unknown		genome
	BH2700	BAB06419	343	10	yes	unknown		genome
	BH0289	BAB04008	346	7	yes	unknown		genome
	BH0272	BAB03991	331	14	yes	unknown		genome
	BH1199	BAB04918	351	16	no	unknown		genome
<i>B. licheniformis</i>	BacS	AAD21212	348	7	yes	<b>Bac-resistance</b>		Neumuller et al. (2001)
<i>B. subtilis</i>	YvcQ	CAB15476	356	15	yes	<b>Bac-inducible</b>		this study, Joseph et al. (2002)
	YbdK	CAB11995	320	19	no	unknown		genome
	YtsB	CAB15017	334	<5	yes	<b>Bac-resistance</b>		this study, Joseph et al. (2002)
	YvqE	CAB15299	360	6	no	<b>Bac-/Van-/Ram-inducible</b>		this study
<b>Clostridium</b>								
<i>C. acetobutylicum</i>	CAC3516	AAK81442	350	11	yes	unknown		genome
	CAC1517	AAK79484	349	9	yes	unknown		genome
	CAC0372	AAK78352	334	8	yes	unknown		genome
	CAC0225	AAK78206	339	15	yes	unknown		genome
<i>C. perfringens</i>	CPE0841	BAB80547	336	<5	no	unknown		genome
<i>Enterococcus faecalis</i>	EF0927	AAO80735	341	8	yes	unknown		genome
<i>Lactobacillus sakei</i>	HPK1	AAD10259	339	14	yes	unknown		genome
<i>Listeria monocytogenes</i>	LMO1741	CAC99819	346	9	yes	unknown		genome
<b>Staphylococcus</b>								
<i>S. aureus</i>	SA0615	BAB94487	346	9	yes	unknown		genome
	SA2417	BAB58786	295	6	yes	unknown		genome
	SaeS	AAD48403	353	7	no	exoprotein prod.		Giraud et al. 1999/2003
	VraS	NP_374992	347	9	no	<b>Bac-/Van-inducible</b>		Kuroda et al. 2003
<i>S. epidermidis</i>	SE2194	AAO05836	298	<5	yes	unknown		genome
	SE0428	AAO04025	346	7	yes	unknown	PsbT dom.	genome
<b>Streptococcus</b>								
<i>S. agalactiae</i>	GBS0964	CAD46623	312	9	yes	unknown		genome
	GBS0430	CAD46074	345	10	no	unknown		genome
	GBS0122	CAD45767	356	6	yes	unknown		genome
<i>S. mutans</i>	MbrD	BAB83946	317	<5	yes	<b>Bac-resistance</b>		Tsuda et al. 2002
<i>S. pneumoniae</i>	HK01 or SP1632	CAB54567	324	<5	no	unknown		Lange et al. (1999)
	HK08 or SP0084	CAB54579	350	10	yes?	unknown		Lange et al. (1999)
<b>Bifidobacterium longum</b>								
BL1001	AAN24809	358	6	no	no	unknown		genome
<b>Streptomyces</b>								
<i>S. avermitis</i>	SAV2971	BAC70682	368	10	no	unknown		genome
	SAV7391	BAC75102	388	5-15	no	unknown		genome
<i>S. coelicolor</i>	SCO5282	CAC04497	375	10	no	unknown		genome
	SCO6424	CAA18911	331	12	no	unknown		genome
	SCO5784	CAA18321	358	8	no	unknown		genome
	SCO6163	CAA22397	303	<5	no	unknown		genome
<b>Anabaena sp.</b>								
ALR3155	BAB74854	344	17	yes	unknown		genome	
<b>Haemophilus influenzae</b>								
ArcB	P44578	325	10	no	no	aerobic respiration?		genome
<b>Ralstonia solanacearum</b>								
RS03089	CAD18605	365	16	yes	yes	unknown		genome
<b>Xenorhabdus nematophilus</b>								
EnvZ	AAB36612	342	8	no	no	osmo-sensing		Tabatabai and Forst (1995)
<b>Thermotoga maritima</b>								
TM1258	AAD36332	319	8	yes	yes	unknown		genome

(1) Estimated number of amino acids between the two putative transmembrane domains

(2) Localization of two-component systems corresponding to the histidine kinases in direct vicinity to genes coding for ABC transporters