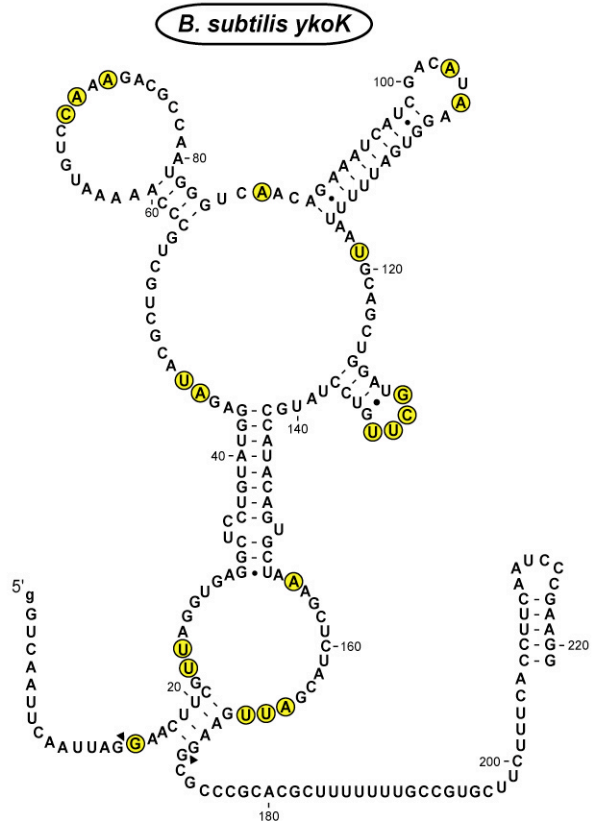
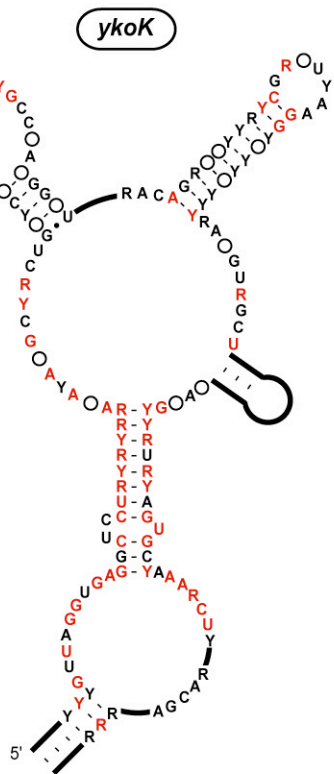


A

Abb	Organism	Accession	Position	Genes
Bacillus/Clostridium				
Ban	<i>Bacillus anthracis</i>	NC_003997.3	+ 1510409 1510555	BA1605 COG0474
Bce	<i>Bacillus cereus</i>	NC_004722.1	+ 1527922 1528069	BC1581 COG0474
Bce	<i>Bacillus cereus</i>	NC_004722.1	+ 4103599 4103748	BC4140 COG0474 BC4141 COG1285
Bha	<i>Bacillus halodurans</i>	NC_002570.1	+ 2041950 2042097	BH1946 COG3464 BH1947 COG2239 BH1948 COG2239
Bha	<i>Bacillus halodurans</i>	NC_002570.1	- 3340848 3340994	BH3226 ----- BH3225 COG1285 BH3224 COG2239
Bha	<i>Bacillus halodurans</i>	NC_002570.1	- 3340396 3340541	BH3225 COG1285 BH3224 COG2239
Bsu	<i>Bacillus subtilis</i>	NC_000964.1	+ 1395090 1395237	ykoK COG2239
Cac	<i>Clostridium acetobutylicum</i>	NC_003030.1	+ 789416 789571	CAC0683 ----- CAC0684 COG2239 CAC0685 COG1914
Cac	<i>Clostridium acetobutylicum</i>	NC_003030.1	- 3501692 3501837	CAC3329 COG1914
Cth	<i>Clostridium thermocellum</i>	NZ_AABG02000025.1	+ 30891 31039	chte1267 COG0598
Efa	<i>Enterococcus faecalis</i>	NC_004668.1	+ 1268274 1268425	EF1304 COG0474
Lga	<i>Lactobacillus gasseri</i>	ZP_00046151.1	+ 78545 78693	Lgas0315 COG0474
Lin	<i>Listeria innocua</i>	NC_003212.1	- 2855176 2855325	lin2836 COG0474 lin2835 COG0772 Lin2834 COG0772
Lmo	<i>Listeria monocytogenes</i>	NC_003210.1	- 2765947 2766095	lmo2689 COG0474 lmo2688 COG0772 lmo2687 COG0772
Tte	<i>Thermoanaerobacter tengcongensis</i>	NC_003869.1	- 2397961 2398107	TTE2510 ----- TTE2509 COG0474
Actinobacteria				
Mbo	<i>Mycobacterium bovis</i>	NC_002945.3	+ 1719531 1719680	Mb1562 -----
Mle	<i>Mycobacterium leprae</i>	NC_002677.1	- 3196999 3197092	ML2667 COG1914
Msm	<i>Mycobacterium smegmatis</i>		- 1484907 1485062	(mgtA) COG0474
	(gnl TIGR_246196 contig:3312:m_smegmatis)			
Mtu	<i>Mycobacterium tuberculosis</i>	NC_000962.1	+ 1735516 1735665	Rv1535 -----
Beta Proteobacteria				
Cvi	<i>Chromobacterium violaceum</i>	NC_005085.1	+ 3525136 3525282	mgtE COG2239
Gamma Proteobacteria				
Vch	<i>Vibrio cholerae</i> chr I	NC_002505.1	+ 1786711 1786862	VC1655 COG2239
COG	Gene	Description		
COG2239	BS_ykoK	Mg/Co/Ni transporter MgtE (contains CBS domain)		
COG1914	mntA	Mn2+ and Fe2+ transporters of the NRAMP family		
COG1285	yhiD	Uncharacterized membrane protein		
COG0474	mgtA	Cation transport ATPase		
COG0772	ftsW	Bacterial cell division membrane protein		
COG0598	corA	Mg2+ and Co2+ transporters		
COG3464	-	Transposase and inactivated derivatives		

C



B. subtilis
ykoK

NR T1 OH -

