



Figure S1. The *pepR* gene cluster is conserved in bacteria. The neighboring loci of *pepR* in the genome were *thpR* (RNA 2',3'-cyclic phosphodiesterase), *pepV* (dipeptidase), *rsuA* (rRNA pseudouridine synthase), *ytgP* (polysaccharide biosynthesis protein), and *ytfP* (NAD(P)/FAD-dependent oxidoreductase). Blue, green, and yellow arrows indicate *pepV*, *pepR*, and *rsuA-ytgP* operon, respectively. The numbers at the ends of the lines represent the locations in the genome for the two end bases.

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Bt : MSAINWTEEVAKRKDDLRDQTQOFLQKSVVEESAKEGAPFEGVEKALSFMLHKGETEGFASKNLEGYAGHLE : 75
Bs : ---MNVEEVIRKKEDLRDQTQOFLRINSVMDETTAGPGKPEEGVNASLTSLLELGELEGFTTKNLDGFFAGHIE : 72
Ldel : -MDLNKELAEAKKDAIRDLDELIAIDSSDELNATEEYPVCKGPDAMTKFLSFAKRDGFDLENFANYAGRNV : 74
Lhel : -MNLDYKLLAAAKDDIRDLDELISIDSSDLNTSABEYFVCGPPVKAMKKFLSFAKRDGFDHKNVDNYAGRVD : 74
Sg : -MTIDSKAEVEKRREALADLFSLEINSEKDDSKADKEHPFEGPPVQALHKFLEIAERDGYETKNVDNYAGHFT : 74
Llac : MTTIDSKAEVEKRKDALMEDLFSLEIRIDSAMDEHADAEENPEGPPRKALDAFLKIAERDGYETKNVDNYVGHFE : 75

Bt : MCQGE---EIVGILCHVDVVPEDGWTTPAYSADIRD-GKIFARGAIDDKGPTMAAYYAMKIVKELGLPLSKRV : 145
Bs : WCEGD---DIIGVILCHVDVVPEDGWTSDFFSABEIRN-GRIYARGAIDDKGPTMAAFYALKIVKDMNLPLSKRV : 142
Ldel : FCAGD---KRLGILCHMDVVPAGEGWTRODFKMEIDEGRITVGRGSADDKGPSLAAYYGMILLKEAGFKPKKKI : 145
Lhel : YCDGE---KRLGILCHMDVVPAGDGWNTDFKMLIKD-GKIIIGRGSADDKGPAALAYYGMILLKEAGFTPKKKI : 144
Sg : FCEGQ---EELGIFAHMDVVPAGSGWNTDFYKPEILD-GKLYARGSSDDKGPTMACYYGLKIIKDLGLFPVSKRV : 144
Llac : YENGANADAELVGLIICHLDVVPAGSGWDSNFEPEPEIRN-GNLYARGASDDKGPTVACYALKIKLKEINLPLSKKI : 149

Bt : RMIIGTDEESNWKVDHYEKNEEMP--TICFAPDADFPIINAEKGISDIOVQ-NGSEEKGTYTELVSEDSGRRL : 217
Bs : RMIIGTDEESDWRQVEHYEKHEEMP--TMCFAPDADFPIINAEKGIIDASLIPHPRNQAEPKAVLVSEFQSGRL : 215
Ldel : DFLVLTNEETNNVGLIDYLLKHEPTP--DIVESPDAEYPIINCEOGITLFSFK--NDDTKDYVLQKEKAGIAT : 216
Lhel : DFLVGTNEETNNVGLIDYLLKHEPTP--DQVESPDAEYPIINCEOGIYTLINFK--DDAQTCSVKLEKFTAGIAE : 215
Sg : REVVGTDDEESGQMDYIEKHVGLPEPDFCESPDAEFPIINCEKGNITEYHF--GNDNTENAKLHSETGGLRE : 216
Llac : RFLVGTNEETGWADMDYIEHCELPDFCESPDAEFPIINCEKGNITEYHF--SGKNACQVVLHSEKAGIAE : 221

Bt : NMVDPDAEAVITGEDVNAITVAYEETIQTAKE---KIGKSTDEGNAVTLQEGISAHGSTPBRKGENAGLLIANEL : 288
Bs : NMVDPDAEAVIEGPKNEETLSSFKDMRTTD---QKGEAAENGQLITRMVGLSCHAMEPNNGINAGILICEFL : 286
Ldel : NVTPQVTRATISGPDLEAVKLAYESTADKE---LDGSFENDESADIVLIGQCAHASAPOVGKNSATFIALREL : 287
Lhel : NVTPQKAYATISGADLANKEQETKFTDNN---LEGNFENNGDEAKIETIGQCAHASAPOVGRNAATFELGKEL : 286
Sg : NMVPESATAVVSGQ-LPDIAGLLDAEAKHK---LQYEISTDEETYTITLICKSAHGSTPDDGINGGTYDALLL : 287
Llac : NMVPESATAVISG--AKDIEAALEKVAEHASKNLRFDLLEADGKA-TITTYCKSAHGAMPEKGINATYITLREL : 293

Bt : TTVSLDGKATATATFATETFTGDIIFGEKATLAYKDEISEPLTVNVGRIST-KENGGNGLNVRYPTTNFE-ET : 361
Bs : QQTELDAGAKREYQVVTDKFSGDTRCKKIDDCEDIEISECLTLNVGTLRYK-EGQGGETGINIRYPVTA---ES : 356
Ldel : DQYAFAGRDKNEHFLAEVEHEDFYCKKIGIFHDDIMCDLASSPSMFDYE-HAGKASLNNVRYPOGTDPDTMI : 361
Lhel : NQDFEAGRDKNYNFLANVEHEDFKCKIGVAHDDIMCDLSAPSIFEQ-ADGDAILKDNIRYPQGTDPNKMV : 360
Sg : NQDFEFGGAASKSYDEVAARVLHEDFTCKKIGLAYTDAKMCSLSMNAGVFHEDSAKADNTIALNIRYPQGTDPK-AI : 361
Llac : NQDFEADGAAAFKVGAEKLLDHECKIGTAFVDELMENTSMNAGVWSED-ENGEKGTALNRFEPQNSPE-RM : 366

Bt : IVKLKEYVGTGHFEVADYSNSRPHVDKDHVILRLTLQRYEEQTEKAELLAIGGGTYARSLKAGVAFGLFPFGK : 436
Bs : KVIRDTFESASEFELGEFKDSKPHVVSADHPLVKTQLQVYEGQLGKKADLISIGGGTYARSLKAGVAFGLFPGR : 431
Ldel : KQVMDKFGSGILDVTYNGFEFP--HYVPGSDPMVQTLKLVYEKQTKPGHEVVIGGGTYCRLFERGVAFGAQFENG : 434
Lhel : KQVEEFSDILTASFNSFEFP--HYVPGDDELVKTLKLVYEHQTKPGHEVVIGGGTYCRLFKHGVAFGAQPEDA : 433
Sg : QASLEKVGAVVSVSLSEHGT-PHYVPADDELVAITLLSVYEKQTKLGHEQVIGGGTYCRLLRGVAFGAMFDPY : 435
Llac : QEILAKLDGVVEVELSKHLHT-PHYVPMSEDELVSTLIDVYEKHGLKGYETIIGGGTYCRLLRGVAYGAMFEGE : 440

Bt : EELAHOKDEYIEIDLLKATAIYAQAITHELAK---- : 468
Bs : PDSAHOKDEYIEIDLLRSTALYAQAIVELAK---- : 463
Ldel : PMVMHAANEPMMLDILSLIAIYAEAIYELTKDEEL : 470
Lhel : PMVMHCAANEPMKVDLILSLIAIYAEAIYELTKEA-- : 467
Sg : VNTMHCAANEPTVDLFRAAAIYAEAIYELTK---- : 467
Llac : PDSMHCAANEPMKPVENIYKAAVIYAEAIYELAK---- : 472

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Figure S2. Comparison of the amino acid sequences revealed a conserved PepV homologs in bacteria. Sequences from *Bacillus thuringiensis* HD73 (Bt) [WP_001274251.1], *Bacillus subtilis* 168 (Bs) [WP_004399126.1], *Lactobacillus delbrueckii* subsp. *Lactis* DSM7290 (Ldel) [WP_014565245.1], *Lactobacillus helveticus* SBT2171 (Lhel) [WP_003626366.1], *Lactococcus lactis* MG1363 (Llac) [WP_011835507.1] and *Streptococcus gordonii* (Sg) [VT24557.1] were aligned with the ClustalW multiple sequence alignment tool according to homology modeling

(grey shading indicates similarity, and black shading indicates identity). Conserved box regions (boxes 1 to 4) are in sequential order and are denoted with single lines. An asterisk (*) indicates the catalytic site, closed circles (●) indicate the zinc-binding sites, and open circles (○) indicate the substrate-binding sites.

Supplementary Table S1. List of species in Figure 1

| Species | Accession | Cover | E-value | Identity |
|---|----------------|-------|----------|----------|
| <i>Bacillus thuringiensis</i> HD73 | WP_000805512.1 | 100% | 2.07E-45 | 100% |
| <i>Bacillus thuringiensis</i> | HDX9497500.1 | 100% | 6.55E-45 | 98.63% |
| <i>Bacillus cereus</i> | HDW3053053.1 | 100% | 7.63E-45 | 98.63% |
| <i>Bacillus cytotoxicus</i> | MCM3734429.1 | 100% | 1.52E-44 | 98.63% |
| <i>Bacillus anthracis</i> | WP_047398659.1 | 100% | 5.04E-43 | 98.63% |
| <i>Ectobacillus funiculus</i> | WP_129727866.1 | 100% | 1.10E-38 | 86.30% |
| <i>Domibacillus indicus</i> | WP_046176652.1 | 100% | 8.47E-38 | 86.30% |
| <i>Ectobacillus panaciterrae</i> | WP_028399761.1 | 100% | 2.74E-37 | 84.93% |
| <i>Ectobacillus</i> | WP_124564370.1 | 100% | 4.40E-37 | 86.30% |
| <i>Domibacillus antri</i> | WP_075399267.1 | 100% | 4.50E-37 | 83.56% |
| <i>Domibacillus epiphyticus</i> | WP_076764548.1 | 100% | 8.04E-37 | 84.93% |
| <i>Thermolongibacillus altinsuensis</i> | WP_132949297.1 | 100% | 3.21E-36 | 79.45% |
| <i>Bacillus kexueae</i> | WP_243385999.1 | 100% | 7.56E-36 | 78.08% |
| <i>Kurthia massiliensis</i> | WP_010288356.1 | 100% | 8.25E-36 | 82.19% |
| <i>Rossellomorea aquimaris</i> | WP_113969813.1 | 100% | 1.41E-35 | 79.45% |
| <i>Aeribacillus pallidus</i> | MDR9796532.1 | 100% | 1.92E-35 | 76.71% |
| <i>Bacillus salacetis</i> | WP_119546235.1 | 100% | 1.99E-35 | 80.82% |
| <i>Bacillus xiapuensis</i> | WP_100331890.1 | 100% | 2.17E-35 | 79.45% |
| <i>Anoxybacillus tepidamans</i> | WP_084279132.1 | 100% | 2.34E-35 | 78.08% |
| <i>Gottfriedia endophyticus</i> | WP_209406692.1 | 100% | 2.82E-35 | 78.08% |
| <i>Heyndrickxia sporothermodurans</i> | GIN88161.1 | 100% | 3.08E-35 | 79.45% |
| <i>Metabacillus litoralis</i> | WP_226670209.1 | 100% | 3.18E-35 | 78.08% |
| <i>Heyndrickxia oleronia</i> | WP_078111183.1 | 100% | 3.26E-35 | 79.45% |
| <i>Anoxybacillus caldiproteolyticus</i> | WP_181554765.1 | 100% | 3.44E-35 | 79.45% |
| <i>Mesobacillus maritimus</i> | WP_251431821.1 | 100% | 4.38E-35 | 79.45% |
| <i>Ectobacillus ponti</i> | WP_254757185.1 | 100% | 4.89E-35 | 80.82% |
| <i>Planococcus</i> sp. ISL-109 | WP_215106009.1 | 100% | 6.02E-35 | 83.56% |
| <i>Sutcliffiella rhizosphaerae</i> | WP_230502367.1 | 100% | 7.75E-35 | 76.71% |
| <i>Rummeliibacillus pycnus</i> | WP_102691013.1 | 100% | 7.75E-35 | 80.82% |
| <i>Metabacillus sediminilitoris</i> | WP_136352094.1 | 100% | 7.92E-35 | 78.08% |
| <i>Bacillus weihaiensis</i> | WP_072578818.1 | 100% | 9.55E-35 | 78.08% |
| <i>Bacillus ectoiniformans</i> | WP_204556568.1 | 100% | 9.76E-35 | 78.08% |
| <i>Anoxybacillus vitaminiphilus</i> | WP_111644448.1 | 100% | 1.04E-34 | 78.08% |
| <i>Kurthia sibirica</i> | WP_109305283.1 | 100% | 1.04E-34 | 80.82% |
| <i>Paenisporosarcina indica</i> | WP_075620108.1 | 100% | 1.11E-34 | 76.71% |
| <i>Sutcliffiella horikoshii</i> | WP_063559844.1 | 100% | 1.26E-34 | 76.71% |
| <i>Psychrobacillus</i> sp. OK028 | WP_093060335.1 | 100% | 1.28E-34 | 79.45% |
| <i>Psychrobacillus insolitus</i> | WP_111437610.1 | 100% | 1.36E-34 | 79.45% |
| <i>Candidatus Kurthia equi</i> | MBQ0139077.1 | 100% | 1.55E-34 | 80.82% |

| Species | Accession | Cover | E-value | Identity |
|---------------------------------------|----------------|-------|----------|----------|
| <i>Psychrobacillus</i> sp. OK032 | WP_093267179.1 | 100% | 1.73E-34 | 79.45% |
| <i>Mangrovibacillus cuniculi</i> | WP_239671949.1 | 100% | 1.97E-34 | 76.71% |
| <i>Bacillus coahuilensis</i> | WP_010174203.1 | 100% | 2.40E-34 | 76.71% |
| <i>Mesobacillus subterraneus</i> | WP_125479558.1 | 100% | 2.48E-34 | 79.45% |
| <i>Mesobacillus persicus</i> | WP_090741696.1 | 100% | 2.71E-34 | 78.08% |
| <i>Anoxybacillus calidus</i> | WP_181537608.1 | 100% | 3.13E-34 | 76.71% |
| <i>Planococcaceae</i> | WP_084246586.1 | 100% | 3.16E-34 | 82.19% |
| <i>Metabacillus iocasae</i> | WP_205188859.1 | 100% | 3.20E-34 | 78.08% |
| <i>Bacillus alveayuensis</i> | WP_044894459.1 | 100% | 3.27E-34 | 76.71% |
| <i>Bacillus massiliglaei</i> | WP_110927274.1 | 100% | 5.59E-34 | 75.34% |
| <i>Jeotgalibacillus proteolyticus</i> | WP_104057185.1 | 100% | 5.87E-34 | 79.17% |
| <i>Jeotgalibacillus salarius</i> | WP_134382991.1 | 100% | 6.21E-34 | 79.17% |
| <i>Oikeobacillus pervagus</i> | WP_307257751.1 | 100% | 6.38E-34 | 75.34% |
| <i>Psychrobacillus psychrodurans</i> | WP_090564512.1 | 100% | 6.89E-34 | 78.08% |
| <i>Bacillota bacterium</i> | MBU0905012.1 | 100% | 8.13E-34 | 75.34% |
| <i>Psychrobacillus vulpis</i> | WP_142643845.1 | 100% | 8.22E-34 | 78.08% |
| <i>Priestia koreensis</i> | WP_242170838.1 | 100% | 8.97E-34 | 75.34% |
| <i>Planococcus</i> sp. MER TA 32b | MCM3611524.1 | 100% | 9.69E-34 | 80.82% |
| <i>Metabacillus arenae</i> | WP_191157570.1 | 100% | 1.12E-33 | 78.08% |
| <i>Bacillus massiliigorillae</i> | WP_042345227.1 | 100% | 1.17E-33 | 75.34% |
| <i>Peribacillus glennii</i> | WP_117320796.1 | 100% | 1.50E-33 | 75.34% |
| <i>Litchfieldia salsa</i> | WP_090849283.1 | 100% | 1.54E-33 | 76.71% |
| <i>Terrabacteria group</i> | WP_142829443.1 | 100% | 1.55E-33 | 80.82% |
| <i>Metabacillus fastidiosus</i> | WP_066234314.1 | 100% | 1.83E-33 | 72.60% |
| <i>Lederbergia panacisoli</i> | WP_257581349.1 | 100% | 1.91E-33 | 75.34% |
| <i>Planococcus salinus</i> | WP_123163543.1 | 100% | 2.02E-33 | 80.82% |
| <i>Mesobacillus foraminis</i> | WP_121611380.1 | 100% | 2.07E-33 | 76.71% |
| <i>Chryseomicrobium aureum</i> | WP_204590502.1 | 100% | 2.11E-33 | 76.71% |
| <i>Falsibacillus pallidus</i> | WP_114745200.1 | 100% | 2.36E-33 | 72.60% |
| <i>Sutcliffeiella halmapala</i> | WP_078379340.1 | 100% | 2.38E-33 | 75.34% |
| <i>Anoxybacillus flavithermus</i> | WP_004888976.1 | 100% | 2.87E-33 | 72.60% |
| <i>Psychrobacillus glaciei</i> | WP_151700651.1 | 100% | 2.94E-33 | 76.71% |
| <i>Geobacillus</i> | WP_023817707.1 | 100% | 3.58E-33 | 76.71% |
| <i>Bacillus chungangensis</i> | WP_307230403.1 | 100% | 3.70E-33 | 75.34% |
| <i>Cytobacillus spongiae</i> | WP_233807561.1 | 100% | 3.99E-33 | 75.34% |
| <i>Bacillus massilionigeriensis</i> | WP_075982639.1 | 100% | 4.26E-33 | 73.97% |
| <i>Bacillus sinesaloumensis</i> | WP_077619127.1 | 100% | 4.29E-33 | 76.39% |
| <i>Geobacillus proteiniphilus</i> | WP_307898757.1 | 100% | 4.56E-33 | 76.71% |
| <i>Bacillus thermotolerans</i> | WP_039234094.1 | 100% | 4.66E-33 | 75.34% |

| Species | Accession | Cover | E-value | Identity |
|---|----------------|-------|----------|----------|
| <i>Priestia megaterium</i> | WP_098658829.1 | 100% | 4.76E-33 | 76.71% |
| <i>Xanthomonas citri</i> | MBD5023001.1 | 100% | 5.14E-33 | 75.34% |
| <i>Litchfieldia alkalitelluris</i> | WP_078544971.1 | 100% | 5.31E-33 | 73.97% |
| <i>Bacillus pumilus</i> | WP_119125252.1 | 100% | 5.55E-33 | 73.97% |
| <i>Bacillus aquiflavi</i> | WP_163242368.1 | 100% | 5.55E-33 | 73.97% |
| <i>Peribacillus loiseleuriae</i> | WP_049682664.1 | 100% | 5.86E-33 | 73.97% |
| <i>Paenisporosarcina</i> sp. HGH0030 | WP_016426574.1 | 100% | 5.86E-33 | 73.97% |
| <i>Bacillus amyloliquefaciens</i> group | WP_165882092.1 | 100% | 6.26E-33 | 73.97% |
| <i>Peribacillus asahii</i> | WP_119116910.1 | 100% | 6.26E-33 | 72.60% |
| <i>Bacillus kwashiorkori</i> | WP_062354866.1 | 100% | 6.54E-33 | 73.97% |
| <i>Cytobacillus purgationiresistens</i> | WP_307477527.1 | 100% | 6.76E-33 | 73.97% |
| <i>Bacillus haynesii</i> | WP_043926249.1 | 100% | 6.99E-33 | 73.97% |
| <i>Heyndrickxia shackletonii</i> | WP_055738983.1 | 100% | 7.63E-33 | 75.34% |
| <i>Ureibacillus thermophilus</i> | WP_208650260.1 | 100% | 8.52E-33 | 75.34% |
| <i>Bacillus amyloliquefaciens</i> | WP_289393838.1 | 100% | 9.00E-33 | 73.97% |
| <i>Cytobacillus horneckiae</i> | WP_066192053.1 | 100% | 9.61E-33 | 73.97% |
| <i>Fredinandcohnia</i> sp. SECRCQ15 | WP_240254714.1 | 100% | 9.93E-33 | 75.34% |
| <i>Metabacillus kandeliae</i> | WP_231787338.1 | 100% | 1.12E-32 | 76.71% |
| <i>Lysinibacillus fusiformis</i> | QDP99819.1 | 100% | 1.15E-32 | 75.34% |
| <i>Paenisporosarcina quisquiliarum</i> | WP_269925438.1 | 100% | 1.18E-32 | 73.97% |
| <i>Robertmurraya massiliosenegalensis</i> | WP_019154908.1 | 100% | 1.25E-32 | 73.97% |
| <i>Planococcus antarcticus</i> | WP_006830850.1 | 100% | 1.31E-32 | 78.08% |
| <i>Neobacillus</i> sp. PS3-12 | WP_308174508.1 | 100% | 1.31E-32 | 75.34% |
| <i>Neobacillus pocheonensis</i> | MCM2531377.1 | 100% | 1.72E-32 | 76.71% |
| <i>Parageobacillus thermantarcticus</i> | WP_090947684.1 | 100% | 1.86E-32 | 73.97% |
| <i>Neobacillus kokaensis</i> | WP_191270063.1 | 100% | 2.05E-32 | 75.34% |
| <i>Heyndrickxia camelliae</i> | WP_101354979.1 | 100% | 2.26E-32 | 73.97% |
| <i>Heyndrickxia acidicola</i> | WP_066270043.1 | 100% | 3.32E-32 | 73.97% |
| <i>Neobacillus mesonae</i> | WP_251471347.1 | 100% | 3.40E-32 | 75.34% |
| <i>Peribacillus deserti</i> | WP_101643144.1 | 100% | 4.09E-32 | 73.97% |
| <i>Neobacillus vireti</i> | WP_024026706.1 | 100% | 4.09E-32 | 75.34% |
| <i>Neobacillus piezotolerans</i> | WP_115452643.1 | 100% | 4.14E-32 | 75.34% |
| <i>Bacillus suaedaesalsae</i> | WP_204201773.1 | 100% | 5.57E-32 | 73.97% |
| <i>Neobacillus soli</i> | WP_084374900.1 | 100% | 5.88E-32 | 73.97% |
| <i>Bacillus litorisediminis</i> | WP_243298092.1 | 100% | 6.42E-32 | 76.71% |
| <i>Edaphobacillus lindanitolerans</i> | WP_076758254.1 | 100% | 7.17E-32 | 75.34% |
| <i>Neobacillus dielmonensis</i> | WP_042459807.1 | 100% | 7.33E-32 | 73.97% |
| <i>Neobacillus terrae</i> | WP_081680106.1 | 100% | 7.33E-32 | 75.34% |
| <i>Siminovitchia thermophila</i> | WP_077111916.1 | 100% | 8.27E-32 | 72.60% |

| Species | Accession | Cover | E-value | Identity |
|--|----------------|-------|----------|----------|
| <i>Sporosarcina psychrophila</i> | HJF31552.1 | 100% | 9.53E-32 | 73.97% |
| <i>Lysinibacillus contaminans</i> | WP_053582402.1 | 100% | 1.05E-31 | 72.60% |
| <i>Robertmurraya kyonggiensis</i> | WP_136832819.1 | 100% | 1.06E-31 | 72.60% |
| <i>Peribacillus psychrosaccharolyticus</i> | WP_040372415.1 | 100% | 1.08E-31 | 71.23% |
| <i>Bacillus renqingensis</i> | WP_199421031.1 | 100% | 1.09E-31 | 73.97% |
| <i>Caldibacillus debilis</i> | WP_020156918.1 | 100% | 1.33E-31 | 73.97% |
| <i>Lederbergia lenta</i> | WP_066145518.1 | 100% | 1.35E-31 | 72.60% |
| <i>Bacillus benzoovorans</i> | WP_184526108.1 | 100% | 1.78E-31 | 73.97% |
| <i>Peribacillus tepidiphilus</i> | WP_153127386.1 | 100% | 1.90E-31 | 72.60% |
| <i>Sporosarcina</i> sp. ANT_H38 | WP_149578880.1 | 100% | 2.01E-31 | 72.60% |
| <i>Bacillus</i> sp. FJAT-29937 | WP_066294579.1 | 100% | 2.20E-31 | 72.60% |
| <i>Lysinibacillus sphaericus</i> | WP_024363739.1 | 100% | 2.24E-31 | 72.60% |
| <i>Sporosarcina limicola</i> | WP_192598170.1 | 100% | 2.71E-31 | 71.23% |
| <i>Rossellomorea vietnamensis</i> | WP_148945767.1 | 100% | 3.05E-31 | 76.71% |
| <i>Neobacillus fumarioli</i> | WP_066366879.1 | 100% | 3.05E-31 | 72.60% |
| <i>Sporosarcina</i> sp. ACRSM | WP_239390431.1 | 100% | 3.22E-31 | 71.23% |
| <i>Bacillus yapensis</i> | WP_126409524.1 | 100% | 3.41E-31 | 71.23% |
| <i>Lysinibacillus alkalisoli</i> | WP_188615505.1 | 100% | 3.89E-31 | 72.60% |
| <i>Bhargavaea cecembensis</i> | WP_008300161.1 | 100% | 4.43E-31 | 71.23% |
| <i>Weizmannia acidilactici</i> | WP_151679414.1 | 100% | 4.89E-31 | 75.34% |
| <i>Bhargavaea beijingensis</i> | WP_092097684.1 | 100% | 5.52E-31 | 71.23% |
| <i>Caldibacillus thermoamylovorans</i> | WP_034771864.1 | 100% | 6.73E-31 | 75.34% |
| <i>Bacillus dakarensis</i> | WP_077214294.1 | 100% | 6.73E-31 | 72.60% |
| <i>Heyndrickxia acidiproducens</i> | WP_018664029.1 | 100% | 6.73E-31 | 75.34% |
| <i>Heyndrickxia ginsengihumi</i> | WP_025729975.1 | 100% | 7.35E-31 | 75.34% |
| <i>Bacillus oleivorans</i> | WP_097158925.1 | 100% | 9.25E-31 | 73.97% |