## Table S1: Overview of TA loci and solitary toxin genes in 126 prokaryotic genomes

| | *relBE* | *parDE* | *higBA* | *vapBC* | *mazEF* | *phd/doc* | *ccdAB* | Total |
|---|---|---|---|---|---|---|---|---|
| **Total in Bacteria** | **129** | **59** | **74** | **139** | **67** | **22** | **5** | **495** |
| **Total in Archaea** | **27** | **0** | **0** | **146** | **0** | **3** | **0** | **176** |
| **Total** | **156** | **59** | **74** | **285** | **67** | **25** | **5** | **671** |
| **Orphan** | **13** | **0** | **2** | **13** | **7** | **2** | **0** | **37** |

| Organism | *relBE* | *parDE* | *higBA* | *vapBC* | *mazEF* | *phd/doc* | *ccdAB* | Total |
|---|---|---|---|---|---|---|---|---|
| **Archaea** | | | | | | | | |
| Aeropyrum_pernix | 1 | 0 | 0 | 7 | 0 | 0 | 0 | **8** |
| Sulfolobus_solfataricus | 0 | 0 | 0 | 22 | 0 | 0 | 0 | **22** |
| Sulfolobus_tokodaii | 2 | 0 | 0 | 25 | 0 | 2 | 0 | **29** |
| Pyrobaculum_aerophilum | 0 | 0 | 0 | 9 | 0 | 0 | 0 | **9** |
| Archaeoglobus_fulgidus | 4 | 0 | 0 | 24 | 0 | 0 | 0 | **28** |
| Halobacterium_sp_NRC_1 | 1 | 0 | 0 | 3 | 0 | 0 | 0 | **4** |
| M.thermoautotrophicum | 0 | 0 | 0 | 2 | 0 | 0 | 0 | **2** |
| Methanococcus_jannaschii | 4 | 0 | 0 | 5 | 0 | 0 | 0 | **9** |
| Methanopyrus_kandleri_AV19 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | **1** |
| Methanosarcina_acetivorans | 8 | 0 | 0 | 3 | 0 | 0 | 0 | **11** |
| Methanosarcina_mazei | 5 | 0 | 0 | 1 | 0 | 1 | 0 | **7** |
| Pyrococcus_furiosus | 1 | 0 | 0 | 14 | 0 | 0 | 0 | **15** |
| Pyrococcus_horikoshii | 1 | 0 | 0 | 11 | 0 | 0 | 0 | **12** |
| Pyrococcus_abyssi | 0 | 0 | 0 | 16 | 0 | 0 | 0 | **16** |
| Thermoplasma_acidophilum | 0 | 0 | 0 | 2 | 0 | 0 | 0 | **2** |
| Thermoplasma_volcanium | 0 | 0 | 0 | 1 | 0 | 0 | 0 | **1** |
| **Bacteria** | | | | | | | | |
| **Gram Positive** | | | | | | | | |
| Bifidobacterium_longum | 2 | 0 | 0 | 3 | 0 | 0 | 0 | **5** |
| C._glutamicum_ATCC | 0 | 0 | 1 | 0 | 0 | 0 | 0 | **1** |
| C.efficiens_YS_314 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | **1** |
| Mycobacterium_leprae | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| M._tuberculosis_H37Rv | 3 | 2 | 1 | 23 | 9 | 0 | 0 | **38** |
| M._tuberculosis_CDC1551 | 3 | 2 | 1 | 23 | 7 | 0 | 0 | **36** |
| S._avermitilis_MA | 1 | 0 | 0 | 1 | 0 | 2 | 0 | **4** |
| S._coelicolor_A32 | 1 | 0 | 0 | 0 | 0 | 2 | 0 | **3** |
| T._whipplei_Twist | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| T._whipplei_TW08_27 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Chlorobium_tepidum_TLS | 0 | 0 | 0 | 0 | 1 | 1 | 0 | **2** |
| Chlamydia_muridarum | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Chlamydia_trachomatis | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| C._caviae_GPIC | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| C._pneumoniae_CWL029 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| C._pneumoniae_TW_183 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| C._pneumoniae_AR39 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| C._pneumoniae_J138 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Nostoc_sp_PCC_7120 | 5 | 0 | 3 | 14 | 4 | 1 | 0 | **27** |
| Prochlorococcus_marinus | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Synechocystis_PCC6803 | 3 | 0 | 1 | 8 | 1 | 0 | 0 | **13** |
| T._elongatus_BP | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Bacillus_anthracis | 0 | 0 | 0 | 0 | 1 | 0 | 0 | **1** |
| Bacillus_cereus | 0 | 0 | 0 | 0 | 1 | 0 | 0 | **1** |
| Bacillus_halodurans | 0 | 0 | 0 | 0 | 2 | 0 | 0 | **2** |
| Bacillus_subtilis | 0 | 0 | 0 | 0 | 1 | 0 | 0 | **1** |
| C._acetobutylicum | 0 | 0 | 0 | 0 | 1 | 0 | 0 | **1** |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Clostridium_perfringens | 0 | 0 | 0 | 0 | 1 | 0 | 0 | **1** |
| Clostridium_tetani_E88 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | **2** |
| E.faecalis_V583 | 1 | 0 | 0 | 0 | 1 | 1 | 0 | **3** |
| Mycoplasma_gallisepticum | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Mycoplasma_genitalium | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Mycoplasma_penetrans | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Mycoplasma_pneumoniae | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Mycoplasma_pulmonis | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Ureaplasma_urealyticum | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Lactobacillus_plantarum | 0 | 0 | 1 | 0 | 1 | 0 | 0 | **2** |
| Lactococcus_lactis | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Listeria_innocua | 0 | 0 | 0 | 0 | 1 | 0 | 0 | **1** |
| Listeria_monocytogenes | 0 | 0 | 0 | 0 | 1 | 0 | 0 | **1** |
| Oceanobacillus_iheyensis | 0 | 0 | 0 | 0 | 1 | 0 | 0 | **1** |
| T._tengcongensis | 3 | 0 | 0 | 2 | 1 | 0 | 0 | **6** |
| S._aureus_MW2 | 2 | 0 | 0 | 0 | 1 | 0 | 0 | **3** |
| S._aureus_N315 | 2 | 0 | 0 | 0 | 1 | 0 | 0 | **3** |
| S._aureus_Mu50 | 2 | 0 | 0 | 0 | 1 | 0 | 0 | **3** |
| S._epidermidis_ATCC_12228 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | **1** |
| S._agalactiae_2603 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | **2** |
| S._agalactiae_NEM316 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | **2** |
| S.mutans_UA159 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | **2** |
| S.pneumonia_TIGR4 | 3 | 0 | 1 | 0 | 0 | 1 | 0 | **5** |
| Streptococcus_pneumonia_R6 | 3 | 0 | 0 | 0 | 0 | 0 | 0 | **3** |
| Streptococcus_pyogenes | 0 | 2 | 0 | 0 | 0 | 0 | 0 | **2** |
| S._pyogenes_MGAS315 | 0 | 2 | 0 | 0 | 0 | 0 | 0 | **2** |
| S._pyogenes_MGAS8232 | 0 | 2 | 0 | 0 | 0 | 0 | 0 | **2** |
| Streptococcus_pyogenes_SSI_1 | 0 | 2 | 0 | 0 | 0 | 0 | 0 | **2** |
| Fusobacterium_nucleatum | 3 | 0 | 0 | 0 | 0 | 0 | 0 | **3** |
| Pirellula_sp | 1 | 2 | 0 | 0 | 0 | 0 | 0 | **3** |
| **Others** | | | | | | | | |
| Aquifex_aeolicus | 0 | 0 | 0 | 2 | 0 | 0 | 0 | **2** |
| Bacteroides_theta_VPI_5482 | 0 | 0 | 2 | 0 | 0 | 0 | 0 | **2** |
| **Gram_Negative** | | | | | | | | |
| Caulobacter_crescentus | 4 | 4 | 1 | 1 | 0 | 1 | 0 | **11** |
| A._tumefaciens_C58 | 6 | 3 | 0 | 2 | 1 | 0 | 0 | **12** |
| A._tumefaciens_C58_linear | 1 | 0 | 0 | 1 | 0 | 0 | 0 | **2** |
| A._tumef._C58_Wash | 6 | 3 | 0 | 2 | 1 | 0 | 0 | **12** |
| A._tumef._C58_Wash_linear | 1 | 0 | 0 | 1 | 0 | 0 | 0 | **2** |
| Bradyrhizobium_japonicum | 0 | 0 | 4 | 1 | 0 | 0 | 0 | **5** |
| Brucella_melitensis_chr_I | 1 | 0 | 0 | 0 | 0 | 1 | 0 | **2** |
| Brucella_melitensis_chr_II | 0 | 0 | 0 | 0 | 1 | 0 | 0 | **1** |
| Brucella_suis_chromosome_I | 1 | 0 | 0 | 0 | 0 | 1 | 0 | **2** |
| Brucella_suis_chromosome_II | 0 | 0 | 0 | 0 | 1 | 0 | 0 | **1** |
| Mesorhizobium_loti | 1 | 3 | 2 | 4 | 0 | 0 | 0 | **10** |
| S._meliloti_1021_chr | 2 | 0 | 3 | 7 | 0 | 0 | 0 | **12** |
| Rickettsia_conorii_Malish | 1 | 0 | 1 | 3 | 1 | 0 | 0 | **6** |
| Rickettsia_prowazekii | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Coxiella_burnetii | 1 | 1 | 3 | 2 | 0 | 0 | 0 | **7** |
| Ralstonia_solanacearum_chr | 2 | 0 | 0 | 2 | 0 | 0 | 0 | **4** |
| Neisseria_meningitidis_MC58 | 0 | 0 | 0 | 1 | 2 | 1 | 0 | **4** |
| Neisseria_meningitidis_Z2491 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | **1** |
| Nitrosomonas_europaea | 9 | 6 | 7 | 13 | 5 | 2 | 1 | **43** |
| Campylobacter_jejuni | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Helicobacter_hepaticus | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Helicobacter_pylori_26695 | 3 | 0 | 0 | 0 | 0 | 0 | 0 | **3** |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Helicobacter_pylori_J99 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | **1** |
| Buchnera_sp_APS | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Buchnera_aphidicola | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Buchnera_aphidicola_Sg | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Escherichia_coli_CFT073 | 1 | 0 | 3 | 0 | 0 | 0 | 1 | **5** |
| Escherichia_coli_K12 | 3 | 0 | 0 | 0 | 2 | 0 | 0 | **5** |
| Escherichia_coli_O157 | 1 | 3 | 1 | 0 | 2 | 0 | 1 | **8** |
| E._coli_O157_H7_EDL933 | 1 | 3 | 1 | 0 | 2 | 0 | 1 | **8** |
| Salmonella_typhimurium_LT2 | 3 | 1 | 2 | 1 | 0 | 1 | 0 | **8** |
| Salmonella_typhi | 1 | 1 | 1 | 2 | 0 | 1 | 0 | **6** |
| Salmonella_typhi_Ty2 | 1 | 1 | 1 | 2 | 0 | 1 | 0 | **6** |
| Shigella_flexneri_2a | 2 | 0 | 0 | 0 | 1 | 0 | 0 | **3** |
| Shigella_flexneri_2a_2457T | 2 | 0 | 0 | 0 | 0 | 0 | 0 | **2** |
| Wigglesworthia_brevipalpis | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Yersinia_pestis_CO92 | 0 | 0 | 4 | 0 | 0 | 1 | 0 | **5** |
| Yersinia_pestis_KIM | 1 | 0 | 3 | 0 | 0 | 1 | 0 | **5** |
| S._oneidensis_MR | 1 | 1 | 0 | 0 | 0 | 0 | 0 | **2** |
| Vibrio_cholerae | 7 | 3 | 2 | 0 | 0 | 1 | 0 | **13** |
| Vibrio_parahaemolyticus | 3 | 1 | 0 | 0 | 0 | 0 | 0 | **4** |
| V.vulnificus_CMCP6_chr_1 | 3 | 1 | 0 | 0 | 0 | 0 | 0 | **4** |
| V.vulnificus_CMCP6_chr_2 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | **1** |
| X_axonopodis_pv_citri_str_306 | 1 | 2 | 0 | 3 | 0 | 1 | 0 | **7** |
| X._campestris_pv_ATCC_33913 | 3 | 1 | 0 | 2 | 0 | 0 | 1 | **7** |
| Xylella_fastidiosa_chr | 4 | 2 | 8 | 2 | 1 | 0 | 0 | **17** |
| Xylella_fastidiosa_Temecula1 | 2 | 1 | 4 | 1 | 0 | 0 | 0 | **8** |
| Haemophilus_influenzae | 1 | 0 | 3 | 2 | 0 | 0 | 0 | **6** |
| Haemophilus_ducreyi_35000HP | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Pasteurella_multocida | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Pseudomonas_aeruginosa | 1 | 1 | 1 | 0 | 0 | 0 | 0 | **3** |
| Pseudomonas_putida_KT2440 | 2 | 0 | 4 | 0 | 1 | 0 | 0 | **7** |
| Pseudomonas_syringae | 3 | 1 | 3 | 2 | 0 | 0 | 0 | **9** |
| Borrelia_burgdorferi | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Leptospira_intrerrogans_I | 0 | 0 | 0 | 3 | 2 | 0 | 0 | **5** |
| Treponema_pallidum | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| Thermotoga_maritima | 0 | 0 | 0 | 0 | 0 | 0 | 0 | **0** |
| D._radiodurans_chr_1 | 0 | 0 | 0 | 3 | 2 | 0 | 0 | **5** |

| **Solitary toxin genes** | 13 | 0 | 2 | 13 | 7 | 2 | 0 | 37 |
|---|---|---|---|---|---|---|---|---|
| Organism | ***relBE*** | ***parDE*** | ***higBA*** | ***vapBC*** | ***mazEF*** | ***phd/doc*** | ***ccdAB*** | **Total** |
| **Archaea** | | | | | | | | |
| Aeropyrum_pernix | 0 | 0 | 0 | 1 | 0 | 0 | 0 | **1** |
| Sulfolobus_solfataricus | 0 | 0 | 0 | 1 | 0 | 0 | 0 | **1** |
| Sulfolobus_tokodaii | 2 | 0 | 0 | 0 | 0 | 1 | 0 | **3** |
| Pyrobaculum_aerophilum | 0 | 0 | 0 | 2 | 0 | 0 | 0 | **2** |
| Methanopyrus_kandleri_AV19 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | **1** |
| Methanosarcina_acetivorans | 0 | 0 | 0 | 1 | 0 | 0 | 0 | **1** |
| Methanosarcina_mazei | 0 | 0 | 0 | 2 | 0 | 0 | 0 | **2** |
| Pyrococcus_furiosus | 0 | 0 | 0 | 2 | 0 | 0 | 0 | **2** |
| Pyrococcus_horikoshii | 2 | 0 | 0 | 0 | 0 | 0 | 0 | **2** |
| Pyrococcus_abyssi | 1 | 0 | 0 | 0 | 0 | 0 | 0 | **1** |
| Thermoplasma_acidophilum | 1 | 0 | 0 | 0 | 0 | 0 | 0 | **1** |
| Thermoplasma_volcanium | 0 | 0 | 0 | 1 | 0 | 0 | 0 | **1** |
| **Bacteria** | | | | | | | | |
| **Gram Positive** | | | | | | | | |
| Bifidobacterium_longum | 0 | 0 | 1 | 0 | 0 | 0 | 0 | **1** |

| Organism | *relBE* | *parDE* | *higBA* | *vapBC* | *mazEF* | *phd/doc* | *ccdAB* | Total |
|---|---|---|---|---|---|---|---|---|
| S._avermitilis_MA | 0 | 0 | 0 | 0 | 1 | 0 | 0 | **1** |
| Nostoc_sp_PCC_7120 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | **2** |
| Synechocystis_PCC6803 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | **1** |
| C._acetobutylicum | 0 | 0 | 0 | 0 | 1 | 0 | 0 | **1** |
| Clostridium_perfringens | 0 | 0 | 0 | 0 | 0 | 1 | 0 | **1** |
| E.faecalis_V583 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | **2** |
| Lactobacillus_plantarum | 0 | 0 | 0 | 0 | 1 | 0 | 0 | **1** |
| S.mutans_UA159 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | **1** |
| **Gram_negative** | | | | | | | | |
| **Rickettsia_conorii_Malish** | 0 | 0 | 0 | 0 | 1 | 0 | 0 | **1** |
| Nitrosomonas_europaea | 1 | 0 | 0 | 1 | 0 | 0 | 0 | **2** |
| Helicobacter_pylori_J99 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | **1** |
| Yersinia_pestis_CO92 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | **1** |
| Yersinia_pestis_KIM | 1 | 0 | 0 | 0 | 0 | 0 | 0 | **1** |
| Pseudomonas_putida_KT2440 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | **1** |
| Leptospira_intrerrogans_I | 1 | 0 | 0 | 0 | 0 | 0 | 0 | **1** |

# Table S2: List of 671 TA loci and 37 solitary toxin genes in 126 genomes

| TA-loci[a)] | Antitoxin/Toxin GIs[b)] | sizes[c)] (codons) | dist.[d)] (bp) | Comments[e)] |
|---|---|---|---|---|
| **Archaea** | | | | |
| **Aeropyrum_pernix[f)] 14600379\|1,669,695** | | | | |
| *relBE*-1 | 984865-985164,14602207 | 100,94 | +49 | New putative *relB* |
| *vapBC*-1 | c199314-199072,14600586 | 81,144 | -20 | New putative *vapB* |
| *vapBC*-2 | 14600594,14600593 | 75,122 | +82 | |
| *vapBC*-3 | c697607-697245,14601184 | 121,139 | -35 | New putative *vapB* |
| *vapBC*-4 | c760494-760258,14602203 | 79,141 | -20 | New putative *vapB* |
| *vapBC*-5 | c1008442-1008167,14601503 | 92,132 | -20 | New putative *vapB* |
| *vapBC*-6 | c1508755-1508399,14602022 | 119,162 | -76 | New putative *vapB* |
| *vapBC*-7 | c1666639-1666448,14602179 | 64,141 | +3 | New putative *vapB* |
| *vapBC*-8 | -,14602218 | -,87 | NA | Solitary *vapB* |
| **Sulfolobus_solfataricus 15896971\|2,992,245** | | | | |
| *vapBC*-1 | 360012-360608,15897346 | 199,145 | -34 | New putative *vapB* |
| *vapBC*-2 | c683385-683083,15897701 | 101,130 | -12 | New putative *vapB* |
| *vapBC*-3 | c725687-725481,15897743 | 69,52 | -8 | New putative *vapB* |
| *vapBC*-4 | 1073660-1073923,15898090 | 88,130 | -8 | New putative *vapB*, *vapBC*-4=*vapBC*-17 |
| *vapBC*-5 | 1340360-1340617,15898313 | 86,148 | -68 | New putative *vapB* |
| *vapBC*-6 | 15898324,15898323 | 100,107 | +61 | |
| *vapBC*-7 | c1503996-1503685,15898469 | 104,131 | -14 | New putative *vapB* |
| *vapBC*-8 | 15898475,15898476 | 79,126 | -35 | |
| *vapBC*-9 | c1577585-1577400,15898541 | 62,90 | +117 | New putative *vapB* |
| *vapBC*-10 | 1582391-1582642,15898547 | 84,131 | +12 | New putative *vapB* |
| *vapBC*-11 | 1620321-1620638,15898585 | 106,143 | -25 | New putative *vapB* |
| *vapBC*-12 | 15898659,15898660 | 115,204 | +17 | |
| *vapBC*-13 | c1734033-1733776,15898712 | 86,137 | -17 | New putative *vapB* |
| *vapBC*-14 | 1742082-1742303,15898722 | 74,131 | -11 | New putative *vapB* |
| *vapBC*-15 | 15898765,15898764 | 91,128 | -14 | |
| *vapBC*-16 | 1783470-1783712,15898766 | 81,132 | -20 | New putative *vapB* |
| *vapBC*-17 | 1784438-1784701,15898767 | 88,130 | -8 | New putative *vapB*, *vapBC*-17=*vapBC*-4 |
| *vapBC*-18 | c1788331-1788080,15898771 | 84,125 | -32 | New putative *vapB* |
| *vapBC*-19 | 1914151-1914375,15898880 | 75,123 | -22 | New putative *vapB* |
| *vapBC*-20 | c2041164-2040874,15898992 | 97,158 | -14 | New putative *vapB* |
| *vapBC*-21 | -,15899310 | -,126 | NA | Solitary *vapB* |
| *vapBC*-22 | 15899784,15899783 | 73,134 | -20 | |
| *vapBC*-23 | 15899834,15899833 | 81,133 | -23 | |
| **Sulfolobus_tokodaii 24473558\|2,694,756** | | | | |
| *relBE-1* | -,15920339 | -,102 | NA | Solitary *relE* |
| *relBE*-2 | 15920437,15920438 | 97,95 | -8 | |
| *relBE-3* | -,15922162 | -,103 | NA | Solitary *relE* |
| *relBE-4* | 15922557,15922558 | 67,105 | +47 | |
| *vapBC*-1 | c2516-2271,15920165 | 82,96 | -14 | New putative *vapB* |
| *vapBC-2* | 15920187,15920188 | 77,129 | +26 | |
| *vapBC*-3 | 15920210,15920209 | 84,128 | -8 | |
| *vapBC*-4 | c397414-397157,15920583 | 86,143 | -34 | New putative *vapB* |
| *vapBC*-5 | c673537-673358,c673011-673379 | 60,123 | -22 | New putative *vapB*; *vapC* corrected (gi\|15920915) |
| *vapBC*-6 | 15920970,15920969 | 79,124 | +13 | |
| *vapBC*-7 | 761620-761892,15921016 | 91,131 | -8 | New putative *vapB* |
| *vapBC*-8 | 15921073,15921074 | 73,133 | -20 | |
| *vapBC*-9 | 15921133,15921134 | 68,125 | +25 | |
| *vapBC*-10 | 15921142,15921141 | 95,115 | +10 | |
| *vapBC*-11 | 15921355,15921356 | 78,107 | +55 | |
| *vapBC*-12 | 15921382,15921381 | 84,125 | -35 | |
| *vapBC*-13 | c1303456-1303313,c1302999-1303355 | 48,119 | -44 | New putative *vapB*; *vapC* corrected (gi\|15921568) |
| *vapBC*-14 | 15921894,15921893 | 125,204 | +13 | |
| *vapBC*-15 | 15921930,15921931 | 88,155 | -65 | |

| | | | | |
|---|---|---|---|---|
| *vapBC*-16 | 15921943,15921942 | 100,109 | +74 | |
| *vapBC*-17 | 15921944,15921945 | 110,134 | -17 | |
| *vapBC*-18 | 15921992,15921991 | 102,144 | -20 | |
| *vapBC*-19 | 1818807-1819082,15922115 | 92,130 | -14 | New putative *vapB* |
| *vapBC*-20 | 15922247,15922248 | 127,185 | -11 | |
| *vapBC*-21 | 15922259,15922260 | 73,133 | -28 | |
| *vapBC-22* | 15922315,2013264-2013695 | 75,144 | -41 | New putative *vapC* |
| *vapBC*-23 | 15922329,15922330 | 70,117 | +56 | |
| *vapBC*-24 | 2138189-2138767,15922464 | 193,162 | -23 | New putative *vapB* |
| *vapBC*-25 | 15922519,15922520 | 81,105 | +61 | |
| *phd/doc*-1 | 1143830-1143531,15921403 | 97,152 | +17 | New putative *doc* |
| *phd/doc-2* | -,c1317467-1317895 | -,143 | NA | Solitary *doc* |
| *phd/doc-3* | 15921597,c1328737-1329249 | 91,171 | -28 | New putative *doc* |

**Pyrobaculum_aerophilum 18311643|2,222,430**

| | | | | |
|---|---|---|---|---|
| *vapBC*-1 | 18311665,18311666 | 66,125 | +13 | |
| *vapBC*-2 | 18311711,18311712 | 75,126 | -26 | |
| *vapBC*-3 | 18311748,18311747 | 77,131 | -17 | |
| *vapBC*-4 | -,18311834 | -,130 | NA | Solitary *vapC* |
| *vapBC*-5 | 18311873,18311874 | 94,146 | -4 | |
| *vapBC*-6 | 335372-335986,18312054 | 204,111 | -1 | New putative *vapB* |
| *vapBC-7* | -,18313350 | -,165 | NA | Solitary *vapC* |
| *vapBC*-8 | 18313510,18313509 | 116,125 | -4 | |
| *vapBC*-9 | 18313566,18313565 | 74,133 | -11 | |
| *vapBC*-10 | 18313617,18313618 | 74,137 | -17 | |
| *vapBC*-11 | 2133278-2133844,18314154 | 189,110 | -1 | New putative *vapB* |

**Archaeoglobus_fulgidus 11497621|2,178,400**

| | | | | |
|---|---|---|---|---|
| *relBE*-1 | 11498680,11498679 | 62,92 | -16 | |
| *relBE*-2 | 11498685,11498684 | 57,86 | -8 | |
| *relBE*-3 | 11498694,11498693 | 72,85 | -4 | |
| *relBE*-4 | 11499924,11499923 | 65,87 | -8 | |
| *vapBC*-1 | 11497686,11497685 | 62,137 | -4 | |
| *vapBC*-2 | C271532-271335,11497909 | 66,151 | -7 | New putative *vapB* |
| *vapBC*-3 | 287426-287674,11497927 | 84,150 | -1 | New putative *vapB* |
| *vapBC*-4 | 11497928,11497929 | 64,143 | -23 | |
| *vapBC*-5 | 289024-289218,11497931 | 64,149 | -4 | New putative *vapB* |
| *vapBC*-6 | 289639-289923,11497932 | 95,151 | -20 | New putative *vapB* |
| *vapBC*-7 | 290594-290764,11497934 | 57,93 | -44 | |
| *vapBC*-8 | 350180-350689,11497997 | 170,166 | +33 | New putative *vapB* |
| *vapBC*-9 | c534011-533655,11498199 | 119,135 | -41 | New putative *vapB* |
| *vapBC*-10 | c556664-556485,11498226 | 60,96 | +72 | New putative *vapB* |
| *vapBC*-11 | 11498682,11498681 | 45,130 | -17 | |
| *vapBC*-12 | c981711-981451,11498689 | 87,141 | -1 | New putative *vapB* |
| *vapBC*-13 | 11498692,11498691 | 61,139 | -17 | |
| *vapBC*-14 | c1236899-1236693,11498981 | 69,149 | -17 | New putative *vapB* |
| *vapBC*-15 | 11499073,11499074 | 71,130 | -14 | |
| *vapBC*-16 | 11499279,11499280 | 73,136 | -11 | |
| *vapBC*-17 | 11499302,11499301 | 71,147 | -14 | |
| *vapBC*-18 | 11499579,11499578 | 73,84 | -35 | |
| *vapBC*-19 | 11499593,11499594 | 86,137 | -35 | |
| *vapBC*-20 | 11499771,11499772 | 72,136 | -14 | |
| *vapBC*-21 | 1978461-1978667,11499795 | 69,72 | +26 | New putative *vapB* |
| *vapBC*-22 | 11499936,11499937 | 75,134 | -4 | |
| *vapBC*-23 | c980157-979951,11500021 | 70,144 | -17 | New putative *vapB* |
| *vapBC*-24 | c550521-550279,11546068 | 81,111 | -17 | New putative *vapB* |

**Halobacterium_sp_NRC_1 15789340|2,014,239**

| | | | | |
|---|---|---|---|---|
| *relBE*-1 | 15789403,15789404 | 65,97 | -11 | |
| *vapBC*-1 | c67955-67662,15789405 | 98,144 | -1 | New putative *vapB* |
| *vapBC*-2 | c1474604-1474407,15790862 | 66,109 | -1 | New putative *vapB* |
| *vapBC*-3 | c1510923-1510639,15790906 | 105,127 | +7 | New putative *vapB* |

**M.thermoautotrophicum 15678031|1,751,377**

| | | | | |
|---|---|---|---|---|
| *vapBC*-1 | 202303-202899,15678290 | 199,119 | +27 | New putative *vapB* |
| *vapBC*-2 | 1698784-1698945,15679850 | 54,171 | +20 | New putative *vapB* |

**Methanococcus_jannaschii 15668172|1,664,970**

| | | | | |
|---|---|---|---|---|
| *relBE*-1 | 15668241,15668242 | 82,90 | -4 | |
| *relBE*-2 | 840765-840947,15669099 | 61,91 | -1 | New putative *vapB* |
| *relBE*-3 | c1043988-1044146,15669291 | 53,88 | -1 | New putative *vapB* |

| | | | | |
|---|---|---|---|---|
| *relBE*-4 | 15669361,15669362 | 84,94 | 0 | |
| *vapBC*-1 | c846334-846143,15669104 | 64,136 | +47 | New putative *vapB* |
| *vapBC*-2 | 15669165,15669164 | 68,149 | -29 | |
| *vapBC*-3 | 15669309,15669308 | 77,94 | -28 | |
| *vapBC*-4 | c1268398-1268213,15669510 | 62,131 | +23 | New putative *vapB* |
| *vapBC*-5 | 1445372-1445695,15669666 | 108,197 | -5 | New putative *vapB* |
| **Methanopyrus_kandleri_AV19 20093440\|1,694,969** | | | | |
| *vapBC-1* | -,20094181 | -,143 | NA | Solitary *vapC* |
| *vapBC*-2 | 1478697-1479293,20094884 | 199,130 | +9 | New putative *vapB* |
| **Methanosarcina_acetivorans 20088899\|5,751,492** | | | | |
| *relBE*-1 | 20088947,20088948 | 74,83 | +68 | Similar to 21228707 |
| *relBE*-2 | 20089272,20089273 | 93,87 | -13 | |
| *relBE*-3 | 1172771-1172992,20089858 | 74,89 | -8 | New putative *relB* |
| *relBE*-4 | 20090545,20090546 | 69,87 | -4 | |
| *relBE*-5 | 20091001,20091002 | 89,64 | +6 | |
| *relBE-6* | 3293160-3293339,3293349-3293555 | 60,69 | +9 | New putative *relBE* |
| *relBE*-7 | 20092309,20092310 | 80,93 | -4 | |
| *relBE*-8 | 20093070,20093069 | 96,92 | +9 | |
| *vapBC-1* | -,20089798 | -,180 | NA | Solitary *vapC* |
| *vapBC*-2 | 1173673-1173882,20089859 | 70,117 | -10 | New putative *vapB* |
| *vapBC*-3 | 20090373,20090374 | 77,133 | -4 | |
| *vapBC*-4 | 4548892-4549509,20092491 | 206,121 | -1 | New putative *vapB* |
| **Methanosarcina_*mazei* 21226102\|4,096,345** | | | | |
| *relBE*-1 | 21227970,21227969 | 88,67 | +14 | |
| *relBE*-2 | 21228652,21228651 | 79,86 | +4 | |
| *relBE*-3 | 21228701,21228702 | 64,93 | -4 | |
| *relBE*-4 | 21228706,21228707 | 63,92 | -1 | Similar to 20088948 |
| *relBE*-5 | 21228783,21228782 | 93,86 | -13 | |
| *vapBC*-1 | 726480-727034,21226697 | 185,121 | -1 | New putative *vapB* |
| *vapBC-2* | -,21228138 | -,189 | NA | Solitary *vapC* |
| *vapBC*-3 | -,21229222 | -,127 | NA | Solitary *vapC*, pseudo vapB |
| *phd/doc*-1 | 21226652,21226651 | 83,134 | -14 | |
| **Pyrococcus_furiosus 18976372\|1,908,256** | | | | |
| *relBE*-1 | c841447-841569,18977239 | 41,103 | -38 | New putative *relB* |
| *vapBC-1* | 33359474,33359473 | 69,151 | +2 | |
| *vapBC*-2 | 18976945,18976946 | 75,133 | -13 | |
| *vapBC*-3 | 18976948,18976947 | 46,112 | +38 | |
| *vapBC*-4 | 18977146,18977145 | 102,31 | -28 | |
| *vapBC*-5 | 768291-768446,18977153 | 52,138 | -1 | New putative *vapB* |
| *vapBC-6* | 18977147,765885-766256 | 107,124 | +24 | Corrected *vapC* GI:33359506 |
| *vapBC*-7 | 18977185,18977184 | 76,138 | -4 | |
| *vapBC*-8 | 18977210,18977211 | 83,126 | -1 | |
| *vapBC-9* | -,33359527 | -,144 | NA | Solitary *vapC* |
| *vapBC-10* | -,33359529 | -,75 | NA | Solitary *vapC* |
| *vapBC*-11 | 1146253-1146840,18977577 | 196,155 | -13 | New putative *vapB* |
| *vapBC*-12 | 18977579,18977578 | 76,156 | -4 | |
| *vapBC*-13 | 1159756-1160004,18977595 | 82,123 | -28 | New putative *vapB* |
| *vapBC*-14 | 18977725,18977724 | 73,134 | -14 | |
| *vapBC*-15 | c1596552-1596223,18978088 | 110,138 | -10 | New putative *vapB* |
| *vapBC*-16 | c1897570-1897358,18978429 | 71,56 | -32 | New putative *vapB* |
| **Pyrococcus_horikoshii 14589963\|1,738,505** | | | | |
| *relBE*-1 | 14590323,14590322 | 67,90 | +9 | |
| *relBE-2* | -,14590326 | -,96 | NA | Solitary *relE* |
| *relBE-3* | -,928619-928915 | -,99 | NA | Solitary *relE*, corrected GI:33359355 |
| *vapBC-1* | 33359257,33359258 | 86,150 | -29 | |
| *vapBC*-2 | c351629-351390,14590297 | 80,134 | -14 | New putative *vapB* |
| *vapBC-3* | c372554-372781,33359290 | 76,92 | +54 | |
| *vapBC*-4 | c452910-452704,14590406 | 69,149 | -22 | New putative *vapB* |
| *vapBC*-5 | 631040-631294,14590586 | 85,156 | -29 | New putative *vapB* |
| *vapBC*-6 | c632499-632206,14590587 | 98,161 | -13 | New putative *vapB* |
| *vapBC*-7 | 14590763,33359341 | 74,80 | -10 | |
| *vapBC*-8 | c821653-821345,14590765 | 103,138 | -1 | New putative *vapB* |
| *vapBC*-9 | c1168172-1168014,14591108 | 54,117 | +30 | New putative *vapB* |
| *vapBC*-10 | 1501435-1501986,14591473 | 184,138 | +43 | New putative *vapB* |
| *vapBC*-11 | 965798-965962,14591761 | 55,111 | +85 | New putative *vapB* |

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|---|---|---|---|---|
| **Pyrococcus_abyssi** | **14518450\|1,765,118** | | | |
| *relBE*-1 | -,33356736 | -,98 | NA | Solitary *relE* |
| *vapBC*-1 | 14520335,14520334 | 74,128 | -4 | |
| *vapBC*-2 | 14520620,14520619 | 79,123 | -31 | |
| *vapBC-3* | c447806-448138,33356691 | 111,172 | -1 | *vapB* corrected GI:14520682 |
| *vapBC*-4 | 14520978,14520979 | 75,136 | -13 | |
| *vapBC*-5 | 761684-761887,14521013 | 68,156 | -17 | New putative *vapB* |
| *vapBC*-6 | 834293-834433,14521081 | 47,96 | -14 | New putative *vapB* |
| *vapBC*-7 | c898293-898093,14521141 | 67,156 | -8 | New putative *vapB* |
| *vapBC*-8 | c1009921-1009637,14521256 | 95,143 | -29 | New putative *vapB* |
| *vapBC*-9 | c1120616-1120338,14521371 | 93,148 | -13 | New putative *vapB* |
| *vapBC*-10 | 14521382,14521383 | 67,133 | 0 | |
| *vapBC*-11 | 1136739-1136951,14521385 | 71,169 | -38 | New putative *vapB* |
| *vapBC*-12 | c1153817-1153542,14521399 | 92,110 | -10 | New putative *vapB* |
| *vapBC*-13 | 1260427-1260705,14521500 | 93,133 | -23 | New putative *vapB* |
| *vapBC*-14 | 1291316-1291903,14521536 | 136,161 | -13 | New putative *vapB* |
| *vapBC*-15 | 1501612-1501827,14521742 | 72,149 | -8 | New putative *vapB* |
| *vapBC*-16 | c1699062-1698781,14521921 | 94,136 | -1 | New putative *vapB* |
| | | | | |
| **Thermoplasma_acidophilum** | **16081186\|1,564,906** | | | |
| *relBE*-1 | -,237926-238222 | -,99 | NA | Solitary *relE* |
| *vapBC*-1 | 38670-38828,16081221 | 54,194 | +28 | New putative *vapB* |
| *vapBC*-2 | 804192-804743,16081834 | 184,120 | -1 | New putative *vapB* |
| | | | | |
| **Thermoplasma_volcanium** | **13540831\|1,584,804** | | | |
| *vapBC*-1 | -,13540951 | -,163 | NA | Solitary *vapC* |
| *vapBC*-2 | c886266-885913,13541682 | 118,121 | +15 | New putative *vapB* |
| | | | | |
| **Gram positive Bacteria:** | | | | |
| | | | | |
| **Bifidobacterium_longum** | **23464628\|2,256,646** | | | |
| *relBE-1* | 1284380-1284766,1284736-1284981 | 129,82 | -31 | New putative *relBE* |
| *relBE*-2 | c1638570-1638836,c1638230-1638535 | 83,102 | +34 | New putative *relB*E |
| *higBA*-1 | -,23465886 | -,94 | NA | Solitary *higB* |
| *vapBC*-1 | 391430-391864,23464899 | 145,139 | +12 | New putative *vapB* |
| *vapBC-2* | c1248957-1249274,c1248539-1248970 | 106,144 | -14 | New putative *vapBC*. A is a confirmed *relB/dinJ* homolog! |
| *vapBC*-3 | 23465958,23465959 | 120,163 | 0 | |
| | | | | |
| **C._glutamicum_ATCC_13032** | **23308765\|3,309,401** | | | |
| *higBA*-1 | 1085714-1086001,1085499-1085777 | 96,93 | +62 | RGO, New putative *higBA* |
| | | | | |
| **C.efficiens_YS_314** | **25026556\|3,147,090** | | | |
| *higBA*-1 | 25029304,25029303 | 102,104 | -4 | RGO |
| | | | | |
| **M._tuberculosis_H37Rv** | **15607142\|4,411,529** | | | |
| *relBE*-1 | 15608387,15608386 | 89,97 | -4 | |
| *relBE*-2 | 15610002,15610003 | 93,87 | +3 | |
| *relBE*-3 | 15610493,15610494 | 91,85 | -4 | |
| *parDE*-1 | 15609097,15609096 | 83,98 | -4 | |
| *parDE*-2 | c2402508-2402720,15609279 | 71,105 | -4 | New putative *parD* |
| *higBA*-1 | 15609093,2201741-2202091 | 149,117 | +41 | RGO, *higB* corrected (GI\|15609092) |
| *vapBC*-1 | 71575-71823,15607207 | 83,133 | -5 | New putative *vapB* |
| *vapBC*-2 | 15607441,15607442 | 73,141 | -4 | |
| *vapBC*-3 | 15607690,15607689 | 88,137 | -4 | |
| *vapBC*-4 | 15607736,15607735 | 85,130 | -4 | |
| *vapBC*-5 | 15607766,15607767 | 86,135 | -4 | |
| *vapBC*-6 | 15607797,15607796 | 51,127 | +94 | |
| *vapBC*-7 | 15607802,15607801 | 122,145 | -4 | |
| *vapBC*-8 | 15607804,15607805 | 90,112 | -4 | |
| *vapBC*-9 | 1073325-1073543,15608100 | 73,127 | -1 | New putative *vapB* |
| *vapBC*-10 | 15608536,15608535 | 85,133 | -4 | |
| *vapBC*-11 | 15608698,15608699 | 72,134 | +5 | |
| *vapBC*-12 | 15608859,15608858 | 72,129 | -4 | |
| *vapBC*-13 | 15608976,15608975 | 87,131 | -4 | |
| *vapBC*-14 | 15609089,15609090 | 71,103 | -4 | |
| *vapBC*-15 | 15609146,15609147 | 80,132 | 0 | |
| *vapBC*-16 | c2506381-2506208,c2505735-2506153 | 59,139 | +56 | New putative *vapBC* |
| *vapBC*-17 | 15609663,15609664 | 75,133 | -4 | |

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|---|---|---|---|---|
| *vapBC*-18 | 15609682,15609683 | 92,137 | +92 | |
| *vapBC*-19 | 15609684,15609685 | 85,125 | -4 | |
| *vapBC*-20 | 15609687,15609686 | 81,131 | -4 | |
| *vapBC*-21 | 15609895,15609894 | 88,138 | -4 | |
| *vapBC*-22 | 15609967,15609966 | 71,130 | -4 | |
| *vapBC*-23 | 3174744-3174989,15610000 | 82,126 | -55 | New putative *vapB* |
| *mazEF-1* | c547345-547515,c547077-547355 | 57,93 | -11 | New putative *mazEF* |
| *mazEF*-2 | 15607800,15607799 | 81,102 | -14 | |
| *mazEF*-3 | c1231289-1231056,15608242 | 77,103 | -1 | New putative *mazE* |
| *mazEF*-4 | 15608632,15608633 | 100,105 | -4 | |
| *mazEF*-5 | c2195345-2195109,15609079 | 78,109 | -4 | New putative *mazE* |
| *mazEF*-6 | c2234644-2234919,15609128 | 92,114 | -4 | New putative *mazE* |
| *mazEF-7* | 2320829-2321059,2321055-2321462 | 77,136 | -5 | New putative *mazEF* |
| *mazEF*-8 | c2547085-2546840,15609411 | 82,105 | +31 | New putative *mazE* |
| *mazEF*-9 | 3110734-3110507,15609938 | 76,118 | -13 | New putative *mazE* |
| | | | | |
| **M._tuberculosis_CDC1551** | **15839372\|4,403,836** | | | |
| *relBE*-1 | c1388510-1388731,15840691 | 89,97 | -4 | New putative *relB* |
| *relBE*-2 | 3171692-3171970,3171946-3172237 | 93,87 | -25 | New putative *relB*E |
| *relBE*-3 | 15842953,15842954 | 91,85 | -4 | |
| *parDE*-1 | 15841430,15841429 | 83,98 | -4 | |
| *parDE*-2 | 15841634,15841633 | 71,105 | -4 | |
| *higBA*-1 | 15841426,2199074-2199424 | 149,117 | +41 | RGO, *higB* corrected (GI: 15841425) |
| *vapBC*-1 | 71570-71806,15839444 | 79,133 | -5 | New putative *vapB* |
| *vapBC*-2 | 363888-364106,15839686 | 73,141 | -1 | New putative *vapB* |
| *vapBC*-3 | 15839947,15839946 | 88,137 | -4 | |
| *vapBC*-4 | 15839999,15839998 | 85,131 | -7 | |
| *vapBC*-5 | 719471-719728,719728-720132 | 86,135 | -4 | New putative *vapBC* |
| *vapBC*-6 | 15840060,15840059 | 51,127 | +94 | |
| *vapBC*-7 | 15840065,15840064 | 126,145 | -4 | |
| *vapBC*-8 | 15840067,15840068 | 108,112 | -89 | |
| *vapBC*-9 | 15840384,15840385 | 73,127 | -4 | |
| *vapBC*-10 | 15840856,15840855 | 89,133 | -4 | |
| *vapBC*-11 | 15841027,15841028 | 72,134 | +5 | |
| *vapBC*-12 | 15841183,15841182 | 75,129 | -4 | |
| *vapBC*-13 | 15841307,15841306 | 87,131 | -4 | |
| *vapBC*-14 | 15841423,15841424 | 75,103 | -4 | |
| *vapBC*-15 | 15841491,15841492 | 80,132 | 0 | |
| *vapBC*-16 | c2503593-2503357,15841724 | 79,139 | +69 | New putative *vapB* |
| *vapBC*-17 | 15842060,15842061 | 75,133 | -4 | |
| *vapBC*-18 | 15842081,15842082 | 92,138 | +89 | |
| *vapBC*-19 | c2866266-2866541,c2865871-2866266 | 92,132 | -1 | New putative *vapBC* |
| *vapBC*-20 | 15842083,15842084 | 90,125 | -4 | |
| *vapBC*-21 | 15842296,15842295 | 88,138 | -4 | |
| *vapBC*-22 | c3131225-3131449,c3130833-3131225 | 79,131 | -1 | New putative *vapBC* |
| *vapBC*-23 | 15842405,15842406 | 64,126 | -4 | |
| *mazEF*-1 | 15840063,15840062 | 83,102 | -14 | |
| *mazEF*-2 | 15840542,15840541 | 78,103 | -1 | |
| *mazEF*-3 | 15840957,15840958 | 100,105 | -4 | |
| *mazEF*-4 | c2192678-2192442,15841413 | 78,117 | -28 | New putative *mazE* |
| *mazEF*-5 | 15841473,15841472 | 82,114 | -7 | |
| *mazEF*-6 | c2544045-2544290,c2543694-2544008 | 82,105 | -4 | New putative *mazEF* |
| *mazEF*-7 | 3105455-3105228,15842339 | 76,117 | -11 | New putative *mazE* |
| | | | | |
| **S._avermitilis_MA_4680** | **29826540\|9,025,608** | | | |
| *relBE*-1 | 29829748,29829747 | 93,84 | -4 | |
| *vapBC*-1 | 29832236,29832237 | 77,135 | -4 | |
| *mazEF*-1 | -,29827212 | -,158 | NA | Solitary *mazF* |
| *phd/doc-1* | 29833628,29833629 | 79,124 | +4 | |
| *phd/doc*-2 | 29827371,29827370 | 74,125 | -1 | |
| | | | | |
| **S._coelicolor_A32_chromosome** | **32141095\|8,667,507** | | | |
| *relBE*-1 | 21220706,21220707 | 87,84 | -4 | |
| *phd/doc*-1 | 21218953,21218954 | 74,127 | -1 | |
| *phd/doc*-2 | 21224247,21224248 | 64,68 | -4 | |
| | | | | |
| **Chlorobium_tepidum_TLS** | **21672841\|2,154** | | | |
| *mazEF*-1 | 947841-948164,21673827 | 108,107 | -37 | New putative *mazE* |
| *phd/doc*-1 | 21673171,21673172 | 75,127 | +3 | |

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|---|---|---|---|---|
| **Nostoc_sp_PCC_7120** | **17227497\|6,413,771** | | | |
| *relBE*-1 | c181989-181630,17227667 | 119,81 | -14 | New putative *relE* |
| *relBE*-2 | -,17228895 | -,80 | NA | Solitary *relE* |
| *relBE*-3 | 17229593,17229592 | 84,91 | -8 | |
| *relBE*-4 | 17231900,17231899 | 104,127 | -32 | |
| *relBE*-5 | 17231962,17231963 | 76,94 | -23 | |
| *relBE*-6 | 17232054,17232053 | 70,87 | -4 | |
| *higBA*-1 | 17228529,17228529 | 108,123 | -4 | RGO |
| *higBA*-2 | 17229893,17229894 | 98,112 | -11 | RGO |
| *higBA*-3 | 17230415,17230416 | 97,99 | -13 | RGO |
| *vapBC*-1 | 17227644,17227645 | 81,128 | -4 | |
| *vapBC*-2 | 17227999,17228000 | 66,155 | -17 | |
| *vapBC*-3 | 17228249,17228248 | 127,131 | -4 | |
| *vapBC*-4 | 17228989,17228988 | 69,129 | -11 | |
| *vapBC*-5 | 17229689,17229688 | 78,132 | -14 | |
| *vapBC*-6 | 17230178,17230177 | 78,129 | -4 | |
| *vapBC*-7 | c3788612-3788415,17230620 | 66,90 | -16 | New putative *vapB* |
| *vapBC*-8 | 17230960,17230961 | 83,128 | -4 | |
| *vapBC*-9 | 17230970,17230971 | 89,149 | -1 | |
| *vapBC*-10 | 17231113,17231114 | 74,140 | -17 | |
| *vapBC*-11 | 17231465,17231464 | 73,133 | -13 | |
| *vapBC*-12 | 17231628,17231627 | 75,128 | -4 | |
| *vapBC*-13 | 17232092,5499145-5499573 | 96,143 | -1 | *vapC* corrected (GI:17232093) |
| *vapBC*-14 | 17232625,17232624 | 102,147 | -20 | |
| *mazEF*-1 | 17227834,17227833 | 61,121 | -20 | |
| *mazEF*-2 | 17228252,17228253 | 69,113 | -14 | |
| *mazEF*-3 | -,17230498 | -,88 | NA | Solitary *vapC* |
| *mazEF*-4 | 17230704,17230703 | 80,146 | -1 | |
| *mazEF*-5 | 17232412,17232413 | 80,115 | +5 | |
| *phd/doc*-1 | 17227997,17227998 | 136,151 | +72 | |
| **Synechocystis_PCC6803** | **16329170\|3,573,470** | | | |
| *relBE-1* | 16330633,1620536-1620793 | 87,86 | -1 | New putative *relE*(*yefM/yoeB*) |
| *relBE-2* | 16331058,2074933-2075211 | 87,93 | -22 | New putative *relE*(*yefM/yoeB*) |
| *relBE*-3 | 16332147,16332148 | 86,120 | -11 | |
| *higBA*-1 | c474208-474432,c474514-474792 | 75,93 | +82 | RGO, new putative *higA*B |
| *vapBC*-1 | 16329605,16329604 | 75,83 | 0 | |
| *vapBC*-2 | 16330048,16330047 | 133,157 | -68 | |
| *vapBC*-3 | 16330685,16330684 | 84,149 | +9 | |
| *vapBC*-4 | 16330930,16330929 | 68,128 | -1 | |
| *vapBC*-5 | -,16331065 | -,61 | NA | Solitary *vapC* |
| *vapBC*-6 | c2516782-2516531,16331422 | 84,125 | +3 | New putative *vapB* |
| *vapBC*-7 | 16331533,16331532 | 85,133 | +2 | |
| *vapBC-8* | c3044422-3044670,c3044058-3044501 | 83,148 | -79 | New putative *vapBC* |
| *vapBC*-9 | 16332080,16332079 | 92,131 | +11 | |
| *mazEF*-1 | 16330121,16330120 | 88,115 | -4 | |
| **Bacillus_anthracis_Ames** | **30260195\|5,227,293** | | | |
| *mazEF*-1 | 30260429,30260430 | 95,116 | +4 | |
| **Bacillus_cereus_ATCC14579** | **30018278\|5,411,809** | | | |
| *mazEF*-1 | 30018502,30018503 | 95,116 | +4 | |
| **Bacillus_halodurans** | **15612563\|4,202,353** | | | |
| *mazEF*-1 | 15613084,15613085 | 95,116 | +3 | |
| *mazEF*-2 | 15616282,15616283 | 81,109 | 0 | |
| **Bacillus_subtilis** | **16077068\|4,214,814** | | | |
| *mazEF*-1 | 16077532,16077533 | 93,116 | +4 | |
| **C._acetobutylicum_ATCC824** | **15893298\|3,940,880** | | | |
| *mazEF*-1 | 15893784,15893785 | 106,122 | -41 | |
| *mazEF-2* | -,15893379 | -,199 | NA | Solitary *mazE*, annotated |
| **Clostridium_perfringens** | **18308982\|3,031,430** | | | |
| *mazEF*-1 | 18309276,18309277 | 80,117 | +5 | |
| *phd/doc*-1 | -,18309825 | -,137 | NA | Solitary *doc* |
| **Clostridium_tetani_E88** | **28209834\|2,799,251** | | | |
| *mazEF*-1 | c2670080-2670397,c2669764-2670117 | 116,118 | -37 | New putative *mazEF* |
| *phd/doc*-1 | c2057481-2057179,28211562 | 101,127 | -1 | New putative *phd* |

| | | | | |
|---|---|---|---|---|
| **Enterococcus_faecalis_V583** | **29374661\|3,218,031** | | | |
| *relBE*-1 | 29375140,29375141 | 88,91 | -8 | |
| *mazEF*-1 | -,29375414 | -,113 | NA | Solitary *mazF* |
| *mazEF*-2 | -,29375438 | -,125 | NA | Solitary *mazF* |
| *mazEF*-3 | 29377704,29377705 | 76,121 | -11 | |
| *phd/doc*-1 | 29375017,29375016 | 79,139 | -4 | |
| **Lactobacillus_plantarum** | **28376974\|3,308,274** | | | |
| *higBA*-1 | 28377334,28377333 | 97,75 | +11 | RGO |
| *mazEF*-1 | -,28377410 | -,130 | NA | Solitary *mazF* |
| *mazEF*-2 | 28379347,28379346 | 82,115 | -1 | |
| **Listeria_innocua** | **16799079\|3,011,208** | | | |
| *mazEF*-1 | 16799959,16799960 | 92,115 | +3 | |
| **Listeria_monocytogenes** | **16802048\|2,944,528** | | | |
| *mazEF*-1 | 16802928,16802929 | 92,115 | +3 | |
| **Oceanobacillus_iheyensis** | **23097455\|3,630,528** | | | |
| *mazEF*-1 | 23098077,23098078 | 94,119 | +4 | |
| **T._tengcongensis** | **20806542\|2,689,445** | | | |
| *relBE*-1 | 867887-868186,20807340 | 99,87 | +1 | New putative *relB* |
| *relBE*-2 | 20808432,20808431 | 79,92 | -26 | |
| *relBE*-3 | 20808957,20808956 | 91,86 | -11 | |
| *vapBC*-1 | 20807534,20807535 | 83,137 | -17 | |
| *vapBC*-2 | 20808932,20808933 | 88,146 | -23 | |
| *mazEF*-1 | 20808551,20808550 | 91,118 | -4 | |
| **S._aureus_MW2** | **21281729\|2,820,462** | | | |
| *relBE*-1 | 21284059,21284058 | 83,88 | -1 | |
| *relBE*-2 | 21284110,21284109 | 85,88 | -1 | |
| *mazEF*-1 | 21283722,21283721 | 56,120 | -4 | |
| **S._aureus_N315** | **29165615\|2,814,816** | | | |
| *relBE*-1 | 15927986,15927985 | 83,88 | -1 | |
| *relBE*-2 | 15928036,15928035 | 85,88 | -1 | |
| *mazEF*-1 | 15927644,15927643 | 56,120 | -4 | |
| **S._aureus_Mu50** | **15922990\|2,878,040** | | | |
| *relBE*-1 | 15925398,15925397 | 83,88 | -1 | |
| *relBE*-2 | 15925447,15925446 | 85,88 | -1 | |
| *mazEF*-1 | 15925059,15925058 | 56,120 | -4 | |
| **S._epidermidis_ATCC_12228** | **27466918\|2,499,279** | | | |
| *mazEF*-1 | 27468591,27468590 | 56,120 | -4 | |
| **S._agalactiae_2603** | **22536185\|2,160,267** | | | |
| *relBE*-1 | 22538144,22538143 | 88,84 | -8 | |
| *parDE*-1 | 22536413,22536412 | 95,111 | -11 | |
| **S._agalactiae_NEM316** | **25010075\|2,211,485** | | | |
| *relBE*-1 | 25010542,25010543 | 97,112 | -4 | |
| *parDE*-1 | 25010297,25010296 | 95,111 | -11 | |
| **Streptococcus_mutans_UA159** | **24378532\|2,030,921** | | | |
| *relBE-1* | -,44407-44676 | -,90 | NA | Solitary *relE*; Corrected GI:24378568 |
| *relBE*-2 | 24379347,24379348 | 90,92 | -14 | |
| *mazEF*-1 | 24378686,24378687 | 81,110 | -7 | |
| **Streptococcus_pneumonia_TIGR4** | **15899949\|2,160,837** | | | |
| *relBE*-1 | 15900209,15900210 | 87,92 | -8 | |
| *relBE*-2 | 15901086,15901085 | 100,84 | +1 | |
| *relBE*-3 | 15901573,15901572 | 84,84 | +3 | |
| *higBA*-1 | 15901010,15901009 | 97,121 | -11 | RGO |
| *phd/doc*-1 | 15900771,15900772 | 78,137 | -4 | |
| **Streptococcus_pneumonia_R6** | **15902044\|2,038,615** | | | |
| *relBE*-1 | 15902296,15902297 | 87,92 | -8 | |

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|---|---|---|---|---|
| *relBE*-2 | 15903147,15903146 | 100,87 | -8 | |
| *relBE*-3 | 15903628,15903627 | 97,84 | +3 | |
| **Streptococcus_pyogenes** | **15674250\|1,852,441** | | | |
| *parDE*-1 | 448399-448676,15674649 | 95,107 | -4 | New putative *parD*, also related to *relE* |
| *parDE*-2 | 15675733,15675734 | 95,111 | -11 | |
| **S._pyogenes_MGAS315** | **21909536\|1,900,521** | | | |
| *parDE*-1 | 21909929,21909930 | 100,101 | -1 | Also related to *relE* |
| *parDE*-2 | 21911197,21911198 | 95,111 | -11 | |
| **S._pyogenes_MGAS8232** | **19745201\|1,895,017** | | | |
| *parDE*-1 | 19745671,19745672 | 100,101 | -1 | Also related to *relE* |
| *parDE*-2 | 19746843,19746844 | 95,111 | -11 | |
| **Streptococcus_pyogenes_SSI_1** | **28894912\|1,894,275** | | | |
| *parDE*-1 | 28896373,28896372 | 100,101 | -1 | Also related to *relE* |
| *parDE*-2 | 28896571,28896572 | 95,113 | -17 | |
| **Fusobacterium_nucleatum** | **19703352\|2,174,500** | | | |
| *relBE*-1 | 19703555,19703556 | 72,88 | +7 | |
| *relBE*-2 | 19703831,19703832 | 73,90 | +1 | |
| *relBE*-3 | 19704434,19704435 | 75,88 | -16 | |
| **Pirellula_sp** | **32470666\|7,145,576** | | | |
| *relBE*-1 | 32472872,32472873 | 89,154 | +27 | |
| *parDE*-1 | 32473225,32473226 | 85,96 | -4 | |
| *parDE*-2 | 32476300,32476299 | 93,103 | -4 | |
| **Others** | | | | |
| **Aquifex_aeolicus** | **15282445\|1,551,335** | | | |
| *vapBC*-1 | 203338-203605,203579-203860 | 88,94 | -26 | New putative *vapBC* |
| *vapBC*-2 | 1338522-1338839,15606926 | 106,135 | +12 | New putative *vapB* |
| **Bacteroides_theta_VPI_5482** | **29345410\|6,260,361** | | | |
| *higBA-1* | 29349640,5572334-5572546 | 64,71 | -23 | RGO, **n**ew putative *higA* |
| *higBA*-2 | 29350141,29350140 | 101,110 | -20 | RGO |
| **Gram-negative Bacteria** | | | | |
| **Caulobacter_crescentus** | **16124256\|4,016,947** | | | |
| *relBE*-1 | 16125056,16125055 | 87,93 | -4 | |
| *relBE*-2 | 16126753,16126752 | 66,88 | -13 | |
| *relBE*-3 | 3102767-3103121,16127112 | 96,92 | -4 | New putative *relB* |
| *relBE*-4 | 3371212-3371388,16127361 | 59,107 | -58 | New putative *relB* |
| *parDE*-1 | 16125127,16125126 | 88,96 | -4 | |
| *parDE-2* | 16125306,1186395-1186610 | 95,72 | -8 | New putative *parE* |
| *parDE*-3 | c2971288-2971506,16126988 | 73,100 | +15 | New putative *parD* |
| *parDE*-4 | 16127215,16127214 | 96,100 | -20 | |
| *higBA*-1 | 16127267,16127268 | 108,65 | -7 | RGO |
| *vapBC*-1 | 16124288,16124287 | 79,128 | 0 | |
| *phd/doc*-1 | c3613552-3613915,16127593 | 121,130 | -1 | New putative *phd* |
| **A._tumefaciens_C58_Cereon_circ** | **15887359\|2,841,581** | | | |
| *relBE*-1 | 15888018,15888017 | 75,89 | -17 | |
| *relBE*-2 | 15888153,15888152 | 93,103 | -11 | |
| *relBE*-3 | c831117-830842,15888171 | 91,99 | +4 | *relB* corrected (GI:15888172) |
| *relBE*-4 | 15888274,15888273 | 91,111 | +4 | |
| *relBE*-5 | c1769363-1769118,15889086 | 81,96 | -4 | *relB* corrected (GI:15888087) |
| *relBE*-6 | c1979782-1979531,15889305 | 83,89 | -4 | *relB* corrected (GI:15888306) |
| *parDE-1* | 15888422,c1070511-1070861 | 89,117 | -44 | New putative *parE* (corrected GI:15888421) |
| *parDE*-2 | 1304512-1304808,15888638 | 98,124 | -4 | *parD* corrected (GI:15888637) |
| *parDE*-3 | 15888836,15888835 | 88,99 | -17 | |
| *vapBC*-1 | 15888348,c1001393-1001007 | 90,129 | -1 | *vapC* corrected(GI:15888347) |
| *vapBC*-2 | 15889422,15889421 | 142,148 | -38 | |
| *mazEF*-1 | 928764-929030,15888280 | 88,120 | -4 | *mazE* corrected (GI:15888281) |
| **A._tumefaciens_C58_Cereon_linear** | **15890089\|2,074,782** | | | |

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|---|---|---|---|---|
| *relBE*-1 | 15890524,15890523 | 78,95 | +5 | |
| *vapBC*-1 | 15891912,15891913 | 87,134 | -4 | |
| **A._tumef._C58_Washn_cir_chr 17933925\|2,841,490** | | | | |
| *relBE*-1 | 17934585,17934584 | 75,89 | -17 | |
| *relBE*-2 | 17934719,c809573-809884 | 93,104 | -5 | *relE* corrected (GI:17934718) |
| *relBE*-3 | 17934843,17934842 | 91,99 | +32 | |
| *relBE*-4 | 17934986,17934985 | 89,103 | -5 | |
| *relBE*-5 | 17935676,17935675 | 81,96 | -4 | |
| *relBE*-6 | 17935904,17935903 | 84,89 | -4 | |
| *parDE-1* | c830914-831318,c830618-830914 | 135,99 | -1 | New putative *parDE* |
| *parDE-2* | 1304610-1304918,1304918-1305289 | 103,124 | -1 | New putative *parDE* |
| *parDE*-3 | 17935410,17935409 | 88,91 | +7 | |
| *vapBC*-1 | 17934913,17934912 | 76,129 | -4 | |
| *vapBC*-2 | 17936025,c2105391-2105804 | 140,138 | -8 | Start of *vapC* corrected, GI:17936024 |
| *mazEF*-1 | 17934847,17934848 | 88,119 | -1 | |
| **A._tumef._C58_Washn_lin_chr 17936711\|2,075,560** | | | | |
| *relBE*-1 | 17938149,17938150 | 74,95 | +5 | |
| *vapBC*-1 | 17936725,17936724 | 87,134 | -4 | |
| **Bradyrhizobium_japonicum 27375111\|9,105,82** | | | | |
| *higBA-1* | 1797159-1797353,1796750-1797079 | 65,110 | +79 | RGO |
| *higBA*-2 | 27377225,2290771-2291367 | 106,124 | -4 | RGO, corrected (GI:27377224) |
| *higBA*-3 | 27378122,27378123 | 102,93 | +13 | RGO |
| *higBA*-4 | 5539812-5540207,27380106 | 132,100 | -11 | RGO, new putative *higA* |
| *vapBC*-1 | 27377546,27377545 | 94,141 | -4 | |
| **Brucella_melitensis_chr_I 17986284\|2,117,144** | | | | |
| *relBE*-1 | 17987808,17987809 | 86,105 | -4 | |
| *phd/doc*-1 | 17987658,17987659 | 76,129 | -4 | |
| **Brucella_melitensis_chr_II 17988344\|1,177,787** | | | | |
| *mazEF*-1 | 197880-198089,17988530 | 70,94 | -1 | New putative *mazE* |
| **Brucella_suis_chromosome_I 23500916\|2,107,792** | | | | |
| *relBE*-1 | 23501312,23501311 | 86,105 | -4 | |
| *phd/doc*-1 | 23501447,23501446 | 76,129 | -4 | |
| **Brucella_suis_chromosome_II 23499767\|1,207,381** | | | | |
| *mazEF*-1 | c1101320-1101529,23500829 | 70,94 | -1 | New putative *mazE* |
| **Mesorhizobium_loti 13470324\|7,036,074** | | | | |
| *relBE*-1 | 250975-251220,251223-251513 | 81,97 | +2 | New putative *relBE* |
| *parDE*-1 | 13471354,13471355 | 81,98 | -1 | |
| *parDE-2* | 1972578-1972823,1972805-1973119 | 82,105 | -19 | New putative *parDE* |
| *parDE*-3 | 13472960,13472959 | 88,94 | +30 | |
| *higBA*-1 | 13471567,13471566 | 102,98 | +8 | RGO |
| *higBA-2* | 4800860-4801012,4800572-4800853 | 51,94 | +6 | RGO |
| *vapBC*-1 | 13471641,13471640 | 91,132 | -1 | |
| *vapBC*-2 | 13473341,13473340 | 89,139 | -23 | |
| *vapBC*-3 | 13474236,13474235 | 98,137 | -4 | |
| *vapBC*-4 | 13474916,13474917 | 99,129 | -4 | |
| **S._meliloti_1021_chr. 15963753\|3,654,135** | | | | |
| *relBE*-1 | 1588987-1588739,15965227 | 83,92 | +6 | New putative *relB* |
| *relBE*-2 | 15966432,15966431 | 91,100 | -4 | |
| *higBA*-1 | 15964803,15964804 | 102,98 | +15 | RGO |
| *higBA*-2 | 15965582,15965582 | 204,196 | +68 | RGO |
| *higBA*-3 | 15966811,15966812 | 88,92 | +9 | RGO |
| *vapBC*-1 | 15964819,15964820 | 77,94 | -4 | |
| *vapBC*-2 | 15965038,15965037 | 71,121 | -7 | |
| *vapBC*-3 | 15965370,15965369 | 79,132 | -4 | |
| *vapBC*-4 | 15966170,15966171 | 90,134 | -4 | |
| *vapBC*-5 | 15966439,15966438 | 77,132 | -1 | |
| *vapBC*-6 | 15966710,15966709 | 81,153 | -4 | |
| *vapBC*-7 | 15967067,15967066 | 86,134 | -4 | |
| **Rickettsia_conorii_Malish 15891923\|1,268,755** | | | | |
| *relBE*-1 | 15892213,15892214 | 102,86 | +10 | |

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|---|---|---|---|---|
| *higBA*-1 | 15893146,15893145 | 142,78 | +49 | RGO, *higB* followed by 4 stop codons |
| *vapBC*-1 | 15892303,15892302 | 99,134 | -10 | |
| *vapBC*-2 | 15892524,15892523 | 83,139 | -44 | |
| *vapBC*-3 | 15893242,15893241 | 81,135 | -4 | |
| *mazEF*-1 | 15891930,15891929 | 93,80 | +21 | |
| *mazEF-2* | -,15893066 | -,67 | NA | Solitary *mazF* |

**Coxiella_burnetii 29732244|1,995,275**

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|---|---|---|---|---|
| *relBE*-1 | 29655274,29655275 | 84,91 | -1 | |
| *parDE*-1 | 29653983,29653982 | 87,112 | +5 | |
| *higBA*-1 | 29653637,29653636 | 106,75 | +3 | RGO |
| *higBA*-2 | 29654781,29654782 | 101,105 | +21 | RGO |
| *higBA*-3 | 29654981,29654981 | 108,56 | -8 | RGO |
| *vapBC*-1 | 29654541,29654540 | 84,128 | +8 | |
| *vapBC*-2 | 29654595,29654594 | 109,125 | -11 | |

**Ralstonia_solanacearum_chr. 17544719|3,716,413**

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|---|---|---|---|---|
| *relBE*-1 | 17547944,17547943 | 88,99 | -1 | |
| *relBE*-2 | 17547995,17547996 | 110,86 | -23 | |
| *vapBC*-1 | 17545591,17545590 | 83,137 | -4 | |
| *vapBC*-2 | 17547775,17547774 | 77,137 | -14 | |

**Neisseria_meningitidis_MC58 15675948|2,272,351**

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|---|---|---|---|---|
| *vapBC*-1 | 15677515,15677514 | 82,128 | -4 | |
| *mazEF*-1 | 15676809,15676808 | 78,115 | +1 | |
| *mazEF*-2 | 15677860,15677861 | 79,107 | -13 | |
| *phd/doc*-1 | c929475-929630,15676812 | 52,122 | -1 | New putative *doc* |

**Neisseria_meningitidis_Z2491 15793034|2,184,406**

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|---|---|---|---|---|
| *mazEF*-1 | 15793408,15793407 | 79,105 | -7 | |

**Nitrosomonas_europaea 30248031|2,812,094**

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|---|---|---|---|---|
| *relBE*-1 | 30248490,30248491 | 73,84 | -23 | |
| *relBE*-2 | 30248712,30248711 | 91,111 | -1 | |
| *relBE*-3 | 30248721,30248722 | 98,84 | -4 | |
| *relBE*-4 | -,30249083 | -,88 | NA | Solitary *relE* |
| *relBE*-5 | 30249325,30249324 | 102,86 | +2 | |
| *relBE*-6 | c1478798-1479043,30249331 | 82,86 | -4 | New putative *relB* |
| *relBE*-7 | 30249531,30249532 | 83,96 | -11 | |
| *relBE*-8 | 30249547,30249546 | 93,98 | -4 | |
| *relBE*-9 | 30249552,30249553 | 82,98 | -11 | |
| *relBE*-10 | 30249567,30249568 | 85,91 | +3 | |
| *parDE*-1 | 30248282,30248281 | 80,97 | 0 | |
| *parDE*-2 | 30248566,30248567 | 95,96 | -4 | |
| *parDE-3* | 1479335-1479618,30249332 | 88,99 | -1 | New putative *parD* |
| *parDE*-4 | 1655892-1656143,30249495 | 83,73 | +3 | New putative *parD* |
| *parDE*-5 | 30249561,30249560 | 80,98 | -4 | |
| *parDE*-6 | 30250055,30250054 | 81,114 | -4 | |
| *higBA*-1 | 30248496,30248497 | 101,95 | +9 | RGO |
| *higBA*-2 | 30248505,30248506 | 105,107 | +12 | RGO |
| *higBA-3* | c1156304-1156630,c1156617-1156871 | 109,85 | -14 | RGO, **n**ew putative *higBA*. Toxin hits into *relE* group |
| *higBA*-4 | 30249099,30249098 | 118,93 | +12 | RGO |
| *higBA*-5 | 30249283,30249284 | 100,92 | +12 | RGO |
| *higBA*-6 | 30249334,30249335 | 106,111 | -8 | RGO |
| *higBA*-7 | 30249348,30249347 | 92,70 | -17 | RGO |
| *vapBC*-1 | c316448-316260,30248306 | 63,134 | -1 | |
| *vapBC*-2 | 30248493,30248494 | 77,133 | -1 | |
| *vapBC*-3 | 30248512,30248513 | 87,136 | -4 | |
| *vapBC*-4 | -,30248568 | -,138 | NA | Solitary *vapC* |
| *vapBC*-5 | 30249061,30249060 | 82,143 | -4 | |
| *vapBC*-6 | 1155550-1155774,30249063 | 75,87 | +33 | New putative *vapB* |
| *vapBC*-7 | 30249207,30249208 | 87,157 | -20 | |
| *vapBC*-8 | 30249329,30249328 | 81,131 | +7 | |
| *vapBC*-9 | 30249350,30249349 | 77,134 | -14 | |
| *vapBC*-10 | 30249551,30249550 | 84,142 | -4 | |
| *vapBC*-11 | 30249559,30249558 | 100,135 | -4 | |
| *vapBC*-12 | 30250051,30250052 | 85,138 | +5 | |
| *vapBC*-13 | 2296994-2297218,30250053 | 75,131 | -1 | New putative *vapB* |
| *vapBC*-14 | 30250109,30250108 | 79,110 | -14 | |

| | | | | |
|---|---|---|---|---|
| *mazEF*-1 | c1002703-1002936,30248925 | 78,116 | -23 | New putative *mazE* |
| *mazEF*-2 | 30248978,30248977 | 81,115 | -1 | |
| *mazEF*-3 | 30249168,30249167 | 80,113 | -8 | |
| *mazEF*-4 | c1427432-1427208,30249285 | 74,108 | -4 | *mazE* with corrected start (GI:30249286) |
| *mazEF*-5 | 30249549,30249548 | 80,112 | -16 | |
| *phd/doc*-1 | c1386501-1386749,30249247 | 83,129 | -1 | New putative *doc* |
| *phd/doc*-2 | 2674530-2674754,30250372 | 75,129 | -1 | New putative *doc* |
| *ccdAB*-1 | 30249070,30249069 | 87,105 | +143 | |
| **Helicobacter_pylori_26695** | **15644634\|1,667,867** | | | |
| *relBE*-1 | 15645511,15645510 | 95,90 | +13 | |
| *relBE*-2 | c946969-946688,15645512 | 93,88 | -20 | *relB* with corrected start (GI:15645513) |
| *relBE-3* | 15645620,1067530-1067742 | 110,71 | +59 | New putative *relE* |
| **Helicobacter_pylori_J99** | **15611071\|1,643,831** | | | |
| *relBE*-1 | -,15611892 | -,100 | NA | Solitary *relE* |
| *relBE*-2 | 15611899,15611898 | 95,90 | +13 | |
| **Escherichia_coli_CFT073** | **26245917\|5,231,428** | | | |
| *relBE*-1 | 26248392,26248391 | 92,84 | -4 | |
| *higBA*-1 | 26247766,26247767 | 94,90 | -1 | RGO, Alt. name: *yddM* |
| *higBA-2* | 26250653,26250652 | 96,103 | 0 | RGO |
| *higBA-3* | 26251283,26251282 | 94,136 | +1 | RGO |
| *ccdAB*-1 | 26245972,26245973 | 77,104 | +2 | |
| **Escherichia_coli_K12** | **16127994\|4,639,221** | | | |
| *relBE*-2 | 16128212,16128211 | 86,92 | +2 | Alt. name:*dinJ yafQ* |
| *relBE*-1 | 16129523,16129522 | 79,95 | -1 | Alt. name: *relB*-I *relE*-I |
| *relBE*-3 | 16129958,c2087233-2087487 | 83,84 | -4 | Alt. name: *yefM yoeB*, new GI in data base: 33347611 |
| *higBA*-1 | 13878954,- | 94,- | NA | Solitary *higA* |
| *mazEF*-1 | 16130690,16130689 | 82,111 | -1 | Alt. name: *chpA* |
| *mazEF*-2 | 16132046,16132047 | 85,116 | -7 | Alt. name: *chpB* |
| **Escherichia_coli_O157** | **15829254\|5,498,450** | | | |
| *relBE*-1 | 15829507,15829506 | 86,86 | +18 | Alt. name: *dinJ yafQ* |
| *parDE*-1 | 15829715,15829716 | 80,93 | -8 | |
| *parDE*-2 | 15830322,15830321 | 63,95 | -1 | |
| *parDE*-3 | 15831534,15831535 | 75,92 | +1 | |
| *higBA*-1 | 15832124,15832123 | 96,112 | -11 | RGO |
| *mazEF*-1 | 15832897,15832896 | 82,111 | -1 | Alt. name: *chpA* |
| *mazEF*-2 | 15834456,15834457 | 85,116 | -7 | Alt. name: *chpB* |
| *ccdAB*-1 | 15829306,15829307 | 77,104 | +2 | |
| **E._coli_O157_H7_EDL933** | **16445223\|5,528,445** | | | |
| *relBE*-1 | 15799931,c283932-284192 | 86,87 | +18 | Alt. name: *dinJ yafQ*, corrected start GI:15799930 |
| *parDE*-1 | 15800137,15800138 | 80,93 | -8 | |
| *parDE-2* | 15800838,c1256683-1256967 | 63,95 | -1 | New putative *parE* |
| *parDE_3* | 15801987,2324393-2324668 | 89,92 | +1 | New putative *parE* |
| *higBA*-1 | 15802545,15802544 | 96,112 | -11 | RGO |
| *mazEF*-1 | 15803304,15803303 | 82,111 | -1 | Alt. name: *chpA* |
| *mazEF*-2 | 15804815,15804816 | 85,116 | -7 | Alt. name: *chpB* |
| *ccdAB*-1 | 15799732,15799733 | 77,104 | +2 | |
| **Shigella_flexneri_2a** | **24111450\|4,607,203** | | | |
| *relBE*-1 | 24112921,24112920 | 79,95 | -1 | Alt. name: *relBE*-I |
| *relBE*-2 | 24113402,24113399 | 90,84 | NA | *yefM yoeB* separated by *insAB* |
| *mazEF*-1 | 24114677,24114678 | 89,121 | -7 | |
| **Shigella_flexneri_2a_2457T** | **30061571\|4,599,354** | | | |
| *relBE*-1 | 30063051,30063050 | 79,95 | -1 | Alt. name: *relBE*-I |
| *relBE*-2 | 30063468,c2077698-2077949 | 90,84 | -4 | Alt. name: *yefM yoeB*, new putative *relE* |
| **Salmonella_typhimurium_LT2** | **16763390\|4,857,432** | | | |
| *relBE*-1 | 16764896,16764895 | 82,94 | -11 | |
| *relBE*-2 | 16766805,16766804 | 86,91 | +2 | |
| *relBE*-3 | 16767695,16767696 | 80,94 | -11 | |

| | | | | |
|---|---|---|---|---|
| *parDE*-1 | c3102440-3102715,c3102178-3102468 | 91,96 | -29 | New putative *parDE* |
| *higBA*-1 | 16767183,16767182 | 113,105 | -4 | RGO |
| *higBA*-2 | 4241948-4242235,4241636-4241944 | 96,103 | 0 | RGO, new putative *higBA* |
| *vapBC*-1 | 16766336,16766335 | 75,132 | -1 | |
| *phd/doc*-1 | 16766845,16766844 | 75,122 | -4 | |
| | | | | |
| **Salmonella_typhi 16758993\|4,809,037** | | | | |
| *relBE*-1 | 16763249,16763250 | 80,94 | -11 | |
| *parDE*-1 | c2958334-2958059,c2957794-2958012 | 91,73 | -74 | New putative *parDE* |
| *higBA*-1 | 16762224,16762225 | 103,120 | -4 | RGO |
| *vapBC*-1 | 16761811,16761810 | 75,132 | -1 | |
| *vapBC*-2 | 16762401,16762400 | 82,124 | -1 | |
| *phd/doc*-1 | 16759892,16759893 | 95,165 | -10 | |
| | | | | |
| **Salmonella_typhi_Ty2 29140543\|4,791,961** | | | | |
| *relBE*-1 | 29144728,29144729 | 80,94 | -11 | |
| *parDE*-1 | c2944229-2943954,c2943689-2943907 | 91,73 | -74 | New putative *parDE* |
| *higBA*-1 | 29143713,29143714 | 113,120 | -4 | RGO |
| *vapBC*-1 | 29143295,29143294 | 75,132 | -1 | |
| *vapBC*-2 | 29143889,29143888 | 82,124 | -1 | |
| *phd/doc*-1 | 29142336,29142335 | 95,165 | -10 | |
| | | | | |
| **Yersinia_pestis_CO92_chr. 16120353\|4,653,728** | | | | |
| *relBE*-1 | -,16121191 | -,86 | NA | Solitary *relE* |
| *higBA*-1 | c964230-964379,16121186 | 50,108 | -5 | RGO, new putative *higBA* |
| *higBA*-2 | 16121389,16121388 | 106,103 | +7 | RGO |
| *higBA*-3 | 16122544,16122545 | 107,104 | -4 | RGO |
| *higBA*-4 | 16123631,16123632 | 103,122 | +23 | RGO |
| *phd/doc*-1 | 16122085,16122086 | 101,158 | +10 | |
| | | | | |
| **Yersinia_pestis_KIM_chr 22123922\|4,600,755** | | | | |
| *relBE*-1 | c3399757-3400077,22126965 | 107,106 | -4 | New putative *relB* |
| *relBE*-2 | -,c3599007-3599264 | -,86 | NA | Solitary *relE* |
| *higBA*-1 | 22124613,22124612 | 103,122 | +13 | RGO |
| *higBA-2* | 22125904,2218599-2218967 | 107,123 | -1 | RGO |
| | | | | |
| *higBA*-3 | c3594262-3594411,c3594407-3594730 | 50,108 | -5 | RGO, new putative *higAB*; GI:22127138 was corrected |
| *phd/doc*-1 | c2738578-2738880,22126357 | 101,158 | +13 | New putative *doc* |
| | | | | |
| **S._oneidensis_MR_1_chr 24371600\|4,969,803** | | | | |
| *relBE*-1 | 24376115,24376114 | 85,101 | -13 | |
| *parDE*-1 | 24373020,24373019 | 102,97 | -38 | |
| | | | | |
| **Vibrio_cholerae_chromosome_2 15600771\|1,072,315** | | | | |
| *relBE*-1 | 15601089,15601088 | 92,98 | -35 | |
| *relBE*-2 | c343886-343602,15601113 | 94,92 | -4 | New putative *relB* |
| *relBE*-3 | 15601185,15601186 | 97,119 | -4 | |
| *relBE*-4 | 15601208,15601207 | 82,96 | -11 | |
| *relBE*-5 | 15601238,15601239 | 90,96 | -14 | |
| *relBE*-6 | 15601249,15601250 | 85,100 | -13 | |
| *relBE*-7 | c433678-433394,15601263 | 94,92 | -4 | New putative *relB* |
| *parDE*-1 | 15601077,15601076 | 80,111 | 0 | |
| *parDE*-2 | 15601124,15601123 | 153,99 | -14 | |
| *parDE*-3 | 15601149,15601148 | 80,111 | 0 | |
| *higBA*-1 | 15601155,15601154 | 105,117 | +10 | RGO, antitoxin *ybaQ* |
| *higBA*-2 | 15601230,15601229 | 104,110 | -14 | RGO |
| *phd/doc*-1 | 418614-418781,15601236 | 56,133 | -1 | New *phd*; GI: 15601235 was corrected |
| | | | | |
| **Vibrio_parahaemolyticus_chr_1 28896774\|3,288,558** | | | | |
| *relBE*-1 | 28898595,28898594 | 99,90 | -11 | |
| *relBE*-2 | 28898603,28898604 | 94,92 | -4 | |
| *relBE*-3 | 1935517-1935800,28898617 | 94,92 | -4 | New putative *relB* |
| *parDE*-1 | 28898659,28898658 | 42,61 | +21 | |
| | | | | |
| **Vibrio_vulnificus_CMCP6_chr_1 27363490\|3,281,945** | | | | |
| *relBE*-1 | 27365728,27365729 | 85,100 | -13 | |
| *relBE*-2 | 27365748,27365749 | 85,100 | -13 | |
| *relBE*-3 | 27365845,27365846 | 93,95 | -4 | |
| *parDE*-1 | 27365829,27365828 | 80,99 | -4 | |

| | | | | |
|---|---|---|---|---|
| **Vibrio_vulnificus_CMCP6_chr_2 27366463\|1,844,853** | | | | |
| *relBE*-1 | 27367843,27367844 | 94,92 | -4 | |
| **X_axonopodis_pv_citri_str_306 21240774\|5,175,554** | | | | |
| *relBE*-1 | 21241894,21241895 | 86,58 | -4 | |
| *parDE*-1 | 21240854,21240855 | 85,99 | -13 | |
| *parDE*-2 | 21243162,21243161 | 92,96 | -13 | |
| *vapBC*-1 | 21242627,21242628 | 82,136 | -4 | |
| *vapBC*-2 | 21242923,21242922 | 79,130 | +7 | |
| *vapBC*-3 | 21245026,21245027 | 84,138 | -4 | |
| *phd/doc*-1 | 21241949,21241948 | 73,145 | -4 | |
| **X._campestris_pv_ATCC_33913 21229478\|5,076,188** | | | | |
| *relBE*-1 | c74344-74069,21229535 | 93,105 | -4 | New putative *relB* |
| *relBE*-2 | 21230492,21230493 | 97,105 | -4 | |
| *relBE*-3 | 21230523,21230524 | 87,102 | +6 | |
| *parDE-1* | c3665126-3665371,21232522 | 82,100 | -1 | New putative *parD* |
| *vapBC*-1 | 21231084,21231085 | 99,131 | -4 | |
| *vapBC*-2 | 21231309,21231310 | 85,135 | -4 | |
| *ccdAB*-1 | 21230189,21230188 | 101,105 | -4 | |
| **Xylella_fastidiosa_chr 15836605\|2,679,306** | | | | |
| *relBE-1* | 15838297,c1620819-1621091 | 98,91 | -17 | New putative *relE* |
| *relBE*-2 | 15838658,15838657 | 90,102 | +3 | |
| *relBE*-3 | 15838666,15838665 | 92,98 | -13 | |
| *relBE*-4 | 15838672,15838671 | 86,93 | -14 | |
| *parDE*-1 | 15838625,15838626 | 83,102 | -4 | |
| *parDE*-2 | 15838662,15838661 | 80,61 | -8 | |
| *higBA-1* | 15837156,c527947-528210 | 114,88 | -17 | RGO, New putative *higB* |
| *higBA*-2 | 15837322,15837323 | 91,105 | -12 | RGO |
| *higBA*-3 | 15838173,15838174 | 93,112 | -4 | RGO |
| *higBA*-4 | 15838197,15838198 | 99,98 | -4 | RGO |
| *higBA*-5 | 15838278,15838279 | 93,112 | -4 | RGO |
| *higBA*-6 | 15838303,15838304 | 101,102 | -4 | RGO |
| *higBA*-7 | 15838310,c1629883-1630197 | 96,105 | +17 | RGO, new putative *higB* |
| *higBA*-8 | 15839352,15839353 | 102,113 | +3 | RGO |
| *vapBC*-1 | 304978-305193,15836896 | 72,144 | -29 | New putative *vapB* |
| *vapBC*-2 | 15838191,15838190 | 86,142 | 0 | |
| *mazEF*-1 | 15838461,15838460 | 73,109 | -10 | |
| **Xylella_fastidiosa_Temecula1 28197945\|2,519,802** | | | | |
| *relBE-1* | 1298015-1298314,1298354-1298761 | 100,136 | +39 | New putative *relBE*; GI:28198992 was corrected |
| *relBE*-2 | 28199073,28199074 | 98,88 | -17 | |
| *parDE*-1 | 28198860,28198859 | 79,102 | -10 | |
| *higBA*-1 | 28198286,28198285 | 91,93 | +10 | RGO |
| *higBA-2* | 28198867,1167816-1168139 | 93,108 | -1 | RGO |
| *higBA-3* | 28199067,28199066 | 101,100 | +3 | RGO |
| *higBA*-4 | 28199225,28199224 | 99,93 | +9 | RGO |
| *vapBC-1* | 303404-303628,28198163 | 75,132 | +7 | |
| **Haemophilus_influenzae 16271976\|1,830,138** | | | | |
| *relBE*-1 | 16272650,16272651 | 98,102 | -1 | |
| *higBA*-1 | 16272602,16272603 | 98,119 | -8 | RGO |
| *higBA*-2 | 16273170,16273169 | 107,101 | +10 | RGO |
| *higBA*-3 | 16273326,16273325 | 97,99 | -4 | RGO |
| *vapBC*-1 | 16272274,16272275 | 78,134 | -4 | |
| *vapBC*-2 | 16272886,16272885 | 77,132 | -1 | |
| **Pseudomonas_aeruginosa 15595198\|6,264,403** | | | | |
| *relBE*-1 | 15595323,15595322 | 75,93 | -4 | |
| *parDE*-1 | 796960-797238,15595926 | 93,115 | +12 | New putative *parD* |
| *higBA*-1 | 15599869,c5242573-5242848 | 101,92 | +11 | New putative *higB* |
| **Pseudomonas_putida_KT2440 26986745\|6,181,863** | | | | |
| *relBE*-1 | 26989222,26989223 | 90,97 | -13 | |
| *relBE*-2 | 26989659,26989658 | 94,84 | +19 | |
| *higBA*-1 | 334364-334672,334049-334360 | 103,104 | +3 | RGO, new putative *higBA* |
| *higBA*-2 | -,26987565 | -,98 | NA | Solitary *higB* |
| *higBA*-3 | 26987933,26987934 | 98,111 | -10 | RGO |

| | | | | |
|---|---|---|---|---|
| *higBA*-4 | c1418120-1418494,26987976 | 125,116 | -40 | RGO, new putative *higA* |
| *higBA*-5 | 26988317,26988318 | 99,92 | +8 | RGO |
| *mazEF*-1 | 26987506,26987507 | 84,115 | -4 | |
| | | | | |
| **Pseudomonas_syringae** | **28867243\|6,397,126** | | | |
| *relBE*-1 | 28867568,28867567 | 92,82 | +25 | |
| *relBE*-2 | 28870831,28870832 | 79,94 | -11 | |
| *relBE*-3 | 28872496,28872495 | 79,96 | -11 | |
| *parDE*-1 | 28867472,28867473 | 83,116 | -12 | |
| *higBA*-1 | 28867446,28867445 | 101,92 | +9 | RGO |
| *higBA*-2 | 28867652,28867653 | 97,92 | +12 | RGO |
| *higBA*-3 | 28872483,28872482 | 114,107 | -4 | RGO |
| *vapBC*-1 | 28868263,28868262 | 76,134 | -1 | |
| *vapBC*-2 | 28869204,28869203 | 83,150 | -1 | |
| | | | | |
| **Leptospira_intrerrogans_I** | **24212700\|4,332,241** | | | |
| *relBE-1* | -,3672435-3672671 | -,79 | NA | Solitary *relE* |
| *vapBC*-1 | 24213637,24213636 | 77,132 | +1 | |
| *vapBC*-2 | 24213702,24213701 | 76,132 | -1 | |
| *vapBC*-3 | 24215974,24215973 | 72,147 | -11 | |
| *mazEF*-1 | 24214480,24214481 | 78,113 | -7 | |
| *mazEF*-2 | 24215544,24215543 | 82,113 | -14 | |
| | | | | |
| **D._radiodurans_chr_1** | **15805042\|2,648,638** | | | |
| *vapBC*-1 | 15805445,15805446 | 85,137 | -4 | |
| *vapBC*-2 | 15806541,15806540 | 81,141 | -4 | |
| *vapBC*-3 | 15807097,15807096 | 71,130 | 0 | |
| *mazEF*-1 | 15805443,15805444 | 80,117 | -7 | |
| *mazEF*-2 | 15805688,15805689 | 84,115 | -10 | |

Footnotes to Table S2:

a) The TA loci belonging to the seven families are listed with the most abundant families first (*vapBC*, *relBE*, etc). To discriminate TA loci belonging to the same TA family and encoded by the same chromosome, all TA loci was designated a number, with the numbers increasing with increasing locus position in a given chromosome. One exception to this rule was *relBE* of *E. coli* which, for historical reasons, was designated *relBE*-1, although the homologous *dinJ yafQ* locus has a lower chromosomal position.

b) Unique identifiers of antitoxin and toxin genes were either GIs or, for un-annotated genes, co-ordinates in the DNA. A “c” in front of a pair of co-ordinates indicates that the gene was located on the chromosomal minus-strand.

c) The sizes of the antitoxin and toxin genes are given by the number of codons predicted from the DNA.

d) dist. gives the distance (in bp) between the antitoxin and toxin genes. A “-“ indicates overlap between the genes.

e) The comments column yields information of peculiarities discovered during the analysis. RGO indicates reversed gene order for the *higBA* loci.

f) Each species name is followed by the GI identifier of its DNA sequence. The size (in bp) of the corresponding chromosome is also given. DB = Data base. Solitary toxin genes are also indicated in the Comments column.

# Table S3: Protein sequences of un-annotated toxins and antitoxins in 126 prokaryotic organisms

**Aeropyrum_pernix**

>relB|14600379:984865-985164, length 100, Aeropyrum_pernix, RelB
MLISVFLMRRVSECVRWKLLFNLHVTYYILADGGLIVSSKKSKVKVEVEVEVPEGDDEGV
YREEFRRELAKRILNVMLDKDVEPAKRAVAKTLREKGGEG

>vapB|14600379:c199314-199072, length 81, Aeropyrum_pernix, VapB
MLLLVVSTVSKVIRVKYEKGVLKPLEPLDLQEGEEVQVIIQPGEPIAEKYYGIARKHRPN
LDKKEFLEVLEEIEDEDIRGH

>vapB|14600379:c697607-697245, length 121, Aeropyrum_pernix, VapB
MAMNIDGDGVVVSTTAGSTAYSLSGGGPIIDPRLDVIVLTPLNPVQLFLRSIVVPSGSRV
TVEASVYSNPLVVNIDGQYVYELEPGGIVDIERCGSGVRIARFRWWEDYYERLYTRLLAY
W

>vapB|14600379:c1008442-1008167, length 92, Aeropyrum_pernix, VapB
MVPPGHDPNDFARGSIKTCQWRGRNINTNIKNTTMGEAVATKKITIEVEVPEDFDEERGV
ERLIELLRKGAPLGVKQKDLRRQRIYASRTRY

>vapB|14600379:c1508755-1508399, length 119, Aeropyrum_pernix, VapB
MAIGTQLDPSVTKADNLVGNVVGKPGELPEPLTTLRIEHHLLEKVVGMKEEARVEPIRRG
EMLMLSVGTAITLGVVTRAGKDEIEVQLRRPVVTWPKARVALSRRIMGRWRLIGWGLIK

>vapB|14600379:c1666639-1666448, length 64, Aeropyrum_pernix, VapB
MSKVIRVRYEKGVLKPIGEVVLREGEELEVVVVRKSFRGFKDEAGKYMFKADRDTVKEFV
EERR

>vapB|14600379:c760494-760258, length 79, Aeropyrum_pernix, VapB
MGWGCAMSKVIRVKYEGGVLKPLEPLVLSEGEEVEVVIRRRVFGEEDYRELVDFLSELPK
GKAELLDLVEELYLEEALR

**Sulfolobus_solfataricus**

>vapB|15896971:360012-360608, length 199, Sulfolobus_solfataricus, VapB
MIRSFDVNKPGTQFNELKGGVIGGSIIQGLFKVDQEIKVLPGLRVEKQGKVSYEPIFTKI
SSIRFGDEEFKEAKPGGLVAIGTYLDPSLTKADNLLGSIITLADAEVPVLWNIRIKYNLL
ERVVGAKEMLKVDPIRAKETLMLSVGSSTTLGIVTSVKKDEIEVELRRPVAVWSNNIRTV
ISRQIAGRWRMIGWGLVEI

>vapB|15896971:1340360-1340617, length 86, Sulfolobus_solfataricus, VapB
MYYLHLKFTMERMISKVTRNFQVTIPYEIRKVLGIKEGDYIEFAIENGKVMIKPVRKVWS
TIRLGREVTVEEIEEIASKAFKDDSS

>vapB|15896971:c683385-683083, length 101, Sulfolobus_solfataricus, VapB
MKEVKTHYFVTLNPPRSITALQPITVSVGALSAIGILAYLLSRLDKGEDNIREVVEKALD
EAIKEKEKERLRETALKIKELMKDVNEEEWATVIRENRNER

>vapB|15896971:c725687-725481, length 69, Sulfolobus_solfataricus, VapB
MSERIKEKIYDTNALIKIHKNKSLLSTTNYVTTSILNVIEYPPIIDLKEKLIIIYPTRSD
YELAIKDNG

>vapB|15896971:c1503996-1503685, length 104, Sulfolobus_solfataricus, VapB
MNFRSDPQSSIQSKLYIHTHLFTFVSKIIRVSEDVKEKLVKISAELELSEGKRVSLNDTI
KYLITLYEEKKSNKNSELLLSLLGSAKGIREEFERSRIEDESSD

>vapB|15896971:c1577585-1577400, length 62, Sulfolobus_solfataricus, VapB
MKEGDILILRVEDGKIVLEPERKVSFDDLKKKMEEHSAKISYANKAKLGDLINVSLEEEF
DN

>vapB|15896971:1582391-1582642, length 84, Sulfolobus_solfataricus, VapB
MGIQNQLMGYIVTVDERGRIVIPKDIRERLNLKEGSKVEISVDEKGRIIIIVRRISVDNI
YGIAGRERVSIEEIEEALGFEDND

>vapB|15896971:1620321-1620638, length 106, Sulfolobus_solfataricus, VapB
MIHLLRIRKFYNIRMSYFLHMPIISIRIDEKLKKKMDELSYINWSEIIRRKIEEVIEEEE
EKRKGKRKDYKKIAEASVRSYEFFLNYGGKSSEEIIREWRDKNWQL

>vapB|15896971:c1734033-1733776, length 86, Sulfolobus_solfataricus, VapB
MFTIKENTMTSTVISIRVDERLKKELEELGIDYPELVRRYLEEVVRKEKMRRELREANGI
REELLKSHGYYSPSAELVREDRDGYH

>vapB|15896971:1783470-1783712, length 81, Sulfolobus_solfataricus, VapB
MYLMEVKVHKKGIIVIPAEVRRRLNIKEGSVIELEVEGDKIILKRKLTLLDAYGIDKEMG
DSAVKELEKLRKEEVEKENSV

>vapB|15896971:1914151-1914375, length 75, Sulfolobus_solfataricus, VapB
MKSTITVSKKVKEVLERKKKEMEIKLNKPLSWDEFFQNIFREEEERIPKLTEEEAEILKD
LTKEDRKNWRIREFV

>vapB|15896971:c2041164-2040874, length 97, Sulfolobus_solfataricus, VapB
MSATNSLLYKDLNAIEIIFVNPIFYYLRSVVIPPKSLILRLEDKGYPQTARVVVDGEVVT

LIKTNQEITVRVSQHKAKILRFFKLDLIGEVLHAYHI

>vapB|15896971:1073660-1073923, length 88, Sulfolobus_solfataricus, VapB
MYENFIYVYLVYIYMSDVISVRVKKELKKKAEELGINVREVVEKALEEAIREKEKEELKD
MTMKIKELMRDVSEYDWVSTVRESRDER

>vapB|15896971:1742082-1742303, length 74, Sulfolobus_solfataricus, VapB
MSTVISVRIKKEIKEELEKHGVDIDQEVRKFLEELYLKVKAKEYINKWIEDLKDVKPSEE
GFSSNSVREDRESH

>vapB|15896971:1784438-1784701, length 88, Sulfolobus_solfataricus, VapB
MYESFIYVYFVYIYMSDVISVRVKKELKKRAEELGINIREVVEKALEEAIREKEKEELKD
IVMRIKELMRDVSEDDWVRAVRESRDER

>vapB|15896971:c1788331-1788080, length 84, Sulfolobus_solfataricus, VapB
MYTSYMKTIMIRDDVYKKLVEIKGDKSFSEIIEELIEESLTLRRRKLEKYFGILNEEEAE
EIMKEIKEVRKITDESINRKLSNY

**Sulfolobus_tokodaii**
>phd|24473558:1143830-1143531, length 97, Sulfolobus_tokodaii, Phd
MTDKKPFALSEVAQRVLIVLGRENRGLTVRELVEKTDTNSGSIKRALEELAKLNLIKEEK
ENVFPYRRLISLTEVGREVAKRVIEIEELVKKVQSNG

>doc|24473558:c1317467-1317895, lebgth 143, Sulfolobus_tokodaii, doc
MENKFRLIVTSLDKSFITWLNDRVLKEEDPSLTSTVINEGNIEGAIYSAVMDFEINHNIS
RSLAVLIHHLVVGHPFADGNKRTATTLLITLISKLYERDVVLEENLMNSLITIIAEISNE
SENDIDKLQKIIEEIMKNLTVHY

>doc|24473558:c1328737-1329249, length 171, Sulfolobus_tokodaii, doc
MYVDRVYFIRLNILLEEKLLKILNALLKEFEAWIRGESEEKPLIIEIHDKLIANDTYSEG
GVINLDDIGIAIYSSIEDLMRNHDVSRSLAVLTYHLVVSHPFVDGNKRTTLGFLLNILHT
LFEDEIEIPQDVVDTLMQTLVEIADNPPEEDEMAINRVRSIIRGLIPVNQD

>vapB|24473558:c673537-673358, length 60, Sulfolobus_tokodaii, VapB
MLERKKKEMEIKLDKPLTWDEFFQEVFKEENIPKLTEEEAETLKKLVLEDRKNWKVREFA

>vapC|24473558:c673379-673011, length 123, Sulfolobus_tokodaii, VapC (gi|15920915 start corrected)
MESKRVCLDTDILIDSFKRDPRKIIGYYTTCVNLYEFLRGLAFIGKNVDEFKVWVEANLN
VLCIDNSSLKIASRIYADLRKKGNLVEDPDLLIASICIANNLVLRTNNKKHFRRLEEYGL
RLM

>vapB|24473558:c2516-2271, length 82, Sulfolobus_tokodaii, VapB
MFSVYVYYYNMKTVYSLRIDKELREEMEKYNIKWNEEIENFIRRRIEELKKEEILKKINEI
LQTMPETNSSSAELVREDRDNN

>vapB|24473558:c397414-397157, length 86, Sulfolobus_tokodaii, VapB
MENYQLLERVVGAKELVKVENIKKGEVLMLTLGSATTLGVAKNIKNDELEVELKRPLVVW
DKDLRVVISRQVSGRWRLVGWGIIKI

>vapB|24473558:761620-761892, length 91, Sulfolobus_tokodaii, VapB
MLLQSDNVMSETIRVSKEVKRELLKIMGELQIERGEKVDFNDVIEYLLSLYRRKNPEILR
RMVGLVPNISYEDLRKERKKELEYEKEKYGI

>vapC|24473558:1818807-1819082, length 92, Sulfolobus_tokodaii, VapB
MLFYVYENFIYTKIVYLIMSTVISVRVRKELKEKAEELGINIREVVEKALEEAIREKEKE
EIKETARKIKELMKDISEDEWITSIREDRYER

>vapB|24473558:2138189-2138767, length 193, Sulfolobus_tokodaii, VapB
MPILGVKFGRRSALLDIRPENIKEALELLQKNKYTIEEYPMLEAKSKNINTIAFNEIAIL
FNNPETVYGSVNIKERKILFEGDGVLIATPQGSWAWSYSATRVLLHKDINGIEITFINPI
IPNIKALIIPQTETILVKLEDKGRTQNVRVISDGEIVGNLISKEDEELTITLSKRKAKIL
RFFNLIEFDGLFT

>vapB|24473558:c1303456-1303313, length 48, Sulfolobus_tokodaii, VapB
MENVSTGSEIIERLKKLGVEEKDLIVEPPQGEEEFQKELKRKSMIQMF

>vapC|24473558:c1302999-1303355, length 119, Sulfolobus_tokodaii, VapC (start corrected)
MSERTKEKIYDTNVLIEIYKNRTLQDKLDFIITSILNVIEYPPILNLRNKLLVVYPTKED
YELALKIMVKLRKIGKPVNVVDIILASIAINHNMIVVTNDRDFDLIKKVEDKLEIQVNP

>vapC|24473558:2013264-2013695, length 144, Sulfolobus_tokodaii, vapC
MEKRLINLSELIVDTSFLLPLVGIKVKGIKDSLLEGKAIYYPNLLLTELLAVIFKEAKKL
KLNKVPEEAMKGLIYVLSNVNLISIEELEIETIYEILNKGWNDIFDAILYTAYKSTKIPL
ITMDKSFYNFLKENGMDVKGIILL

**Pyrobaculum_aerophilum**
>vapB|18311643:335372-335986 , length 204, Pyrobaculum_aerophilum, VapB
MLGGDGTLLEAIRRHPCVLESVVIHLGLGKVNFYKSAEITLPIDEAVSRVLKGEYKVLEL
STLESDGCIALNEAAVYRRDPGRLLSFKITTDEGQIAGRADGIIVSTPHGASGYVVSTFG
PVVDYRADVIVVSFVAPYTLYLRPMVLTSKRVVIETREDAVLVCDGREARMGRVFEVAKG
QRRLKLAIFGDFQFIQRVAERLRSL

>vapB|18311643:2133278-2133844, length 189, Pyrobaculum_aerophilum, VapB

MREAERALLELRVGLKDKFYLISGRRLAAWKYTYETHVDLMPLTSVGAEGQFTPHHLSRI
LTMSSYEAVRDALYNYLEIADIEDVRVGLVKTGRIALYVKKGGLWTNGYNAGNYTKAVLP
VLLQMLLANEGSSVFIDDVDLAVPSGRAEVLLSALFEIARKRNLQLVASAKEPGFAEIAE
KLGFTIAKL

**Archaeoglobus_fulgidus**

>vapB|11497621:289024-289218, length 64, Archaeoglobus_fulgidus, VapB
MPKIIEAIYENGVFKPLQKVNFRPGSKVRIVIQEDKKEILRKYKGVFGKAEVEELREYEG
EVML

>vapB|11497621:c271532-271335, length 66, Archaeoglobus_fulgidus, VapB
MPRVIEVIYENGMFKPLEKVDLPEGSRFKILIEDFSEIDRIHEHVKKIAGEASKEKILEL
LDEVWI

>vapB|11497621:290594-290764, length 57, Archaeoglobus_fulgidus, VapB
MSMEKIFIDTNVIIDLLRGKKSVVSFFRDVEDGEIHGLTNKNGVSGNCLRLPDPYNG

>vapB|11497621:1978461-1978667, length 69, Archaeoglobus_fulgidus, VapB
MGHGCLRRYFVCDILLIKTDKTEKAIELFNRLNPIASVTVYEESFYTGLRIIAQKRLNIK
NMLMLSGIL

>vapB|11497621:289639-289923, length 95, Archaeoglobus_fulgidus, VapB
MFLRLLSLRGNLFLFSDPQSICQKSSKLYMRTELFKPLQKVDLKEGEKIRLRLDERGYID
HSLIRELEVLLKNAPKTKIDLRELERLHDVGKMLY

>vapB|11497621:287426-287674, length 83, Archaeoglobus_fulgidus, VapB
MSNQKRLQPKPISSFMQTNNMPKVIEAIYENGVFKPLQKVELREGEKVKVIVDRGLTQLF
GMFRHRRKTDLDEDMDLMITERA

>vapB|11497621:350180-350689, length 170, Archaeoglobus_fulgidus, VapB
MVNVTFENDDVGHVAAAIAVNGTYFILDQHLPPFDPQGYFIKWLRDGKRIEKAEIIDNNT
TIPLNLSIGYVASDRDAKSLESRIRQYFKGTGIREDPRLNGEKLPLGYREGYTLKLSLEM
AEYYHPEFERQYAEHIYKLLEESIEGRFKAFNLHLSIKGDVMEIVLYLAR

>vapB|11497621:c534011-533655, length 119, Archaeoglobus_fulgidus, VapB
MGIATKLDPTLTKSDALVGNVVGHPGNLPDVLTSFTMEVNLLERVVGLDEEMEVEKIKMN
EPLMLAVGTAITLGVVTSARDDIVEVKLRRPVCADKGSRVAISRRVGSRWRLIGAGIIR

>vapB|11497621:c550521-550279, length 60, Archaeoglobus_fulgidus, VapB
MLNSQRNMCMPNITLSLPEDLYRKMKKYGEIRWSEVVRKAIAEYLEKLEEIETEVGSKEL

>vapB|11497621:c980157-979951, length 70, Archaeoglobus_fulgidus, VapB
MSGGLSFWRLLNSNFQRNPFLLPRKITDMPKIIEAVYENGVFKPLQKVDLREGEKVKIIA
GNLVERLRKYRVKVDSDIVAEFISERR

>vapB|11497621:c1236899-1236693, length 69, Archaeoglobus_fulgidus, VapB
MRDALGIKPGTVMNVHLEGKKIILEPSPEPPDIFVDLGERSEQILKESRKIDEERMRKLL
RDLGVEGGD

>vapB|11497621:c981711-981451, length 87, Archaeoglobus_fulgidus, VapB
MANLIHTKPFSSFSANHQHAKNHRSCLRKRSLQAFAEGGFEGGGENKASHRGGNRRRYKG
IQQKSRPRRFGGIPKGEKMIVIDTSVFIDALFRFNEKRSNMANEIFEIAQHRQIAVVEPE
IFRMEIIGQLVRRTPKSEAITLYEGIV

>vapB|11497621:c556664-556485, length 81, Archaeoglobus_fulgidus, VapB
MGKVIQIEVPDRVNEKLINKLKEMLADKILDEIGKDYADIDLYNLYLTLKFPKTEDVTFD
TDKELEYLRKMKEKEKKRVWS

**Halobacterium_sp_NRC_1**

>vapB|15789340:c67955-67662, length 98, Halobacterium_sp_NRC_1, VapB
MSKAVKVDEDAKSRLEELQAEIRLETGESVTQQELLSRLIDDAYQDREAVIDSFRSSTVP
LSDAEKARMVEGRVSSGVEIREEDIDDILYGGPEDV

>vapB|15789340:c1474604-1474407, length 66, Halobacterium_sp_NRC_1, VapB
MMGSDGTELGMLYNITMDLKSGTLEHLLVEQTEESVAADFPIGDDGRYRVPVSRVQAVKD
YIVVRR

>vapB|15789340:c1510923-1510639, length 105, Halobacterium_sp_NRC_1, VapB
MPPTWESFEMDVDLLERLVGAADGEQIDDISTGEPLMLTVGTATTVGSVTSARDGECEVA
LKRPVCAPAGAKIAINRRVGARWRLIGVGTLTESE

**M.thermoautotrophicum**

>vapB|15678031:202303-202899, length 199, M.thermoautotrophicum, VapB
MYVARSFDINKPGADPEHLAGGVIGGSLVQGRLRVGDEIEIRPGIQVKKDGKQTWMSLHS
TITGLVAGGEEMEEVGPGGLVGVGTLLDPALTKADSLSGSVAGEPGTLPPVRHSFTMETH
LLERVVGTKEETKVEPIKTGEPLMINVGTTTTVGVVKSARADDADVVLKLPACAEEGQRI
ALSRRVGARWRLIGYGIIK

>vapB|15678031:1698784-1698945, length 54, M.thermoautotrophicum, VapB
MRFCGNTFSCQPGYHSAALKTLRMETDIHIFAGIFPGAVQLIAFFLFIISGYIY

**Methanococcus_jannaschii**

>relB|15668172:840765-840947, length 61, Methanococcus_jannaschii, RelB
MSIVQSYITDEKGNIKGVILDYKTFKKIEELLLDYGLLKAMEEVENEEEIDLETAKKLLEQ

>relB|15668172:c1043988-1044146, length 53, Methanococcus_jannaschii, RelB
MRLKKRFKKFFISRKEYEKIEEILDIGLAKAMEETKDDELLTYDEIKELLGDK

>vapB|15668172:1445372-1445695, length 108, Methanococcus_jannaschii, VapB
MVQGPVIIPLISTLGLSFLAILLAYKISFSVIGFINSTLPTTLFPSKPYMLFVKISTISP
LTCPSLIILTPALTWSLTALSMAYLYSSYKPNTFFTLSKNVSSFLTTG

>vapB|15668172:c846334-846143, length 64, Methanococcus_jannaschii, VapB
MISAKSKTKRITITFEIPEDIDAKKFKDDVKRYVRYKLLANKLYELLEGENIEEIEEEIR
KRRE

>vapB|15668172:c1268398-1268213, length 62, Methanococcus_jannaschii, VapB
MNESIMQLLYDLTKMNYSALYGEGRYLRIPAPIHYADKFVKALGKNWKIDEELLKHGFLY
FI

**Methanopyrus_kandleri_AV19**
>vapB|20093440:1478697-1479293, length 199, Methanopyrus_kandleri_AV19, VapB
MYIARSFDVNKPGTRPSDLKGGVIGGAIVQGEVEIGDEIEIRPGIRVERYGRTEWEPVYT
EVVSLHANVTPVERARPGGLVGIGTKLDPTMTKADRLSGQVAGEPDTLPPVRHELLLEVE
LLERVVGTEEERKVEPIRTNEVLMLTVGTATTVGVVTSARDDEIEIKLKQPVCAEEGDRV
AISRRIQRWRLIGHGVIKG

**Methanosarcina_acetivorans**
>relB|20088899:3293160-3293339, lenth 60, Methanosarcina_acetivorans, relB
MTETELLKKISDDLDFLKTKILEIEESLELIDSELHPIREEYKRLDEIKKQRGNYFRKRI

>relE|20088899:3293349-3293555, length 69, Methanosarcina_acetivorans, relE
MRGKALRYSYEISRHLERDLEKIQKKDRERFEILLDKMSEILDNPHRFKPLMHDMEGLMV
NLYLIGIIY

>relB|20088899:1172771-1172992, length 74, Methanosarcina_acetivorans, RelB
MNAIIAIVTIMSETTTIQISKDTRDELKAIGKMGDDYNTVIRKLIHEHNCNKLIEEGDRL
IREHRDEFVSIDEL

>vapB|20088899:1173673-1173882, length 70, Methanosarcina_acetivorans, VapB
MIFMGSTAEIEKRLIELDKEIHSILNMVRKKEGKSSKEIVESACGAWGYDVESEEFVDQL
RKSSRLDWVE

>vapB|20088899:4548892-4549509, length 206, Methanosarcina_acetivorans, VapB
MDKPASMLIARSFDINKPGASIDEIRGGVIGGTLTEGVLHPGDELEIRPGIKVTTEGSTK
WIPIVTTISSIYAGPTKVEEATPGGLLAVGTYLDPTLTKGDSLTGQIAGVPGTLPETRHQ
FVMELHLLDRVVGVTREEKINEIKTSEPLMLNIGTATTVGIVTSARKNEAQVALKRPISA
AVGAMVAISRRIDSRWRLIGVGVIKS

**Methanosarcina_mazei**
>vapB|21226102:726480-727034, length 185, Methanosarcina_mazei, VapB
MEEIRGGVIGGTLTEGVLHPGDELEIRPGIKVTTEGSTRWIPILTTVSSIYAGATKVDEA
TPGGLLAVGTYLDPTLTKGDSLTGQMAGVPGTLPETRHQFVMELHLLDRVVGVTREEKIN
EIKTSEPLMLNIGTATTVGVVTSARKNEAQVALKRPISAAIGAMVAISRRVDSRWRLIGV
GVIKS

**Pyrococcus_furiosus**
>vapB|18976372:765885-766256, length 124, Pyrococcus_furiosus, corrected gi:33359506, vapC
MKRKRLGKVIPYLDPDLEPHAVDMLTIETTNVIGKYMKKYKLITREQAIGLYKQMVKLIR
EEVIMLEPGEKYLQEALKIAMDYDISIYDGLFLAQARNLKAKLITSDKRQGDVAREIGVE
VAYI

>vapB|18976372:1159756-1160004, length 82, Pyrococcus_furiosus, VapB
MFLSVHPNSITLKYDACIQCIMVSIMVKTITISDDVYNELLRIKGNKSFSEVLRELLKER
KGNKEVLKRIFGILSEEEYQEVKKRLKELEGEFEKWEQSLTQM

>relB|18976372:841569-841447, length 41, Pyrococcus_furiosus, RelB
MWLIFAQNYCHNNKSLRKRYIVVNLTFLHVKSHGALQEISC

>vapB|18976372:c1897570-1897358, length 71, Pyrococcus_furiosus, VapB
MIRSLRRLTMNHFELFVDSSVLVGLNLGDEKAKALVKSLIERGLTLVQSFSLKRLIRLCL
PGPSRWIEGCL

>vapB|18976372:768291-768446, length 52, Pyrococcus_furiosus, VapB
MKGDEVVVIEEEGKVEILPRDVDLSKYVDSVEVDVDNFGDYHELRKELREKK

>vapB|18976372:1146253-1146840, length 196, Pyrococcus_furiosus, VapB
MHANEILDGKDLPLLYVAFSPCFRKEAGTAGKDTKGIFRVHQFHKVEQFVYSRPEESWEW
HERLVRNAEELFQELEIPYRVVNICTGDLGYVAAKKYDIEAWMPGQGRFREVVSASNCTD
WQARRLNIRFRDRTDEKPRYVHTLNSTAIATSRAIVAILENHQQEDGTVKIPRALWKYTG
FKEIVPVEKKEGCCKA

>vapB|18976372:c1596552-1596223, length 110, Pyrococcus_furiosus, VapB
MTKGDLMAGNVVGKPGKLPPVWTDLRLEVHLLERVVGTEQELNVEPIKRKEVLLLNVGTA
RTMGLVTALGKDEIELKLQIPVCAEPGERVAISRQIGSRWRLIGYGIIKE

**Pyrococcus_horikoshii**
>relE|14589963:928619-928915, length 99, Pyrococcus_horikoshii, gi:33359355, relE

MSLREEYRRFKTSTGSVKASIAKSILKELIKFSGEEPYWERVEGELKIKEYEAKEVLLFL
ESIGEIKIRRSKNGRRLYVLTLKNLRKNPITLDKWIKVQ

>vapB|14589963:c372554-372781, length 76, Pyrococcus_horikoshii, vapB
MFGVGCLSKVVTIRVPEWVDEEKLREIINMALAEISPRIMSINKLREILGVEEVEEEISD
DVYVREKEKERVKWLY

>vapB|14589963:631040-631294, length 85, Pyrococcus_horikoshii, VapB
MKTIAVDEETWEAIKKLKARLDAKSYDEVLKKLIQAWHTLELETKAESISLDDEEAELVL
SVIKERGRFVQEGNKNDSNASKNLL

>vapB|14589963:c351629-351390, length 20,Pyrococcus_horikoshii, VapB
MVIKVVCMEVISFRIPSELKKEMKKIDINWSEEIRKFIEAKVREYKRKKALEEIDAMLEN
LPRTEKGTARKYVREDRDSN

>vapB|14589963:c452910-452704, length 69, Pyrococcus_horikoshii, VapB
MKTIAVDETTWKKIKMLKDKMEARSYDEVLQKLIETWHLVELDKKVDKVMVNDEEMKILM
SILKKKKGS

>vapB|14589963:c632499-632206, length 98, Pyrococcus_horikoshii, VapB
MEAWMPGQGKFREVVSASNCTDWQARRLNIRFRDRTDEKPRYVHTLNSTAIATSRAIVAI
LENHQEEDGTVRIPKVLWKYTGFKEIVPVEKKERCCAT

>vapB|14589963:c821653-821345, length 103, Pyrococcus_horikoshii, VapB
MAGLGVAVALKMSSMEGFQIIVMMLMLPMMFLSGAFYPVRTMPNWMQWLAKINPLTYAVD
GARYYLAGVTPTFGIMQDWIVLILLALVFAGFAGLEFRKAYLS

>vapB|14589963:c1168172-1168014, length 53, Pyrococcus_horikoshii, VapB
MRVQKTLAPGLIWNIHPLINKPTHITPDFSGLSLPRKPILHHSTPLYNKRRGK

>vapB|14589963:1501435-1501986, length 184, Pyrococcus_horikoshii, VapB
MYPWDIGWSGIFSPMGGEERFVGVEFEYRGKKFTVINPTPYKKGLFPYINGNSEWMKELN
DDLNNLYMGWAAMVNLALWSAWSDKNVLVPQQGTWSDGTHSWEWETRPDGEITFSGVTFR
VINAEWKYSGEPEGIKLSGNGKFAPEIFIPLSVEGWFSSKDPKTGENIEIYGAYELQDIK
LEEI

>vapB|14589963:965798-965962, length 55, Pyrococcus_horikoshii, VapB
MYFVHTCTYEVTSMSKTITIADDVYYELVKMKGKRSFSEVLRELIGKKKEGISTY

**Pyrococcus_abyssi**
>vapB|14518450:c447806-448138, length 111, Pyrococcus_abyssi, VapB
MNLALWSAWSDKNVLVPQHGSWSDGLHSWKWKTNPDGNVELSGMTFRVVNAEWNYSGGPE
NIDLSGKGRFSPKIPIPLYIEGRFYSKDPETGEEVEVYGEYELEDMKLEEI

>vapB|14518450:834293-834433, length 43, Pyrococcus_abyssi, VapB
MVIYLDANVIVGYLIYTDKTEEIKELLEKDEIFVTTINTLFWDEINL

>vapB|14518450:761684-761887, length 68, Pyrococcus_abyssi, VapB
MWLEALFLYGENMEVIKVEIPRELEEDVKRYIKLLKKRREVLKKTFGILKTEKTAKELKV
EIYDELYD

>vapB|14518450:c898293-898093, length 67, Pyrococcus_abyssi, VapB
MKTIAVDEETWEAIKRLKAKLDAKSYTEVLKKLIEVWHSVELEMKAEKVTIEDDKAEMII
SLLENSE

>vapB|14518450:c1009921-1009637, length 95, Pyrococcus_abyssi, VapB
MYQYVHYMQIYGDINMNVEVKRIDSQGRIVLPKEWRKKWGSEVILIELDDRIEILPRKKP
KLSEFFDIIEVEDIGEDIEKDLLKELGEDINEVHR

>vapB|14518450:c1120616-1120338, length 93, Pyrococcus_abyssi, VapB
MVIRMVTTKKVKIVQTEVDLGTYHTLRAIAVHRGVPLKEVIREILRNYAETYKRELIKEI
HEDPIWKGIGLLNTGDPRASEKDDWGVVKWSSE

>vapB|14518450:1136739-1136951, length 71, Pyrococcus_abyssi, VapB
MRKVKNVGKVVITLNVPDGMEDVVKSLLEREARVIMRRLSRADFKSTFGILKGKRKSVDE
IEADIYDEWEV

>vapB|14518450:c1153817-1153542, length 92, Pyrococcus_abyssi, VapB
MASLINFRNLKSHWMIVTFGGHMSKVITIEVPEWVDEERLKTILNKVLMELSPKVMPVDK
LREMLGVVELEEEITDHTYVREKEKERIKWLY

>vapB|14518450:1260427-1260705, length 93, Pyrococcus_abyssi, VapB
MVTSVVSIRLKVGPKGQIVIPKVFREAYGIKEGGEVIIEPTDKGLVIKAPLDVKTLMEKL
KERRKNMKGVGIQAKLGDLKDVDLEDEFNEDIP

>vapB|14518450:1291316-1291903, length 196, Pyrococcus_abyssi, VapB
MHANEILDGKDLPLLYVGISPCFRKEAGTAGKDTKGIFRVHQFHKVEQFVYSRPEESWEW
HERIIRNAEELFQKLEIPYRVVNICTGDLGYVAAKKYDIEAWMPGQGRFREVVSASNCTD
WQARRLNIRFRDRTDEKPRYVHTLNSTAIATSRAIVAILENHQEEDGTVKIPKVLWKYTG
FKEIVPVEKKERCCSS

>vapB|14518450:1501612-1501827, length 72, Pyrococcus_abyssi, VapB
MKTIAVDESTWKKIKMLKDKLEAKSYDEVLQKLIETWHLVELDKKVDKVVVKEEEAETLL
SVLNKIKKKGES

>vapB|14518450:c1699062-1698781, length 94, Pyrococcus_abyssi, VapB
MILLVSIRLKVGPKGQIVIPKVFREAYGIKEGGEVVLEPTDKGLIIRAPIRVDDLIKKIR
EERKKMNPKRRPKPGELRGISLEDEYEEEWRSEE

**Thermoplasma_acidophilum**
>relE|16081186:237926-238222, length 99, Thermoplasma_acidophilum, Solitary RelE
MEDNAFKEKWTVFMNYIVESTETFEREFFKNHKDKKEWLQHMIERLEQEPQSGKPLRGKL
HGLWQLRIGPFRVWYEINERERKVILRAILHKDEAKKYY

>vapB|16081186:38670-38828, length 54, Thermoplasma_acidophilum, VapB
MTHVHFAGYRRWWGIYGKDLIAICWFEPVNILLVPVPDPLFFHLIYVYIHSDL

>vapB|16081186:804192-804743, length 184, Thermoplasma_acidophilum, VapB
MSGYIARNTDIDIVLSSDYLREFLRPFAPQESHLETSVYDAWKFYGDMSDDNIIRGYLDQ
ARPIMGGINRVIARALANGEDLIIESLYFVPDMMDEMVLKNAFLAYVYIDDPDLHRSRLE
DRINYTHRNSPGSRLAAHLKEYRTIMDYSMDMARGRGIGLYSTDDYALARQRLLDDFRKF
VDRR

**Thermoplasma_volcanium**
>vapB|13540831:c886266-885913, length 118, Thermoplasma_volcanium, VapB
MDRILIRAIENGENLILETLYFLPEMLSEKARNNVHMFYLYIGDEKLHRDRLVDRINYTH
KNSPGTRLAEHLYEYRNIMEYSMMRSSEYNVKIIDTSNYEEARRTILEMIVKGESRYA

**Gram-positive Bacteria:**

**Bifidobacterium_longum**
>relB|23464628:1638836-1638570, length 83, Bifidobacterium_longum, RelB
MPRMQTRSDGREGRGAAPVQVRQSHQRAGAARAEPRQGRGNTPDQDTGRHEPMAQGKLRV
RGQPQADQQLAQPGQTPQLETRR

>relE|23464628:1638535-1638230, length 102, Bifidobacterium_longum, RelE
MEIKQSAEYRKWFKKLRDHKAKAAIQARLDACKLAGRPFGDIKPVGGPVSEMRFHTGAGY
RVYFAMQGNVLMLLLAGGDKSTQQTDIRQAHDILNDYKEQRQ

>relB|23464628:1284380-1284766, length 129, Bifidobacterium_longum, relB
MRIRQAIWSLRERPALSLPPSSSPAMSIRPRSRAVASSSSSSMGAKEPSSTWRWSVSSAS
SMRCSSSAVRSPARPRARAWAREPAMSSSAKRQSNCVDLDSRANSGDGPDVKRPPHRARC
SLFSVMKAP

>relE|23464628:1284736-1284981, length 82, Bifidobacterium_longum, relE
MFVVLSHEGSLKPWIANKSDCLSDYQRWATYRWIQVVRIPWRQCQGYWSRRIDEKNRIVY
RITGNDVQNLEIAVCRTHYGEH

>vapB|23464628:391589-391864, length 92, Bifidobacterium_longum, VapB
MIRRLREDPVQAQKADAHDAYPPFFMRAYLITRTASKTTAPHASIMTATRRCIMATLTIR
KIPDEQIQQLKEVAEKNNRSMESQVRSILEEWLAGTVAHEITRKTNFYDEIREFMKNMDF
EGLDKGELPLSERNSADSRPPVSFE

>vapB|23464628:c1248957-1249274, length 106, Bifidobacterium_longum, vapB, a relB/dinJ homolog
MTMAMVTARVNAERKRDAEKVLKRNGRTYSDLIRDLTDYLADTGELPEFERLTLSLIQER
ERRKKQELIQRFADRNLPEAEGDLSDEEILAQARMERFGGRDETAV

>vapC|23464628:c1248539-1248970, length 144, Bifidobacterium_longum, vapC
MKLLFDTNILLDLCNDKRAPFHKQCVDLLMEAVAQPNIEIMAPVSSLNDVYCVLRKHYGE
ERAARDDIGGLMELFDIRPLMERHACMSYRSDEPDFEDGLIRAVAEDNDADVIVTRDVEA
FHHSSVRSMDAEQCRALLLADSKA

**C._glutamicum_ATCC_13032**
>higB|23308765:1085499-1085777, length 93, C._glutamicum_ATCC_13032, upstream HigB toxin
MIRSFADRDTELVWLREGAKRVDPRIHKVANRKLHLLDAATTLDALRVTPGNRLETLEGD
RVGQYSIRVNDQWRICFRWNDSGPENVEIVDYH

>higA|23308765:1085714-1086001, length 96, C._glutamicum_ATCC_13032, downstream antitoxin HigA
MADLLPLERLGPRKRRDRGLSLRRRRWLRSSTRRFTLVRFSWRTSSRASASHRTRSPYRS
GCLRDASTRSCTASDPSRPIRLCVSGGTSVSTRSSG

**M._tuberculosis_H37Rv**
>parD|15607142:c2402508-2402720, length 71, M._tuberculosis_H37Rv, ParD
MVVNRALLASVDALSRDEQIELVEHINGNLAEGMHISEANQALIEARANDTDDAHWSTID
DFDKRIRARLG

>mazE|15607142:c547345-547515, length 57, Mycobacterium_tuberculosis_H37Rv, mazE
MTTYYYVLLSVTTWVGLRHEAKRELVYRGRRSIGRMPREWACRRSRRFAANGVDAAR

>mazF|15607142:c547077-547355, length 93, Mycobacterium_tuberculosis_H37Rv, mazF
MLRGEIWQVDLDPARGSAANMRRPAVIVSNDRANAAAIRLDRGVVPVVPVTSNTEKVPIP
GVVAGSERWPGRRFEGAGPAGWIRRCATSPLPS

>mazF|15607142:2320829-2321059, length 77, Mycobacterium_tuberculosis_H37Rv, mazE
MSTSTTIRVSTQTRDRLAAQARERGISMSALLTELAAQAERQAIFRAEREASHAETTTQA
VRDEDREWEGTVGDGLG

>mazF|15607142:2321055-2321462, length 136, Mycobacterium_tuberculosis_H37Rv, mazF
MAEPRRGDLWLVSLGAARAGEPGKHRPAVVVSVDELLTGIDDELVVVVPVSSSRSRTPLR
PPVAPSEGVAADSVAVCRGVRAVARARLVERLGALKPATMRAIENALTLILGLPTGPERG
EAATHSPVRWTGGRDP

>mazE|15607142:3110734-3110507, length 76, M._tuberculosis_H37Rv, MazE
MKLSVSLSDDDVAILDAYVKRAGLPSRSAGLQHAIRVLRYPTLEDDYANAWQEWSAAGDT
DAWEQTVGDGVGDAPR

>mazE|15607142:2234919-2234644, length 92, M._tuberculosis_H37Rv, MazE
MEVIPGYTICMKTAISLPDETFDRVSRRASELGMSRSEFFTKAAQRYLHELDAQLLTGQI
DRALESIHGTDEAEALAVANAYRVLETMDDEW

>mazE|15607142:2547085-2546840, length 82, M._tuberculosis_H37Rv, MazE
MAEPETLPGRWLPECACLAETVSWEQSRLWSRLLCRPHFRHALPGLTGGSASRPSARSAR
LVRQPRMTLFSLDHRDGVDARC

>mazE|15607142:c1231289-1231056, length 77, M._tuberculosis_H37Rv, MazE (gi|put_here corrected start)
MYLPWGVVLAGGANGFGAGAYQTGTICE VSTQIAVRLPDEIVAFIDDEVRGQHARSRAAVVLRALERERRRRLAERDAEI
LATNTSATGDLDTLAGHCARTALDID

>mazE|15607142:c2195345-2195109, length 78, M._tuberculosis_H37Rv, mazE (gi|put_here corrected start)
MKTARLQVTLRCAVDLINSSSDQCFARIEHVASDQADPRPGVWHSSG MNRIRLSTTVDAALLTSARDMRAGITDAALIDE
ALAALLARHRSAEVDASYAAYDKHPVDEPDEWGDLASWRRAAGDS

>higB|15607142:2201741-2202091, corrected start, length 117, M._tuberculosis_H37Rv, HigB
MGTWKFFRASVDGRPVFKKEFDKLPDQARAALIVLMQRYLVGDLAAGSIKPIRGDILELR
WHEANNHFRVLFFRWGQHPVALTAFYKNQQKTPKTKIETALDRQKIWKRAFGDTPPI

>vapB|15607142:71575-71823, length 83, M._tuberculosis_H37Rv, VapB
MNSAMATIQVRDLPEDVAETYRRRATAAGQSLQTYMRTKLIEGVRGRDKAEAIEILEQAL
ASTASPGISRETIEASRRELRGG

>vapB|15607142:1073325-1073543, length 73, M._tuberculosis_H37Rv, VapB
MKTLYLRNVPDDVVERLERLAELAKTSVSAVAVRELTEASRRADNPALLGDLPDIGIDTT
ELIGGIDAERAGR

>vapB|15607142:3174744-3174989, length 82, M._tuberculosis_H37Rv, VapB
MLSDEEREAFRQQAAAQQMSLSNWLRQAGLRQLEAQRQRPLRTAQELREFFASRPDETGA
EPDWQAHLQVMAESRRRGLPAP

>vapB|15607142:c2506381-2506208, length 59, M._tuberculosis_H37Rv, VapB
MALWYQAMIAKFGEQVVDAKVWAPAKRVGVHEAKTRLSELLRLVYGGQRLRLPAAASR

>vapC|15607142:c2506381-2506208, length 139, M._tuberculosis_H37Rv, VapC
MT MACTACPTIWTLRCQTTCSNAFTGEALPHRHPRLAADAVNETRAIVQDVRNSILLSAA
SAWEIAINYRLGKLPPPEPSASYVPDRMRRCGTSPLSVDHAHTAHRRASGSPSTSIRPCA
HRPGTAAWPDDHHRRRPVSCL

**M._tuberculosis_CDC1551**

>relB|15839372:c1388510-1388731, length 86, M._tuberculosis_CDC1551, RelB
MPTTWRSPRQRHATCNAYPKRSPPHVSSLFSDRCLTTRIGWASRCAMTLKASTQPAAVIT
ASSTPSTTATTESRSSTSLVAVPATE

>relB|15839372:3171692-3171970, length 93, M._tuberculosis_CDC1551, RelB
MRILPISTIKGKLNEFVDAVSSTQDQITITKNGAPAAVLVGADEWESLQETLYWLAQPGI
RESIAEADADIASGRTYGEDEIRAEFGVPRRPH

>relE|15839372:3171947-3172237, length 87, M._tuberculosis_CDC1551, RelE
MRRPATPPLSGALHRAVHHNRASRPPQAATANPRGSGRIRVRRSVARAPAGGQAPSARVG
RHVQRASRNVPPAVPD

>mazE|15839372:c2544045-2544290, length 82, M._tuberculosis_CDC1551, MazE
MAEPETLPGRWLPECACLAETVSWEQSRLWSRLLCRPHFRHALPGLTGGSASRPSARSAR
LVRQPRMTLFSLDHRDGVDARC

>vapB|15839372:719471-719728, length 86, M._tuberculosis_CDC1551, VapB
MVGMSEVASRELRNDTAGVLRRVRAGEDVTITVSGRPVAVLTPVRPRRRRWLSKTEFLSR
LRGAQADPGLRNDLAVLAGDTTEDLGPIR

>mazE|15839372:3105455-3105228, length 76, M._tuberculosis_CDC1551, MazE
MKLSVSLSDDDVAILDAYVKRAGLPSRSAGLQHAIRVLRYPTLEDDYANAWQEWSAAGDT
DAWEQTVGDGVGDAPR

>vapB|15839372:363648-364106, length 141, M._tuberculosis_CDC1551, VapB
MPIHSGPGPRGSLGDGGGGRATQRHAAAGTRAVASCCRARCATRQRGRGRPTRGCLGRDS
SALLALSPAKIPDIARYHRKMSDVLIRDIPDDVLASLDAIAARLGLSRTEYIRRRLAQDA
QTARVTVTAADLRRLRGAVAGLGDPELMRQAWR

>mazE|15839372:c2192678-2192442, length 78, corrected start, M._tuberculosis_CDC1551, MazE
MKTARLQVTLRCAVDLINSSSDQCFARIEHVASDQADPRPGVWHSSG MNRIRLSTTVDAALLTSARDMRAGITDAALIDE
ALAALLARHRSAEVDASYAAYDKHPVDEPDEWGDLASWRRAAGDS

>vapB|15839372:71570-71806, length 79, M._tuberculosis_CDC1551, VapB

MATIQVRDLPEDVAETYRRRATAAGQSLQTYMRTKLIEGVRGRDKAEAIEILEQALASTA
SPGISRETIEASRRELRGG

>vapB|15839372:c2503593-2503357, length 79, M._tuberculosis_CDC1551, VapB
MGACEAGRRSRGEDTPVRAAAARLRRAEVEIARRGEPVAKLVPLHPHETRRLGIDHGVYR
VPDDLDAPLSDDVLERFHR

>vapB|15839372:c2866266-2866541, length 92, M._tuberculosis_CDC1551, VapB
MRFSATDVYSIMLVAYICHVKRLQIYIDEDVDRALAVEARRRRTSKAALIREYVAEHLRQ
PGPDPVDAFVGSFVGEADLSASVDDVVYGKHE

>vapC|15839372:c2865871-2866266, length 132, M._tuberculosis_CDC1551, VapC
MIFVDTSFWAALGNAGDARHGTAKRLWASKPPVVMTSNHVLGETWTLLNRRCGHRAAVAA
AAIRLSTVVRVEHVTADLEEQAWEWLVRHDEREYSFVDATSFAVMRKKGIQNAYAFDGDF
SAAGFVEVRPE

>vapB|15839372:c3131225-3131449, length 79, M._tuberculosis_CDC1551, VapB
MTRKMTATEVKAKILSLLDEVAQGEEIEITKHGRTVARLVAATGPHALKGRFSGVAMAAV
DDDELFTTGVSWNVS

>vapC|15839372:c3130833-3131225, length 131, M._tuberculosis_CDC1551, VapC
MTTVLLDSHVAYWWSAEPQRLSMAASQAIEHADELAVAAISWFELAWLAEQERIQL
AIPVLSWLQQLAEHVRTVGITPSVAATAVALPSSFPGDPADRLIYATAIEHGWRLVTKDR
RLRSHRHPRPVTVW

>higB|15839372:2199074-2199424, length 117, corrected start, M._tuberculosis_CDC1551, HigB
MGTWKFFRASVDGRPVFKKEFDKLPDQARAALIVLMQRYLVGDLAAGSIKPIRGDILELR
WHEANNHFRVLFFRWGQHPVALTAFYKNQQKTPKTKIETALDRQKIWKRAFGDTPPI

**Chlorobium_tepidum_TLS**
>mazE|21672841:947841-948164, length 108, Chlorobium_tepidum_TLS, MazE
MLLEGSIGLLPDALLNNEEPEQNTGYNSSARCIVNREDQAGITRKETIGASVWFGLVCVT
DESVAYRYDGLAARSLRLWTTPSLKKQQIAKAGTHEKGIGGHDCLAGQ

**Nostoc_sp_PCC_7120**
>relB|17227497:c181989-181630, length 119, corrected start, Nostoc_sp_PCC_7120, RelB
MLSNTYTYTQARDRLSELCDKVTSERDFVVITRRNAENVALIPVDELSSLLETAHLLRSPRNAERLLRAL
DRAKSGVVESQSLDDIRKELGFDQKEESQKPIKRRSSSNSKAKKNSVST

>vapB|17227497:c3788612-3788415, length 66, Nostoc_sp_PCC_7120, VapB
MRDRFNLPQILIIKPYVKLVMLLIDTSVWISVFRNRSGQVRQQLETLVANRQNSLGSPSL
NCCKVV

>vapB|17227497:5499145-5499573, length 143, Nostoc_sp_PCC_7120, VapC (start corrected)
MSIKYLLDTNIISEATRQSPNVNVVKKLTQHQLETATGSVVMHELLFGCLRLVESQKRRL
LLEYINQIPLKMTILNYDLKAAQWHAQERARLSKMGKTPAFIDGQIASIAYSNNLILVTN
NVSDFESFNDLAVENWFVNSGEG

**Synechocystis_PCC6803**
>relE|16329170:1620536-1620793, length 86, Synechocystis_PCC6803, relE/yoeB
MKEVVLDSQAIEDIKWWIQQDKKLALKIMELIETLPKSPFAGKGKPEKLRFNLSGFWPRR
ITQEHRLVYEVTDDFIRVVSCRYHYR

>relE|16329170:2074933-2075211, length 93, Synechocystis_PCC6803, relE/yoeB
MTRFIGTVKIAFTELSWHDYLWFQQNDKKLLKRINLLIKAIARDPFDGIGKPEPLKANLS
GYWSRRINSEHRLVYTIADRDLLIISCRFHYQR

>vapB|16329170:c2516782-2516531, length 74, Synechocystis_PCC6803, VapB
MDTKSKLRSNPMTDTALLEKINALPDAMKIEVEHFVEFLLTKQPPVSPVTNDGQKKYRQA
GVLKGKIWMADDFDAPLEEMQEYM

>vapB|16329170:c3044422-3044670, length 83, Synechocystis_PCC6803, vapB
MEQNRMKQITPTELRGNLYNLLDEVLATGIPLEINRGGKRLRILPVEEPDKFKNLVHRPG
VIIGDPEELVTIDWEGEIELDLP

>vapC|16329170:c3044058-3044501, length 148, Synechocystis_PCC6803, vapB
MVQGLSLATRKSWSPLIGRERLSSIYLDTHIVVWLYCGLTEKFSSLAKSLINSNDLTFSP
IVRLELKYLLEIERITASPEAILTTLENNIGLCSCTKNFDQVVYQALTLDWTRDPFDRLI
TAQSALTDSLLLTKDQKILAHYDYARWS

>higA|16329170:c474208-474432, length 75, Synechocystis_PCC6803, HigA
MNTAQISTDGTHQIVILPENFTIAGSEVYIKKIGSTIILIAKNNPWQSLIESLDQFSDDF
MKTREQPPLDIREEF

>higB|16329170:c474514-474792, length 92, Synechocystis_PCC6803, HigB
MKIAWSPKSLRSFKRLIPKNPNLRPMIEQILHQLATDPFHPSLRTHKLKGELANVWSCSID
YNYRLLFEFVNNPEDKEEAILLLNLGSHDEVY

**Clostridium_tetani_E88**
>phd|28209834:2057179-2057481, length 101, Clostridium_tetani_E88, Phd
MILGLIYPKIVYNITIEEVLFMQVNINNLVSISEANQNFSRVARMVDENGAAIILKNNAP
RYVLIDYSKFQQDTIADDATVEEAANNILNKHLKAFEELAK

>mazE|28209834:c2670080-2670397, length 116, Clostridium_tetani_E88, MazE

MAGSKRVGVSLSETLNNEFNKALKEDSKKRSEFIRELIILYIEDKKKLREIEQMKKGYLE
MGKLNLEIAEVGFASDINSLKEYEAKLSESDWSDDNDSEKRRYILC

>mazF|28209834:c2669764-2670117, length 118, Clostridium_tetani_E88, MazF
MTTIVKRGDI YYASLSPVVG SEQGGIRPVI IIQNDVGNRY SPTVIVAAITSQ INKAKLPTHV
EISSEEYGLN KDSVVLLEQI RTLDKRRLKE KIGRMTNGDM RKVDDALLVSIG LKEK

**T._tengcongensis**
>relB|20806542:867887-868186, length 99, corrected start, T._tengcongensis, relB
MISVSDLGRGKASKIIEKVAKKKEHYIVVKNNKPQAVIIPIEEYDELIEAQEDLELLQLAIERTKNLKEG
ETLPFEEILKEDGLTKEELKKYIDIVEIE

**Streptococcus_mutans_UA159**
>relE|24378532:44407-44676, length 90, Streptococcus_mutans_UA159, relE, gi corrected:24378568
MLYTIVILAIGILKLFFFINLLKSPLQAGFSFWFEKLMVLTIQDSKALIGNIKDFWHYRV
GHYRIICRIEDEGLIIVAINGGHRKDVYKK

**Streptococcus_pyogenes**
>parD|15674250:448399-448676, length 95, corrected start, parD [Streptococcus pyotoxin or antitoxins]
MAKTGTLNLRVDDSVKSAADDILKRLGIPMSTAIDMFLNQIILTGGIPFDVSLPEAPQRVNVDYMSQEKF
YDKLITSFEDAKTCNPQDVGKFYFQ

**Others:**

**Aquifex_aeolicus**
>vapB|15282445:203338-203605, length 91, Aquifex_aeolicus, VapB
MICMVGKDEIVVKVLPKGQITLPKRIREKLGIREGDILIVEEKEGKLEIRKPKSLRDFYG
FLKGKKSINRENIERVIEEVVKERELEKDSR

>vapC|15282445:203579-203860, length 94, Aquifex_aeolicus, VapC
MNLKKIVVDTSVFIRLFTRNDEKKFEKAEKLIDDASKGKIQLFVPFIVVAEIVWVLEKVY
KVNRENIRDVVEALINTRPRSNYSIGKLYSFFYV

>vapB|15282445:1338522-1338839, length 166, Aquifex_aeolicus, VapB
MNKRFEQVDKRFEQVDKRFEQINNELNRLIQIMVGIFAGQIALVAAVIGFAWWDRRTIIR
KSKEETFEEMEKELRPEKFKKLLNALREKAKTDKELEAILKKYGLL

**Bacteroides_theta_VPI_5482**
>higB|29345410:5572334-5572546, length 71, Bacteroides_thetaiotaomicron_VPI_5482, higB
MLAGGCGGWLKGLKRLKIKKHSMNIYGAFFIFDEGNIVMLFNGFQKKTQKTPESEIEKAV
KLKNEYYASKP

**Gram-negative bacteria:**

**Caulobacter_crescentus**
>relB|16124256:3102767-3103121, length 96, corrected start, Caulobacter_crescentus, RelB
MALTITIPAELASRLRASAEAEGKDVDAYAIDALHVMSDEDWGYTDDDAYWRELRAHSDEVRRDGGIPL
EDVKRWVASWDTENELPPPEPRIKARG

>relB|16124256:3371212-3371388, length 59, Caulobacter_crescentus, RelB
MAEPDPDIFDEDDEAILAADAEADADFEAGRTVPHERVGEWLKTLGTPHQTPPPYSWRK

>parE|16124256:1186395-1186610, length 72, Caulobacter_crescentus, parE
MRVTWTDSASRDLRFAYAWIAQDRPTAALKQVRRIWEFAAKLSDFPNLGRPGRRPGTRNW
SCRAAPSLSLTE

>parD|16124256:c2971506-2971288, length 73, Caulobacter_crescentus, ParD
MMNKPAKPAADDVDDLFGRPLTPAEEDTWFEHNREAIGQLVDEAWAEFERGEYDERSFAE
IIAQGVAEHNAKR

>phd|16124256:3613915-3613552, length 121, Caulobacter_crescentus, Phd
MAFEEGFEFLVGDVGIDGHDAGMRERALAVKGAVRYNVCSNVWSAAMIALKLSQIGNSVG
VVLPKEALVKLGVEKGDTLYLTDAPGGGMQIAPYDPDVARQIALGEEIMDEYRDTFRALAK

**A._tumefaciens_Cereon_C58_circ_chr**
>relB|15887359:c831117-830842, length 91, corrected start, A._tumefaciens_Cereon_C58_circ_chr, RelB
MKTATIPSLRVTADFREAAESVLKDGETLSAFMEEAVRKQVEIRKSQAEFIKQGLAAREESKRTGVYHKA
EDVLAELKAMLDEKLAEDNDK

>relB|15887359:c1769363-1769118, length 81, corrected start, A._tumefaciens_Cereon_C58_circ_chr, RelB
MTAFTVRLPDEVAEKLDQLAEKLDRSRSYMAVQAIEDFVAREEWQLAEIEAGLAEADRGEFGTPEDLAN
IVGRYVKTARPL

>relB|15887359:c1979782-1979531, length 83, corrected start, A._tumefaciens_Cereon_C58_circ_chr, RelB
MANVRFTEFRQNFATHFDRVLETRAPLLVTRQGKEAVVVLAEGEYESMQETLHLLSNPANASRLRASMGE
LERGDTIERDPTEE

>mazE|15887359:928764-929030, length 88, corrected start,  A._tumefaciens_Cereon_C58_circ_chr, MazE
MKMCYICCTMQERRRMTVTTKIRRQGGAAVMTIPPALLKMLGLEIGEQLTLEVDNGALVASPVRLEKKRFTLAELLDGAE
EVAALNARERAWDTAPPVGKEAL

>parE|15887359:c1070511-1070861, length 117, A.tumefaciens_str_C58_Cereon_circ_chr, parE
MSNAFPPSKKRGPIIKIRTPIWTTRARRDLAEDHAYIETENPVAADRLVLDIYNKIESIA
AIGLTGVSRHGYGTGLRSIAYRDRVIFFRVNNGELTVMRVLHGHQDISADDFKQEEN

>parD|15887359:1304512-1304808, length 98, corrected start, A._tumefaciens_Cereon_C58_circ_chr, ParD
MPTRNVVLTQHHEEIIDDLVKSGRYQNASEVLREGLRLIERRERLEATRLETLKVAAQQGFCDLDQGRYI
DVSDDALDDFISAFGREAEVRLTKSDDK

>vapC|15887359:c1001393-1001007, length 129, corrected start, A._tumefaciens_Cereon_C58_circ_chr, VapC
MIVVDTSVWIDWFQNKQTPQVATLSDINDLSDVIIGDIILLEILQGERNERRAAAIESRL
KVFELVSMLTPEFAVAAAANYRKLRGLGKTVRKTADLIIGTYCIEHGHKLLQNDRDFQPM
ADHLGLQFV

**A._tumef._C58_Washn_cir_chr**
>relE|17933925:c809884-809573, length 104, A._tumef._C58_Washn_cir_chr, RelE (starts at ATG or GTG codon)
M VTTKLVWTPRARSDVKKIYVDIGKSQPLAAERYFARFRAKAESLIDHPHLGERHPEIFP
SARMLVEAPYVILYETVPDTDDDEIRCVEIVRVNDGRRDLRTLF

>parD|17933925:c830914-831318, length 135, A.tumefaciens__str_C58_U_Wash_circ_chr, parD
MIWCSADVKPVYLPQGPRLQGFAFDLSLPMTDLMHRNCNAGRRSMKTATIPSLRVTADFR
EAAESVLKDGETLSAFMEEAVRKQVEIRKSQAEFIKQGLAAREESKRTGVYHKAEDVLAE
LKAMLDEKLAEDNDK

>parE|17933925:c830618-830914, length 99, A.tumefaciens__str_C58_U_Wash_circ_chr, parE
MTFQVFLADRARDNITRLYAHLLRQDKYAAKRAYRAIEKGIAALADFPLSCRKVDAENPF
LREFLIPFGSSGYVVLFEIESAEKVTILAIRHQREDDYH

>parD|17933925:1304610-1304918, length 103, A.tumefaciens__str_C58_U_Wash_circ_chr, parD
MVEAPMPTRNVVLTQHHEEIIDDLVKSGRYQNASEVLREGLRLIERRERLEATRLETLKV
AAQQGFCDLDQGRYIDVSDDALDDFISAFGREAEVRLTKSDDK

>parE|17933925:1304918-1305289, length 124, A.tumefaciens__str_C58_U_Wash_circ_chr, parE
MTTYRLSDAAQSDIIEILGWTHATFGAAARKRYEKLLATALRDVAVDPLRAGTNIRAELG
EDVRSYHLRYSRERAKSETGLVKNPRHLLLYRALRPGLVGVGRVLHDSMEIERHLPDDYG
DITF

>vapC|17933925:c2105391-2105804, length 138, A.tumefaciens__str_C58_U_Wash_circ_chr, vapC
MSDGFLLDTCAVIWMSQGEPVSDEAVSALNQSYRAGDPVCVSAVTAWEMGMLVAKGRISE
TKSPQRWYDDFKREAEVIEQPVTADIFIASCFLPQLVHKDPIDRILITTAREHDLTIITR
DRVILAYGEAGHVKTLAC

**Bradyrhizobium_japonicum**
>higB|27375111:1797159-1797353, length 65, Bradyrhizobium_japonicum, HigB
MLTAARLIRAPSLMKFYSTSGSLRPRLQKRWDSRQHLHDILAEKKPVSPNVAARIGKPVG
NGPAI

>higA|27375111:1796750-1797079, length 110, Bradyrhizobium_japonicum, HigA
MTTTRIGRSQRLAISCDLRQYGRATSGEPAASTRECTSASRSHPDCRAIGVRLDTLNEAV
NSSELKLTGNDFHKLAGKSVRYTIHINGPWCITFEFEGGDAFKVDFEQYH

>higB|27375111:2290771-2291367, length 124, Bradyrhizobium_japonicum, corrected start HigB
MDRIGEVVDGQWRKFAIYRPVRKPLQNYSSSAIREGR MTTQKPVVWIGSSKDDLRAFPDEVRRVMGFAINDAQNGDEHPR
AKALKGFGGRSVLEVIDDEDGDTFRAVYTVRFAGVIYVLHAFQKKSKKGIETPKHDILVIQARLKAAEAHYQENYGKGGK
K

>higA|27375111:5539812-5540207, length 132, Bradyrhizobium_japonicum, HigA
MTTQKPVVWIGSSKDDLRAFPDEVRRVMGFAINDAQNGDEHPRAKALKGFGGRSVLEVID
DEDGDTFRAVYTVRFAGVIYVLHAFQKKSKKGIETPKHDILVIQARLKAAEAHYQENYGK
GGKK

**Brucella_melitensis_chr_II**
>mazE|17988344:197880-198089, length 70, Brucella_melitensis_chr_II, MazE
MEAETIPREGRRTSRSFARLRFALDPDLGAGRAFSSFRDEAHRQSLTVASRSHAADDLAF
INSVSDWSDE

**Brucella_suis_chromosome_II**
>mazE|23499767:1101529-1101320, length 70, Brucella_suis_chromosome_II, MazE
MEAETIPREGRRTSRSFARLRFALDPDLGAGRAFSSFRDEAHRQSLTVASRSHAADDLAF
INSVSDWSDE

**Mesorhizobium_loti**
>higB|13470324:4800860-4801012, length 55, Mesorhizobium_loti, higB
MTGEMTSGNVFADLGFDNSEEELSKAKLAVRSAPSLCVGASLKRNRLNCLL

>higA|13470324:4800572-4800853, length 94, Mesorhizobium_loti, higA
MSASSWVLQSTMPKMASSILGVKALKRFGGRILAVVDDLDRILIARPCRRFAGVICIFAS
RRRAGTRPSAKSISLQRLKVAGTHDRENYGKGHD

>relB|13470324:250975-251220, length 81, Mesorhizobium_loti, RelB
MAMTAFTVRLSDDTTDRLDQLAEKLDRSRSYVAAQAIEDFVTRQEWQLAEIEAGLAEAER
GEFANEQELAAVIAKYIKPAG

>relE|13470324:251223-251513, length 97, Mesorhizobium_loti, RelE
MSHKTIRWTKRALRRLDEIGAHIEKDSPEAASRVIARILSAAELLTQQPAMGRVGRIKAT
RELVLVDIPYIVPYRVSGNTVEILTVIHAAQQWPRTL

>parD|13470324:1972578-1972823, length 82, Mesorhizobium_loti, parD
MMAMTAFTVRLSDDTTDRLDQLAEKLDRSRSYVAAQAIEDFVTRQEWQLAEIEAGLAEAE
RGEFANEQELAAVIAKYIKPAG

>parE|13470324:1972805-1973119, length 113, Mesorhizobium_loti, parE
MYQARRLIVSHKTIRWTKRALRRLDEIGAHIEKDSPEAASRVIARILSAAELLTQQPAMG
RVGRIKATRELVLVDIPYIVPYRVSGNTVEILTVIHAAQQWPRTL

**S._meliloti_1021_chr**
>relB|15963753:c1588987-1588739, length 83, S._meliloti_1021_chr, RelB
MRHPRNGLRPPGRQPRDLHGPGPDRRTELAGRVLRQSSARADQAVPQPDPALIRNNSKRR
RPAFMAGRFVLYSKPKPRRNSPF

**Neisseria_meningitidis_MC58**
>phd|15675948:c929630-929475, length 52, Neisseria_meningitidis_MC58, Phd
MPANRQGAAMQNQNTRPVKIELKGEAGKRVLLAAARRIAKTHQKAVKALADK

**Nitrosomonas_europaea**
>higB|30248031:c1156617-1156871, length 85, Nitrosomonas_europaea, higB, also hits into relE
MNRIIWKTKAIKQVLKLPRQTAQVIRDTVEEKLSVFPDCNSIKKLTNHRYPYRLRAGDYR
VFFDFDGEIHIINIQEVKKRDETTY

>higA|30248031:c1156304-1156630, length 109, Nitrosomonas_europaea, higA
MRPLTNYQTINDVDGRPAFVVIPYADFVHSQVYVPKDGAPHAVVSKAINGMSMLQAWREY
LMLTQEEMAKRMEITQAGYAQIEAAKRPRKATLEKAAAAMGITLEQLAY

>relB|30248031:1479043-1478798, length 82, Nitrosomonas_europaea, RelB
MYMAILNATEARARLYALIDEAAETHQPIVIKGKRSSAVLLSEEDWNAINETLYLVSIPG
MRESIMEGMKTDVDECSRELDW

>parD|30248031:1479335-1479618, length 88, Nitrosomonas_europaea, parD
MKSSTIPSLRVTPEFRRDAESVLREGESLSAFVEESLRQHIERRRTQQEFIARGLTAREA
AKSSGQYASKAEVMSSLHSILDEQRSKE

>mazE|30248031:c1427432-1427208, length 74, corrected start, Nitrosomonas_europaea, MazE
MNSHRGQMMSKDATALLHVTCVFRHNVACNASGGLHMGTTHVNARVKKHRDTLRMAGLRPVQIWVPDTRRPDFAEECRRQ
CLLIAQADKADTSMQQFMDEALADSDGWTE

>mazE|30248031:1002936-1002703, length 78, Nitrosomonas_europaea, MazE
MKMTIIAKVTSKGQTTIPADIRAALRIKPGDLIIWEMSDDGSARIRRVQPLDIEYLKAVE
GTLSEWAGAADEEAYREL

>parD|30248031:1655892-1656143, length 83, corrected start, Nitrosomonas_europaea, ParD
MATVRKTISLTNQQDAWITAQVEAGRFTNDSELIRDLIRREQERMAEIDNIRAALIDGEQSGEPQPFDFD
QFKRHKLAQHKPG

>phd|30248031:1386749-1386501, length 83, Nitrosomonas_europaea, Phd
MVITLGYEMIELKVRKFGNSLGIVLPKEVVNHLRTGDGQRLFLTEASDGRYLITPYDPSF
GEKMAKVEDICNRYRNTLHVLTK

>phd|30248031:2674530-2674754, length 75, Nitrosomonas_europaea, Phd
MVELKVRKLGNSLGVVLPKEVINHLRTGDGQRLFLTEASDGGYLITPYDPAFEEKMVKVE
NICDRYRNTLRILAK

>vapB|30248031:1155550-1155774, length 75, Nitrosomonas_europaea, VapB
MGHRRCGSGVPPLARTGTACGLHLMLLLDTNVISELLKVRAGKADPHVTTWGRTVPGASL
YVSVITVQELEIGTL

>vapB|30248031:2296994-2297218, length 75, Nitrosomonas_europaea, VapB
MKNIPDDVYERLKAAAEIHRRSLNSEIIVCLETVLMPTRISPSERLERARQLRAGLNPKK
FQACDIAIMKRQGRP

>vapB|30248031:c316448-316260, length 63, Nitrosomonas_europaea, VapB
MASTFRLSSLCCIARRTAAVVRALPCNICPIIPPVSVANHTIHHHNAGPNNYLLIRRAWN
SER

**Helicobacter_pylori_26695**
>relB|15644634:c946969-946688, length 93, corrected start, Helicobacter_pylori_26695, RelB
MQNDRISFKEKMAKELEKRDQNFKDKIDALNELLQKISQAFDDKRDCCLGHEIPNIETQQAMRDVGNKET
DLIVEDFSSYSNERKRALGVEAQS

>relE|15644634:1067530-1067742, length 71, Helicobacter_pylori_26695, relE
MTESDVTSIVDCLKKQKPLQQKYCDHALSGNLKGLRECHVKPNLLLIYEIKKQENELVLL
RLDTHSELFKK

**Escherichia_coli_K12**
>yoeB|16127994:c2087233-2087487, length 84, Escherichia_coli_K12, RelE/YoeB, new gi|33347611
MKLIWSEESWDDYLYWQETDKRIVKKINELIKDTRRTPFEGKGKPEPLKHNLSGFWSRRI
TEEHRLVYAVTDDSLLIAACRYHY

**E._coli_O157_H7_EDL933**
>relE|16445223:c283932-284192, length 88, E._coli_O157_H7_EDL933, RelE/YafQ
MLNSGQFSKDVKLAQKRHKDMNKLKYLMTLLINNTLPLPAVYKDHPLQGSWKGYRDAHVE
PDWILIYKLTDKLLRFERTGTHAALFG

>parE|16445223:2324393-2324668, length 92, E._coli_O157_H7_EDL933, parE
MLPVLWLESADTDLDDITSYIARFDIDAAERLWQRLRGCVLPLSEHPYLYPPSDRVPGLR
EIVAHPNYIILYRVTTSSVEVVNVIHARRQFP

>parE|16445223:c1256683-1256967, length 95, E._coli_O157_H7_EDL933, parE
MLPILWLPSARDDLRQIITYIAKENPPAARRLKIRIETSVLPLSEHPYLYPPSERVSGLR
EIVTHPNYIILYRVAASSIEIVSVTHSRRQFPFSI

**Shigella_flexneri_2a_2457T**
>relE| 30061571:c2077698-2077949, length 84, Shigella_flexneri_2a_2457T, RelE/YoeB
MKLIWSEESWDDYLYWQETDKRIVKKINELIKDTRRTPFEGKGKPEPLKHNLSGFWSRRI
TEEHRLVYAVTDDSLLIAACRYHY

**Salmonella_typhimurium_LT2**
>parD|16763390:c3102440-3102715, length 91, Salmonella_typhimurium_LT2, ParD
MTVDLGDELREFIESLIESGDYRTQSEVIRESLRLLREKQAESRLQALRELLAEGLNSGE
PQAWEKDAFLRKVKTGMIKPDENGKINAKGQ

>parE|16763390:c3102178-3102468, length 96, Salmonella_typhimurium_LT2, ParE
MRMVKLTPKASEDLENIWHYGWQHFGEIQADRYINHLSEIFSIMSANNIGTPRPELGEYI
YALPFKRHIIYFIQSVTEVIVIRILSQNQDAGKHVNWL

>higB|16763390:4241948-4242235, length 103, Salmonella_typhimurium_LT2, HigB
MQFIETELFTEDVKKLLDDDEYHKLQVFMAQHPDCGDVIQETGGLRKMRWGARGKGKRSG
VRIIYFHRSQRYEIRLLLIYQKGIKDDLTPQEKAVLRMLNERW

>higA|16763390:4241636-4241944, length 96, Salmonella_typhimurium_LT2, HigA
MDKVLFERLTQSMSQMNEIIEGTREPSRTFHIDAMKIKEIRQASGLSQSKFAELISVNVD
TLRNWEQGRRSPTGPAKALLRAIANDPRNVIQALRY

**Salmonella_typhi**
>parD|16758993:c2958334-2958059, length 91, corrected start, Salmonella_typhi, ParD
MTVDLGDELREFIESLIESGDYRTQSEVIRESLRLLREKQAESRLQALRELLAEGLNSGE
PQAWEKDAFLRKVKTGMIKPDENGKINAKGQ

>parE|16758993:c2957794-2958012, length 73, Salmonella_typhi, ParE
MRTVKLTPKASEDLENIWHYGWQHFGEIQADRYIHHLSEIFSIMSANNIGTPRPELGEYI
YALPFERHIIYFI

**Salmonella_typhi_Ty2**
>parD|29140543:c2944229-2943954, length 91, corrected start, Salmonella_typhi_Ty2, ParD
MTVDLGDELREFIESLIESGDYRTQSEVIRESLRLLREKQAESRLQALRELLAEGLNSGEPQAWEKDAFL
RKVKTGMIKPDENGKINAKGQ

>parE|29140543:c2943689-2943907, length 73, Salmonella_typhi_Ty2, ParE
MRTVKLTPKASEDLENIWHYGWQHFGEIQADRYIHHLSEIFSIMSANNIGTPRPELGEYI
YALPFERHIIYFI

**Yersinia_pestis_CO92_chr.**
>higA|16120353:c964230-964379, length 50, Yersinia_pestis_CO92_chr., HigA
MDNKRQPPSLSHEQVVARMLKKPAVRAEYERLERQDFAIIDETLKGIHSE

**Yersinia_pestis_KIM_chr**
>relE|22123922:c3599007-3599225, length 86, Yersinia_pestis_KIM_chr, solitary RelE
MVKVDWSRKAVKQLLSIDARYRKPISEKVNKLTNFPAVDLDIKKLQMGDSQFRMRVGNYR
VIFQIVEGTPVICTIQEVKRRTTATY

>relB|22123922:c3399757-3400077, length 107, Yersinia_pestis_KIM_chr, RelB
MLMKTIKHYLTPEGRDLYMEYLKSLRDSIAKAKISSRVNRIASGNFGDHKPCREGVWELR
IDQGPGYRVYYSLVDGEVVLLLLGGDKRSQNADIDQAIVCLKDYLTR

>higA|22123922:c3594262-3594411, length 50, Yersinia_pestis_KIM_chr, HigA
MDNKRQPPSLSHEQVVARMLKKPAVRAEYERLERQDFAIIDETLKGIHSE

>higB|22123922:c3599007-3599264, length 108, Yersinia_pestis_KIM_chr, HigB
MNYTIEYYDDDVITQLLAQPISLQANFISLAKRMKRYGIKMVDAVPMHYHEDVFELCFYE
PKGWNRVIFMAQIDWQIVILHIVVQKTAYMPWKEKGKAAKRMKELRFG

>higA|22123922:2218599-2218967, length 123, Yersinia_pestis_KIM_chr, HigA
MVSLIPFFTEQGRLMYKISLLRLAQRELVRLPVGIQAVLIKAMDELEACGHELREPYVRD
MGQGLKELRVSAKEGIGRGFFFCHLHRQVYIIHLLQKKTQKTPRRTLILAYRRMKELKRR
LQS

>phd|22123922:2738880-2738578, length 101, Yersinia_pestis_KIM_chr, Phd
MQLIRYSLSYTLCINKNGYNPFTTAENSMCQRFSIYNSEDNVMSHALKNADRLYIPPRDK
GTKAYPRASMDTSSTHADQVKNAFAFGFSRYEKAMEELSKV

**Vibrio_cholerae_chromosome_2**
>relB|15600771:c343886-343602, length 94, corrected start, Vibrio_cholerae_chromosome_2, RelB
MDTRIQFRVDEETKRLAQQMAESQGRTLSDACRELTEQLAEQQRKALSHDAWLTEQVNQAFEKFDSGKA
VFIEHDIAKARMAERKAKIRNRGHA

>relB|15600771:c433678-433394, length 94, corrected start, Vibrio_cholerae_chromosome_2, RelB

MDTRIQFRVDEETKRLAQQMAESQGRTLSDACRELTEQLAEQQRKALSHDAWLTEQVNQAFEKFDSGKA
VFIEHDIAKARMAERKAKIRNRGHA

>phd|15600771:418614-418781, length 56, Vibrio_cholerae_chromosome_2, phd, corrected GI:15601235
MNRKVEAYGVDAVERPKIKASKKLDLTGDAGRQIVKSETKLALRTHQKTFTKLADM

**Vibrio_parahaemolyticus_chr_1**
>relB|28896774:1935517-1935800, length 94, corrected start, Vibrio_parahaemolyticus_chr_1, RelB
MDTRIQFRVDEETKRLAQQMAESQGRTLSDACRELTEQLAEQQRKTLSHDAWLTEQVNLAFEKFDSGKS
VFLEHQTAKSRMEERKARIRNRGKQ

**X._campestris_pv_ATCC_33913**
>relB|21240774:c74344-74069, length 93, corrected start, X_axonopodis_pv_citri_str_306, RelB
MGMPLDVLHVDAARWDAEGGKTKRRPERSEAMNVKELDARYAVSLRTQTEHALADPRPALSSAQAKQQME
TLKTQQRAALEAALAAKGTRA

>parD|21240774:c3665126-3665371, length 82, X_axonopodis_pv_citri_str_306, parD
MSPGRRKMPELRRTALSSTPLRKKSRRTSAALHSMPKRSNAGLLSKAATTRCPGRTYAST
CSSLLTERTPRHRSPAPSSADR

**Xylella_fastidiosa_chr**
>relE|15836605:c1620819-1621091, length 91, Xylella_fastidiosa_chr, relE
MAWTIDYTDTAKQQLRKLDKHMARRIVDFMDERIAGLENPRSSGKALTGPLGGFWRYRVG
DFRVVCAIQDSVLRVLVVGVGHRGEMYRREC

>higA|15836605:c527947-528210, length 88, Xylella_fastidiosa_chr, higA
MKVLRFLGDSLMCLRQFPEDACSDAGYQLDKIQRGEQPKDFKPMPSIGKGVEELRIWDDS
GTYRVVYTARLADAVYVLHAFQKKTQATSKRDVELAKRRYTELTKGAK

>higB|15836605:1630197-1629883, length 105, Xylella_fastidiosa_chr, HigB
MIRCSGTCSVRKTFFSGQIKVPVEALLQRLAGGAASMAPRPARIKMPHEAERWYQKMPQR
DVRVLVGTDTRTTSYFDHQSLNLGRDRCRLKSNIITITLSVIVVY

>vapB|15836605:304978-305193, length 72, Xylella_fastidiosa_chr, VapB
MDATVAERGQITLPKRVRDALGLTKGTVLKVELEGGRIILRKSVDDAIARARGRFILDDF
GCSAIATKTDKQ

**Xylella_fastidiosa_Temecula1**
>relB|28197945:1298015-1298314, length 100, Xylella_fastidiosa_Temecula1, relB
MYRLAQVVDAIKRLSGVHVHSAHAQQLGGTHWAVSCGGFSEGSMHLAMTQSECLGIIELQ
CSSFLTGYRRIALCLQTQLSVPALTRTSKKKHQPCWRRWA

>relE|28197945:1298354-1298761, length 136, Xylella_fastidiosa_Temecula1, relE
MPARRRCRSSRWCRTKLPSQPCVKPVLVTSRALIVLRRSWRTCMRRISQTGQFKRDYKRE
AKGQHRATLDEELIHVLEALTCDHPLEPRHHDHALTGDWKDHRDCHIKPDLVLIYRKPDN
ETLQLVRIGSHSELGL

>higA|28197945:1167816-1168139, length 108, Xylella_fastidiosa_Temecula1, higA
MKVLRFLGDSLMCLRQFPEDACSDAGYQLDKIQRGEQPKDFKPMPSIGKGVEELRIWDDS
GTYRVVYTARLADAVYVLHAFQKKTQATSKRDVELAKRRYTELTKGAK

>vapB|28197945:303404-303628, length 75, Xylella_fastidiosa_Temecula1, vapB
MDATVAERGQITLPKRVRDALGLTKGTVLKVELEGGRIILRKSVDDAIARARGRFILDDL
DDFGCSATATKTDKQ

**Pseudomonas_aeruginosa**
>parD|15595198:796960-797238, length 93, Pseudomonas_aeruginosa, ParD
MFPQQWRYRLMRVETISYLKRHAADLDLSEPMVVTQNGVPAYVVESYAERKQRDEAIALV
KLLAIGSRQYAEGKHRSVDDLKARLSRRFAQPE

>higB|15595198:c5242573-5242848, length 92, Pseudomonas_aeruginosa, HigB
MILTFRCDETRQLFETGLSRRWGAILTVATRKLAMLHAATELRDLRSPPGNRLEPLQGKR
AGQHSIRINDQWRVCFVWTDAGPEEVEIVDYH

**Pseudomonas_putida_KT2440**
>higA|26986745:334364-334672, length 103, Pseudomonas_putida_KT2440, HigA
MRSSWHPCRPQYCISPWLRRIQYGQDPERPIKSLTESVGAGAIELIINGSPAFRCVYVAK
FADMVVVLHSFVKTTNRSERHAMQVAEQRMKELKQELRKMGYRV

>higB|26986745:334049-334360, length 104, Pseudomonas_putida_KT2440, HigB
MPGVWVITIWIGEPASFEGRVRVVRKPSLSSMSIMASKVNFSILPFASSDMRDWVTFSLA
AASCCLRPIFLMQSVMKMDKSIFKAILLAVSASWVAWKGLSWN

>higA|26986745:c1418120-1418494, length 125, Pseudomonas_putida_KT2440, HigA
MFAFHNEKAPESFRFQGLDLVWRRDRDLNPRYCCQYNGFRIRPVRPLRHLSNAAHHTSVL
LKRKSFFQKNRVVSGACVNVPLTAARPGAWQLLRRLRSRRPGPGGSGPCPSSCGFPCPTG
GSRPG

**Leptospira_intrerrogans_I**
>relE|24212700:3672435-3672671, length 79, Leptospira_intrerrogans_I, relE
MSKFWPSLKNNSTQGIPIEQNYYKIRIPIASKGKGKSGGARVISCVVFVEKTVFLVSIYD
KSEKENISDKDLEKIIKNL

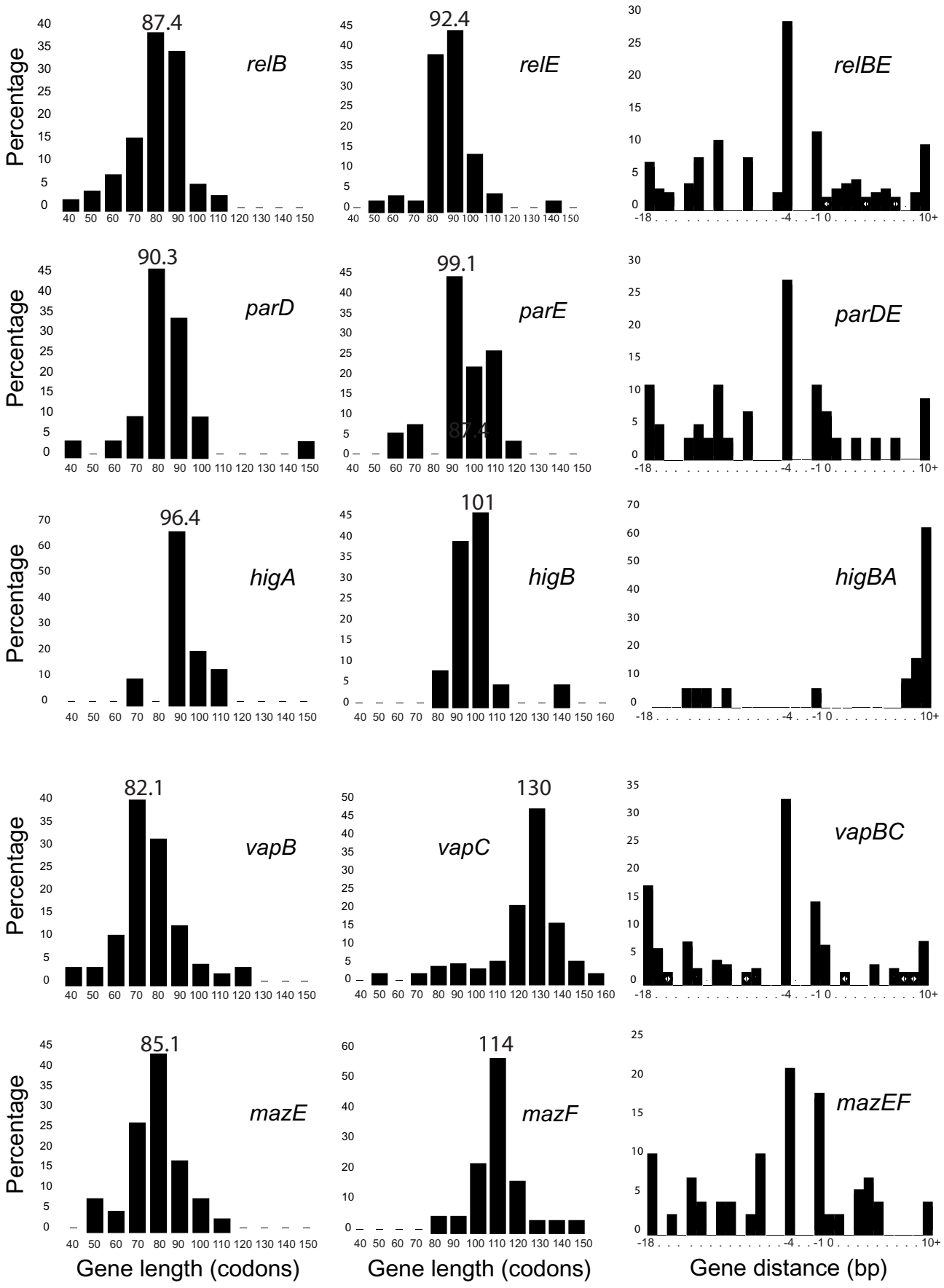
Percentage
87.4
relB
92.4
relE
relBE
90.3
parD
99.1
parE
87.4
parDE
96.4
higA
101
higB
higBA
82.1
vapB
130
vapC
vapBC
85.1
mazE
114
mazF
mazEF
Gene length (codons)
Gene length (codons)
Gene distance (bp)

Figure S1

**Legend to Figure S1**

**Fig. S1. Gene length distributions and distances.** Statistical analysis of the five most abundant TA gene families. The first and second columns show the antitoxin and toxin gene length distributions (in codons) and the third column shows the distances between the genes. Number at each insert is average of gene length. The statistics shown was based on 633 TA loci (from Table S2).