Table S1. Reference strains and sample source of *Bacillus subtilis*

| *Bacillus subtilis* trains | Source | |
|---|---|---|
| *Bacillus subtilis* strain AMR1 (BSAMR1) | | https://www.ncbi.nlm.nih.gov/nuccore/NZ_CP050319 |
| *Bacillus subtilis* strain A10 (BSA10) | | https://www.ncbi.nlm.nih.gov/nuccore/NZ_CP054050 |
| *Bacillus subtilis* strain ATCC 11774 (BS11774) | | https://www.ncbi.nlm.nih.gov/nuccore/NZ_CP026010 |
| *Bacillus subtilis* strain BS16045 (BS16045) | | https://www.ncbi.nlm.nih.gov/nuccore/NZ_CP017112 |
| *Bacillus subtilis* strain DKU_NT_02 (BSDKU) | | https://www.ncbi.nlm.nih.gov/nuccore/NZ_CP022890 |
| *Bacillus subtilis* strain LIN78 | milk powder | |

Table S2. LIN78 protein functional annotation via the Non-Redundant Protein Database

| Gene id | Identity | E value | Subject id | Subject description |
|---|---|---|---|---|
| BSLIN78GL000001 | 100 | 6.80E-254 | WP_003242674.1 | MULTISPECIES: chromosomal replication initiator protein DnaA [Bacillales] |
| BSLIN78GL000002 | 100 | 4.50E-206 | WP_003226811.1 | MULTISPECIES: DNA polymerase III subunit beta [Bacillus |
| BSLIN78GL000003 | 100 | 1.20E-32 | WP_003226810.1 | MULTISPECIES: ribosome maturation protein RlbA [Bacillales] |
| BSLIN78GL000004 | 100 | 4.00E-207 | WP_003226809.1 | MULTISPECIES: DNA replication/repair protein RecF [Bacillus |
| BSLIN78GL000005 | 100 | 6.60E-38 | WP_003219266.1 | MULTISPECIES: extracellular matrix regulator RemB [Bacillales] |
| BSLIN78GL000006 | 99.8 | 0.00E+00 | WP_258996692.1 | DNA topoisomerase (ATP-hydrolyzing) subunit B [Bacillus subtilis] |
| BSLIN78GL000007 | 100 | 1.40E-11 | EHA31815.1 | hypothetical protein BSSC8_00720 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000008 | 93.8 | 0.00E+00 | WP_223061589.1 | DNA gyrase subunit A [Bacillus sp. YC2] |
| BSLIN78GL000009 | 100 | 3.70E-85 | AKE21963.1 | hypothetical protein BsLM_0164 [Bacillus sp. LM 4-2] |
| BSLIN78GL000010 | 100 | 5.30E-184 | AIC96660.1 | hypothetical protein Q433_00070 [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL000011 | 100 | 2.60E-275 | WP_003226803.1 | MULTISPECIES: IMP dehydrogenase [Bacillales |
| BSLIN78GL000012 | 100 | 2.90E-238 | WP_032676922.1 | MULTISPECIES: D-alanyl-D-alanine carboxypeptidase [Bacillus |
| BSLIN78GL000013 | 100 | 5.00E-160 | WP_003226799.1 | MULTISPECIES: pyridoxal 5'-phosphate synthase lyase subunit PdxS [Bacillus |
| BSLIN78GL000014 | 100 | 2.70E-106 | WP_003226797.1 | MULTISPECIES: pyridoxal 5'-phosphate synthase glutaminase subunit PdxT |
| BSLIN78GL000015 | 99.5 | 4.00E-254 | AHA75969.1 | Seryl-tRNA synthetase [Bacillus subtilis PY79 |
| BSLIN78GL000016 | 100 | 2.70E-123 | WP_003226792.1 | MULTISPECIES: deoxyadenosine/deoxycytidine kinase [Bacillales |
| BSLIN78GL000017 | 100 | 4.50E-115 | WP_003226790.1 | MULTISPECIES: deoxyguanosine kinase [Bacillus |
| BSLIN78GL000018 | 100 | 6.60E-246 | WP_003226788.1 | MULTISPECIES: glycoside hydrolase family 18 protein [Bacillus |
| BSLIN78GL000019 | 100 | 1.50E-92 | WP_259266293.1 | isochorismatase family cysteine hydrolase [Bacillus subtilis |
| BSLIN78GL000020 | 100 | 6.40E-85 | WP_003226784.1 | MULTISPECIES: tRNA adenosine(34) deaminase TadA [Bacillus] |
| BSLIN78GL000021 | 100 | 0.00E+00 | WP_029317164.1 | MULTISPECIES: DNA polymerase III subunit gamma/tau [Bacillus |
| BSLIN78GL000022 | 100 | 2.80E-52 | AGA21853.1 | Hypothetical protein YaaK [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL000023 | 100 | 7.80E-109 | WP_003225425.1 | MULTISPECIES: recombination protein RecR [Bacillales] |
| BSLIN78GL000024 | 100 | 3.10E-34 | WP_003242387.1 | MULTISPECIES: YaaL family protein [Bacillales |
| BSLIN78GL000025 | 100 | 1.30E-39 | WP_029726362.1 | MULTISPECIES: sigma-K factor-processing regulator BofA [Bacillus] |
| BSLIN78GL000026 | 100 | 3.70E-85 | AKE21963.1 | hypothetical protein BsLM_0164 [Bacillus sp. LM 4-2] |
| BSLIN78GL000027 | 100 | 1.20E-32 | QHF55833.1 | hypothetical protein Bateq7PJ16_0027 [Bacillus subtilis] |
| BSLIN78GL000028 | 100 | 3.80E-94 | EHA31802.1 | hydrolysis of 5-bromo 4-chloroindolyl phosphate (X-phos) [Bacillus subtilis subsp. |
| BSLIN78GL000029 | 100 | 5.80E-209 | WP_029726396.1 | MULTISPECIES: toxic anion resistance protein [Bacillus] |
| BSLIN78GL000030 | 100 | 2.60E-275 | WP_029726395.1 | MULTISPECIES: aminotransferase class I/II-fold pyridoxal phosphate-dependent |
| BSLIN78GL000031 | 100 | 6.60E-114 | WP_003243137.1 | MULTISPECIES: dTMP kinase [Bacillales] |
| BSLIN78GL000032 | 100 | 1.60E-52 | AGE61896.1 | hypothetical protein C663_0030 [Bacillus subtilis XF-1] |
| BSLIN78GL000033 | 100 | 2.30E-73 | WP_326253868.1 | YaaR family protein [Bacillus subtilis] |
| BSLIN78GL000034 | 100 | 1.50E-184 | WP_003244417.1 | MULTISPECIES: DNA polymerase III subunit delta' [Bacillales |
| BSLIN78GL000035 | 100 | 1.30E-154 | WP_003243571.1 | MULTISPECIES: competence/sporulation regulator complex protein RicT |
| BSLIN78GL000036 | 100 | 3.00E-63 | WP_003218308.1 | MULTISPECIES: replication initiation-control protein YabA [Bacillales |
| BSLIN78GL000037 | 100 | 1.00E-137 | WP_003244526.1 | MULTISPECIES: tRNA1(Val) (adenine(37)-N6)-methyltransferase [Bacillales |
| BSLIN78GL000038 | 100 | 7.90E-32 | AHA75990.1 | UPF0213 protein yazA [Bacillus subtilis PY79] |
| BSLIN78GL000039 | 100 | 6.40E-157 | WP_268549257.1 | 16S rRNA (cytidine(1402)-2'-O)-methyltransferase [Bacillus subtilis |
| BSLIN78GL000040 | 100 | 3.90E-45 | WP_003226760.1 | MULTISPECIES: transition state genes transcriptional regulator AbrB [Bacillales] |
| BSLIN78GL000041 | 100 | 0.00E+00 | WP_029726394.1 | MULTISPECIES: methionine--tRNA ligase [Bacillus |
| BSLIN78GL000042 | 100 | 7.40E-144 | WP_029726393.1 | MULTISPECIES: TatD family hydrolase [Bacillus |
| BSLIN78GL000043 | 100 | 5.30E-243 | WP_029726392.1 | MULTISPECIES: ubiquitin-like domain-containing protein [Bacillus] |
| BSLIN78GL000044 | 100 | 4.00E-99 | WP_015253010.1 | MULTISPECIES: ribonuclease M5 [Bacillus] |
| BSLIN78GL000045 | 100 | 6.00E-158 | WP_014662482.1 | MULTISPECIES: 16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))- |
| BSLIN78GL000046 | 100 | 8.10E-160 | WP_015382563.1 | MULTISPECIES: sporulation-specific protease PrtG [Bacillus |
| BSLIN78GL000047 | 100 | 4.10E-41 | AGE61911.1 | hypothetical protein C663_0045 [Bacillus subtilis XF-1] |
| BSLIN78GL000048 | 100 | 3.00E-23 | AEP84820.1 | small, acid-soluble spore protein F [Bacillus spizizenii TU-B-10] |
| BSLIN78GL000049 | 100 | 4.90E-160 | WP_003226742.1 | MULTISPECIES: 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase |
| BSLIN78GL000050 | 100 | 1.40E-148 | AGE61914.1 | hypothetical protein C663_0048 [Bacillus subtilis XF-1] |
| BSLIN78GL000051 | 100 | 1.40E-63 | WP_003226738.1 | MULTISPECIES: 2-iminobutanoate/2-iminopropanoate deaminase [Bacillales] |
| BSLIN78GL000052 | 100 | 1.30E-38 | WP_003218346.1 | MULTISPECIES: septation regulator SpoVG [Bacillales] |
| BSLIN78GL000053 | 89.9 | 1.70E-236 | WP_276351540.1 | MULTISPECIES: bifunctional UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase GlmU [Bacillus |
| BSLIN78GL000054 | 100 | 7.70E-175 | WP_003218353.1 | MULTISPECIES: ribose-phosphate diphosphokinase [Bacillales] |
| BSLIN78GL000055 | 100 | 6.70E-111 | AGE61919.1 | 50S ribosomal protein L25/general stress protein Ctc [Bacillus subtilis XF-1] |
| BSLIN78GL000056 | 100 | 2.10E-103 | WP_003226727.1 | MULTISPECIES: aminoacyl-tRNA hydrolase [Bacillales |
| BSLIN78GL000057 | 100 | 1.80E-26 | WP_120027699.1 | anti-sigma-F factor Fin [Bacillus subtilis] |
| BSLIN78GL000058 | 98.5 | 0.00E+00 | WP_060397771.1 | transcription-repair coupling factor [Bacillus inaquosorum] |
| BSLIN78GL000059 | 100 | 2.20E-100 | BAI83503.2 | transcriptional regulator [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL000060 | 100 | 3.90E-296 | WP_003243709.1 | MULTISPECIES: polysaccharide biosynthesis protein [Bacillales |
| BSLIN78GL000061 | 99.8 | 1.00E-279 | WP_326253867.1 | nucleoside triphosphate pyrophosphohydrolase [Bacillus subtilis] |
| BSLIN78GL000062 | 100 | 4.80E-39 | WP_003226716.1 | MULTISPECIES: S4 domain-containing protein [Bacillales] |
| BSLIN78GL000063 | 100 | 1.20E-49 | WP_003226714.1 | MULTISPECIES: sporulation protein YabP [Bacillales] |
| BSLIN78GL000064 | 100 | 4.10E-116 | WP_003226711.1 | MULTISPECIES: spore cortex biosynthesis protein YabQ [Bacillus |
| BSLIN78GL000065 | 100 | 1.20E-65 | AGA22453.1 | Cell division protein DivIC [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL000066 | 100 | 1.50E-65 | WP_003218379.1 | MULTISPECIES: S1 domain-containing RNA-binding protein [Bacillales] |
| BSLIN78GL000067 | 99.9 | 0.00E+00 | EHA31762.1 | serine phosphatase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000068 | 100 | 2.50E-133 | WP_003226706.1 | MULTISPECIES: VWA domain-containing protein [Bacillus] |
| BSLIN78GL000069 | 100 | 1.40E-173 | AHA76022.1 | putative serine/threonine-protein kinase yabT [Bacillus subtilis PY79] |
| BSLIN78GL000070 | 100 | 5.30E-284 | WP_156581679.1 | tRNA lysidine(34) synthetase TilS [Bacillus subtilis |
| BSLIN78GL000071 | 100 | 1.70E-94 | WP_003226700.1 | MULTISPECIES: hypoxanthine phosphoribosyltransferase [Bacillales |
| BSLIN78GL000072 | 100 | 0.00E+00 | AGE61936.1 | cell-division protein and general stress protein [Bacillus subtilis XF-1] |
| BSLIN78GL000073 | 100 | 5.20E-142 | AEP89140.1 | transcriptional activator, Baf family protein [Bacillus subtilis subsp. subtilis str. RO- |
| BSLIN78GL000074 | 100 | 3.10E-162 | WP_003226695.1 | MULTISPECIES: redox-regulated molecular chaperone HslO [Bacillales] |
| BSLIN78GL000075 | 100 | 6.80E-165 | WP_024571698.1 | MULTISPECIES: peptidyl-prolyl cis-trans isomerase [Bacillus |
| BSLIN78GL000076 | 100 | 4.20E-170 | AGA21503.1 | Cysteine synthase [Bacillus subtilis subsp. subtilis str. BSP1] |

|  |  |  |  |  |
|---|---|---|---|---|
| BSLIN78GL000077 | 100 | 5.10E-290 | AEP89144.1 | para-aminobenzoate synthase component 1 [Bacillus subtilis subsp. subtilis str. RO- |
| BSLIN78GL000078 | 100 | 6.00E-109 | EHA31751.1 | para-aminobenzoate/anthranilate synthase glutamine amidotransferase component II |
| BSLIN78GL000079 | 100 | 7.10E-167 | AIC96724.1 | 4-amino-4-deoxychorismate lyase [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL000080 | 100 | 7.50E-144 | WP_029317175.1 | MULTISPECIES: dihydropteroate synthase [Bacillus |
| BSLIN78GL000081 | 100 | 1.50E-62 | WP_014478613.1 | MULTISPECIES: dihydroneopterin aldolase [Bacillus |
| BSLIN78GL000082 | 100 | 1.30E-88 | WP_003226679.1 | MULTISPECIES: 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine |
| BSLIN78GL000083 | 100 | 4.30E-30 | WP_003226678.1 | MULTISPECIES: helix-turn-helix transcriptional regulator [Bacillales |
| BSLIN78GL000085 | 99.7 | 1.90E-192 | AGA21511.1 | tRNA-dihydrouridine synthase 1 [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL000086 | 94.8 | 1.70E-277 | WP_032872208.1 | MULTISPECIES: lysine--tRNA ligase [Bacillus |
| BSLIN78GL000087 | 100 | 3.70E-85 | AKE21963.1 | hypothetical protein BsLM_0164 [Bacillus sp. LM 4-2] |
| BSLIN78GL000088 | 100 | 2.30E-19 | BAO93215.1 | hypothetical protein BSNT_06368 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL000089 | 98.1 | 5.00E-54 | QHF55815.1 | hypothetical protein Bateq7PJ16_0009 [Bacillus subtilis] |
| BSLIN78GL000091 | 100 | 4.20E-78 | WP_003225724.1 | MULTISPECIES: transcriptional regulator CtsR [Bacillales] |
| BSLIN78GL000092 | 100 | 8.00E-67 | WP_085187881.1 | MULTISPECIES: protein-arginine kinase activator protein McsA [Bacillus |
| BSLIN78GL000093 | 100 | 1.40E-193 | WP_003235007.1 | MULTISPECIES: protein arginine kinase [Bacillales] |
| BSLIN78GL000094 | 99.8 | 0.00E+00 | WP_213383247.1 | ATP-dependent Clp protease ATP-binding subunit [Bacillus subtilis] |
| BSLIN78GL000095 | 100 | 3.10E-257 | WP_029727024.1 | DNA repair protein RadA [Bacillus subtilis] |
| BSLIN78GL000096 | 100 | 1.10E-198 | WP_003225736.1 | MULTISPECIES: DNA integrity scanning diadenylate cyclase DisA [Bacillales |
| BSLIN78GL000097 | 100 | 5.00E-202 | WP_003235014.1 | MULTISPECIES: PIN/TRAM domain-containing protein [Bacillales |
| BSLIN78GL000098 | 100 | 2.40E-125 | WP_046664350.1 | MULTISPECIES: 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase [Bacillus |
| BSLIN78GL000099 | 100 | 1.40E-87 | AGA20733.1 | 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (MECPS; MECDP-synthase) |
| BSLIN78GL000100 | 100 | 3.20E-281 | WP_029727023.1 | MULTISPECIES: glutamate--tRNA ligase [Bacillus] |
| BSLIN78GL000101 | 100 | 4.90E-117 | WP_003235025.1 | MULTISPECIES: serine O-acetyltransferase [Bacillus |
| BSLIN78GL000102 | 100 | 2.80E-274 | WP_038427269.1 | MULTISPECIES: cysteine--tRNA ligase [Bacillus |
| BSLIN78GL000103 | 100 | 5.00E-73 | WP_014475597.1 | MULTISPECIES: mini-ribonuclease 3 [Bacillus] |
| BSLIN78GL000104 | 100 | 4.20E-119 | WP_327841896.1 | 23S rRNA (guanosine(2251)-2'-O)-methyltransferase RlmB [Bacillus subtilis] |
| BSLIN78GL000105 | 100 | 2.00E-89 | WP_003235032.1 | MULTISPECIES: ribosome-dependent mRNA decay endonuclease Rae1/YacP |
| BSLIN78GL000106 | 100 | 5.00E-117 | WP_003225758.1 | MULTISPECIES: RNA polymerase sporulation sigma factor SigH [Bacillales] |
| BSLIN78GL000107 | 100 | 7.00E-23 | EHA28651.1 | preprotein translocase subunit SecE [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000108 | 100 | 2.30E-96 | AFI26641.1 | transcription antitermination protein NusG [Bacillus sp. JS] |
| BSLIN78GL000109 | 100 | 2.30E-51 | AEB61660.1 | 50S ribosomal protein L11 [Bacillus amyloliquefaciens LL3] |
| BSLIN78GL000110 | 100 | 4.80E-126 | WP_003235040.1 | MULTISPECIES: 50S ribosomal protein L1 [Bacillales] |
| BSLIN78GL000111 | 100 | 5.20E-82 | WP_003235042.1 | MULTISPECIES: 50S ribosomal protein L10 [Bacillales] |
| BSLIN78GL000112 | 100 | 2.50E-60 | AGA20719.1 | 50S ribosomal protein L7 / L12 [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL000113 | 100 | 1.00E-108 | QAV86759.1 | class I SAM-dependent methyltransferase [Bacillus subtilis] |
| BSLIN78GL000114 | 100 | 0.00E+00 | AFI26647.1 | DNA-directed RNA polymerase subunit beta [Bacillus sp. JS] |
| BSLIN78GL000115 | 95.3 | 0.00E+00 | WP_226567652.1 | DNA-directed RNA polymerase subunit beta' [Bacillus stratosphericus] |
| BSLIN78GL000116 | 100 | 4.90E-36 | AGA20715.1 | Putative ribosomal protein L7Ae-like protein [Bacillus subtilis subsp. subtilis str. |
| BSLIN78GL000117 | 100 | 8.00E-42 | AGE61976.1 | 30S ribosomal protein [Bacillus subtilis XF-1] |
| BSLIN78GL000118 | 100 | 7.60E-83 | WP_003225784.1 | MULTISPECIES: 30S ribosomal protein S7 [Bacillales] |
| BSLIN78GL000119 | 95.8 | 0.00E+00 | WP_003328292.1 | MULTISPECIES: elongation factor G [Bacillus] |
| BSLIN78GL000120 | 100 | 3.10E-226 | WP_003235058.1 | MULTISPECIES: elongation factor Tu [Bacillales] |
| BSLIN78GL000121 | 100 | 4.40E-186 | WP_147797795.1 | alpha/beta hydrolase [Bacillus subtilis] |
| BSLIN78GL000122 | 100 | 2.70E-49 | WP_003156464.1 | MULTISPECIES: 30S ribosomal protein S10 [Bacteria] |
| BSLIN78GL000123 | 100 | 9.40E-113 | WP_004399671.1 | MULTISPECIES: 50S ribosomal protein L3 [Bacillales] |
| BSLIN78GL000124 | 99 | 4.40E-44 | WP_326195074.1 | 50S ribosomal protein L4 [Bacillus mojavensis] |
| BSLIN78GL000125 | 100 | 6.50E-45 | WP_003156467.1 | MULTISPECIES: 50S ribosomal protein L23 [Bacteria] |
| BSLIN78GL000126 | 100 | 7.50E-158 | WP_003225795.1 | MULTISPECIES: 50S ribosomal protein L2 [Bacillales] |
| BSLIN78GL000127 | 100 | 2.10E-43 | AGE61986.1 | 50S ribosomal protein [Bacillus subtilis XF-1] |
| BSLIN78GL000128 | 100 | 5.90E-118 | WP_003242001.1 | MULTISPECIES: 30S ribosomal protein S3 [Bacillus] |
| BSLIN78GL000129 | 100 | 1.50E-26 | AEB61679.1 | 50S ribosomal protein L16 [Bacillus amyloliquefaciens LL3] |
| BSLIN78GL000130 | 100 | 7.30E-27 | WP_003156482.1 | MULTISPECIES: 50S ribosomal protein L29 [Bacteria] |
| BSLIN78GL000131 | 100 | 2.50E-30 | WGD65037.1 | 30S ribosomal protein S17 [Bacillus subtilis] |
| BSLIN78GL000132 | 100 | 2.30E-51 | WP_003156486.1 | MULTISPECIES: 50S ribosomal protein L24 [Bacteria] |
| BSLIN78GL000133 | 100 | 6.40E-94 | WP_003225809.1 | MULTISPECIES: 50S ribosomal protein L5 [Bacillales] |
| BSLIN78GL000134 | 100 | 4.00E-26 | WP_003156488.1 | MULTISPECIES: 30S ribosomal protein S14 [Bacillales] |
| BSLIN78GL000135 | 100 | 9.80E-56 | WP_003241998.1 | MULTISPECIES: 30S ribosomal protein S8 [Bacillales] |
| BSLIN78GL000136 | 100 | 7.50E-98 | AGA20693.1 | 50S ribosomal protein L6 [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL000137 | 100 | 8.60E-24 | AGE61996.1 | 50S ribosomal protein [Bacillus subtilis XF-1] |
| BSLIN78GL000138 | 100 | 1.50E-84 | WP_003328273.1 | MULTISPECIES: 30S ribosomal protein S5 [Bacteria] |
| BSLIN78GL000139 | 100 | 6.70E-24 | WP_003156497.1 | MULTISPECIES: 50S ribosomal protein L30 [Bacteria] |
| BSLIN78GL000140 | 100 | 4.90E-76 | WP_003225819.1 | MULTISPECIES: 50S ribosomal protein L15 [Bacillales] |
| BSLIN78GL000141 | 100 | 3.80E-227 | WP_004399662.1 | MULTISPECIES: preprotein translocase subunit SecY [Bacillales] |
| BSLIN78GL000142 | 100 | 1.20E-118 | WP_029727021.1 | MULTISPECIES: adenylate kinase [Bacillus |
| BSLIN78GL000143 | 100 | 8.40E-134 | WP_019713059.1 | type I methionyl aminopeptidase [Bacillus spizizenii |
| BSLIN78GL000144 | 100 | 3.50E-25 | WP_015382593.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL000145 | 100 | 3.30E-33 | WP_003156508.1 | MULTISPECIES: translation initiation factor IF-1 [Bacteria] |
| BSLIN78GL000146 | 100 | 6.70E-14 | WP_003156543.1 | MULTISPECIES: 50S ribosomal protein L36 [Bacteria] |
| BSLIN78GL000147 | 100 | 9.10E-60 | WP_003235095.1 | MULTISPECIES: 30S ribosomal protein S13 [Bacillales] |
| BSLIN78GL000148 | 100 | 1.30E-28 | WP_010332782.1 | MULTISPECIES: 30S ribosomal protein S11 [Bacillus] |
| BSLIN78GL000149 | 100 | 6.00E-172 | WP_003225835.1 | MULTISPECIES: DNA-directed RNA polymerase subunit alpha [Bacillales |
| BSLIN78GL000150 | 100 | 8.80E-51 | AGE62008.1 | 50S ribosomal protein [Bacillus subtilis XF-1] |
| BSLIN78GL000151 | 100 | 2.70E-155 | WP_029727020.1 | MULTISPECIES: energy-coupling factor ABC transporter ATP-binding protein |
| BSLIN78GL000152 | 100 | 1.10E-159 | WP_029727019.1 | energy-coupling factor ABC transporter ATP-binding protein [Bacillus subtilis] |
| BSLIN78GL000153 | 100 | 6.50E-143 | WP_004399656.1 | MULTISPECIES: energy-coupling factor transporter transmembrane protein EcfT |
| BSLIN78GL000154 | 100 | 1.90E-141 | WP_004399657.1 | MULTISPECIES: tRNA pseudouridine(38-40) synthase TruA [Bacillales |
| BSLIN78GL000155 | 100 | 2.10E-45 | AEP89218.1 | ribosomal protein L13 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL000156 | 100 | 1.30E-55 | AGE62014.1 | 30S ribosomal protein [Bacillus subtilis XF-1] |
| BSLIN78GL000157 | 100 | 3.30E-144 | WP_004399665.1 | MULTISPECIES: class I SAM-dependent methyltransferase [Bacillales |
| BSLIN78GL000158 | 100 | 5.70E-80 | WP_003235118.1 | MULTISPECIES: YbaK family protein [Bacillales |

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|---|---|---|---|---|
| BSLIN78GL000159 | 100 | 4.20E-133 | WP_004399672.1 | MULTISPECIES: N-acetylmuramoyl-L-alanine amidase CwlD [Bacillales |
| BSLIN78GL000160 | 100 | 1.40E-198 | WP_019712637.1 | MULTISPECIES: iron-sulfur carrier protein/transcriptional regulator SalA [Bacillus] |
| BSLIN78GL000161 | 100 | 1.50E-98 | WP_003235126.1 | MULTISPECIES: spore germination lipoprotein GerD [Bacillales] |
| BSLIN78GL000162 | 100 | 3.40E-121 | RAP04007.1 | hypothetical protein HS3_04324 [Bacillus subtilis] |
| BSLIN78GL000163 | 100 | 1.20E-141 | WP_029727017.1 | polysaccharide deacetylase family sporulation protein PdaB [Bacillus subtilis] |
| BSLIN78GL000164 | 100 | 3.70E-85 | AKE21963.1 | hypothetical protein BsLM_0164 [Bacillus sp. LM 4-2] |
| BSLIN78GL000165 | 97.9 | 2.00E-18 | QHF55894.1 | hypothetical protein Bateq7PJ16_0088 [Bacillus subtilis] |
| BSLIN78GL000166 | 100 | 3.70E-85 | AKE21963.1 | hypothetical protein BsLM_0164 [Bacillus sp. LM 4-2] |
| BSLIN78GL000167 | 100 | 3.70E-38 | WP_003234987.1 | MULTISPECIES: hypothetical protein [Bacilli |
| BSLIN78GL000168 | 99.6 | 1.80E-260 | WP_042975706.1 | SulP family inorganic anion transporter [Bacillus subtilis] |
| BSLIN78GL000169 | 100 | 2.90E-174 | AIC96806.1 | hypothetical protein Q433_01015 [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL000170 | 100 | 6.80E-142 | WP_038427276.1 | MULTISPECIES: alpha/beta hydrolase [Bacillus] |
| BSLIN78GL000171 | 100 | 1.30E-183 | WP_029726921.1 | MULTISPECIES: iron ABC transporter permease FeuC [Bacillus] |
| BSLIN78GL000172 | 100 | 5.20E-182 | WP_015715127.1 | MULTISPECIES: iron ABC transporter permease [Bacillus] |
| BSLIN78GL000173 | 100 | 5.90E-175 | WP_014475620.1 | MULTISPECIES: iron ABC transporter substrate-binding protein FeuA [Bacillus |
| BSLIN78GL000174 | 100 | 2.2e-310 | WP_029726922.1 | MULTISPECIES: bacillibactin transport transcriptional regulator Btr [Bacillus] |
| BSLIN78GL000175 | 100 | 3.10E-240 | WP_015252972.1 | MULTISPECIES: exo-beta-N-acetylmuramidase NamZ domain-containing protein |
| BSLIN78GL000176 | 100 | 0.00E+00 | WP_029726923.1 | MULTISPECIES: beta-N-acetylhexosaminidase [Bacillus |
| BSLIN78GL000177 | 100 | 7.20E-256 | WP_029726924.1 | MULTISPECIES: N-acetylmuramoyl-L-alanine amidase [Bacillus |
| BSLIN78GL000178 | 100 | 2.50E-251 | WP_014475625.1 | MULTISPECIES: PTS transporter subunit EIIC [Bacillus |
| BSLIN78GL000179 | 100 | 8.20E-152 | WP_029726925.1 | MULTISPECIES: MurR/RpiR family transcriptional regulator [Bacillus] |
| BSLIN78GL000180 | 100 | 1.50E-147 | WP_029726926.1 | MULTISPECIES: N-acetylmuramic acid 6-phosphate etherase [Bacillus |
| BSLIN78GL000181 | 100 | 4.40E-86 | WP_029726927.1 | MULTISPECIES: GNAT family N-acetyltransferase [Bacillus |
| BSLIN78GL000182 | 100 | 2.40E-78 | WP_003234960.1 | MULTISPECIES: DUF523 domain-containing protein [Bacillales] |
| BSLIN78GL000183 | 100 | 3.10E-99 | WP_326253294.1 | RNA polymerase sigma factor SigW [Bacillus subtilis] |
| BSLIN78GL000184 | 100 | 4.30E-118 | WP_015252964.1 | MULTISPECIES: anti-sigma-W factor RsiW [Bacillus |
| BSLIN78GL000185 | 100 | 1.80E-154 | AGE62039.1 | hypothetical protein C663_0174 [Bacillus subtilis XF-1] |
| BSLIN78GL000186 | 100 | 5.50E-273 | WP_029726928.1 | MULTISPECIES: CdaA regulatory protein CdaR [Bacillus] |
| BSLIN78GL000187 | 99.8 | 1.50E-253 | WP_014112449.1 | MULTISPECIES: phosphoglucosamine mutase [Bacillus] |
| BSLIN78GL000188 | 97.7 | 2.70E-14 | AGI27451.1 | hypothetical protein I653_00905 [Bacillus subtilis subsp. subtilis str. BAB-1] |
| BSLIN78GL000189 | 99.8 | 0.00E+00 | WP_049140335.1 | glutamine--fructose-6-phosphate transaminase (isomerizing) [Bacillus subtilis] |
| BSLIN78GL000190 | 100 | 1.10E-175 | WP_147797776.1 | DNA-3-methyladenine glycosidase II [Bacillus subtilis |
| BSLIN78GL000191 | 100 | 2.30E-122 | WP_147797777.1 | bifunctional transcriptional activator/DNA repair enzyme AdaA [Bacillus subtilis] |
| BSLIN78GL000192 | 100 | 4.70E-91 | WP_326214300.1 | methylated-DNA--[protein]-cysteine S-methyltransferase [Bacillus subtilis |
| BSLIN78GL000193 | 100 | 1.50E-286 | WP_038427277.1 | NADH dehydrogenase subunit 5 [Bacillus subtilis] |
| BSLIN78GL000194 | 99.9 | 0.00E+00 | WP_326253292.1 | YbcC family protein [Bacillus subtilis] |
| BSLIN78GL000195 | 99.5 | 5.20E-119 | AKE21994.1 | hypothetical protein BsLM_0195 [Bacillus sp. LM 4-2] |
| BSLIN78GL000196 | 98 | 3.60E-46 | WP_017694954.1 | MULTISPECIES: DUF6407 family protein [Bacillus |
| BSLIN78GL000197 | 100 | 1.30E-39 | WP_087961888.1 | DUF2294 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL000198 | 100 | 5.20E-15 | AKN12260.1 | hypothetical protein ABU16_1184 [Bacillus subtilis] |
| BSLIN78GL000199 | 100 | 2.70E-49 | WP_003234907.1 | MULTISPECIES: metalloregulator ArsR/SmtB family transcription factor [Bacillales |
| BSLIN78GL000200 | 100 | 3.60E-214 | WP_029726935.1 | MULTISPECIES: MFS transporter [Bacillus] |
| BSLIN78GL000202 | 100 | 1.30E-182 | WP_015715149.1 | MULTISPECIES: S8 family serine peptidase [Bacillus |
| BSLIN78GL000203 | 100 | 0.00E+00 | WP_015715150.1 | MULTISPECIES: lantibiotic dehydratase [Bacillus |
| BSLIN78GL000204 | 100 | 2.60E-253 | WP_015715151.1 | MULTISPECIES: lanthionine synthetase C family protein [Bacillus |
| BSLIN78GL000205 | 99.2 | 2.10E-62 | WP_015715152.1 | MULTISPECIES: DUF5823 family protein [Bacillus |
| BSLIN78GL000206 | 100 | 0.00E+00 | WP_015715153.1 | MULTISPECIES: ABC transporter ATP-binding protein [Bacillus] |
| BSLIN78GL000207 | 100 | 3.50E-183 | WP_015715154.1 | MULTISPECIES: alpha/beta hydrolase [Bacillus] |
| BSLIN78GL000208 | 100 | 7.40E-124 | WP_029726937.1 | MULTISPECIES: two-component system response regulator YbdJ [Bacillus |
| BSLIN78GL000209 | 100 | 3.60E-183 | WP_029726938.1 | MULTISPECIES: two-component system sensor histidine kinase YbdK [Bacillus |
| BSLIN78GL000210 | 100 | 6.70E-28 | RAP04840.1 | hypothetical protein HS3_03515 [Bacillus subtilis] |
| BSLIN78GL000211 | 100 | 1.20E-141 | WP_029726940.1 | MULTISPECIES: protein kinase [Bacillus] |
| BSLIN78GL000212 | 100 | 4.10E-159 | WP_029726941.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL000213 | 100 | 3.20E-223 | WP_029726942.1 | MULTISPECIES: DUF4885 domain-containing protein [Bacillus] |
| BSLIN78GL000214 | 99.8 | 9.40E-270 | WP_074794539.1 | MULTISPECIES: amino acid permease [Bacillus] |
| BSLIN78GL000215 | 100 | 1.60E-39 | WP_014478667.1 | MULTISPECIES: sigma-G-dependent sporulation-specific acid-soluble spore protein |
| BSLIN78GL000216 | 100 | 1.30E-30 | WP_147797778.1 | YbxH family protein [Bacillus subtilis] |
| BSLIN78GL000217 | 100 | 3.50E-152 | WP_029726944.1 | class D beta-lactamase [Bacillus subtilis] |
| BSLIN78GL000218 | 100 | 4.90E-246 | WP_029726945.1 | fatty-acid peroxygenase [Bacillus subtilis] |
| BSLIN78GL000219 | 100 | 4.70E-42 | WP_003234883.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL000220 | 100 | 0.00E+00 | RAP04850.1 | hypothetical protein HS3_03525 [Bacillus subtilis] |
| BSLIN78GL000221 | 100 | 6.00E-166 | WP_029726947.1 | MULTISPECIES: glycerophosphodiester phosphodiesterase [Bacillus |
| BSLIN78GL000222 | 100 | 1.20E-261 | WP_003246460.1 | MULTISPECIES: glycerol-3-phosphate transporter [Bacillales |
| BSLIN78GL000223 | 100 | 1.50E-37 | WP_003234879.1 | MULTISPECIES: YbeF family protein [Bacillales |
| BSLIN78GL000224 | 99.7 | 2.80E-174 | AHA76173.1 | Putative HTH-type DNA-binding domain-containing acetyltransferase ybfA [Bacillus |
| BSLIN78GL000225 | 100 | 1.20E-236 | AGA23883.1 | Hypothetical protein YbfB [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL000226 | 98.7 | 9.40E-78 | WP_250621743.1 | hypothetical protein, partial [Bacillus subtilis] |
| BSLIN78GL000227 | 100 | 0.00E+00 | WP_015252935.1 | MULTISPECIES: glycoside hydrolase domain-containing protein [Bacillus |
| BSLIN78GL000228 | 100 | 8.80E-168 | WP_003234873.1 | MULTISPECIES: DMT family transporter [Bacillales |
| BSLIN78GL000229 | 100 | 2.00E-158 | WP_003246321.1 | MULTISPECIES: AraC family transcriptional regulator [Bacillales] |
| BSLIN78GL000230 | 99.2 | 1.10E-212 | WP_326256068.1 | phosphoribosylglycinamide formyltransferase 2 [Bacillus subtilis |
| BSLIN78GL000231 | 99.7 | 1.20E-188 | AGE62073.1 | extracellular metalloprotease [Bacillus subtilis XF-1] |
| BSLIN78GL000232 | 99.1 | 1.10E-56 | WP_033883172.1 | MULTISPECIES: YbfJ family protein [Bacillus] |
| BSLIN78GL000233 | 99.7 | 2.10E-163 | ANY31209.1 | carboxylesterase [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL000234 | 100 | 5.20E-93 | WP_009966430.1 | MULTISPECIES: CDP-diacylglycerol--serine O-phosphatidyltransferase [Bacillales |
| BSLIN78GL000235 | 100 | 3.60E-88 | WP_003234861.1 | MULTISPECIES: DedA family protein [Bacillales |
| BSLIN78GL000236 | 100 | 3.00E-148 | WP_003246344.1 | MULTISPECIES: phosphatidylserine decarboxylase [Bacillales |
| BSLIN78GL000237 | 100 | 7.40E-46 | WP_021481898.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL000238 | 100 | 7.00E-22 | RPK08114.1 | hypothetical protein EH5_04209 [Bacillus subtilis] |
| BSLIN78GL000239 | 100 | 2.00E-191 | WP_003246287.1 | MULTISPECIES: rhodanese-related sulfurtransferase [Bacillales |

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|---|---|---|---|---|
| BSLIN78GL000240 | 100 | 1.90E-226 | WP_003234847.1 | MULTISPECIES: glutamate-aspartate/proton symporter GltP [Bacillales] |
| BSLIN78GL000241 | 100 | 0.00E+00 | WP_015252925.1 | MULTISPECIES: glucose-specific PTS transporter subunit IIBC [Bacillus] |
| BSLIN78GL000242 | 100 | 2.60E-138 | WP_032722871.1 | MULTISPECIES: glucosamine-6-phosphate deaminase [Bacillus] |
| BSLIN78GL000243 | 100 | 1.20E-127 | WP_003234841.1 | MULTISPECIES: transcriptional regulator GamR [Bacillales] |
| BSLIN78GL000244 | 100 | 2.10E-45 | WP_032722873.1 | MULTISPECIES: DUF1648 domain-containing protein [Bacillus] |
| BSLIN78GL000245 | 97.4 | 3.80E-15 | QHF56099.1 | hypothetical protein Bateq7PJ16_0293 [Bacillus subtilis] |
| BSLIN78GL000246 | 100 | 1.50E-206 | ADV95167.1 | branched-chain amino acid aminotransferase [Bacillus subtilis BSn5] |
| BSLIN78GL000247 | 100 | 1.90E-259 | WP_015715174.1 | MULTISPECIES: S-methylmethionine permease [Bacillus] |
| BSLIN78GL000248 | 100 | 4.10E-170 | WP_038428310.1 | homocysteine S-methyltransferase [Bacillus subtilis] |
| BSLIN78GL000249 | 100 | 8.90E-268 | WP_032722877.1 | MULTISPECIES: alanine/glycine:cation symporter family protein [Bacillus] |
| BSLIN78GL000250 | 100 | 1.10E-187 | WP_003234829.1 | MULTISPECIES: glutaminase [Bacillales] |
| BSLIN78GL000251 | 100 | 4.30E-256 | ADV95172.1 | two-component sensor histidine kinase [Bacillus subtilis BSn5] |
| BSLIN78GL000252 | 100 | 3.50E-172 | WP_003234824.1 | MULTISPECIES: glutamine utilization two-component system response regulator |
| BSLIN78GL000254 | 100 | 3.70E-174 | EHA28813.1 | 5-dehydro-4-deoxyglucarate dehydratase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000255 | 100 | 1.70E-277 | AIX05962.1 | Aldehyde dehydrogenase, thermostable [Bacillus subtilis] |
| BSLIN78GL000256 | 100 | 3.50E-261 | WP_038428315.1 | glucarate transporter GudP [Bacillus subtilis] |
| BSLIN78GL000257 | 99.8 | 6.10E-266 | WP_046664304.1 | MULTISPECIES: glucarate dehydratase [Bacillus] |
| BSLIN78GL000258 | 100 | 1.10E-125 | WP_003234813.1 | MULTISPECIES: FadR/GntR family transcriptional regulator [Bacillus] |
| BSLIN78GL000259 | 100 | 1.10E-295 | WP_029726963.1 | galactarate dehydratase [Bacillus subtilis] |
| BSLIN78GL000260 | 100 | 1.60E-16 | AHA76211.1 | Hypothetical Protein U712_01285 [Bacillus subtilis PY79] |
| BSLIN78GL000261 | 100 | 5.10E-176 | WP_029726965.1 | macrolide 2'-phosphotransferase MphK [Bacillus subtilis] |
| BSLIN78GL000262 | 100 | 1.80E-23 | WP_003234807.1 | MULTISPECIES: anti-TRAP regulator [Bacillales] |
| BSLIN78GL000263 | 100 | 3.20E-144 | CAF1761603.1 | hypothetical protein NRS6103_03201 [Bacillus subtilis] |
| BSLIN78GL000264 | 96.9 | 1.60E-26 | CAF1827218.1 | hypothetical protein NRS6131_02656 [Bacillus subtilis] |
| BSLIN78GL000265 | 100 | 5.70E-127 | AMR48465.1 | DNA-binding response regulator [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL000266 | 100 | 1.70E-171 | WP_015252907.1 | MULTISPECIES: two-component system sensor histidine kinase YcbM [Bacillus] |
| BSLIN78GL000267 | 100 | 1.80E-168 | WP_029726967.1 | ABC transporter ATP-binding protein [Bacillus subtilis] |
| BSLIN78GL000268 | 100 | 8.70E-120 | WP_080348100.1 | ABC transporter permease [Bacillus subtilis] |
| BSLIN78GL000269 | 100 | 3.70E-70 | BAI83711.2 | hypothetical protein BSNT_06572 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL000270 | 100 | 1.60E-20 | AKN12334.1 | hypothetical protein ABU16_1258 [Bacillus subtilis] |
| BSLIN78GL000271 | 100 | 6.60E-87 | BAI83713.2 | cell wall hydrolase [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL000272 | 99.6 | 1.60E-149 | AII34389.1 | hypothetical protein M036_01440 [Bacillus subtilis TO-A] |
| BSLIN78GL000273 | 100 | 4.60E-25 | WP_019712346.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL000274 | 100 | 0.00E+00 | WP_014475691.1 | MULTISPECIES: alkaline phosphatase PhoD [Bacillus] |
| BSLIN78GL000275 | 100 | 2.40E-31 | AGE62114.1 | component of the twin-arginine pre-protein translocation pathway [Bacillus subtilis |
| BSLIN78GL000276 | 100 | 6.80E-131 | WP_014475692.1 | MULTISPECIES: twin-arginine translocase subunit TatC [Bacillus] |
| BSLIN78GL000277 | 100 | 2.20E-120 | WP_038427317.1 | MULTISPECIES: pyroglutamyl-peptidase I [Bacillus] |
| BSLIN78GL000278 | 100 | 2.00E-211 | WP_050258602.1 | aminotransferase class V-fold PLP-dependent enzyme [Bacillus subtilis] |
| BSLIN78GL000279 | 100 | 8.10E-269 | WP_032728901.1 | MULTISPECIES: lincomycin efflux MFS transporter Lmr(B) [Bacillus] |
| BSLIN78GL000280 | 100 | 2.30E-102 | WP_038428320.1 | transcriptional regulator LmrA [Bacillus subtilis] |
| BSLIN78GL000281 | 97.7 | 2.70E-17 | AHA76231.1 | Hypothetical Protein U712_01385 [Bacillus subtilis PY79] |
| BSLIN78GL000282 | 100 | 5.30E-207 | WP_072175248.1 | asparaginase AnsZ [Bacillus subtilis] |
| BSLIN78GL000283 | 99.5 | 3.80E-120 | BAI83725.2 | lipase [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL000284 | 100 | 3.50E-59 | WP_029317228.1 | MULTISPECIES: RDD family protein [Bacillus] |
| BSLIN78GL000285 | 100 | 4.90E-202 | WP_003234762.1 | MULTISPECIES: helix-turn-helix domain-containing protein [Bacillus] |
| BSLIN78GL000286 | 100 | 1.80E-179 | WP_046380763.1 | MULTISPECIES: two-component system sensor histidine kinase NatK [Bacillus] |
| BSLIN78GL000287 | 100 | 3.00E-128 | WP_003234759.1 | MULTISPECIES: two-component system response regulator NatR [Bacillales] |
| BSLIN78GL000288 | 100 | 4.30E-133 | WP_015252894.1 | MULTISPECIES: sodium ABC transporter ATP-binding protein NatA [Bacillus] |
| BSLIN78GL000289 | 100 | 8.10E-211 | WP_147797780.1 | sodium ABC transporter permease NatB [Bacillus subtilis] |
| BSLIN78GL000290 | 100 | 8.30E-174 | WP_147797781.1 | aldo/keto reductase [Bacillus subtilis] |
| BSLIN78GL000291 | 100 | 2.00E-195 | WP_003234750.1 | MULTISPECIES: DUF4352 domain-containing protein [Bacillales] |
| BSLIN78GL000292 | 100 | 3.10E-281 | WP_147797783.1 | YcdB/YcdC domain-containing protein [Bacillus subtilis] |
| BSLIN78GL000293 | 99.8 | 1.40E-292 | UBZ17261.1 | hypothetical protein JS609_00321 [Bacillus subtilis] |
| BSLIN78GL000294 | 100 | 5.10E-72 | WP_017695036.1 | MULTISPECIES: peptidoglycan L-alanyl-D-glutamate endopeptidase CwlK |
| BSLIN78GL000295 | 100 | 2.10E-216 | WP_015715201.1 | MULTISPECIES: response regulator aspartate phosphatase RapJ [Bacillus] |
| BSLIN78GL000296 | 100 | 4.50E-141 | WP_029726977.1 | MULTISPECIES: SDR family oxidoreductase [Bacillus] |
| BSLIN78GL000297 | 100 | 0.00E+00 | WP_029726978.1 | alpha-glucosidase [Bacillus subtilis] |
| BSLIN78GL000298 | 100 | 8.50E-182 | WP_029726979.1 | metal ABC transporter substrate-binding protein [Bacillus subtilis] |
| BSLIN78GL000299 | 100 | 6.50E-131 | WP_014475714.1 | MULTISPECIES: zinc ABC transporter ATP-binding protein ZnuC [Bacillus] |
| BSLIN78GL000300 | 100 | 7.30E-145 | WP_003246340.1 | MULTISPECIES: zinc ABC transporter permease ZnuB [Bacillales] |
| BSLIN78GL000301 | 99.1 | 3.00E-193 | QHF56155.1 | 1,2-monooxygenase [Bacillus subtilis] |
| BSLIN78GL000302 | 100 | 3.20E-110 | WP_017695039.1 | MULTISPECIES: TerD family protein [Bacillus] |
| BSLIN78GL000303 | 100 | 6.00E-106 | WP_003234723.1 | MULTISPECIES: TerD family protein [Bacillales] |
| BSLIN78GL000304 | 100 | 8.40E-108 | AGA22525.1 | Hypothetical protein YceE [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL000305 | 100 | 2.50E-130 | QHF56159.1 | membrane protein [Bacillus subtilis] |
| BSLIN78GL000306 | 100 | 0.00E+00 | WP_029726981.1 | YceG family protein [Bacillus subtilis] |
| BSLIN78GL000307 | 100 | 1.10E-198 | WP_003234715.1 | MULTISPECIES: toxic anion resistance protein [Bacillales] |
| BSLIN78GL000308 | 100 | 7.80E-225 | WP_326253276.1 | niacin permease NiaP [Bacillus subtilis] |
| BSLIN78GL000309 | 100 | 5.30E-218 | WP_003246304.1 | MULTISPECIES: MFS transporter [Bacillales] |
| BSLIN78GL000310 | 100 | 1.40E-44 | WP_010886398.1 | MULTISPECIES: metalloregulator ArsR/SmtB family transcription factor [Bacillales] |
| BSLIN78GL000311 | 84.6 | 3.30E-14 | AFI26843.1 | hypothetical protein MY9_0304 [Bacillus sp. JS] |
| BSLIN78GL000312 | 100 | 3.40E-231 | WP_003246301.1 | MULTISPECIES: glycine/proline betaine ABC transporter ATP-binding protein |
| BSLIN78GL000313 | 100 | 1.80E-151 | WP_003234703.1 | MULTISPECIES: glycine/proline betaine ABC transporter permease subunit OpuAB |
| BSLIN78GL000314 | 100 | 2.30E-165 | WP_003234700.1 | MULTISPECIES: glycine/proline betaine ABC transporter substrate-binding protein |
| BSLIN78GL000315 | 100 | 1.20E-219 | WP_003234698.1 | MULTISPECIES: M20 peptidase aminoacylase family protein [Bacillus] |
| BSLIN78GL000316 | 99.8 | 1.50E-267 | AGE62149.1 | hypothetical protein C663_0292 [Bacillus subtilis XF-1] |
| BSLIN78GL000317 | 99.3 | 8.50E-79 | AGE62150.1 | hypothetical protein C663_0293 [Bacillus subtilis XF-1] |
| BSLIN78GL000318 | 100 | 0.00E+00 | WP_003234692.1 | MULTISPECIES: alpha-amylase [Bacillales] |
| BSLIN78GL000319 | 100 | 4.60E-16 | AHA76268.1 | Hypothetical Protein U712_01570 [Bacillus subtilis PY79] |
| BSLIN78GL000320 | 100 | 5.00E-182 | WP_003234685.1 | MULTISPECIES: L-lactate dehydrogenase [Bacillales] |

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| BSLIN78GL000321 | 100 | 5.70E-303 | WP_003246465.1 | MULTISPECIES: L-lactate permease [Bacillales] |
| BSLIN78GL000322 | 100 | 8.30E-288 | WP_003246377.1 | MULTISPECIES: multidrug efflux MFS transporter Bmr3 [Bacillales] |
| BSLIN78GL000323 | 100 | 1.30E-73 | AGE62155.1 | putative transcriptional regulator [Bacillus subtilis XF-1] |
| BSLIN78GL000324 | 100 | 2.00E-115 | WP_003246469.1 | MULTISPECIES: LysE family translocator [Bacillales] |
| BSLIN78GL000325 | 100 | 5.20E-150 | WP_003246374.1 | MULTISPECIES: YqcI/YcgG family protein [Bacillales] |
| BSLIN78GL000326 | 100 | 1.40E-254 | WP_029727057.1 | MULTISPECIES: amino acid permease [Bacillus] |
| BSLIN78GL000327 | 100 | 7.40E-121 | AHA76276.1 | Uncharacterized protein ycgI [Bacillus subtilis PY79] |
| BSLIN78GL000328 | 100 | 1.70E-160 | AGE62160.1 | NAD synthetase [Bacillus subtilis XF-1] |
| BSLIN78GL000329 | 98.1 | 2.10E-112 | RUS03968.1 | hypothetical protein EFW59_03959 [Bacillus subtilis] |
| BSLIN78GL000330 | 100 | 9.30E-104 | WP_003246473.1 | MULTISPECIES: shikimate kinase [Bacillales] |
| BSLIN78GL000331 | 100 | 8.00E-163 | WP_160245387.1 | class I SAM-dependent methyltransferase [Bacillus subtilis] |
| BSLIN78GL000332 | 100 | 1.10E-179 | WP_038427340.1 | LysR family transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL000333 | 100 | 9.10E-184 | WP_029727060.1 | MULTISPECIES: cephalosporin C deacetylase [Bacillus] |
| BSLIN78GL000334 | 99.3 | 1.70E-160 | ADV95249.1 | hypothetical protein BSn5_13175 [Bacillus subtilis BSn5] |
| BSLIN78GL000335 | 100 | 7.70E-172 | AIC96950.1 | proline dehydrogenase [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL000336 | 100 | 2.90E-296 | WP_003234655.1 | MULTISPECIES: L-glutamate gamma-semialdehyde dehydrogenase [Bacillales] |
| BSLIN78GL000337 | 100 | 1.50E-270 | AII34448.1 | proline:sodium symporter [Bacillus subtilis TO-A] |
| BSLIN78GL000338 | 100 | 1.70E-230 | WP_003234651.1 | MULTISPECIES: proline utilization transcriptional regulator PutR [Bacillales] |
| BSLIN78GL000339 | 100 | 2.80E-168 | WP_046380772.1 | MULTISPECIES: TIGR03943 family protein [Bacillus] |
| BSLIN78GL000340 | 100 | 1.60E-161 | WP_003234647.1 | MULTISPECIES: permease [Bacillus] |
| BSLIN78GL000341 | 99.6 | 3.80E-151 | WP_163131182.1 | MULTISPECIES: alpha/beta hydrolase [Bacillus] |
| BSLIN78GL000342 | 100 | 1.60E-191 | WP_163131180.1 | MULTISPECIES: ferredoxin--NADP(+) reductase [Bacillus] |
| BSLIN78GL000343 | 100 | 2.40E-281 | WP_101172118.1 | MULTISPECIES: uroporphyrinogen-III C-methyltransferase [Bacillus |
| BSLIN78GL000344 | 100 | 3.80E-57 | EHA28727.1 | assimilatory nitrite reductase (subunit) [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000345 | 100 | 0.00E+00 | WP_086343433.1 | NADPH-nitrite reductase [Bacillus subtilis] |
| BSLIN78GL000346 | 100 | 0.00E+00 | WP_088467517.1 | assimilatory nitrate reductase catalytic subunit [Bacillus subtilis] |
| BSLIN78GL000347 | 100 | 0.00E+00 | WP_032722896.1 | assimilatory nitrate reductase electron transfer subunit NasB [Bacillus subtilis] |
| BSLIN78GL000348 | 100 | 3.80E-227 | WP_032722897.1 | nitrate/nitrite transporter [Bacillus subtilis] |
| BSLIN78GL000349 | 100 | 4.00E-173 | WP_032722899.1 | GTP cyclohydrolase FolE2 [Bacillus subtilis] |
| BSLIN78GL000350 | 100 | 4.80E-105 | KFC29009.1 | L,D-transpeptidase [Bacillus subtilis] |
| BSLIN78GL000351 | 100 | 5.00E-27 | WP_326253271.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL000352 | 100 | 2.30E-229 | WP_003234625.1 | MULTISPECIES: zinc metallochaperone ZinU [Bacillales] |
| BSLIN78GL000353 | 100 | 6.00E-121 | AIX06053.1 | Inner membrane amino-acid ABC transporter permease protein YecS [Bacillus |
| BSLIN78GL000354 | 100 | 1.00E-157 | WP_029727074.1 | MULTISPECIES: transporter substrate-binding domain-containing protein [Bacillus] |
| BSLIN78GL000355 | 100 | 6.60E-19 | AHA76304.1 | Hypothetical Protein U712_01750 [Bacillus subtilis PY79] |
| BSLIN78GL000356 | 100 | 7.30E-78 | WP_029727075.1 | MULTISPECIES: RDD family protein [Bacillus] |
| BSLIN78GL000357 | 100 | 8.00E-70 | EHA28715.1 | hypothetical protein BSSC8_39880 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000358 | 100 | 3.50E-285 | RAP04982.1 | Beta-glucosidase [Bacillus subtilis] |
| BSLIN78GL000359 | 100 | 8.10E-70 | WP_015715226.1 | MULTISPECIES: DNA-entry nuclease inhibitor [Bacillus] |
| BSLIN78GL000360 | 100 | 1.50E-80 | WP_003234608.1 | MULTISPECIES: DNA-entry nuclease [Bacillus] |
| BSLIN78GL000361 | 99.8 | 3.30E-298 | WP_029727077.1 | MULTISPECIES: methyl-accepting chemotaxis protein TlpC [Bacillus] |
| BSLIN78GL000362 | 100 | 1.30E-97 | WP_003234605.1 | MULTISPECIES: 6-phospho-3-hexuloisomerase [Bacillus] |
| BSLIN78GL000363 | 100 | 6.30E-109 | WP_003234604.1 | MULTISPECIES: 3-hexulose-6-phosphate synthase [Bacillus] |
| BSLIN78GL000364 | 100 | 7.20E-62 | EHA28708.1 | positive regulator of hxlAB expression [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000365 | 97.4 | 2.60E-13 | AEP89419.1 | hypothetical protein I33_0399 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL000366 | 99.9 | 0.00E+00 | WP_282914531.1 | surfactin non-ribosomal peptide synthetase SrfAA [Bacillus subtilis] |
| BSLIN78GL000367 | 99.4 | 0.00E+00 | QPF45238.1 | surfactin non-ribosomal peptide synthetase SrfAB [Bacillus subtilis] |
| BSLIN78GL000368 | 100 | 0.00E+00 | WP_326253834.1 | surfactin non-ribosomal peptide synthetase SrfAC [Bacillus subtilis] |
| BSLIN78GL000369 | 100 | 9.80E-138 | WP_003234568.1 | MULTISPECIES: surfactin biosynthesis thioesterase SrfAD [Bacillales] |
| BSLIN78GL000370 | 100 | 1.60E-230 | WP_038427360.1 | MFS transporter [Bacillus subtilis] |
| BSLIN78GL000371 | 100 | 9.60E-101 | WP_038427362.1 | YcxB family protein [Bacillus subtilis] |
| BSLIN78GL000372 | 100 | 5.30E-168 | WP_041850685.1 | MULTISPECIES: DMT family transporter [Bacillus] |
| BSLIN78GL000373 | 100 | 8.50E-19 | KIL29382.1 | hypothetical protein B4067_0372 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL000374 | 100 | 6.80E-254 | WP_195727647.1 | PLP-dependent aminotransferase family protein [Bacillus subtilis] |
| BSLIN78GL000375 | 100 | 1.30E-128 | WP_195727646.1 | 4'-phosphopantetheinyl transferase [Bacillus subtilis] |
| BSLIN78GL000376 | 99.5 | 1.00E-117 | WP_003234545.1 | MULTISPECIES: YitT family protein [Bacillus] |
| BSLIN78GL000377 | 100 | 3.90E-134 | WP_003234543.1 | MULTISPECIES: cystine ABC transporter ATP-binding protein TcyC [Bacillus |
| BSLIN78GL000378 | 100 | 2.90E-126 | WP_003234541.1 | MULTISPECIES: cystine ABC transporter permease TcyB [Bacillales] |
| BSLIN78GL000379 | 100 | 1.40E-148 | WP_032726543.1 | MULTISPECIES: cystine ABC transporter substrate-binding lipoprotein TcyA |
| BSLIN78GL000380 | 100 | 8.10E-163 | WP_003234533.1 | MULTISPECIES: transcriptional regulator BsdA [Bacillus] |
| BSLIN78GL000381 | 99.5 | 1.00E-111 | AGE62212.1 | aromatic acid decarboxylase [Bacillus subtilis XF-1] |
| BSLIN78GL000382 | 99.8 | 5.30E-281 | WP_003234529.1 | MULTISPECIES: phenolic acid decarboxylase BsdC [Bacillus] |
| BSLIN78GL000383 | 100 | 8.50E-30 | WP_173613898.1 | phenolic acid decarboxylase subunit BsdD [Bacillus subtilis] |
| BSLIN78GL000384 | 100 | 9.70E-80 | WP_015482788.1 | pyridoxamine 5'-phosphate oxidase family protein [Bacillus subtilis] |
| BSLIN78GL000385 | 100 | 1.50E-161 | WP_029726572.1 | MULTISPECIES: alpha/beta hydrolase [Bacillus] |
| BSLIN78GL000386 | 99.8 | 6.80E-246 | WP_029726571.1 | MULTISPECIES: peptide MFS transporter [Bacillus] |
| BSLIN78GL000387 | 100 | 0.00E+00 | WP_029726570.1 | MULTISPECIES: right-handed parallel beta-helix repeat-containing protein [Bacillus] |
| BSLIN78GL000388 | 100 | 2.80E-32 | WP_015252828.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL000389 | 99.8 | 6.10E-305 | WP_041336865.1 | MULTISPECIES: spore germination protein GerKA [Bacillus] |
| BSLIN78GL000390 | 100 | 4.40E-228 | WP_041336863.1 | spore germination protein GerKC [Bacillus subtilis] |
| BSLIN78GL000391 | 99.7 | 2.90E-205 | WP_101172128.1 | spore germination protein GerKB [Bacillus subtilis] |
| BSLIN78GL000392 | 100 | 4.90E-123 | WP_014662766.1 | MULTISPECIES: ABC transporter ATP-binding protein [Bacillus] |
| BSLIN78GL000393 | 100 | 5.30E-268 | WP_326253830.1 | ABC transporter permease [Bacillus subtilis] |
| BSLIN78GL000394 | 100 | 7.20E-150 | TWG78854.1 | DNA-binding response OmpR family regulator [Bacillus subtilis J27] |
| BSLIN78GL000395 | 100 | 1.50E-267 | WP_009969263.1 | MULTISPECIES: two-component system sensor histidine kinase YclK [Bacillales] |
| BSLIN78GL000396 | 100 | 2.90E-224 | AGE62227.1 | Response regulator aspartate phosphatase C [Bacillus subtilis XF-1] |
| BSLIN78GL000397 | 100 | 3.60E-13 | WP_003224994.1 | MULTISPECIES: phosphatase RapC inhibitor PhrC [Bacillales] |
| BSLIN78GL000398 | 100 | 1.20E-13 | KIU10900.1 | hypothetical protein SC09_Contig25orf00769 [Bacillus subtilis] |
| BSLIN78GL000399 | 100 | 4.80E-12 | WP_032678937.1 | MULTISPECIES: YjcZ family sporulation protein [Bacillus] |
| BSLIN78GL000400 | 100 | 1.10E-254 | WP_029726569.1 | aspartate kinase [Bacillus subtilis] |

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| BSLIN78GL000401 | 100 | 1.40E-168 | WP_014475804.1 | MULTISPECIES: petrobactin ABC transporter permease YclN [Bacillus] |
| BSLIN78GL000402 | 100 | 1.40E-168 | WP_014475805.1 | MULTISPECIES: petrobactin ABC transporter permease YclO [Bacillus] |
| BSLIN78GL000403 | 100 | 6.60E-137 | WP_015252819.1 | MULTISPECIES: petrobactin ABC transporter ATP-binding protein YclP [Bacillus] |
| BSLIN78GL000404 | 100 | 1.80E-176 | WP_015252818.1 | MULTISPECIES: petrobactin ABC transporter substrate-binding protein YclQ |
| BSLIN78GL000405 | 96.6 | 1.20E-253 | WP_174229086.1 | MDR family MFS transporter [Bacillus tequilensis] |
| BSLIN78GL000406 | 100 | 7.60E-164 | KIL29346.1 | hypothetical protein B4067_0336 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL000407 | 100 | 2.90E-137 | WP_014475811.1 | MULTISPECIES: oxygen-insensitive NADPH nitroreductase [Bacillus] |
| BSLIN78GL000408 | 100 | 4.50E-46 | WP_003234477.1 | MULTISPECIES: putative quinol monooxygenase [Bacilli] |
| BSLIN78GL000409 | 100 | 1.00E-51 | WP_003234476.1 | MULTISPECIES: metalloregulator ArsR/SmtB family transcription factor [Bacillales] |
| BSLIN78GL000410 | 100 | 1.70E-274 | WP_015252815.1 | MULTISPECIES: transcriptional regulator GabR [Bacillus] |
| BSLIN78GL000411 | 99.1 | 9.00E-254 | AFQ56327.1 | 4-aminobutyrate aminotransferase [Bacillus subtilis QB928] |
| BSLIN78GL000412 | 100 | 6.00E-269 | AGA23705.1 | Succinate-semialdehyde dehydrogenase [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL000413 | 100 | 2.60E-153 | WP_026009827.1 | MULTISPECIES: glucose uptake protein GlcU [Bacillus] |
| BSLIN78GL000414 | 100 | 2.30E-145 | AFQ56330.1 | Glucose 1-dehydrogenase [Bacillus subtilis QB928] |
| BSLIN78GL000415 | 99.5 | 7.10E-113 | EHA28974.1 | hypothetical protein BSSC8_39280 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000416 | 100 | 0.00E+00 | WP_326253840.1 | copper transporter YcnJ [Bacillus subtilis] |
| BSLIN78GL000417 | 100 | 7.00E-107 | WP_024573246.1 | MULTISPECIES: copper uptake transcriptional regulator YcnK [Bacillus] |
| BSLIN78GL000418 | 100 | 8.00E-61 | WP_003234445.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL000419 | 99.8 | 4.60E-264 | WP_129110443.1 | PTS mannitol transporter subunit IICB [Bacillus subtilis] |
| BSLIN78GL000420 | 100 | 1.90E-72 | AFQ56336.1 | Phosphotransferase system (PTS) mannitol-specific enzyme [Bacillus subtilis QB928] |
| BSLIN78GL000421 | 100 | 3.00E-210 | WP_003234438.1 | MULTISPECIES: mannitol-1-phosphate 5-dehydrogenase [Bacillus] |
| BSLIN78GL000422 | 100 | 1.40E-201 | WP_003234436.1 | MULTISPECIES: tartrate dehydrogenase [Bacillales] |
| BSLIN78GL000423 | 100 | 6.30E-100 | WP_014475826.1 | signal peptidase I [Bacillus subtilis] |
| BSLIN78GL000424 | 97.6 | 7.80E-115 | QHF56281.1 | hypothetical protein Bateq7PJ16_0475 [Bacillus subtilis] |
| BSLIN78GL000425 | 100 | 1.20E-71 | AFQ56341.1 | Putative hydroxymyristoyl-(acyl carrier protein)dehydratase [Bacillus subtilis QB928 |
| BSLIN78GL000426 | 100 | 1.20E-24 | WP_134982047.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL000427 | 100 | 4.50E-138 | WP_003234424.1 | MULTISPECIES: phosphoglycolate phosphatase [Bacillales] |
| BSLIN78GL000428 | 100 | 1.00E-140 | WP_003234423.1 | MULTISPECIES: 5-oxoprolinase subunit PpxA [Bacillales] |
| BSLIN78GL000429 | 100 | 5.90E-220 | WP_014478854.1 | MULTISPECIES: NRAMP family divalent metal transporter [Bacillus] |
| BSLIN78GL000430 | 100 | 1.10E-150 | PLV34728.1 | hypothetical protein BSP4_16280 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL000431 | 100 | 2.00E-135 | WP_041351806.1 | MULTISPECIES: 5-oxoprolinase subunit B [Bacillus] |
| BSLIN78GL000432 | 100 | 7.10E-187 | ADV95342.1 | putative hydrolase subunit antagonist of KipI [Bacillus subtilis BSn5] |
| BSLIN78GL000433 | 100 | 5.20E-134 | AOA53069.1 | HTH-type transcriptional regulator KipR [Bacillus subtilis] |
| BSLIN78GL000434 | 100 | 5.80E-118 | WP_029317305.1 | MULTISPECIES: spore germination lipase LipC [Bacillus] |
| BSLIN78GL000435 | 100 | 3.10E-38 | AFQ56351.1 | YczI [Bacillus subtilis QB928] |
| BSLIN78GL000436 | 100 | 3.30E-49 | WP_029726562.1 | MULTISPECIES: antibiotic biosynthesis monooxygenase [Bacillus] |
| BSLIN78GL000437 | 100 | 0.00E+00 | AIC97039.1 | penicillin-binding protein [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL000438 | 100 | 2.30E-173 | WP_003234411.1 | MULTISPECIES: aldo/keto reductase family oxidoreductase [Bacillus] |
| BSLIN78GL000439 | 100 | 0.00E+00 | WP_029726559.1 | mannitol operon transcriptional activator MtlR [Bacillus subtilis] |
| BSLIN78GL000440 | 100 | 1.90E-21 | AHA76383.1 | Hypothetical Protein U712_02160 [Bacillus subtilis PY79] |
| BSLIN78GL000441 | 100 | 4.50E-294 | WP_024572566.1 | class I adenylate-forming enzyme family protein [Bacillus subtilis] |
| BSLIN78GL000442 | 100 | 3.90E-108 | WP_003234403.1 | MULTISPECIES: methyltransferase domain-containing protein [Bacillales] |
| BSLIN78GL000443 | 100 | 1.40E-162 | WP_003246648.1 | MULTISPECIES: SDR family oxidoreductase [Bacillales] |
| BSLIN78GL000444 | 100 | 8.30E-96 | WP_003234400.1 | MULTISPECIES: D-lyxose ketol-isomerase [Bacillales] |
| BSLIN78GL000445 | 100 | 8.50E-102 | WP_003246691.1 | MULTISPECIES: GNAT family protein [Bacillales] |
| BSLIN78GL000446 | 100 | 4.70E-76 | WP_003234396.1 | MULTISPECIES: pyridoxamine 5'-phosphate oxidase family protein [Bacillales] |
| BSLIN78GL000447 | 99.6 | 2.00E-144 | WP_038427391.1 | lipid II flippase Amj [Bacillus subtilis] |
| BSLIN78GL000448 | 100 | 2.20E-48 | WP_015252794.1 | MULTISPECIES: DUF3817 domain-containing protein [Bacillus] |
| BSLIN78GL000449 | 100 | 4.10E-81 | QHF56306.1 | transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL000450 | 100 | 0.00E+00 | WP_029317313.1 | MULTISPECIES: DNA topoisomerase III [Bacillus] |
| BSLIN78GL000451 | 99.2 | 3.20E-212 | AFQ56366.1 | Putative glycosyl hydrolase lipoprotein [Bacillus subtilis QB928] |
| BSLIN78GL000452 | 100 | 5.50E-156 | WP_113713036.1 | cyclic-di-GMP receptor EpsK [Bacillus subtilis] |
| BSLIN78GL000453 | 100 | 0.00E+00 | RAP05068.1 | hypothetical protein HS3_03754 [Bacillus subtilis] |
| BSLIN78GL000454 | 100 | 2.20E-235 | WP_029726554.1 | glycosyltransferase family 2 protein [Bacillus subtilis] |
| BSLIN78GL000455 | 100 | 0.00E+00 | CAF1764565.1 | hypothetical protein NRS6103_03385 [Bacillus subtilis] |
| BSLIN78GL000456 | 97.6 | 7.40E-17 | KIL29485.1 | hypothetical protein B4067_0474 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL000457 | 100 | 0.00E+00 | WP_003234374.1 | MULTISPECIES: potassium transporter KimA [Bacillus] |
| BSLIN78GL000458 | 100 | 1.70E-79 | WP_205423225.1 | MULTISPECIES: NUDIX hydrolase [Bacillus] |
| BSLIN78GL000459 | 100 | 0.00E+00 | WP_003246569.1 | MULTISPECIES: pyruvate oxidase [Bacillales] |
| BSLIN78GL000460 | 100 | 1.70E-51 | QHF56317.1 | membrane protein [Bacillus subtilis] |
| BSLIN78GL000461 | 100 | 2.70E-231 | WP_003234364.1 | MULTISPECIES: Nramp family divalent metal transporter [Bacillales] |
| BSLIN78GL000462 | 100 | 5.30E-41 | EHA28926.1 | hypothetical protein BSSC8_38800 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000463 | 100 | 9.70E-92 | AFQ56377.1 | YdaT [Bacillus subtilis QB928] |
| BSLIN78GL000464 | 100 | 2.30E-151 | WP_003246628.1 | MULTISPECIES: EcsC family protein [Bacillales] |
| BSLIN78GL000465 | 100 | 7.80E-67 | WP_003246542.1 | MULTISPECIES: glucose starvation-inducible protein GsiB [Bacillales] |
| BSLIN78GL000466 | 100 | 3.00E-57 | AFQ56380.1 | Putative enzyme [Bacillus subtilis QB928] |
| BSLIN78GL000467 | 100 | 7.80E-61 | WP_017697013.1 | MULTISPECIES: YdbC family protein [Bacillus] |
| BSLIN78GL000468 | 100 | 9.00E-156 | WP_029726549.1 | manganese catalase family protein [Bacillus subtilis] |
| BSLIN78GL000469 | 100 | 9.00E-201 | WP_029726548.1 | C4-dicarboxylate TRAP transporter substrate-binding protein DctB [Bacillus subtilis] |
| BSLIN78GL000470 | 100 | 1.20E-300 | WP_003234348.1 | MULTISPECIES: two-component system sensor histidine kinase DctS [Bacillales] |
| BSLIN78GL000471 | 100 | 6.00E-121 | WP_003234347.1 | MULTISPECIES: two-component system response regulator DctR [Bacillales] |
| BSLIN78GL000472 | 100 | 5.70E-234 | AFQ56386.1 | C4-dicarboxylate transport protein [Bacillus subtilis QB928] |
| BSLIN78GL000473 | 100 | 5.30E-193 | WP_003246523.1 | MULTISPECIES: AI-2E family transporter [Bacillales] |
| BSLIN78GL000474 | 100 | 1.40E-23 | WP_009966597.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL000475 | 100 | 1.50E-170 | WP_003246573.1 | MULTISPECIES: ABC transporter ATP-binding protein [Bacillales] |
| BSLIN78GL000476 | 100 | 4.80E-132 | WP_003246631.1 | MULTISPECIES: ABC transporter permease [Bacillales] |
| BSLIN78GL000477 | 100 | 3.30E-13 | QHF56333.1 | hypothetical protein Bateq7PJ16_0527 [Bacillus subtilis] |
| BSLIN78GL000478 | 100 | 2.30E-44 | QHF56334.1 | hypothetical protein Bateq7PJ16_0528 [Bacillus subtilis] |
| BSLIN78GL000479 | 100 | 2.70E-219 | WP_003234334.1 | MULTISPECIES: acyl-CoA dehydrogenase family protein [Bacillales |
| BSLIN78GL000480 | 100 | 4.20E-26 | WP_010886410.1 | MULTISPECIES: Fur-regulated basic protein FbpB [Bacillales] |

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| BSLIN78GL000481 | 100 | 2.60E-22 | WP_003225157.1 | MULTISPECIES: Fur-regulated basic protein FbpA [Bacillales |
| BSLIN78GL000482 | 100 | 9.90E-161 | WP_029726541.1 | cation diffusion facilitator family transporter [Bacillus subtilis] |
| BSLIN78GL000483 | 100 | 5.40E-56 | WP_003234326.1 | MULTISPECIES: thioredoxin family protein [Bacillales |
| BSLIN78GL000484 | 99.7 | 4.10E-201 | WP_029726540.1 | D-alanine--D-alanine ligase [Bacillus subtilis] |
| BSLIN78GL000485 | 100 | 2.20E-274 | RAP05097.1 | UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanine |
| BSLIN78GL000486 | 100 | 1.70E-266 | WP_142302775.1 | ATP-dependent RNA helicase CshA [Bacillus subtilis] |
| BSLIN78GL000487 | 100 | 1.40E-84 | WP_003234318.1 | MULTISPECIES: PH domain-containing protein [Bacillales] |
| BSLIN78GL000488 | 100 | 9.80E-278 | RAP05100.1 | hypothetical protein HS3_03786 [Bacillus subtilis] |
| BSLIN78GL000489 | 100 | 1.20E-109 | WP_003246687.1 | MULTISPECIES: rhomboid family intramembrane serine protease [Bacillales] |
| BSLIN78GL000490 | 100 | 1.60E-59 | WP_015252768.1 | MULTISPECIES: holo-ACP synthase [Bacillus |
| BSLIN78GL000491 | 100 | 2.10E-208 | AIX06186.1 | Sporulation protein YdcC [Bacillus subtilis] |
| BSLIN78GL000492 | 100 | 1.20E-222 | WP_029727188.1 | MULTISPECIES: alanine racemase [Bacillus] |
| BSLIN78GL000493 | 100 | 1.40E-38 | AGE62318.1 | antitoxin MazF [Bacillus subtilis XF-1] |
| BSLIN78GL000494 | 100 | 7.50E-56 | AGE62319.1 | hypothetical protein C663_0464 [Bacillus subtilis XF-1] |
| BSLIN78GL000495 | 100 | 1.30E-146 | WP_009966610.1 | MULTISPECIES: RsbT co-antagonist protein RsbRA [Bacillales |
| BSLIN78GL000496 | 100 | 4.80E-49 | EHA29030.1 | antagonist of RsbT [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000497 | 100 | 6.90E-63 | WP_003225192.1 | MULTISPECIES: serine/threonine-protein kinase RsbT [Bacillus |
| BSLIN78GL000498 | 100 | 6.80E-190 | WP_003234295.1 | MULTISPECIES: phosphoserine phosphatase RsbU [Bacillales] |
| BSLIN78GL000499 | 100 | 7.50E-53 | BBK71129.1 | anti-sigma-B factor antagonist [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL000500 | 100 | 3.40E-86 | WP_003234299.1 | MULTISPECIES: anti-sigma B factor RsbW [Bacillales] |
| BSLIN78GL000501 | 100 | 6.00E-141 | AAA22713.1 | 37 kd minor sigma factor (rpoF, sigB; ttg start codon) [Bacillus subtilis] |
| BSLIN78GL000502 | 100 | 2.30E-108 | WP_003246608.1 | MULTISPECIES: phosphoserine phosphatase RsbX [Bacillales] |
| BSLIN78GL000503 | 100 | 0.00E+00 | WP_015252761.1 | MULTISPECIES: Tex family protein [Bacillus |
| BSLIN78GL000504 | 100 | 1.20E-15 | WP_003225207.1 | MULTISPECIES: cortex morphogenetic protein CmpA [Bacillales] |
| BSLIN78GL000505 | 100 | 6.00E-85 | WP_015252760.1 | MULTISPECIES: SprT family protein [Bacillus |
| BSLIN78GL000506 | 100 | 3.00E-31 | BEV38903.1 | hypothetical protein BSB_19760 [Bacillus stercoris] |
| BSLIN78GL000508 | 100 | 1.20E-92 | WP_015252758.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL000509 | 100 | 7.10E-119 | RAP05125.1 | hypothetical protein HS3_03818 [Bacillus subtilis] |
| BSLIN78GL000510 | 100 | 4.20E-95 | WP_046664266.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL000511 | 100 | 2.60E-97 | WP_113713038.1 | MULTISPECIES: HNH endonuclease [Bacillus] |
| BSLIN78GL000512 | 100 | 3.90E-137 | WP_015252754.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL000513 | 100 | 4.60E-91 | WP_015252753.1 | MULTISPECIES: DUF4944 domain-containing protein [Bacillus] |
| BSLIN78GL000514 | 100 | 4.30E-203 | WP_015252752.1 | MULTISPECIES: amidase domain-containing protein [Bacillus] |
| BSLIN78GL000515 | 100 | 1.60E-28 | WP_231940254.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL000516 | 100 | 1.20E-17 | WP_214285398.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL000517 | 100 | 4.70E-39 | ADV95415.1 | hypothetical protein BSn5_14035 [Bacillus subtilis BSn5] |
| BSLIN78GL000518 | 100 | 1.90E-23 | WP_009966645.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL000519 | 100 | 3.60E-123 | WP_015252750.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL000520 | 100 | 5.70E-112 | WP_003234249.1 | MULTISPECIES: type 1 glutamine amidotransferase family protein [Bacillales |
| BSLIN78GL000521 | 100 | 4.10E-30 | WP_003234247.1 | MULTISPECIES: cold shock protein CspC [Bacillales] |
| BSLIN78GL000522 | 100 | 1.00E-82 | AGA21930.1 | Hypothetical protein YdeB [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL000523 | 100 | 2.70E-26 | KAF2421418.1 | hypothetical protein B6K89_22455 [Bacillus subtilis] |
| BSLIN78GL000524 | 100 | 5.90E-147 | WP_015252748.1 | MULTISPECIES: DMT family transporter [Bacillus] |
| BSLIN78GL000525 | 100 | 1.90E-167 | WP_015252747.1 | MULTISPECIES: AraC family transcriptional regulator [Bacillus] |
| BSLIN78GL000526 | 99.4 | 1.10E-187 | EHA29119.1 | hypothetical protein BSSC8_38280 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000527 | 100 | 3.50E-166 | WP_019712424.1 | MULTISPECIES: AraC family transcriptional regulator [Bacillus] |
| BSLIN78GL000528 | 100 | 2.80E-266 | AWM19790.1 | PLP-dependent aminotransferase family protein [Bacillus subtilis] |
| BSLIN78GL000529 | 100 | 1.10E-232 | WP_026009831.1 | MULTISPECIES: MFS transporter [Bacillus] |
| BSLIN78GL000530 | 100 | 2.80E-68 | WAE48942.1 | hypothetical protein ORP33_02775 [Bacillus subtilis] |
| BSLIN78GL000531 | 100 | 2.30E-108 | WP_019712427.1 | MULTISPECIES: YdeI family protein [Bacillus |
| BSLIN78GL000532 | 99.5 | 1.60E-109 | WP_029725814.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL000533 | 100 | 3.30E-110 | WP_029317369.1 | MULTISPECIES: rRNA adenine N-6-methyltransferase family protein [Bacillus |
| BSLIN78GL000534 | 100 | 3.10E-125 | TDY56192.1 | DNA-binding response OmpR family regulator [Bacillus subtilis] |
| BSLIN78GL000535 | 100 | 6.20E-197 | WP_029725815.1 | MULTISPECIES: HAMP domain-containing sensor histidine kinase [Bacillus] |
| BSLIN78GL000536 | 100 | 6.10E-112 | WP_231940253.1 | MULTISPECIES: VTT domain-containing protein [Bacillus] |
| BSLIN78GL000537 | 100 | 4.00E-15 | WP_237983720.1 | HPr family phosphocarrier protein [Bacillus subtilis] |
| BSLIN78GL000538 | 98.1 | 1.90E-22 | AKE22330.1 | hypothetical protein BsLM_0531 [Bacillus sp. LM 4-2] |
| BSLIN78GL000539 | 100 | 6.70E-99 | WP_015252737.1 | MULTISPECIES: TetR/AcrR family transcriptional regulator [Bacillus |
| BSLIN78GL000540 | 100 | 5.90E-158 | WP_029725816.1 | MULTISPECIES: DMT family transporter [Bacillus] |
| BSLIN78GL000541 | 100 | 5.80E-272 | WP_029725817.1 | MULTISPECIES: PLP-dependent aminotransferase family protein [Bacillus |
| BSLIN78GL000542 | 100 | 1.30E-73 | AGE62350.1 | putative dehydratase [Bacillus subtilis XF-1] |
| BSLIN78GL000543 | 100 | 2.30E-105 | WP_003234219.1 | MULTISPECIES: alpha/beta hydrolase [Bacillales] |
| BSLIN78GL000544 | 100 | 2.30E-157 | WP_029725818.1 | MULTISPECIES: YitT family protein [Bacillus |
| BSLIN78GL000545 | 99.5 | 2.40E-221 | EHA29105.1 | hypothetical protein BSSC8_38140 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000546 | 100 | 9.70E-107 | WP_003234206.1 | TetR/AcrR family transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL000547 | 100 | 7.90E-28 | WP_003244283.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL000548 | 100 | 1.60E-35 | AGE62358.1 | transcriptional regulator (metals sensing ArsR-SmtB repressors family) [Bacillus |
| BSLIN78GL000549 | 96.5 | 1.40E-232 | WP_134155659.1 | arsenic transporter [Bacillus subtilis] |
| BSLIN78GL000550 | 92.5 | 8.20E-12 | OAY86603.1 | hypothetical protein AWM78_18485 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL000551 | 100 | 4.10E-150 | WP_082359965.1 | MULTISPECIES: GNAT family N-acetyltransferase [Bacillus |
| BSLIN78GL000552 | 100 | 2.90E-160 | WP_220396588.1 | EamA family transporter [Bacillus subtilis] |
| BSLIN78GL000553 | 100 | 1.80E-243 | WP_119899055.1 | PLP-dependent aminotransferase family protein [Bacillus subtilis] |
| BSLIN78GL000554 | 100 | 1.00E-105 | WP_063336124.1 | flavin reductase family protein [Bacillus subtilis] |
| BSLIN78GL000555 | 99.6 | 5.70E-127 | EHA29095.1 | hypothetical protein BSSC8_38040 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000556 | 99.3 | 2.00E-77 | WP_029725825.1 | MULTISPECIES: carboxymuconolactone decarboxylase family protein [Bacillus |
| BSLIN78GL000557 | 100 | 5.70E-18 | WP_014478971.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL000558 | 100 | 8.40E-216 | AIC97135.1 | histidine kinase [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL000559 | 100 | 1.80E-111 | WP_046664259.1 | MULTISPECIES: two-component system response regulator YdfI [Bacillus |
| BSLIN78GL000560 | 100 | 0.00E+00 | WP_326253811.1 | MMPL family transporter [Bacillus subtilis] |
| BSLIN78GL000561 | 99.6 | 3.90E-145 | WP_213414853.1 | alpha/beta hydrolase [Bacillus subtilis] |

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| BSLIN78GL000562 | 100 | 3.00E-120 | WP_033883509.1 | MULTISPECIES: DUF554 domain-containing protein [Bacillus] |
| BSLIN78GL000563 | 100 | 7.30E-150 | WP_015715309.1 | MULTISPECIES: MerR family transcriptional regulator [Bacillus] |
| BSLIN78GL000564 | 100 | 2.90E-160 | WP_038428417.1 | MULTISPECIES: manganese transporter MneP [Bacillus] |
| BSLIN78GL000565 | 100 | 1.70E-111 | BAA19382.1 | ydfN [Bacillus subtilis] [Bacillus subtilis subsp. subtilis str. 168] |
| BSLIN78GL000566 | 100 | 1.80E-184 | WP_038427440.1 | ring-cleaving dioxygenase [Bacillus subtilis] |
| BSLIN78GL000567 | 100 | 6.80E-60 | WP_003234169.1 | MULTISPECIES: DoxX family protein [Bacillales] |
| BSLIN78GL000568 | 100 | 3.20E-30 | EHA29082.1 | putative thioredoxin or thiol-disulfide isomerase [Bacillus subtilis subsp. subtilis str. |
| BSLIN78GL000569 | 100 | 1.20E-29 | WP_041351246.1 | spore germination protein [Bacillus subtilis] |
| BSLIN78GL000570 | 100 | 7.10E-14 | AHA76501.1 | Hypothetical Protein U712_02750 [Bacillus subtilis PY79] |
| BSLIN78GL000571 | 97.8 | 6.20E-17 | AGI27816.1 | hypothetical protein I653_02755 [Bacillus subtilis subsp. subtilis str. BAB-1] |
| BSLIN78GL000572 | 100 | 1.40E-19 | EHA29077.1 | hypothetical protein BSSC8_37860 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000573 | 100 | 1.30E-100 | WP_003234158.1 | MULTISPECIES: DUF421 domain-containing protein [Bacillales] |
| BSLIN78GL000574 | 100 | 1.20E-124 | WP_003234156.1 | MULTISPECIES: DUF421 domain-containing protein [Bacillales] |
| BSLIN78GL000575 | 100 | 2.80E-76 | WP_015715315.1 | MULTISPECIES: spore coat protein CotP [Bacillus] |
| BSLIN78GL000576 | 100 | 1.30E-38 | WP_003234151.1 | MULTISPECIES: spore germination protein [Bacillales] |
| BSLIN78GL000577 | 99.5 | 4.40E-104 | WP_019712445.1 | MULTISPECIES: TetR/AcrR family transcriptional regulator [Bacillus |
| BSLIN78GL000578 | 99.1 | 6.20E-55 | QJD02995.1 | YdgD [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL000579 | 100 | 3.90E-87 | WP_003234145.1 | MULTISPECIES: GNAT family N-acetyltransferase [Bacillales |
| BSLIN78GL000580 | 100 | 0.00E+00 | WP_046664255.1 | MULTISPECIES: ABC-F type ribosomal protection protein VmlR [Bacillus |
| BSLIN78GL000581 | 100 | 2.70E-261 | WP_014475969.1 | MULTISPECIES: amino acid permease [Bacillus] |
| BSLIN78GL000582 | 100 | 4.70E-103 | BAI84074.2 | nuclease inhibitor [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL000583 | 100 | 1.80E-90 | AIC38942.1 | MarR family transcriptional regulator [Bacillus subtilis subsp. subtilis str. JH642 |
| BSLIN78GL000584 | 100 | 0.00E+00 | WP_032722939.1 | MMPL family transporter [Bacillus subtilis] |
| BSLIN78GL000585 | 100 | 5.50E-113 | WP_003234135.1 | MULTISPECIES: nitroreductase family protein [Bacillales |
| BSLIN78GL000586 | 100 | 3.50E-77 | QHF56461.1 | HTH-type transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL000587 | 100 | 1.90E-218 | WP_015382899.1 | MULTISPECIES: Bcr/CflA family efflux MFS transporter [Bacillus |
| BSLIN78GL000588 | 100 | 6.40E-129 | WP_003234130.1 | MULTISPECIES: sulfite exporter TauE/SafE family protein [Bacillales |
| BSLIN78GL000589 | 100 | 1.10E-124 | WP_029725842.1 | MULTISPECIES: GntR family transcriptional regulator [Bacillus |
| BSLIN78GL000590 | 100 | 3.90E-243 | WP_024571334.1 | MULTISPECIES: glycoside hydrolase family 18 protein [Bacillus |
| BSLIN78GL000591 | 100 | 1.10E-226 | WP_029725843.1 | MULTISPECIES: glycosyltransferase [Bacillus |
| BSLIN78GL000592 | 99.2 | 5.90E-138 | KIL30054.1 | hypothetical protein B4067_0611 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL000593 | 100 | 2.00E-264 | WP_029725845.1 | MULTISPECIES: alkaline phosphatase PhoB [Bacillus] |
| BSLIN78GL000594 | 98.5 | 2.90E-75 | KIN50764.1 | hypothetical protein B4146_0204 [Bacillus subtilis] |
| BSLIN78GL000595 | 100 | 1.00E-72 | CAF1766614.1 | hypothetical protein NRS6103_03531 [Bacillus subtilis] |
| BSLIN78GL000596 | 100 | 6.90E-69 | WP_080477812.1 | MULTISPECIES: GNAT family N-acetyltransferase [Bacillus |
| BSLIN78GL000597 | 100 | 4.90E-185 | WP_029725847.1 | MULTISPECIES: HD domain-containing protein [Bacillus] |
| BSLIN78GL000598 | 100 | 1.30E-114 | KIN50760.1 | hypothetical protein B4146_0200 [Bacillus subtilis] |
| BSLIN78GL000599 | 100 | 4.00E-210 | WP_003234105.1 | MULTISPECIES: purine transporter PbuE [Bacillales] |
| BSLIN78GL000600 | 100 | 3.30E-40 | EHA29048.1 | oligo-alpha-mannoside phosphotransferase system enzyme IIA [Bacillus subtilis |
| BSLIN78GL000601 | 100 | 6.80E-54 | WP_003234101.1 | MULTISPECIES: PTS lactose/cellobiose transporter subunit IIA [Bacillus |
| BSLIN78GL000602 | 100 | 7.30E-248 | WP_015715334.1 | MULTISPECIES: PTS cellobiose transporter subunit IIC [Bacillus |
| BSLIN78GL000603 | 100 | 2.10E-285 | WP_128992460.1 | MULTISPECIES: 6-phospho-beta-glucosidase GmuD [Bacillus |
| BSLIN78GL000604 | 100 | 1.20E-132 | WP_024571322.1 | MULTISPECIES: transcriptional regulator GmuR [Bacillus] |
| BSLIN78GL000605 | 99.7 | 1.80E-170 | WP_326145349.1 | fructokinase GmuE [Bacillus subtilis] |
| BSLIN78GL000606 | 100 | 4.60E-188 | WP_003242491.1 | MULTISPECIES: mannose-6-phosphate isomerase, class I [Bacillales] |
| BSLIN78GL000607 | 99.7 | 6.50E-218 | EHA29041.1 | hypothetical protein BSSC8_37500 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000608 | 99.3 | 2.10E-82 | WP_195727921.1 | manganese catalase family protein [Bacillus subtilis] |
| BSLIN78GL000609 | 100 | 7.50E-29 | CAF1787499.1 | putative manganese catalase [Bacillus subtilis] |
| BSLIN78GL000610 | 100 | 3.70E-85 | AKE21810.1 | hypothetical protein BsLM_0009 [Bacillus sp. LM 4-2] |
| BSLIN78GL000611 | 100 | 5.40E-184 | WP_195727920.1 | thiamine-phosphate kinase [Bacillus subtilis] |
| BSLIN78GL000612 | 100 | 4.30E-86 | WP_015715341.1 | MULTISPECIES: tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex |
| BSLIN78GL000613 | 100 | 6.20E-126 | WP_003234078.1 | MULTISPECIES: tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex |
| BSLIN78GL000614 | 100 | 2.50E-83 | WP_003243019.1 | MULTISPECIES: ribosomal protein S18-alanine N-acetyltransferase [Bacillales |
| BSLIN78GL000615 | 100 | 4.40E-192 | WP_003234076.1 | MULTISPECIES: tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex |
| BSLIN78GL000616 | 100 | 0.00E+00 | WP_003244150.1 | MULTISPECIES: ABC-F family ATP-binding cassette domain-containing protein |
| BSLIN78GL000617 | 100 | 3.10E-96 | AEP89690.1 | molybdenum cofactor biosynthesis protein C [Bacillus subtilis subsp. subtilis str. RO- |
| BSLIN78GL000618 | 100 | 2.50E-116 | WP_003234073.1 | MULTISPECIES: redox-sensing transcriptional repressor Rex [Bacillales] |
| BSLIN78GL000619 | 100 | 1.90E-23 | WP_003234072.1 | MULTISPECIES: sec-independent protein translocase protein TatAY [Bacillales |
| BSLIN78GL000620 | 100 | 1.50E-133 | AHA76550.1 | Sec-independent protein translocase protein tatCy [Bacillus subtilis PY79] |
| BSLIN78GL000621 | 100 | 9.70E-29 | WP_044052618.1 | DUF4305 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL000622 | 100 | 1.60E-132 | WP_003234069.1 | MULTISPECIES: type II CAAX endopeptidase family protein [Bacillales |
| BSLIN78GL000623 | 100 | 5.30E-51 | AFQ56521.1 | Chaperonin small subunit [Bacillus subtilis QB928] |
| BSLIN78GL000624 | 93.2 | 1.20E-279 | WP_231791074.1 | chaperonin GroEL [Metabacillus kandeliae] |
| BSLIN78GL000625 | 96.9 | 1.70E-09 | RPJ97632.1 | hypothetical protein BSBH6_01429 [Bacillus subtilis] |
| BSLIN78GL000626 | 100 | 1.50E-56 | WP_041336754.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL000627 | 100 | 0.00E+00 | WP_069703743.1 | MULTISPECIES: T7SS effector LXG polymorphic toxin [Bacillus |
| BSLIN78GL000628 | 100 | 2.20E-120 | WP_041336758.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL000629 | 99.5 | 1.20E-99 | AXP50608.1 | DUF420 domain-containing protein [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL000630 | 100 | 2.40E-22 | KIN35282.1 | hypothetical protein B4071_0607 [Bacillus subtilis] |
| BSLIN78GL000631 | 100 | 2.20E-100 | WP_041336762.1 | MULTISPECIES: restriction endonuclease subunit S [Bacillus] |
| BSLIN78GL000632 | 100 | 4.10E-306 | WP_041336764.1 | MULTISPECIES: type I restriction-modification system subunit M [Bacillus |
| BSLIN78GL000633 | 100 | 3.80E-224 | WP_195727919.1 | restriction endonuclease subunit S [Bacillus subtilis] |
| BSLIN78GL000634 | 100 | 0.00E+00 | WP_041336768.1 | MULTISPECIES: HsdR family type I site-specific deoxyribonuclease [Bacillus |
| BSLIN78GL000635 | 100 | 0.00E+00 | WP_217024697.1 | MULTISPECIES: glucitol operon transcriptional regulator GutR [Bacillus] |
| BSLIN78GL000636 | 99.2 | 2.00E-214 | QHF56502.1 | dehydrogenase [Bacillus subtilis] |
| BSLIN78GL000637 | 99.8 | 2.20E-263 | KFC28587.1 | major facilitator transporter [Bacillus subtilis] |
| BSLIN78GL000638 | 100 | 6.10E-169 | KIO55113.1 | Fructokinase [Bacillus subtilis] |
| BSLIN78GL000639 | 100 | 2.30E-120 | AOA53246.1 | Phage shock protein A like protein [Bacillus subtilis] |
| BSLIN78GL000640 | 100 | 7.90E-191 | AKN12703.1 | Primosomal protein N' (replication factor Y) - superfamily II helicase [Bacillus |
| BSLIN78GL000641 | 100 | 7.60E-141 | WP_015252670.1 | MULTISPECIES: YgcG family protein [Bacillus |

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| BSLIN78GL000642 | 100 | 1.50E-186 | WP_003234032.1 | MULTISPECIES: SPFH domain-containing protein [Bacillus] |
| BSLIN78GL000643 | 100 | 8.50E-196 | WP_029726585.1 | potassium channel family protein [Bacillus subtilis] |
| BSLIN78GL000644 | 100 | 7.50E-18 | QAR60659.1 | hypothetical protein BS11774_09270 [Bacillus subtilis] |
| BSLIN78GL000645 | 100 | 7.40E-270 | AGA20631.1 | Major myo-inositol transporter iolT [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL000646 | 100 | 3.30E-195 | WP_003234015.1 | MULTISPECIES: (R,R)-butanediol dehydrogenase [Bacillales |
| BSLIN78GL000647 | 100 | 7.30E-65 | WP_003234013.1 | MULTISPECIES: cell wall metabolism protein WalM [Bacillales] |
| BSLIN78GL000648 | 100 | 2.80E-194 | WP_038427474.1 | PD40 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL000649 | 100 | 8.00E-21 | WP_038427476.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL000650 | 100 | 9.90E-35 | WP_003234008.1 | MULTISPECIES: cold-shock protein [Bacillales |
| BSLIN78GL000651 | 100 | 1.60E-157 | WP_029317396.1 | MULTISPECIES: alpha/beta hydrolase [Bacillus] |
| BSLIN78GL000652 | 100 | 3.90E-196 | KIN49540.1 | hypothetical protein B4146_0672 [Bacillus subtilis] |
| BSLIN78GL000653 | 100 | 0.00E+00 | AGE62493.1 | spore coat protein A [Bacillus subtilis XF-1] |
| BSLIN78GL000654 | 100 | 1.10E-262 | WP_113713046.1 | GABA permease [Bacillus subtilis] |
| BSLIN78GL000655 | 100 | 1.30E-157 | WP_015382984.1 | MULTISPECIES: manganese transporter MneS [Bacillus] |
| BSLIN78GL000656 | 100 | 9.80E-178 | WP_003233978.1 | MULTISPECIES: MoxR family ATPase [Bacillus |
| BSLIN78GL000657 | 100 | 9.80E-228 | WP_029726592.1 | MULTISPECIES: DUF58 domain-containing protein [Bacillus] |
| BSLIN78GL000658 | 100 | 0.00E+00 | WP_147797763.1 | transglutaminase domain-containing protein [Bacillus subtilis] |
| BSLIN78GL000659 | 100 | 3.00E-15 | WP_003233972.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL000660 | 97.5 | 2.40E-295 | WP_014469845.1 | glutamine-hydrolyzing GMP synthase [Bacillus amyloliquefaciens |
| BSLIN78GL000661 | 100 | 3.80E-241 | WP_003243780.1 | MULTISPECIES: hypoxanthine/guanine permease PbuG [Bacillales |
| BSLIN78GL000662 | 99.6 | 2.50E-153 | BAI84151.2 | hypothetical protein BSNT_07013 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL000663 | 100 | 1.10E-23 | AFQ56559.1 | YebD [Bacillus subtilis QB928] |
| BSLIN78GL000664 | 100 | 7.60E-98 | AFQ56560.1 | YebE [Bacillus subtilis QB928] |
| BSLIN78GL000665 | 100 | 7.60E-29 | WP_003219403.1 | MULTISPECIES: NETI motif-containing protein [Bacillales |
| BSLIN78GL000666 | 100 | 1.40E-84 | WP_088467550.1 | 5-(carboxyamino)imidazole ribonucleotide mutase [Bacillus subtilis] |
| BSLIN78GL000667 | 99.7 | 5.80E-217 | WP_088467551.1 | 5-(carboxyamino)imidazole ribonucleotide synthase [Bacillus subtilis] |
| BSLIN78GL000668 | 94.4 | 8.10E-236 | WP_061418190.1 | adenylosuccinate lyase [Bacillus altitudinis] |
| BSLIN78GL000669 | 100 | 1.90E-133 | WP_041337795.1 | MULTISPECIES: phosphoribosylaminoimidazolesuccinocarboxamide synthase |
| BSLIN78GL000670 | 100 | 3.60E-39 | WP_003219409.1 | MULTISPECIES: phosphoribosylformylglycinamidine synthase subunit PurS |
| BSLIN78GL000671 | 100 | 2.30E-128 | WP_014663062.1 | MULTISPECIES: phosphoribosylformylglycinamidine synthase subunit PurQ |
| BSLIN78GL000672 | 100 | 0.00E+00 | WP_029726601.1 | phosphoribosylformylglycinamidine synthase subunit PurL [Bacillus subtilis |
| BSLIN78GL000673 | 100 | 1.00E-271 | AGA23732.1 | Amidophosphoribosyltransferase precursor [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL000674 | 100 | 4.30E-195 | WP_003233945.1 | MULTISPECIES: phosphoribosylformylglycinamidine cyclo-ligase [Bacillus |
| BSLIN78GL000675 | 100 | 1.00E-105 | WP_015252651.1 | MULTISPECIES: phosphoribosylglycinamide formyltransferase [Bacillus |
| BSLIN78GL000676 | 100 | 4.40E-289 | WP_003244516.1 | MULTISPECIES: bifunctional phosphoribosylaminoimidazolecarboxamide |
| BSLIN78GL000677 | 100 | 2.10E-236 | WP_029726602.1 | MULTISPECIES: phosphoribosylamine--glycine ligase [Bacillus |
| BSLIN78GL000678 | 100 | 4.30E-62 | WP_251188019.1 | Lrp/AsnC family transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL000680 | 100 | 1.30E-249 | EHA29400.1 | hypothetical protein BSSC8_36800 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000681 | 100 | 7.40E-32 | QHF56547.1 | membrane protein [Bacillus subtilis] |
| BSLIN78GL000682 | 100 | 0.00E+00 | WP_003233929.1 | MULTISPECIES: adenine deaminase [Bacillales] |
| BSLIN78GL000683 | 100 | 3.20E-192 | WP_003233927.1 | MULTISPECIES: DUF3048 domain-containing protein [Bacillales] |
| BSLIN78GL000684 | 100 | 2.30E-51 | WP_003219429.1 | MULTISPECIES: YerC/YecD family TrpR-related protein [Bacillales |
| BSLIN78GL000685 | 100 | 3.70E-307 | WP_003233925.1 | MULTISPECIES: FMN-binding glutamate synthase family protein [Bacillales |
| BSLIN78GL000686 | 100 | 3.10E-125 | WP_029726604.1 | MULTISPECIES: heptaprenylglyceryl phosphate synthase [Bacillus |
| BSLIN78GL000687 | 100 | 0.00E+00 | WP_015383008.1 | MULTISPECIES: DNA helicase PcrA [Bacillus] |
| BSLIN78GL000688 | 99.7 | 0.00E+00 | WP_015715451.1 | MULTISPECIES: NAD-dependent DNA ligase LigA [Bacillus |
| BSLIN78GL000689 | 100 | 3.50E-21 | EHA29390.1 | hypothetical protein BSSC8_36700 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000690 | 100 | 8.80E-193 | EHA29389.1 | hypothetical protein BSSC8_36690 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000691 | 100 | 8.10E-199 | WP_003233909.1 | MULTISPECIES: phosphotransferase enzyme family protein [Bacillus |
| BSLIN78GL000692 | 100 | 2.40E-125 | AEP89752.1 | protein SapB [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL000693 | 99.8 | 1.10E-273 | WP_072173414.1 | proline transporter OpuE [Bacillus subtilis] |
| BSLIN78GL000694 | 100 | 1.20E-49 | AAB72183.1 | YedA [Bacillus subtilis] |
| BSLIN78GL000695 | 90.7 | 6.30E-253 | WP_144626151.1 | Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatA [Bacillus altitudinis |
| BSLIN78GL000696 | 100 | 5.00E-271 | WP_003219444.1 | MULTISPECIES: Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatB |
| BSLIN78GL000697 | 100 | 1.90E-153 | AII34751.1 | TetR family transcriptional regulator [Bacillus subtilis TO-A] |
| BSLIN78GL000698 | 100 | 0.00E+00 | AWM19936.1 | efflux RND transporter permease subunit [Bacillus subtilis] |
| BSLIN78GL000699 | 100 | 2.70E-169 | WP_003233894.1 | MULTISPECIES: diacylglycerol kinase [Bacillales |
| BSLIN78GL000700 | 100 | 5.80E-272 | WP_113713048.1 | 23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD [Bacillus subtilis] |
| BSLIN78GL000701 | 100 | 3.10E-57 | WP_250622025.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL000702 | 100 | 3.30E-189 | WP_250622026.1 | recombinase family protein [Bacillus subtilis] |
| BSLIN78GL000703 | 97.5 | 6.20E-13 | WP_162920073.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL000704 | 100 | 0.00E+00 | WP_326253334.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL000705 | 100 | 1.30E-93 | WP_113713054.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL000706 | 100 | 6.90E-226 | WP_181456322.1 | DUF3578 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL000707 | 100 | 8.60E-51 | WP_113713055.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL000708 | 98.5 | 9.70E-71 | AGE62547.1 | hypothetical protein C663_0704 [Bacillus subtilis XF-1] |
| BSLIN78GL000709 | 100 | 0.00E+00 | RAP04441.1 | hypothetical protein HS3_04023 [Bacillus subtilis] |
| BSLIN78GL000710 | 100 | 1.20E-194 | WP_113713058.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL000711 | 100 | 4.70E-205 | WP_088467558.1 | response regulator aspartate phosphatase RapH [Bacillus subtilis] |
| BSLIN78GL000712 | 100 | 1.30E-24 | WP_038427496.1 | phosphatase RapH inhibitor PhrH [Bacillus subtilis] |
| BSLIN78GL000713 | 100 | 5.70E-130 | WP_003233863.1 | MULTISPECIES: YebC/PmpR family DNA-binding transcriptional regulator |
| BSLIN78GL000714 | 100 | 2.60E-87 | WP_113713059.1 | spore coat protein [Bacillus subtilis] |
| BSLIN78GL000715 | 98 | 3.60E-107 | AGE62556.1 | putative transcriptional regulator (TetR family) [Bacillus subtilis XF-1] |
| BSLIN78GL000716 | 100 | 3.90E-81 | WP_038427500.1 | MULTISPECIES: nuclear transport factor 2 family protein [Bacillus] |
| BSLIN78GL000717 | 99.6 | 8.40E-157 | AWM19955.1 | NAD-dependent epimerase/dehydratase family protein [Bacillus subtilis |
| BSLIN78GL000718 | 100 | 1.30E-19 | WP_088467559.1 | spore coat-associated protein CotJA [Bacillus subtilis] |
| BSLIN78GL000719 | 100 | 2.40E-46 | WP_003219491.1 | MULTISPECIES: spore coat protein CotJB [Bacillales] |
| BSLIN78GL000720 | 100 | 7.20E-104 | WP_003233850.1 | MULTISPECIES: spore coat protein CotJC [Bacillales] |
| BSLIN78GL000721 | 100 | 4.20E-101 | WP_087614410.1 | GNAT family N-acetyltransferase [Bacillus subtilis |
| BSLIN78GL000722 | 100 | 1.60E-45 | QCY76166.1 | hypothetical protein CAH07_17480 [Bacillus subtilis] |

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| BSLIN78GL000723 | 100 | 1.50E-110 | WP_088467560.1 | YesL family protein [Bacillus subtilis] |
| BSLIN78GL000724 | 100 | 0.00E+00 | WP_088467561.1 | two-component system sensor histidine kinase YesM [Bacillus subtilis] |
| BSLIN78GL000725 | 100 | 4.90E-205 | WP_029726627.1 | MULTISPECIES: two-component system response regulator YesN [Bacillus] |
| BSLIN78GL000726 | 99.8 | 1.60E-244 | WP_029726628.1 | MULTISPECIES: ABC transporter substrate-binding protein [Bacillus] |
| BSLIN78GL000727 | 100 | 1.30E-174 | WP_003233835.1 | MULTISPECIES: sugar ABC transporter permease [Bacillales] |
| BSLIN78GL000728 | 100 | 1.90E-167 | WP_015252615.1 | MULTISPECIES: carbohydrate ABC transporter permease [Bacillus] |
| BSLIN78GL000729 | 99.7 | 3.80E-199 | EHA29349.1 | hypothetical protein BSSC8_36290 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000730 | 99.9 | 0.00E+00 | WP_029726629.1 | MULTISPECIES: transcriptional regulator YesS [Bacillus] |
| BSLIN78GL000731 | 100 | 1.30E-131 | WP_080477801.1 | MULTISPECIES: rhamnogalacturonan acetylesterase [Bacillus] |
| BSLIN78GL000732 | 100 | 5.20E-130 | WP_029726631.1 | MULTISPECIES: YesU family protein [Bacillus] |
| BSLIN78GL000733 | 100 | 1.60E-117 | WP_029726632.1 | MULTISPECIES: YesL family protein [Bacillus] |
| BSLIN78GL000734 | 99.8 | 0.00E+00 | WP_080477802.1 | MULTISPECIES: rhamnogalacturonan lyase [Bacillus] |
| BSLIN78GL000735 | 100 | 0.00E+00 | WP_046664337.1 | MULTISPECIES: rhamnogalacturonan exolyase [Bacillus] |
| BSLIN78GL000736 | 100 | 1.40E-122 | WP_003233813.1 | MULTISPECIES: rhamnogalacturonan acetylesterase [Bacillus] |
| BSLIN78GL000737 | 100 | 0.00E+00 | WP_029726635.1 | MULTISPECIES: beta-galactosidase YesZ [Bacillus] |
| BSLIN78GL000738 | 100 | 0.00E+00 | WP_029726636.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL000739 | 100 | 1.20E-291 | SMF41272.1 | carbohydrate ABC transporter substrate-binding protein, CUT1 family [Bacillus |
| BSLIN78GL000740 | 100 | 1.50E-181 | WP_015482931.1 | MULTISPECIES: sugar ABC transporter permease [Bacillus] |
| BSLIN78GL000741 | 100 | 1.50E-164 | WP_003242715.1 | MULTISPECIES: carbohydrate ABC transporter permease [Bacillales] |
| BSLIN78GL000742 | 99.8 | 2.50E-256 | WP_033883224.1 | alpha-galacturonidase LplD [Bacillus subtilis] |
| BSLIN78GL000743 | 100 | 1.50E-124 | WP_015252601.1 | MULTISPECIES: DUF421 domain-containing protein [Bacillus] |
| BSLIN78GL000744 | 100 | 7.60E-52 | KAF2425214.1 | antibiotic biosynthesis monooxygenase [Bacillus subtilis] |
| BSLIN78GL000745 | 100 | 7.90E-64 | WP_033883226.1 | MULTISPECIES: VOC family protein [Bacillus] |
| BSLIN78GL000746 | 100 | 1.80E-98 | KIL30178.1 | hypothetical protein B4067_0786 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL000747 | 99.7 | 2.30E-185 | BAI84241.2 | hypothetical protein BSNT_07104 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL000748 | 100 | 1.70E-21 | WP_003244522.1 | MULTISPECIES: YezD family protein [Bacilli] |
| BSLIN78GL000749 | 100 | 3.10E-105 | WP_038427515.1 | MULTISPECIES: Bax inhibitor-1 family protein [Bacillus] |
| BSLIN78GL000750 | 100 | 3.20E-15 | WP_015715486.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL000751 | 100 | 3.40E-89 | WP_015252596.1 | MULTISPECIES: transcriptional regulator YetL [Bacillus] |
| BSLIN78GL000752 | 98.9 | 4.90E-213 | QHF56639.1 | synthase [Bacillus subtilis] |
| BSLIN78GL000753 | 100 | 3.80E-285 | WP_046664328.1 | MULTISPECIES: excalibur calcium-binding domain-containing protein [Bacillus] |
| BSLIN78GL000754 | 100 | 4.40E-203 | WP_014479133.1 | MULTISPECIES: DUF3900 domain-containing protein [Bacillus] |
| BSLIN78GL000755 | 100 | 0.00E+00 | WP_029726664.1 | MULTISPECIES: bifunctional P-450/NADPH--P450 reductase [Bacillus] |
| BSLIN78GL000756 | 100 | 6.50E-19 | AHA76681.1 | Hypothetical Protein U712_03665 [Bacillus subtilis PY79] |
| BSLIN78GL000757 | 100 | 0.00E+00 | AGE62594.1 | hypothetical protein C663_0752 [Bacillus subtilis XF-1] |
| BSLIN78GL000758 | 100 | 5.40E-147 | WP_029726884.1 | MULTISPECIES: glucose-1-phosphate cytidylyltransferase [Bacillus |
| BSLIN78GL000759 | 100 | 8.30E-185 | WP_032679065.1 | MULTISPECIES: GDP-mannose 4,6-dehydratase [Bacillus] |
| BSLIN78GL000760 | 99.7 | 4.10E-181 | AGE62597.1 | putative glycosyltransferase [Bacillus subtilis XF-1] |
| BSLIN78GL000761 | 100 | 4.10E-226 | WP_003233779.1 | MULTISPECIES: glycosyltransferase family 2 protein [Bacillales] |
| BSLIN78GL000762 | 100 | 5.20E-178 | AHA76688.1 | Uncharacterized protein yfnD [Bacillus subtilis PY79] |
| BSLIN78GL000763 | 100 | 2.90E-227 | WP_003243467.1 | MULTISPECIES: MFS transporter [Bacillales] |
| BSLIN78GL000764 | 99.2 | 9.20E-136 | AGE62601.1 | putative hydrolase [Bacillus subtilis XF-1] |
| BSLIN78GL000765 | 100 | 1.50E-256 | WP_003233771.1 | MULTISPECIES: amino acid permease [Bacillus] |
| BSLIN78GL000766 | 99.8 | 1.00E-279 | AGA22396.1 | Hypothetical protein YfmT [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL000767 | 100 | 1.20E-150 | WP_003233767.1 | MULTISPECIES: methyl-accepting chemotaxis protein [Bacillales] |
| BSLIN78GL000768 | 100 | 0.00E+00 | WP_003244423.1 | MULTISPECIES: ABC-F family ATP-binding cassette domain-containing protein |
| BSLIN78GL000769 | 100 | 1.60E-77 | WP_003243426.1 | MULTISPECIES: YfmQ family protein [Bacillales] |
| BSLIN78GL000770 | 99.4 | 1.50E-92 | ARW30458.1 | HTH-type transcriptional regulator YfmP [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL000771 | 100 | 6.40E-219 | WP_015715492.1 | MULTISPECIES: MFS transporter [Bacillus] |
| BSLIN78GL000772 | 100 | 6.40E-24 | WP_153912164.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL000773 | 98.3 | 1.30E-24 | AID00393.1 | hypothetical protein Q433_04180 [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL000774 | 100 | 4.40E-14 | RAP04500.1 | hypothetical protein HS3_04085 [Bacillus subtilis] |
| BSLIN78GL000775 | 100 | 1.40E-298 | WP_014476110.1 | MULTISPECIES: ABC-F family ATP-binding cassette domain-containing protein |
| BSLIN78GL000776 | 100 | 1.50E-209 | WP_015715493.1 | MULTISPECIES: DEAD/DEAH box helicase [Bacillus] |
| BSLIN78GL000777 | 100 | 6.70E-81 | WP_015252579.1 | MULTISPECIES: GNAT family N-acetyltransferase [Bacillus] |
| BSLIN78GL000778 | 100 | 1.10E-190 | EHA29299.1 | putative oxidoreductase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000779 | 98.2 | 1.40E-23 | AHA76704.1 | Hypothetical Protein U712_03780 [Bacillus subtilis PY79] |
| BSLIN78GL000780 | 100 | 1.70E-24 | AIY92037.1 | hypothetical protein QU35_04255 [Bacillus subtilis subsp. subtilis str. 168] |
| BSLIN78GL000781 | 100 | 1.80E-224 | WP_003233743.1 | MULTISPECIES: MFS transporter [Bacillales] |
| BSLIN78GL000782 | 100 | 4.80E-293 | WP_003244287.1 | MULTISPECIES: formylglycine-generating enzyme family protein [Bacillales |
| BSLIN78GL000783 | 100 | 1.50E-14 | AHA76707.1 | Hypothetical Protein U712_03795 [Bacillus subtilis PY79] |
| BSLIN78GL000784 | 100 | 2.30E-12 | AHA76708.1 | Hypothetical Protein U712_03800 [Bacillus subtilis PY79] |
| BSLIN78GL000785 | 100 | 3.60E-149 | WP_003233737.1 | MULTISPECIES: Fe(3+)-citrate ABC transporter ATP-binding protein YfmF |
| BSLIN78GL000786 | 100 | 2.40E-179 | WP_003243506.1 | MULTISPECIES: Fe(3+)-citrate ABC transporter permease YfmE [Bacillales] |
| BSLIN78GL000787 | 100 | 2.80E-172 | WP_046664325.1 | MULTISPECIES: Fe(3+) dicitrate ABC transporter permease FecD [Bacillus] |
| BSLIN78GL000788 | 99.7 | 9.50E-170 | WP_003243996.1 | MULTISPECIES: Fe(3+)-citrate ABC transporter substrate-binding protein YfmC |
| BSLIN78GL000789 | 100 | 2.80E-64 | AIX06518.1 | hypothetical protein OB04_00832 [Bacillus subtilis] |
| BSLIN78GL000790 | 100 | 4.30E-59 | WP_003233729.1 | MULTISPECIES: general stress protein [Bacillales] |
| BSLIN78GL000791 | 100 | 3.10E-248 | WP_003244025.1 | MULTISPECIES: pectate lyase [Bacillales] |
| BSLIN78GL000792 | 100 | 3.60E-280 | AOA53382.1 | Putative malate transporter YflS [Bacillus subtilis] |
| BSLIN78GL000793 | 100 | 7.40E-303 | WP_038427521.1 | two-component sensor histidine kinase CitS [Bacillus subtilis] |
| BSLIN78GL000794 | 99.5 | 1.40E-108 | WP_038427522.1 | MULTISPECIES: two-component response regulator CitT [Bacillus] |
| BSLIN78GL000795 | 100 | 2.50E-181 | WP_029946126.1 | MULTISPECIES: tripartite tricarboxylate transporter substrate binding protein |
| BSLIN78GL000796 | 100 | 2.30E-15 | WP_003233716.1 | MULTISPECIES: hypothetical protein [Bacilli] |
| BSLIN78GL000797 | 100 | 3.60E-239 | WP_003233714.1 | MULTISPECIES: citrate transporter CitM [Bacillus] |
| BSLIN78GL000798 | 100 | 1.40E-150 | WP_003233712.1 | MULTISPECIES: MBL fold metallo-hydrolase [Bacillus] |
| BSLIN78GL000799 | 100 | 7.90E-216 | WP_003233711.1 | MULTISPECIES: nitric oxide synthase [Bacillus] |
| BSLIN78GL000800 | 100 | 4.00E-44 | BAI84280.2 | hypothetical protein BSNT_07142 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL000801 | 100 | 8.10E-123 | WP_038427523.1 | MULTISPECIES: MOSC domain-containing protein [Bacillus] |
| BSLIN78GL000802 | 100 | 1.40E-18 | WP_003233704.1 | MULTISPECIES: YflJ family protein [Bacillales] |

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| BSLIN78GL000803 | 98.3 | 5.60E-26 | CAF1858022.1 | hypothetical protein NRS6167_03625 [Bacillus subtilis] |
| BSLIN78GL000804 | 100 | 4.60E-52 | WP_003233700.1 | MULTISPECIES: DUF3243 domain-containing protein [Bacillus] |
| BSLIN78GL000805 | 100 | 1.20E-138 | WP_003223067.1 | MULTISPECIES: type I methionyl aminopeptidase [Bacillus |
| BSLIN78GL000806 | 100 | 5.80E-264 | EHA29274.1 | phosphotransferase system (PTS) N-acetylglucosamine-specific enzyme IICB |
| BSLIN78GL000807 | 100 | 0.00E+00 | WP_003233694.1 | MULTISPECIES: lipoteichoic acid synthase [Bacillales |
| BSLIN78GL000808 | 100 | 1.90E-18 | WP_072557053.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL000809 | 100 | 2.00E-68 | AEP89862.1 | YflB [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL000810 | 99.8 | 1.70E-277 | AEP89863.1 | YflA [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL000811 | 100 | 1.70E-199 | WP_038427524.1 | endospore germination permease [Bacillus subtilis] |
| BSLIN78GL000812 | 100 | 2.80E-31 | WP_003233686.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL000813 | 99.7 | 9.60E-209 | WP_038427525.1 | Ger(x)C family spore germination protein [Bacillus subtilis] |
| BSLIN78GL000814 | 100 | 6.20E-291 | WP_015715500.1 | MULTISPECIES: spore germination protein [Bacillus] |
| BSLIN78GL000815 | 100 | 1.10E-262 | WP_003233682.1 | MULTISPECIES: PTS system trehalose-specific EIIBC component [Bacillales |
| BSLIN78GL000816 | 100 | 0.00E+00 | WP_119899129.1 | alpha,alpha-phosphotrehalase [Bacillus subtilis] |
| BSLIN78GL000817 | 100 | 5.50E-133 | WP_003233679.1 | MULTISPECIES: trehalose operon repressor [Bacillales] |
| BSLIN78GL000818 | 100 | 3.30E-124 | WP_003243096.1 | MULTISPECIES: NAD(P)H-dependent oxidoreductase [Bacillales] |
| BSLIN78GL000819 | 99.9 | 0.00E+00 | WP_147797766.1 | multifunctional 2',3'-cyclic-nucleotide 2'-phosphodiesterase/3'-nucleotidase/5' |
| BSLIN78GL000820 | 100 | 7.50E-92 | WP_032726651.1 | MULTISPECIES: general stress protein 18 [Bacillus] |
| BSLIN78GL000821 | 100 | 7.80E-217 | WP_003243812.1 | MULTISPECIES: MFS transporter [Bacillales] |
| BSLIN78GL000822 | 100 | 4.00E-24 | AGE62649.1 | hypothetical protein C663_0809 [Bacillus subtilis XF-1] |
| BSLIN78GL000823 | 100 | 5.20E-19 | KIL31111.1 | hypothetical protein B4067_0842 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL000824 | 100 | 3.40E-74 | WP_003243480.1 | MULTISPECIES: protein-tyrosine-phosphatase [Bacillales |
| BSLIN78GL000825 | 100 | 1.20E-52 | WP_003233665.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL000826 | 100 | 1.70E-149 | WP_014479170.1 | MULTISPECIES: YihY family inner membrane protein [Bacillus] |
| BSLIN78GL000827 | 100 | 1.00E-224 | WP_003243008.1 | MULTISPECIES: MFS transporter [Bacillus] |
| BSLIN78GL000828 | 100 | 1.20E-18 | WP_009966796.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL000829 | 100 | 5.50E-190 | WP_003242902.1 | MULTISPECIES: calcium/proton exchanger [Bacillales] |
| BSLIN78GL000830 | 100 | 3.90E-148 | WP_003233657.1 | MULTISPECIES: YfkD famly protein [Bacillales |
| BSLIN78GL000831 | 100 | 1.20E-152 | WP_010886444.1 | MULTISPECIES: mechanosensitive ion channel protein MscC [Bacillales |
| BSLIN78GL000832 | 100 | 7.10E-220 | WP_003233655.1 | MULTISPECIES: radical SAM/CxCxxxxC motif protein YfkAB [Bacillales |
| BSLIN78GL000833 | 100 | 2.30E-27 | WP_003223132.1 | MULTISPECIES: SE1561 family protein [Bacillales |
| BSLIN78GL000834 | 100 | 4.90E-151 | WP_014479173.1 | MULTISPECIES: delta-lactam-biosynthetic de-N-acetylase [Bacillus |
| BSLIN78GL000835 | 100 | 4.40E-153 | WP_046380859.1 | MULTISPECIES: NAD(P)-dependent oxidoreductase [Bacillus |
| BSLIN78GL000836 | 100 | 1.30E-190 | AFQ56717.1 | Putative divalent cation transport protein [Bacillus subtilis QB928] |
| BSLIN78GL000837 | 100 | 7.70E-166 | WP_003233646.1 | MULTISPECIES: DNA-3-methyladenine glycosylase [Bacillales |
| BSLIN78GL000838 | 100 | 7.90E-269 | WP_029726868.1 | 23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD [Bacillus subtilis] |
| BSLIN78GL000839 | 100 | 9.40E-178 | WP_003243992.1 | MULTISPECIES: tRNA-dihydrouridine synthase [Bacillales |
| BSLIN78GL000840 | 100 | 6.60E-84 | WP_003233638.1 | MULTISPECIES: DUF6884 domain-containing protein [Bacillales] |
| BSLIN78GL000841 | 100 | 3.00E-15 | EHA29239.1 | hypothetical protein BSSC8_35190 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000842 | 100 | 1.00E-193 | WP_003233633.1 | MULTISPECIES: acetoin:2,6-dichlorophenolindophenol oxidoreductase subunit |
| BSLIN78GL000843 | 100 | 3.80E-188 | EHA29237.1 | acetoin dehydrogenase E1 component (TPP-dependent beta subunit) [Bacillus subtilis |
| BSLIN78GL000844 | 100 | 7.50E-220 | WP_003233630.1 | MULTISPECIES: acetoin dehydrogenase complex dihydrolipoyllysine-residue |
| BSLIN78GL000845 | 100 | 4.70E-258 | WP_003233626.1 | MULTISPECIES: acetoin dehydrogenase complex dihydrolipoyl dehydrogenase |
| BSLIN78GL000846 | 100 | 9.70E-13 | AEP89901.1 | hypothetical protein I33_0909 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL000847 | 100 | 0.00E+00 | WP_326253315.1 | acetoin dehydrogenase operon transcriptional activator AcoR [Bacillus subtilis] |
| BSLIN78GL000848 | 100 | 3.20E-26 | WP_003233621.1 | MULTISPECIES: small acid-soluble spore protein H [Bacillus] |
| BSLIN78GL000849 | 100 | 2.90E-57 | AFQ56730.1 | Putative membrane protein [Bacillus subtilis QB928] |
| BSLIN78GL000850 | 100 | 9.60E-101 | WP_003233617.1 | MULTISPECIES: YfjD family protein [Bacillus] |
| BSLIN78GL000851 | 100 | 3.00E-145 | WP_003233615.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL000852 | 99.8 | 1.30E-230 | EHA29229.1 | hypothetical protein BSSC8_35090 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000853 | 100 | 2.80E-49 | WP_014476174.1 | MULTISPECIES: WXG100 family type VII secretion target [Bacillus |
| BSLIN78GL000854 | 100 | 2.60E-261 | WP_032726629.1 | maltose-6'-phosphate glucosidase [Bacillus subtilis] |
| BSLIN78GL000855 | 99.6 | 1.20E-144 | AGE62679.1 | transcriptional activator of the Mal operon [Bacillus subtilis XF-1] |
| BSLIN78GL000856 | 100 | 3.20E-303 | WP_042978116.1 | MULTISPECIES: PTS maltose transporter subunit IIBC [Bacillus |
| BSLIN78GL000857 | 100 | 0.00E+00 | WP_038427533.1 | MULTISPECIES: peptidase G2 autoproteolytic cleavage domain-containing protein |
| BSLIN78GL000858 | 100 | 0.00E+00 | WP_326253312.1 | ABC transporter ATP-binding protein [Bacillus subtilis] |
| BSLIN78GL000859 | 98.5 | 0.00E+00 | WP_217001835.1 | ABC transporter ATP-binding protein [Bacillus subtilis] |
| BSLIN78GL000860 | 100 | 7.20E-72 | AGE62683.1 | catechol-2,3-dioxygenase membrane subunit [Bacillus subtilis XF-1] |
| BSLIN78GL000861 | 100 | 1.10E-161 | WP_003233597.1 | MULTISPECIES: catechol 2,3-dioxygenase [Bacillales |
| BSLIN78GL000862 | 94.2 | 1.40E-21 | KIN49733.1 | hypothetical protein B4146_0872 [Bacillus subtilis] |
| BSLIN78GL000863 | 100 | 9.80E-217 | WP_205423213.1 | sensor histidine kinase [Bacillus subtilis] |
| BSLIN78GL000864 | 100 | 4.30E-122 | EHA29219.1 | two-component response regulator YfiJ [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000865 | 100 | 1.30E-19 | AHA76791.1 | Hypothetical Protein U712_04215 [Bacillus subtilis PY79] |
| BSLIN78GL000866 | 100 | 3.50E-172 | WP_003233591.1 | linearmycin resistance ATP-binding protein LnrL [Bacillus subtilis |
| BSLIN78GL000867 | 100 | 1.70E-219 | WP_003233590.1 | MULTISPECIES: linearmycin resistance permease LnrM [Bacillus |
| BSLIN78GL000868 | 100 | 5.60E-223 | WP_250903007.1 | linearmycin resistance permease LnrN [Bacillus sp. C21] |
| BSLIN78GL000869 | 100 | 6.70E-99 | WP_003233588.1 | MULTISPECIES: transcriptional regulator PadR [Bacillales] |
| BSLIN78GL000870 | 100 | 8.40E-16 | AHA76796.1 | Hypothetical Protein U712_04240 [Bacillus subtilis PY79] |
| BSLIN78GL000871 | 100 | 1.00E-111 | WP_003233586.1 | MULTISPECIES: esterase EstB [Bacillus] |
| BSLIN78GL000872 | 100 | 1.10E-206 | WP_003233584.1 | MULTISPECIES: acyltransferase family protein [Bacillus |
| BSLIN78GL000873 | 100 | 6.00E-100 | WP_029726848.1 | MULTISPECIES: bacillithiol transferase BstA [Bacillus] |
| BSLIN78GL000874 | 100 | 1.10E-292 | AOA53458.1 | putative MFS-type transporter YfiU [Bacillus subtilis] |
| BSLIN78GL000875 | 100 | 5.00E-82 | WP_003233577.1 | MULTISPECIES: MarR family transcriptional regulator [Bacillus] |
| BSLIN78GL000876 | 100 | 0.00E+00 | WP_003233575.1 | MULTISPECIES: bifunctional lysylphosphatidylglycerol flippase/synthetase MprF |
| BSLIN78GL000877 | 99.1 | 2.40E-187 | AFQ56761.1 | Putative iron(III) dicitrate transporter bindinglipoprotein [Bacillus subtilis QB928] |
| BSLIN78GL000878 | 100 | 1.40E-182 | WP_003233570.1 | MULTISPECIES: iron ABC transporter permease [Bacillus] |
| BSLIN78GL000879 | 100 | 3.00E-185 | WP_003233568.1 | MULTISPECIES: iron ABC transporter permease [Bacillus] |
| BSLIN78GL000880 | 99.7 | 1.00E-165 | WP_003242763.1 | MULTISPECIES: PhzF family phenazine biosynthesis protein [Bacillales |
| BSLIN78GL000881 | 100 | 2.70E-106 | WP_003243940.1 | MULTISPECIES: nitroreductase [Bacillales] |
| BSLIN78GL000882 | 100 | 2.80E-28 | WP_003233561.1 | MULTISPECIES: YfhD family protein [Bacillales |

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| BSLIN78GL000883 | 100 | 5.30E-15 | AEP89946.1 | conserved hypothetical protein [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL000884 | 99.7 | 3.10E-173 | EHA29200.1 | hypothetical protein BSSC8_34800 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000885 | 100 | 5.30E-145 | WP_003233555.1 | MULTISPECIES: recombination regulator RecX [Bacillus] |
| BSLIN78GL000886 | 100 | 6.00E-52 | WP_003233553.1 | MULTISPECIES: YfhH family protein [Bacillus] |
| BSLIN78GL000887 | 100 | 1.20E-211 | WP_080010604.1 | MULTISPECIES: MFS transporter [Bacillus] |
| BSLIN78GL000888 | 100 | 1.50E-21 | WP_003223241.1 | MULTISPECIES: small, acid-soluble spore protein K [Bacillales] |
| BSLIN78GL000889 | 100 | 8.60E-44 | WP_003243789.1 | MULTISPECIES: YfhJ family protein [Bacillales] |
| BSLIN78GL000890 | 98.3 | 1.60E-97 | EHA29194.1 | hypothetical protein BSSC8_34740 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000891 | 100 | 2.90E-61 | AOA53476.1 | uncharacterized protein BSHJ0_00883 [Bacillus subtilis] |
| BSLIN78GL000892 | 100 | 3.30E-169 | WP_029726839.1 | MULTISPECIES: epoxide hydrolase EphM [Bacillus] |
| BSLIN78GL000893 | 100 | 2.00E-186 | WP_003244113.1 | MULTISPECIES: glycosyltransferase family 2 protein [Bacillales] |
| BSLIN78GL000894 | 100 | 0.00E+00 | WP_029726838.1 | MULTISPECIES: YfhO family protein [Bacillus] |
| BSLIN78GL000895 | 100 | 4.80E-188 | WP_003244136.1 | MULTISPECIES: metal-dependent hydrolase [Bacillales] |
| BSLIN78GL000896 | 100 | 3.40E-225 | AKN12943.1 | A/G-specific adenine glycosylase [Bacillus subtilis] |
| BSLIN78GL000897 | 100 | 3.30E-36 | WP_003233542.1 | MULTISPECIES: hypothetical protein [Bacillales] |
| BSLIN78GL000898 | 100 | 5.20E-134 | WP_003223262.1 | MULTISPECIES: enoyl-[acyl-carrier-protein] reductase FabL [Bacillales |
| BSLIN78GL000899 | 100 | 3.60E-39 | BAI84385.2 | small acid-soluble spore protein, gamma-type [Bacillus subtilis subsp. natto |
| BSLIN78GL000900 | 100 | 9.50E-50 | ADV95848.1 | hypothetical protein BSn5_16200 [Bacillus subtilis BSn5] |
| BSLIN78GL000901 | 100 | 6.70E-104 | WP_003223272.1 | MULTISPECIES: DUF402 domain-containing protein [Bacillales] |
| BSLIN78GL000902 | 100 | 0.00E+00 | WP_010886448.1 | ABC transporter ATP-binding protein [Bacillus subtilis] |
| BSLIN78GL000903 | 100 | 1.70E-194 | WP_003233537.1 | MULTISPECIES: aromatic acid exporter family protein [Bacillales] |
| BSLIN78GL000904 | 99.8 | 5.10E-246 | KDE24853.1 | glutamate-1-semialdehyde aminotransferase [Bacillus subtilis] |
| BSLIN78GL000905 | 100 | 1.10E-86 | WP_326253305.1 | thioredoxin-dependent thiol peroxidase [Bacillus subtilis] |
| BSLIN78GL000906 | 100 | 2.10E-79 | WP_003223285.1 | MULTISPECIES: peroxide-responsive transcriptional repressor PerR [Bacillales] |
| BSLIN78GL000907 | 100 | 8.10E-61 | AGA20927.1 | Hypothetical protein YgzB [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL000908 | 100 | 5.50E-167 | WP_003243727.1 | MULTISPECIES: nucleotidyltransferase-like protein [Bacillales] |
| BSLIN78GL000909 | 98.1 | 5.00E-54 | QHF55815.1 | hypothetical protein Bateq7PJ16_0009 [Bacillus subtilis] |
| BSLIN78GL000911 | 100 | 1.50E-144 | WP_029726361.1 | MULTISPECIES: sporulation control protein Spo0M [Bacillus] |
| BSLIN78GL000912 | 100 | 2.30E-28 | AGE62734.1 | hypothetical protein C663_0899 [Bacillus subtilis XF-1] |
| BSLIN78GL000913 | 100 | 2.50E-22 | AHA76841.1 | Spore coat protein F-like protein YgzC [Bacillus subtilis PY79] |
| BSLIN78GL000914 | 98.9 | 4.90E-165 | AII34910.1 | peptidase [Bacillus subtilis TO-A] |
| BSLIN78GL000915 | 100 | 0.00E+00 | WP_017697515.1 | MULTISPECIES: phosphomethylpyrimidine synthase ThiC [Bacillus |
| BSLIN78GL000916 | 100 | 7.10E-267 | WP_038427541.1 | FAD-binding oxidoreductase [Bacillus subtilis] |
| BSLIN78GL000917 | 100 | 7.10E-30 | ARB36283.1 | transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL000918 | 99.8 | 4.90E-290 | WP_015252505.1 | catalase KatA [Bacillus subtilis] |
| BSLIN78GL000919 | 100 | 2.60E-14 | WP_284675367.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL000920 | 100 | 3.20E-139 | WP_021479704.1 | MULTISPECIES: ABC transporter ATP-binding protein [Bacillus] |
| BSLIN78GL000921 | 100 | 1.30E-185 | WP_003233463.1 | MULTISPECIES: aliphatic sulfonate ABC transporter substrate-binding protein |
| BSLIN78GL000922 | 100 | 1.10E-150 | WP_003233461.1 | MULTISPECIES: ABC transporter permease [Bacillus] |
| BSLIN78GL000923 | 100 | 1.50E-217 | AGA24458.1 | Alkanesulfonate monooxygenase SsuD [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL000924 | 100 | 4.00E-96 | WP_326253462.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL000925 | 100 | 2.00E-43 | WP_003233455.1 | MULTISPECIES: 30S ribosomal protein S14 [Bacillales] |
| BSLIN78GL000926 | 100 | 3.80E-82 | WP_003233453.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL000927 | 100 | 2.60E-33 | AFQ56808.1 | Putative HTH-type transcriptional regulator [Bacillus subtilis QB928] |
| BSLIN78GL000928 | 100 | 4.90E-114 | WP_003233449.1 | MULTISPECIES: B3/4 domain-containing protein [Bacillus] |
| BSLIN78GL000929 | 100 | 4.50E-236 | BAI84415.2 | hypothetical protein BSNT_07301 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL000930 | 100 | 1.30E-179 | AIC97448.1 | hypothetical protein Q433_05080 [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL000931 | 100 | 4.70E-88 | WP_003233442.1 | MULTISPECIES: tRNA (uridine(34)/cytosine(34)/5-carboxymethylaminomethyluridine(34)-2'-O)-methyltransferase TrmL [Bacillus] |
| BSLIN78GL000932 | 100 | 9.60E-113 | WP_015715554.1 | MULTISPECIES: YhbD family protein [Bacillus] |
| BSLIN78GL000933 | 99.6 | 9.80E-127 | WP_038427542.1 | polymer-forming cytoskeletal protein [Bacillus subtilis] |
| BSLIN78GL000934 | 100 | 3.00E-131 | WP_038427543.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL000935 | 97.4 | 2.60E-13 | KIL33794.1 | hypothetical protein B4067_1171 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL000936 | 100 | 0.00E+00 | AFQ56816.1 | Serine protein kinase [Bacillus subtilis QB928] |
| BSLIN78GL000937 | 100 | 1.80E-229 | WP_003233432.1 | MULTISPECIES: sporulation protein YhbH [Bacillales] |
| BSLIN78GL000938 | 100 | 2.50E-78 | WP_003233431.1 | MULTISPECIES: MarR family transcriptional regulator [Bacillales] |
| BSLIN78GL000939 | 100 | 5.40E-119 | WP_014476241.1 | MULTISPECIES: HlyD family efflux transporter periplasmic adaptor subunit |
| BSLIN78GL000940 | 100 | 1.20E-300 | WP_003233429.1 | MULTISPECIES: MFS transporter [Bacillales] |
| BSLIN78GL000941 | 100 | 5.50E-98 | WP_015252498.1 | MULTISPECIES: NAD(P)H-dependent oxidoreductase [Bacillus] |
| BSLIN78GL000942 | 100 | 1.20E-62 | WP_003233427.1 | MULTISPECIES: hypothetical protein [Bacillales] |
| BSLIN78GL000943 | 100 | 5.40E-22 | WP_003233426.1 | MULTISPECIES: hypothetical protein [Bacillales] |
| BSLIN78GL000944 | 98.5 | 6.50E-151 | AFQ56824.1 | Putative integral inner membrane protein [Bacillus subtilis QB928] |
| BSLIN78GL000945 | 100 | 2.40E-60 | WP_015252495.1 | MULTISPECIES: GntR family transcriptional regulator [Bacillus] |
| BSLIN78GL000946 | 100 | 1.80E-125 | WP_015252494.1 | MULTISPECIES: ABC transporter ATP-binding protein [Bacillus] |
| BSLIN78GL000947 | 99.7 | 2.60E-167 | EHA30324.1 | hypothetical protein BSSC8_34210 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL000948 | 100 | 3.20E-173 | WP_038427544.1 | MULTISPECIES: ABC transporter permease [Bacillus] |
| BSLIN78GL000949 | 100 | 2.20E-35 | AGE62770.1 | major cold shock protein [Bacillus subtilis XF-1] |
| BSLIN78GL000950 | 99.6 | 1.90E-153 | AFQ56830.1 | Putative ABC transporter (binding lipoprotein) [Bacillus subtilis QB928] |
| BSLIN78GL000951 | 100 | 1.70E-202 | WP_003233417.1 | MULTISPECIES: diguanylate cyclase DgcK [Bacillus] |
| BSLIN78GL000952 | 100 | 4.70E-239 | WP_128441470.1 | L-cystine transporter TcyP [Bacillus subtilis] |
| BSLIN78GL000953 | 100 | 1.30E-79 | WP_041520516.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL000954 | 100 | 1.60E-103 | WP_003245125.1 | MULTISPECIES: YhcN/YlaJ family sporulation lipoprotein [Bacillales] |
| BSLIN78GL000955 | 99.7 | 4.20E-170 | WP_283934180.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL000956 | 99.4 | 0.00E+00 | WP_181216918.1 | endonuclease YhcR [Bacillus subtilis] |
| BSLIN78GL000957 | 100 | 1.90E-107 | WP_029317530.1 | MULTISPECIES: sortase SrtA [Bacillus] |
| BSLIN78GL000958 | 100 | 8.40E-171 | WP_029726346.1 | MULTISPECIES: RluA family pseudouridine synthase [Bacillus] |
| BSLIN78GL000959 | 100 | 5.80E-68 | WP_015252484.1 | MULTISPECIES: YhcU family protein [Bacillus] |
| BSLIN78GL000960 | 100 | 5.10E-70 | AFQ56840.1 | Putative oxidoreductase [Bacillus subtilis QB928] |
| BSLIN78GL000961 | 100 | 9.90E-121 | WP_003233396.1 | MULTISPECIES: HAD family hydrolase [Bacillus] |
| BSLIN78GL000962 | 100 | 1.30E-304 | WP_003245514.1 | MULTISPECIES: bifunctional GNAT family N-acetyltransferase/carbon-nitrogen |

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| BSLIN78GL000963 | 100 | 9.00E-27 | AWX21440.1 | hypothetical protein CXF51_05840 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL000964 | 100 | 6.20E-263 | WP_031600324.1 | MULTISPECIES: aspartate aminotransferase family protein [Bacillus] |
| BSLIN78GL000965 | 100 | 1.30E-103 | WP_003233388.1 | MULTISPECIES: glycerol uptake operon antiterminator GlpP [Bacillales |
| BSLIN78GL000966 | 100 | 5.90E-155 | WP_003233386.1 | MULTISPECIES: glycerol uptake facilitator protein GlpF [Bacillales |
| BSLIN78GL000967 | 99.2 | 4.30E-289 | WEY95518.1 | glycerol kinase GlpK [Bacillus subtilis] |
| BSLIN78GL000968 | 99.6 | 0.00E+00 | KIU11869.1 | glycerol-3-phosphate dehydrogenase [Bacillus subtilis |
| BSLIN78GL000969 | 100 | 0.00E+00 | WP_014479288.1 | MULTISPECIES: phosphoglucomutase [Bacillus] |
| BSLIN78GL000970 | 100 | 9.30E-212 | WP_326253357.1 | two-component system sensor histidine kinase YhcY [Bacillus subtilis] |
| BSLIN78GL000971 | 100 | 6.10E-115 | WP_041335631.1 | MULTISPECIES: two-component system response regulator YhcZ [Bacillus |
| BSLIN78GL000972 | 100 | 1.60E-89 | WP_326253359.1 | FMN-dependent NADPH-azoreductase [Bacillus subtilis] |
| BSLIN78GL000973 | 100 | 2.60E-39 | WP_003233373.1 | MULTISPECIES: YhdB family protein [Bacillales |
| BSLIN78GL000974 | 100 | 7.80E-55 | WP_003233371.1 | MULTISPECIES: YqzG/YhdC family protein [Bacillales |
| BSLIN78GL000975 | 100 | 3.50E-267 | WP_326253361.1 | peptidoglycan endopeptidase LytF [Bacillus subtilis |
| BSLIN78GL000976 | 100 | 2.90E-76 | WP_014479293.1 | MULTISPECIES: nitric oxide-sensing transcriptional repressor NsrR [Bacillus] |
| BSLIN78GL000977 | 100 | 6.30E-272 | BAI84481.2 | hypothetical protein BSNT_07371 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL000978 | 100 | 1.40E-278 | WP_003233364.1 | MULTISPECIES: stage V sporulation protein SpoVR [Bacillales] |
| BSLIN78GL000979 | 100 | 9.90E-264 | WP_082359951.1 | MULTISPECIES: alkaline phosphatase PhoA [Bacillus] |
| BSLIN78GL000980 | 100 | 4.00E-182 | WP_015715576.1 | MULTISPECIES: peptidoglycan endopeptidase LytE [Bacillus |
| BSLIN78GL000981 | 100 | 2.80E-163 | WP_003233357.1 | MULTISPECIES: transcriptional regulator CitR [Bacillales] |
| BSLIN78GL000982 | 100 | 5.20E-207 | WP_029726338.1 | MULTISPECIES: citrate synthase CitA [Bacillus |
| BSLIN78GL000983 | 100 | 1.50E-164 | WP_072175832.1 | SDR family oxidoreductase [Bacillus subtilis] |
| BSLIN78GL000984 | 100 | 3.00E-260 | WP_003233350.1 | MULTISPECIES: branched-chain amino acid transporter BcaP [Bacillus] |
| BSLIN78GL000985 | 100 | 7.70E-242 | WP_003233348.1 | MULTISPECIES: sodium-dependent transporter [Bacillus] |
| BSLIN78GL000986 | 100 | 2.40E-273 | WP_029726335.1 | MULTISPECIES: PLP-dependent aminotransferase family protein [Bacillus |
| BSLIN78GL000987 | 100 | 4.40E-83 | AEP90048.1 | acetyltransferase family protein [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL000988 | 100 | 3.50E-46 | WP_003233341.1 | MULTISPECIES: anti-sigma-M factor [Bacillales] |
| BSLIN78GL000989 | 100 | 1.80E-204 | WP_015252469.1 | MULTISPECIES: anti-sigma factor [Bacillus] |
| BSLIN78GL000990 | 100 | 8.20E-88 | WP_003224177.1 | MULTISPECIES: RNA polymerase sigma factor SigM [Bacillales] |
| BSLIN78GL000991 | 100 | 4.00E-190 | WP_029726334.1 | MULTISPECIES: aldo/keto reductase AkrN [Bacillus] |
| BSLIN78GL000992 | 100 | 2.70E-109 | WP_003233335.1 | MULTISPECIES: 1-acylglycerol-3-phosphate O-acyltransferase [Bacillales |
| BSLIN78GL000993 | 100 | 5.70E-245 | AGE62810.1 | putative transporter or sensor [Bacillus subtilis XF-1] |
| BSLIN78GL000994 | 100 | 7.40E-98 | AEP90055.1 | HTH-type transcriptional regulator CueR [Bacillus subtilis subsp. subtilis str. RO-NN- |
| BSLIN78GL000995 | 100 | 1.60E-222 | WP_029726333.1 | MULTISPECIES: pyridoxal phosphate-dependent aminotransferase [Bacillus |
| BSLIN78GL000996 | 100 | 5.70E-18 | AKE22797.1 | hypothetical protein BsLM_0998 [Bacillus sp. LM 4-2] |
| BSLIN78GL000997 | 100 | 2.40E-257 | WP_029726332.1 | MULTISPECIES: hemolysin family protein [Bacillus |
| BSLIN78GL000998 | 100 | 1.20E-59 | WP_029726331.1 | MULTISPECIES: fluoride efflux transporter CrcB [Bacillus |
| BSLIN78GL000999 | 100 | 3.70E-67 | WP_029726330.1 | MULTISPECIES: CrcB family protein [Bacillus] |
| BSLIN78GL001000 | 100 | 6.00E-135 | WP_021479659.1 | MULTISPECIES: glycerophosphodiester phosphodiesterase family protein [Bacillus] |
| BSLIN78GL001001 | 100 | 1.30E-17 | AGE62817.1 | hypothetical protein C663_0986 [Bacillus subtilis XF-1] |
| BSLIN78GL001002 | 100 | 3.30E-209 | WP_015383218.1 | MULTISPECIES: small-conductance mechanosensitive channel protein MscY |
| BSLIN78GL001003 | 100 | 3.10E-139 | WP_029726329.1 | MULTISPECIES: sirtuin NAD-dependent deacetylase [Bacillus |
| BSLIN78GL001004 | 100 | 2.90E-157 | WP_029726328.1 | MULTISPECIES: polysaccharide deacetylase family protein [Bacillus |
| BSLIN78GL001005 | 99.3 | 6.50E-160 | AGE62820.1 | D-alanine aminotransferase [Bacillus subtilis XF-1] |
| BSLIN78GL001006 | 100 | 4.20E-251 | WP_029726327.1 | MULTISPECIES: Na+/H+ antiporter NhaC [Bacillus] |
| BSLIN78GL001007 | 100 | 1.00E-85 | ASB92533.1 | Stress response protein NhaX [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL001008 | 100 | 8.40E-41 | AHA76935.1 | Uncharacterized protein yheJ [Bacillus subtilis PY79] |
| BSLIN78GL001009 | 99.3 | 0.00E+00 | WP_015383224.1 | multidrug ABC transporter ATP-binding protein BmrC [Bacillus subtilis] |
| BSLIN78GL001010 | 100 | 0.00E+00 | WP_029726326.1 | MULTISPECIES: multidrug resistance ABC transporter ATP-binding |
| BSLIN78GL001011 | 100 | 1.70E-111 | WP_029726325.1 | MULTISPECIES: SDR family oxidoreductase [Bacillus |
| BSLIN78GL001012 | 100 | 6.10E-16 | WP_003245136.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL001013 | 100 | 1.80E-28 | WP_003233287.1 | MULTISPECIES: beta type acid-soluble spore protein SspB [Bacillales |
| BSLIN78GL001014 | 100 | 6.80E-36 | WP_029726324.1 | YheE family protein [Bacillus subtilis] |
| BSLIN78GL001015 | 100 | 3.20E-267 | WP_003233284.1 | MULTISPECIES: spore coat associated protein YheD [Bacillus] |
| BSLIN78GL001016 | 100 | 5.60E-214 | WP_003245845.1 | MULTISPECIES: spore coat associated protein SpaC [Bacillales] |
| BSLIN78GL001017 | 100 | 8.20E-208 | WP_014479323.1 | MULTISPECIES: DUF445 domain-containing protein [Bacillus] |
| BSLIN78GL001018 | 100 | 2.40E-57 | WP_003224239.1 | MULTISPECIES: YlbF family regulator [Bacillales] |
| BSLIN78GL001019 | 100 | 8.60E-207 | WP_046664065.1 | MULTISPECIES: DNA alkylation repair protein [Bacillus] |
| BSLIN78GL001020 | 100 | 1.80E-159 | WP_003233277.1 | MULTISPECIES: Cof-type HAD-IIB family hydrolase [Bacillales |
| BSLIN78GL001021 | 100 | 1.30E-296 | AGA24362.1 | Oxygen-independent coproporphyrinogen III oxidase [Bacillus subtilis subsp. subtilis |
| BSLIN78GL001022 | 100 | 2.50E-218 | CAA74453.1 | hypothetical protein [Bacillus subtilis subsp. subtilis str. 168] |
| BSLIN78GL001023 | 100 | 3.10E-87 | WP_003233269.1 | MULTISPECIES: K(+)/H(+) antiporter subunit KhtT [Bacillales] |
| BSLIN78GL001024 | 100 | 4.80E-61 | QHF56909.1 | hypothetical protein Bateq7PJ16_1103 [Bacillus subtilis] |
| BSLIN78GL001025 | 100 | 8.40E-146 | AKE22826.1 | enoyl-CoA hydratase [Bacillus sp. LM 4-2 |
| BSLIN78GL001026 | 100 | 2.30E-27 | WP_003233264.1 | MULTISPECIES: YhzD family protein [Bacillales |
| BSLIN78GL001027 | 100 | 4.20E-167 | WP_003233262.1 | MULTISPECIES: ABC transporter ATP-binding protein [Bacillales] |
| BSLIN78GL001028 | 100 | 1.30E-225 | WP_003244912.1 | MULTISPECIES: ABC transporter permease [Bacillales] |
| BSLIN78GL001029 | 100 | 1.10E-239 | WP_046380897.1 | MULTISPECIES: exonuclease SbcCD subunit D [Bacillus] |
| BSLIN78GL001030 | 100 | 0.00E+00 | WP_082098092.1 | MULTISPECIES: DNA repair/recombination ATPase SbcE [Bacillus] |
| BSLIN78GL001031 | 100 | 2.80E-177 | WP_003245698.1 | MULTISPECIES: 3'-5' exoribonuclease YhaM [Bacillales |
| BSLIN78GL001032 | 100 | 4.40E-37 | WP_194418433.1 | sporulation protein YhaL [Bacillus subtilis] |
| BSLIN78GL001033 | 100 | 2.70E-158 | WP_029726316.1 | MULTISPECIES: peptidylprolyl isomerase PrsA [Bacillus |
| BSLIN78GL001034 | 100 | 2.40E-15 | AEP90096.1 | conserved hypothetical protein [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL001035 | 100 | 8.30E-21 | AEP85945.1 | conserved hypothetical protein [Bacillus spizizenii TU-B-10 |
| BSLIN78GL001036 | 100 | 1.20E-86 | WP_015715601.1 | MULTISPECIES: DUF3267 domain-containing protein [Bacillus] |
| BSLIN78GL001037 | 100 | 2.00E-46 | AGE62851.1 | hypothetical protein C663_1021 [Bacillus subtilis XF-1] |
| BSLIN78GL001038 | 99.5 | 3.40E-112 | AGE62852.1 | transcriptional regulator Hpr [Bacillus subtilis XF-1] |
| BSLIN78GL001039 | 100 | 1.90E-66 | AFQ56916.1 | Putative membrane protein [Bacillus subtilis QB928] |
| BSLIN78GL001040 | 100 | 2.00E-26 | WP_014476318.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL001041 | 100 | 1.80E-85 | WP_015715602.1 | MULTISPECIES: tryptophan transporter TrpP [Bacillus] |
| BSLIN78GL001042 | 100 | 8.10E-205 | WP_029726314.1 | MULTISPECIES: 3-phosphoserine/phosphohydroxythreonine transaminase [Bacillus] |

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| BSLIN78GL001043 | 100 | 5.60E-80 | WP_003233231.1 | MULTISPECIES: HIT family protein [Bacillales] |
| BSLIN78GL001044 | 100 | 3.80E-137 | AFQ56921.1 | ABC transporter (ATP-binding protein) [Bacillus subtilis QB928] |
| BSLIN78GL001045 | 100 | 4.60E-225 | WP_017695369.1 | MULTISPECIES: ABC transporter permease EcsB [Bacillus] |
| BSLIN78GL001046 | 100 | 1.50E-127 | WP_029726313.1 | MULTISPECIES: EcsC family protein [Bacillus] |
| BSLIN78GL001047 | 100 | 7.90E-219 | WP_046664068.1 | MULTISPECIES: N-acetyl amino acid acetylase SndC [Bacillus] |
| BSLIN78GL001048 | 93 | 1.40E-15 | GAK79837.1 | hypothetical protein BSMD_017450 [Bacillus subtilis Miyagi-4] |
| BSLIN78GL001049 | 100 | 2.10E-258 | WP_080348079.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL001050 | 100 | 1.60E-42 | AOL28137.1 | hypothetical protein BGM23_16605 [Bacillus sp. FJAT-14266] |
| BSLIN78GL001051 | 99.4 | 9.70E-92 | AFQ56927.1 | Heme-degrading monooxygenase [Bacillus subtilis QB928] |
| BSLIN78GL001052 | 100 | 0.00E+00 | WP_029726309.1 | MULTISPECIES: transglycosylase domain-containing protein [Bacillus] |
| BSLIN78GL001053 | 99.2 | 2.10E-205 | QHF56936.1 | decarboxylase [Bacillus subtilis] |
| BSLIN78GL001054 | 100 | 3.00E-176 | WP_021479633.1 | MULTISPECIES: ferrochelatase [Bacillus] |
| BSLIN78GL001055 | 100 | 4.00E-268 | WP_029726307.1 | MULTISPECIES: protoporphyrinogen oxidase [Bacillus] |
| BSLIN78GL001056 | 100 | 8.90E-102 | QHF56939.1 | HTH-type transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL001057 | 100 | 0.00E+00 | WP_029726305.1 | MULTISPECIES: YhgE/Pip domain-containing protein [Bacillus] |
| BSLIN78GL001058 | 100 | 2.10E-183 | WP_029726304.1 | MULTISPECIES: beta-ketoacyl-ACP synthase III FabHB [Bacillus |
| BSLIN78GL001059 | 100 | 1.60E-141 | WP_003233198.1 | MULTISPECIES: YhfC family intramembrane metalloprotease [Bacillales] |
| BSLIN78GL001060 | 100 | 6.50E-25 | WP_003245634.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL001061 | 100 | 4.20E-195 | EHA30212.1 | hypothetical protein BSSC8_33090 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001062 | 100 | 6.80E-72 | WP_015252434.1 | MULTISPECIES: ASCH domain-containing protein [Bacillus] |
| BSLIN78GL001063 | 100 | 1.40E-235 | WP_003245579.1 | MULTISPECIES: glutamate/proton symporter GltT [Bacillales] |
| BSLIN78GL001064 | 100 | 4.30E-52 | KKB92818.1 | hypothetical protein WB24_04145 [Bacillus sp. CMAA 1185] |
| BSLIN78GL001065 | 100 | 3.60E-140 | WP_046160237.1 | MULTISPECIES: MBL fold metallo-hydrolase [Bacillus] |
| BSLIN78GL001066 | 100 | 1.00E-190 | WP_014479356.1 | MULTISPECIES: lipoate--protein ligase LplJ [Bacillus] |
| BSLIN78GL001067 | 98.2 | 1.50E-116 | BAI84576.2 | hypothetical protein BSNT_07463 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL001068 | 100 | 7.30E-300 | WP_032725337.1 | long-chain-fatty-acid--CoA ligase LcfB [Bacillus subtilis] |
| BSLIN78GL001069 | 100 | 1.30E-70 | AFQ56944.1 | YhfM [Bacillus subtilis QB928] |
| BSLIN78GL001070 | 100 | 3.50E-247 | WP_003233175.1 | MULTISPECIES: M48 family metallopeptidase [Bacillales] |
| BSLIN78GL001071 | 100 | 1.60E-211 | WP_015715621.1 | MULTISPECIES: subtilisin AprE [Bacillus] |
| BSLIN78GL001072 | 100 | 3.20E-22 | AHA76999.1 | Hypothetical Protein U712_05255 [Bacillus subtilis PY79] |
| BSLIN78GL001073 | 100 | 6.30E-79 | WP_019712916.1 | MULTISPECIES: GNAT family N-acetyltransferase [Bacillus] |
| BSLIN78GL001074 | 100 | 6.80E-182 | WP_019712915.1 | MULTISPECIES: acryloyl-CoA reductase [Bacillus] |
| BSLIN78GL001075 | 100 | 9.00E-17 | AHA77002.1 | Hypothetical Protein U712_05270 [Bacillus subtilis PY79] |
| BSLIN78GL001076 | 100 | 4.90E-177 | WP_032721272.1 | MULTISPECIES: ABC transporter substrate-binding protein [Bacillus] |
| BSLIN78GL001077 | 100 | 6.40E-108 | WP_003233157.1 | MULTISPECIES: phosphatase PhoE [Bacillales] |
| BSLIN78GL001078 | 100 | 1.00E-202 | WP_019712349.1 | MULTISPECIES: acetyl-CoA C-acyltransferase [Bacillus |
| BSLIN78GL001079 | 99.8 | 7.80E-280 | WP_019712350.1 | acyl-CoA synthetase [Bacillus subtilis] |
| BSLIN78GL001080 | 100 | 1.40E-96 | WP_019712351.1 | MULTISPECIES: biotin transporter BioY [Bacillus] |
| BSLIN78GL001081 | 100 | 1.20E-248 | QHF56964.1 | aerotactic transducer HemAT [Bacillus subtilis] |
| BSLIN78GL001082 | 100 | 0.00E+00 | AFQ56955.1 | Putative Rieske [2Fe-2S] oxygenase [Bacillus subtilis QB928] |
| BSLIN78GL001083 | 100 | 2.20E-160 | AFQ56956.1 | Putative oxidoreductase [Bacillus subtilis QB928] |
| BSLIN78GL001084 | 100 | 1.40E-34 | AFQ56957.1 | YhzC [Bacillus subtilis QB928] |
| BSLIN78GL001085 | 99.5 | 8.20E-114 | AFQ56958.1 | Competence transcription factor (CTF) [Bacillus subtilis QB928] |
| BSLIN78GL001086 | 100 | 2.70E-169 | AKE22885.1 | oxidoreductase [Bacillus sp. LM 4-2] |
| BSLIN78GL001087 | 100 | 3.30E-17 | AHA77014.1 | Hypothetical Protein U712_05330 [Bacillus subtilis PY79] |
| BSLIN78GL001088 | 100 | 2.00E-43 | WP_003233136.1 | MULTISPECIES: excalibur calcium-binding domain-containing protein [Bacillales] |
| BSLIN78GL001089 | 100 | 4.50E-275 | WP_017695341.1 | MULTISPECIES: sodium:solute symporter [Bacillus] |
| BSLIN78GL001090 | 100 | 1.70E-28 | WP_043857242.1 | DUF3311 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL001091 | 99.2 | 3.10E-60 | WP_121591604.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001092 | 100 | 7.10E-113 | WP_010886465.1 | MULTISPECIES: VTT domain-containing protein [Bacillales] |
| BSLIN78GL001093 | 99.4 | 3.70E-94 | AFQ56965.1 | Type I signal peptidase [Bacillus subtilis QB928] |
| BSLIN78GL001095 | 99 | 9.30E-284 | WP_072692641.1 | monooxygenase [Bacillus subtilis] |
| BSLIN78GL001096 | 100 | 4.30E-98 | EHA30179.1 | putative transcriptional regulator [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001097 | 96.6 | 4.70E-07 | AEP90156.1 | hypothetical protein I33_1185 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL001098 | 100 | 6.60E-224 | WP_229762443.1 | MULTISPECIES: glucose/mannose transporter GlcP [Bacillus] |
| BSLIN78GL001099 | 100 | 1.20E-181 | WP_131227290.1 | glucose-6-phosphate 3-dehydrogenase NdtC [Bacillus subtilis] |
| BSLIN78GL001100 | 100 | 4.60E-163 | WP_032721285.1 | kanosamine-6-phosphate phosphatase [Bacillus subtilis] |
| BSLIN78GL001101 | 100 | 1.00E-254 | WP_131227291.1 | 3-dehydro-glucose-6-phosphate--glutamate transaminase [Bacillus subtilis] |
| BSLIN78GL001102 | 100 | 3.70E-188 | WP_003245736.1 | MULTISPECIES: NTD biosynthesis operon transcriptional regulator NtdR [Bacillus] |
| BSLIN78GL001103 | 100 | 5.60E-212 | WP_061891216.1 | MULTISPECIES: AbrB family transcriptional regulator [Bacillus] |
| BSLIN78GL001104 | 100 | 8.10E-222 | WP_069704122.1 | MULTISPECIES: MFS transporter [Bacillus] |
| BSLIN78GL001105 | 99.1 | 0.00E+00 | AFQ56975.1 | YhjP [Bacillus subtilis QB928] |
| BSLIN78GL001106 | 98.7 | 1.50E-80 | RAP06563.1 | hypothetical protein HS3_03256 [Bacillus subtilis] |
| BSLIN78GL001107 | 100 | 3.60E-79 | WP_003245806.1 | MULTISPECIES: ferritin family protein [Bacillales] |
| BSLIN78GL001108 | 99.9 | 0.00E+00 | WP_069704118.1 | MULTISPECIES: helicase-exonuclease AddAB subunit AddB [Bacillus] |
| BSLIN78GL001109 | 100 | 0.00E+00 | WP_160216283.1 | MULTISPECIES: helicase-exonuclease AddAB subunit AddA [Bacillus] |
| BSLIN78GL001110 | 100 | 2.70E-222 | WP_069704117.1 | MULTISPECIES: exonuclease subunit SbcD [Bacillus] |
| BSLIN78GL001111 | 100 | 0.00E+00 | WP_069704116.1 | MULTISPECIES: exonuclease subunit SbcC [Bacillus] |
| BSLIN78GL001112 | 100 | 7.60E-52 | WP_015252406.1 | MULTISPECIES: HNH nuclease-like protein HlpB [Bacillus] |
| BSLIN78GL001113 | 100 | 3.30E-33 | AFQ56983.1 | Spore germination protein [Bacillus subtilis QB928] |
| BSLIN78GL001114 | 100 | 3.40E-56 | ADV96053.1 | spore germination protein [Bacillus subtilis BSn5] |
| BSLIN78GL001115 | 100 | 3.00E-24 | WP_003233093.1 | MULTISPECIES: spore germination protein GerPD [Bacillales] |
| BSLIN78GL001116 | 100 | 4.10E-116 | EHA30159.1 | spore germination protein GerPC [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001117 | 100 | 1.70E-35 | AFQ56987.1 | Spore germination protein [Bacillus subtilis QB928] |
| BSLIN78GL001118 | 100 | 8.90E-34 | WP_003233088.1 | MULTISPECIES: spore germination protein [Bacillales] |
| BSLIN78GL001119 | 100 | 1.60E-24 | AKE22915.1 | hypothetical protein BsLM_1116 [Bacillus sp. LM 4-2] |
| BSLIN78GL001120 | 100 | 7.00E-23 | WP_003233086.1 | MULTISPECIES: aspartyl-phosphate phosphatase YisI [Bacillales] |
| BSLIN78GL001121 | 100 | 2.20E-174 | WP_046380911.1 | MULTISPECIES: CotH kinase family protein [Bacillus] |
| BSLIN78GL001122 | 100 | 7.10E-170 | WP_003233084.1 | MULTISPECIES: fumarylacetoacetate hydrolase family protein [Bacillus] |
| BSLIN78GL001123 | 100 | 7.50E-53 | QHF57005.1 | hypothetical protein Bateq7PJ16_1199 [Bacillus subtilis] |

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| BSLIN78GL001124 | 100 | 0.00E+00 | WP_069704115.1 | MULTISPECIES: cell wall-associated protease WprA [Bacillus |
| BSLIN78GL001125 | 99.5 | 7.40E-115 | AKE22921.1 | hypothetical protein BsLM_1122 [Bacillus sp. LM 4-2] |
| BSLIN78GL001126 | 100 | 0.00E+00 | WP_029726288.1 | MULTISPECIES: asparagine synthase (glutamine-hydrolyzing) [Bacillus |
| BSLIN78GL001127 | 100 | 1.00E-93 | WP_046380914.1 | DinB family protein [Bacillus subtilis] |
| BSLIN78GL001128 | 99.6 | 8.60E-151 | WP_326144905.1 | farnesyl diphosphate phosphatase [Bacillus subtilis] |
| BSLIN78GL001129 | 100 | 6.50E-252 | WP_014476390.1 | MULTISPECIES: MATE family efflux transporter [Bacillus |
| BSLIN78GL001130 | 100 | 1.10E-164 | WAE49480.1 | AraC family transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL001131 | 99.7 | 3.90E-185 | AFQ57000.1 | Transcriptional regulator (LacI family) [Bacillus subtilis QB928] |
| BSLIN78GL001132 | 100 | 1.30E-16 | AKE22928.1 | hypothetical protein BsLM_1129 [Bacillus sp. LM 4-2] |
| BSLIN78GL001133 | 99.7 | 8.90E-190 | WP_046380917.1 | MULTISPECIES: scyllo-inositol 2-dehydrogenase [Bacillus |
| BSLIN78GL001134 | 99.4 | 1.20E-94 | RPK17361.1 | hypothetical protein EH2_02669 [Bacillus subtilis] |
| BSLIN78GL001135 | 100 | 1.30E-111 | AOR97519.1 | Putative amino-acid transporter YisU [Bacillus subtilis] |
| BSLIN78GL001136 | 100 | 1.60E-280 | WP_085186299.1 | PLP-dependent aminotransferase family protein [Bacillus subtilis] |
| BSLIN78GL001137 | 100 | 2.00E-118 | WP_003233060.1 | MULTISPECIES: pentapeptide repeat-containing protein [Bacillales |
| BSLIN78GL001138 | 100 | 1.60E-166 | AFQ57006.1 | Putative hydrolase [Bacillus subtilis QB928] |
| BSLIN78GL001139 | 100 | 2.90E-111 | WP_003245829.1 | MULTISPECIES: adenylyl-sulfate kinase [Bacillales |
| BSLIN78GL001140 | 100 | 1.60E-230 | WP_003233054.1 | MULTISPECIES: sulfate adenylyltransferase [Bacillales |
| BSLIN78GL001141 | 100 | 3.20E-141 | WP_003244757.1 | MULTISPECIES: phosphoadenylyl-sulfate reductase [Bacillales |
| BSLIN78GL001142 | 100 | 3.10E-125 | AFQ57010.1 | 2-phosphosulfolactate phosphatase [Bacillus subtilis QB928] |
| BSLIN78GL001143 | 100 | 1.70E-140 | WP_003233048.1 | MULTISPECIES: phosphosulfolactate synthase [Bacillales |
| BSLIN78GL001144 | 100 | 3.10E-122 | AEP90202.1 | sporulation membrane protein YitE [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL001145 | 100 | 3.50E-219 | WP_003245056.1 | MULTISPECIES: mandelate racemase/muconate lactonizing enzyme family protein |
| BSLIN78GL001146 | 100 | 8.00E-236 | WP_003245414.1 | MULTISPECIES: MFS transporter [Bacillales] |
| BSLIN78GL001147 | 100 | 1.80E-159 | WP_029726280.1 | MULTISPECIES: GNAT family N-acetyltransferase [Bacillus |
| BSLIN78GL001148 | 100 | 2.30E-81 | AXV60865.1 | GNAT family N-acetyltransferase [Bacillus subtilis |
| BSLIN78GL001149 | 100 | 0.00E+00 | WP_029726278.1 | MULTISPECIES: bifunctional homocysteine S- |
| BSLIN78GL001150 | 100 | 2.70E-17 | AKN13190.1 | hypothetical protein ABU16_2114 [Bacillus subtilis] |
| BSLIN78GL001151 | 100 | 2.30E-82 | WP_003233034.1 | MULTISPECIES: YajQ family cyclic di-GMP-binding protein [Bacillales |
| BSLIN78GL001152 | 100 | 1.20E-169 | AFQ57019.1 | RNA-binding protein [Bacillus subtilis QB928] |
| BSLIN78GL001153 | 100 | 3.60E-92 | EHA30124.1 | hypothetical protein BSSC8_32210 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001154 | 100 | 2.00E-175 | WP_003233028.1 | MULTISPECIES: sporulation-delaying protein SdpB family protein [Bacillales |
| BSLIN78GL001155 | 100 | 2.10E-106 | AFQ57022.1 | YitP [Bacillus subtilis QB928] |
| BSLIN78GL001156 | 100 | 1.10E-40 | WP_069837423.1 | MULTISPECIES: PadR family transcriptional regulator [Bacillus] |
| BSLIN78GL001157 | 100 | 1.60E-101 | WP_003233023.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL001158 | 100 | 3.50E-46 | WP_003233021.1 | MULTISPECIES: DUF3784 domain-containing protein [Bacillales] |
| BSLIN78GL001159 | 100 | 2.90E-304 | WP_120027970.1 | neutral protease NprB [Bacillus subtilis] |
| BSLIN78GL001160 | 99.7 | 5.70E-164 | AFQ57027.1 | YitS [Bacillus subtilis QB928] |
| BSLIN78GL001161 | 100 | 3.30E-167 | AFQ57028.1 | Putative integral inner membrane protein [Bacillus subtilis QB928] |
| BSLIN78GL001162 | 100 | 5.40E-81 | EHA30115.1 | intracellular proteinase inhibitor BsuPI [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001163 | 100 | 8.40E-28 | WP_003233010.1 | MULTISPECIES: DUF3813 domain-containing protein [Bacillus] |
| BSLIN78GL001164 | 100 | 5.80E-155 | WP_003233007.1 | MULTISPECIES: 5-amino-6-(5-phospho-D-ribitylamino)uracil phosphatase YitU |
| BSLIN78GL001165 | 100 | 2.50E-144 | WP_003233006.1 | MULTISPECIES: prolyl oligopeptidase family serine peptidase [Bacillales |
| BSLIN78GL001166 | 100 | 1.70E-51 | WP_003232998.1 | MULTISPECIES: metal-sulfur cluster assembly factor [Bacillales |
| BSLIN78GL001167 | 100 | 1.70E-24 | WP_003232996.1 | MULTISPECIES: YqaE/Pmp3 family membrane protein [Bacillales] |
| BSLIN78GL001168 | 100 | 5.80E-275 | AFQ57034.1 | Putative FMN/FAD-binding oxidoreductase [Bacillus subtilis QB928] |
| BSLIN78GL001169 | 100 | 3.10E-96 | WP_003232993.1 | MULTISPECIES: MFS transporter [Bacillales] |
| BSLIN78GL001170 | 100 | 4.90E-199 | WP_003232991.1 | MULTISPECIES: N-acetyl-gamma-glutamyl-phosphate reductase [Bacillus |
| BSLIN78GL001171 | 100 | 3.70E-230 | WP_003232989.1 | MULTISPECIES: bifunctional ornithine acetyltransferase/N-acetylglutamate synthase |
| BSLIN78GL001172 | 100 | 3.60E-138 | WP_003232987.1 | MULTISPECIES: acetylglutamate kinase [Bacillales |
| BSLIN78GL001173 | 100 | 3.10E-218 | WP_003232985.1 | MULTISPECIES: acetylornithine transaminase [Bacillales |
| BSLIN78GL001174 | 100 | 7.90E-205 | WP_003232984.1 | MULTISPECIES: carbamoyl phosphate synthase small subunit [Bacillales |
| BSLIN78GL001175 | 100 | 0.00E+00 | WP_003232982.1 | MULTISPECIES: carbamoyl phosphate synthase large subunit [Bacillales |
| BSLIN78GL001176 | 100 | 3.10E-176 | WP_003232980.1 | MULTISPECIES: ornithine carbamoyltransferase [Bacillales |
| BSLIN78GL001177 | 100 | 2.40E-40 | AGE62980.1 | hypothetical protein C663_1153 [Bacillus subtilis XF-1] |
| BSLIN78GL001178 | 100 | 3.80E-12 | AGE62981.1 | hypothetical protein C663_1154 [Bacillus subtilis XF-1] |
| BSLIN78GL001179 | 100 | 4.50E-146 | EHA30098.1 | hypothetical protein BSSC8_31950 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001180 | 100 | 3.20E-21 | AHA77107.1 | Hypothetical Protein U712_05795 [Bacillus subtilis PY79] |
| BSLIN78GL001181 | 100 | 1.60E-103 | WP_003232974.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL001182 | 100 | 3.60E-188 | EHA30095.1 | positive regulator of comK [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001183 | 100 | 1.50E-26 | WP_003224559.1 | MULTISPECIES: ComG operon transcriptional repressor ComZ [Bacillales] |
| BSLIN78GL001184 | 100 | 7.80E-36 | WP_003232972.1 | MULTISPECIES: spore coat protein YjzB [Bacillales] |
| BSLIN78GL001185 | 100 | 4.90E-174 | WP_003232971.1 | MULTISPECIES: beta-ketoacyl-ACP synthase III [Bacillales |
| BSLIN78GL001186 | 97.1 | 1.10E-229 | WP_254503005.1 | beta-ketoacyl-ACP synthase II [Bacillus halotolerans |
| BSLIN78GL001187 | 98.9 | 3.70E-154 | QHF57068.1 | hypothetical protein Bateq7PJ16_1262 [Bacillus subtilis] |
| BSLIN78GL001188 | 100 | 5.00E-185 | WP_003232965.1 | MULTISPECIES: oligopeptide ABC transporter ATP-binding protein AppD |
| BSLIN78GL001189 | 100 | 3.50E-186 | WP_003232964.1 | MULTISPECIES: oligopeptide ABC transporter ATP-binding protein AppF |
| BSLIN78GL001190 | 100 | 0.00E+00 | WP_003245082.1 | MULTISPECIES: peptide-binding protein [Bacillales |
| BSLIN78GL001191 | 100 | 2.00E-175 | WP_003245828.1 | MULTISPECIES: oligopeptide ABC transporter permease AppB [Bacillales |
| BSLIN78GL001192 | 100 | 2.50E-167 | WP_003232961.1 | MULTISPECIES: oligopeptide ABC transporter permease AppC [Bacillales |
| BSLIN78GL001193 | 100 | 5.30E-147 | WP_003239298.1 | MULTISPECIES: YjbA family protein [Bacillales |
| BSLIN78GL001194 | 100 | 8.00E-194 | AHA77120.1 | Tryptophanyl-tRNA synthetase [Bacillus subtilis PY79 |
| BSLIN78GL001195 | 99.8 | 0.00E+00 | WP_003232957.1 | MULTISPECIES: oligopeptide ABC transporter substrate-binding protein OppA |
| BSLIN78GL001196 | 100 | 3.10E-165 | AGE62997.1 | oligopeptide ABC transporter (permease) [Bacillus subtilis XF-1] |
| BSLIN78GL001197 | 100 | 2.50E-170 | WP_003232954.1 | MULTISPECIES: oligopeptide ABC transporter permease OppC [Bacillales] |
| BSLIN78GL001198 | 100 | 1.30E-199 | AHA77124.1 | Oligopeptide transport ATP-binding protein OppD [Bacillus subtilis PY79] |
| BSLIN78GL001199 | 100 | 8.30E-174 | AAA62692.1 | sporulation protein [Bacillus subtilis] |
| BSLIN78GL001200 | 100 | 7.70E-217 | AHA77127.1 | putative MFS-type transporter yjbB [Bacillus subtilis PY79 |
| BSLIN78GL001201 | 100 | 3.20E-107 | WP_003244921.1 | MULTISPECIES: GNAT family N-acetyltransferase [Bacillales |
| BSLIN78GL001202 | 100 | 9.90E-68 | WP_003245483.1 | MULTISPECIES: transcriptional regulator Spx [Bacillales] |
| BSLIN78GL001203 | 100 | 1.40E-114 | WP_003232944.1 | MULTISPECIES: TerC family protein [Bacillales |

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|---|---|---|---|---|
| BSLIN78GL001204 | 100 | 2.80E-120 | WP_015383354.1 | MULTISPECIES: adaptor protein MecA [Bacillus] |
| BSLIN78GL001205 | 99.7 | 7.40E-225 | WP_029726275.1 | competence protein CoiA [Bacillus subtilis] |
| BSLIN78GL001206 | 99.9 | 0.00E+00 | AEP90257.1 | oligoendopeptidase F [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL001207 | 100 | 3.20E-14 | QHF57090.1 | membrane protein [Bacillus subtilis] |
| BSLIN78GL001208 | 100 | 7.30E-18 | EHA30068.1 | hypothetical protein BSSC8_31640 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001209 | 100 | 1.70E-154 | WP_003245184.1 | MULTISPECIES: protease adaptor protein SpxH [Bacillales] |
| BSLIN78GL001210 | 100 | 5.60E-71 | WP_003232928.1 | MULTISPECIES: group 2 truncated hemoglobin YjbI [Bacillales] |
| BSLIN78GL001211 | 100 | 4.40E-130 | WP_029726274.1 | MULTISPECIES: bifunctional muramidase/murein lytic transglycosylase [Bacillus] |
| BSLIN78GL001212 | 100 | 3.00E-102 | WP_014479452.1 | MULTISPECIES: CYTH domain-containing protein [Bacillus] |
| BSLIN78GL001213 | 100 | 6.80E-63 | WP_014479453.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL001214 | 100 | 7.80E-115 | AFI27803.1 | (p)ppGpp synthetase [Bacillus sp. JS] |
| BSLIN78GL001215 | 100 | 1.90E-150 | WP_003232918.1 | MULTISPECIES: NAD kinase [Bacillales] |
| BSLIN78GL001216 | 100 | 5.40E-170 | WP_003244860.1 | MULTISPECIES: RluA family pseudouridine synthase [Bacillales] |
| BSLIN78GL001217 | 100 | 3.60E-140 | WP_003244765.1 | MULTISPECIES: bis(5'-nucleosyl)-tetraphosphatase PrpE [Bacillales] |
| BSLIN78GL001218 | 100 | 0.00E+00 | WP_003232910.1 | MULTISPECIES: monovalent cation:proton antiporter family protein [Bacillales] |
| BSLIN78GL001219 | 100 | 1.10E-138 | WP_003232909.1 | MULTISPECIES: thiaminase II [Bacillales] |
| BSLIN78GL001220 | 100 | 1.80E-108 | WP_003232908.1 | MULTISPECIES: thiazole tautomerase TenI [Bacillales] |
| BSLIN78GL001221 | 100 | 1.80E-215 | WP_029726273.1 | MULTISPECIES: glycine oxidase ThiO [Bacillus] |
| BSLIN78GL001222 | 100 | 8.40E-31 | AEP90272.1 | thiamine biosynthesis protein ThiS [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL001223 | 100 | 2.80E-135 | WP_003232902.1 | MULTISPECIES: thiazole synthase [Bacillus] |
| BSLIN78GL001224 | 100 | 7.60E-189 | WP_003232900.1 | MULTISPECIES: thiazole biosynthesis adenylyltransferase ThiF [Bacillus |
| BSLIN78GL001225 | 100 | 4.30E-150 | WP_014479462.1 | MULTISPECIES: bifunctional hydroxymethylpyrimidine |
| BSLIN78GL001226 | 100 | 2.00E-147 | QHF57109.1 | reductase [NADH] [Bacillus subtilis] |
| BSLIN78GL001227 | 100 | 1.80E-125 | WP_072692635.1 | MULTISPECIES: spore coat protein CotO [Bacillus] |
| BSLIN78GL001228 | 100 | 7.70E-21 | AKE23027.1 | hypothetical protein BsLM_1228 [Bacillus sp. LM 4-2] |
| BSLIN78GL001229 | 100 | 2.50E-83 | WP_014479464.1 | MULTISPECIES: spore coat protein CotZ [Bacillus] |
| BSLIN78GL001230 | 100 | 6.20E-105 | BAI84731.2 | spore coat protein Y [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL001231 | 100 | 2.00E-89 | WP_015252341.1 | MULTISPECIES: spore coat protein CotX [Bacillus] |
| BSLIN78GL001232 | 100 | 3.60E-52 | WP_015252340.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL001233 | 100 | 6.20E-65 | AGA21613.1 | Spore coat protein V [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL001234 | 100 | 5.20E-60 | WP_014476457.1 | MULTISPECIES: sporulation protein YjcA [Bacillus] |
| BSLIN78GL001235 | 100 | 8.20E-35 | KFC31678.1 | hypothetical protein ZQL_01685 [Bacillus subtilis] |
| BSLIN78GL001236 | 100 | 4.50E-32 | WP_017695696.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL001237 | 100 | 4.30E-21 | WP_015252337.1 | MULTISPECIES: sporulation protein YjcZ [Bacillus] |
| BSLIN78GL001238 | 100 | 4.70E-39 | WP_003232870.1 | MULTISPECIES: sporulation-specific transcription regulator SopVIF [Bacillales] |
| BSLIN78GL001239 | 100 | 0.00E+00 | WP_029726268.1 | ATP-dependent helicase [Bacillus subtilis] |
| BSLIN78GL001240 | 100 | 8.60E-41 | WP_003232866.1 | MULTISPECIES: hypothetical protein [Bacillales] |
| BSLIN78GL001241 | 100 | 7.50E-74 | WP_029726267.1 | MULTISPECIES: GNAT family N-acetyltransferase [Bacillus] |
| BSLIN78GL001242 | 100 | 4.00E-93 | WP_003232861.1 | MULTISPECIES: YjcG family protein [Bacillales] |
| BSLIN78GL001243 | 100 | 1.70E-137 | WP_029726266.1 | MULTISPECIES: esterase family protein [Bacillus] |
| BSLIN78GL001244 | 100 | 1.90E-19 | AFI27832.1 | hypothetical protein MY9_1294 [Bacillus sp. JS] |
| BSLIN78GL001245 | 100 | 2.00E-217 | AHA77173.1 | Cystathionine gamma-synthase [Bacillus subtilis PY79] |
| BSLIN78GL001246 | 100 | 9.40E-212 | EHA30029.1 | cystathionine beta-lyase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001247 | 100 | 3.30E-98 | WP_015383377.1 | MULTISPECIES: GNAT family protein [Bacillus] |
| BSLIN78GL001248 | 100 | 2.40E-218 | EHA30027.1 | hypothetical protein BSSC8_31240 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001249 | 100 | 5.60E-22 | AKN13288.1 | hypothetical protein ABU16_2212 [Bacillus subtilis] |
| BSLIN78GL001250 | 100 | 5.00E-51 | WP_003232848.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL001251 | 100 | 2.80E-70 | WP_003232847.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL001252 | 100 | 0.00E+00 | EHA30023.1 | yqcG [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001253 | 100 | 4.00E-139 | WP_003232844.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL001254 | 100 | 3.50E-25 | WP_015715690.1 | MULTISPECIES: YolD-like family protein [Bacillus] |
| BSLIN78GL001255 | 100 | 6.30E-91 | WP_014476481.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL001256 | 100 | 6.40E-16 | AKN13297.1 | hypothetical protein ABU16_2221 [Bacillus subtilis] |
| BSLIN78GL001257 | 100 | 2.80E-28 | ADV96194.1 | hypothetical protein BSn5_17930 [Bacillus subtilis BSn5] |
| BSLIN78GL001258 | 97.5 | 1.40E-60 | EHA30018.1 | hypothetical protein BSSC8_31150 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001259 | 99.3 | 2.50E-161 | AFQ57117.1 | Putative acyl-carrier protein oxidoreductase [Bacillus subtilis QB928] |
| BSLIN78GL001260 | 100 | 1.50E-56 | WP_015715694.1 | MULTISPECIES: Ig-like domain-containing protein [Bacillus] |
| BSLIN78GL001261 | 100 | 0.00E+00 | WP_015715695.1 | MULTISPECIES: mannose transport/utilization transcriptional regulator ManR |
| BSLIN78GL001262 | 100 | 0.00E+00 | WP_038427604.1 | MULTISPECIES: PTS mannose transporter subunit IIABC [Bacillus] |
| BSLIN78GL001263 | 100 | 1.90E-186 | WP_015715697.1 | MULTISPECIES: mannose-6-phosphate isomerase, class I [Bacillus] |
| BSLIN78GL001264 | 100 | 1.00E-70 | TWH26971.1 | Protein of unknown function (DUF2992) [Bacillus subtilis J22] |
| BSLIN78GL001265 | 100 | 7.90E-94 | WP_029726260.1 | GNAT family N-acetyltransferase [Bacillus subtilis] |
| BSLIN78GL001266 | 100 | 1.90E-81 | WP_128422178.1 | Cys-tRNA(Pro) deacylase [Bacillus subtilis] |
| BSLIN78GL001267 | 100 | 2.00E-29 | AFI27854.1 | hypothetical protein MY9_1317 [Bacillus sp. JS] |
| BSLIN78GL001268 | 100 | 1.00E-54 | WP_003232822.1 | MULTISPECIES: YjdJ family protein [Bacillales] |
| BSLIN78GL001270 | 100 | 2.50E-14 | ADV96207.1 | hypothetical protein BSn5_17995 [Bacillus subtilis BSn5] |
| BSLIN78GL001271 | 100 | 1.40E-187 | WP_072692652.1 | MULTISPECIES: heme o synthase [Bacillus] |
| BSLIN78GL001272 | 100 | 6.70E-58 | ARB36605.1 | spore coat protein [Bacillus subtilis] |
| BSLIN78GL001273 | 100 | 7.10E-270 | WP_003245023.1 | MULTISPECIES: peptidoglycan-N-acetylmuramic acid deacetylase PdaC [Bacillales |
| BSLIN78GL001274 | 100 | 5.60E-86 | WP_032678796.1 | MULTISPECIES: YjfA family protein [Bacillus] |
| BSLIN78GL001275 | 100 | 7.70E-22 | WP_014476499.1 | MULTISPECIES: YjfB family protein [Bacillus] |
| BSLIN78GL001276 | 100 | 2.60E-13 | AOL27932.1 | hypothetical protein BGM23_15515 [Bacillus sp. FJAT-14266] |
| BSLIN78GL001277 | 100 | 4.10E-170 | WP_029726258.1 | MULTISPECIES: DUF2268 domain-containing protein [Bacillus] |
| BSLIN78GL001278 | 98.8 | 1.50E-86 | AOR97672.1 | putative membrane protein YjgA [Bacillus subtilis] |
| BSLIN78GL001279 | 100 | 4.60E-106 | WP_014476503.1 | MULTISPECIES: YjgB family protein [Bacillus] |
| BSLIN78GL001280 | 99.5 | 0.00E+00 | WP_213414424.1 | formate dehydrogenase subunit alpha [Bacillus subtilis] |
| BSLIN78GL001281 | 100 | 9.00E-99 | WP_029726254.1 | MULTISPECIES: DUF1641 domain-containing protein [Bacillus] |
| BSLIN78GL001282 | 100 | 2.70E-115 | WP_029726253.1 | MULTISPECIES: DUF4352 domain-containing protein [Bacillus] |
| BSLIN78GL001283 | 100 | 9.70E-118 | WP_080477798.1 | MULTISPECIES: NUDIX hydrolase [Bacillus] |
| BSLIN78GL001284 | 100 | 1.60E-43 | WP_029726251.1 | MULTISPECIES: hypothetical protein [Bacillus] |

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| BSLIN78GL001285 | 99 | 1.60E-233 | KIN56728.1 | hypothetical protein B4146_1325 [Bacillus subtilis] |
| BSLIN78GL001286 | 100 | 3.30E-220 | WP_038427605.1 | MULTISPECIES: glycosyltransferase [Bacillus |
| BSLIN78GL001287 | 100 | 3.90E-30 | WP_003232781.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL001288 | 99.6 | 8.00E-152 | AFQ57144.1 | Putative enzyme [Bacillus subtilis QB928] |
| BSLIN78GL001289 | 100 | 6.60E-129 | WP_029726247.1 | MULTISPECIES: iron export ABC transporter permease subunit FetB [Bacillus] |
| BSLIN78GL001290 | 100 | 1.90E-136 | AFQ57146.1 | Putative phosphate ABC transporter (ATP-bindingprotein) [Bacillus subtilis QB928] |
| BSLIN78GL001291 | 100 | 2.00E-144 | WP_268553255.1 | multidrug resistance efflux transporter family protein [Bacillus subtilis] |
| BSLIN78GL001292 | 98.1 | 6.90E-51 | ADV96228.1 | hypothetical protein BSn5_18100 [Bacillus subtilis BSn5] |
| BSLIN78GL001293 | 100 | 1.50E-92 | WP_038427606.1 | MULTISPECIES: cupin domain-containing protein [Bacillus] |
| BSLIN78GL001294 | 100 | 5.80E-16 | AEP90351.1 | hypothetical protein I33_1382 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL001295 | 100 | 7.30E-69 | AFQ57149.1 | YjlC [Bacillus subtilis QB928] |
| BSLIN78GL001296 | 100 | 1.10E-218 | WP_326253389.1 | NAD(P)/FAD-dependent oxidoreductase [Bacillus subtilis] |
| BSLIN78GL001297 | 75 | 9.20E-09 | ADM37301.1 | hypothetical protein BSUW23_06260 [Bacillus spizizenii str. W23 |
| BSLIN78GL001298 | 99 | 4.00E-284 | CJR52041.1 | glucuronate isomerase [Streptococcus pneumoniae] |
| BSLIN78GL001299 | 100 | 3.40E-256 | WP_119899268.1 | MFS transporter [Bacillus subtilis] |
| BSLIN78GL001300 | 100 | 3.90E-193 | WP_119899270.1 | ureidoglycolate dehydrogenase [Bacillus subtilis] |
| BSLIN78GL001301 | 100 | 1.00E-193 | WP_041333924.1 | zinc-binding alcohol dehydrogenase family protein [Bacillus subtilis |
| BSLIN78GL001302 | 98.6 | 1.10E-214 | BAI84823.2 | mannonate dehydratase [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL001303 | 100 | 5.00E-154 | WP_003245605.1 | MULTISPECIES: SDR family oxidoreductase [Bacillales |
| BSLIN78GL001304 | 100 | 4.70E-236 | WP_003245531.1 | MULTISPECIES: MFS transporter [Bacillales] |
| BSLIN78GL001305 | 100 | 2.30E-185 | WP_029726237.1 | MULTISPECIES: LacI family DNA-binding transcriptional regulator [Bacillus |
| BSLIN78GL001306 | 100 | 2.00E-283 | WP_029726236.1 | MULTISPECIES: tagaturonate reductase [Bacillus] |
| BSLIN78GL001307 | 100 | 4.70E-288 | WP_003245409.1 | MULTISPECIES: UxaA family hydrolase [Bacillales |
| BSLIN78GL001308 | 100 | 2.40E-134 | WP_003245643.1 | MULTISPECIES: sulfite exporter TauE/SafE family protein [Bacillales |
| BSLIN78GL001309 | 100 | 1.40E-81 | WP_003245144.1 | MULTISPECIES: DinB family protein [Bacillales |
| BSLIN78GL001310 | 100 | 1.20E-250 | AFQ57163.1 | ATPase possibly involved in protein degradation [Bacillus subtilis QB928] |
| BSLIN78GL001311 | 100 | 9.60E-217 | WP_010886491.1 | MULTISPECIES: response regulator aspartate phosphatase RapA [Bacillales] |
| BSLIN78GL001312 | 100 | 2.70E-13 | AGE63096.1 | secreted inhibitor of the activity of phosphatase [Bacillus subtilis XF-1] |
| BSLIN78GL001313 | 100 | 3.90E-41 | WP_003232731.1 | MULTISPECIES: YciI family protein [Bacillales |
| BSLIN78GL001314 | 100 | 7.20E-167 | WP_003244876.1 | MULTISPECIES: N-acetylmuramoyl-L-alanine amidase [Bacillales |
| BSLIN78GL001315 | 99.2 | 1.30E-61 | AGA20874.1 | Hypothetical protein YjqA [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL001316 | 100 | 6.50E-111 | WP_003244789.1 | MULTISPECIES: poly-gamma-glutamate hydrolase family protein [Bacillales |
| BSLIN78GL001317 | 100 | 2.80E-160 | WP_003245071.1 | MULTISPECIES: manganese catalase family protein [Bacillales] |
| BSLIN78GL001318 | 100 | 1.20E-112 | WP_003232721.1 | MULTISPECIES: ImmA/IrrE family metallo-endopeptidase [Bacillales |
| BSLIN78GL001319 | 100 | 1.60E-58 | WP_003232719.1 | MULTISPECIES: HTH-type transcriptional regulator Xre [Bacillales |
| BSLIN78GL001320 | 100 | 6.50E-27 | WP_003232712.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL001321 | 99.6 | 6.00E-149 | WP_151870280.1 | MULTISPECIES: phage portal protein [Bacillus] |
| BSLIN78GL001322 | 100 | 2.90E-114 | AHA77250.1 | Phage-like element PBSX protein xkdC [Bacillus subtilis PY79] |
| BSLIN78GL001323 | 100 | 5.70E-25 | WP_003245588.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL001324 | 98.2 | 3.40E-56 | QHF57206.1 | element PBSX protein [Bacillus subtilis] |
| BSLIN78GL001325 | 100 | 1.10E-30 | WP_003244900.1 | MULTISPECIES: phage-like element PBSX protein XtrA [Bacillales |
| BSLIN78GL001326 | 98.9 | 1.90E-96 | BAI84850.2 | positive control sigma-like factor [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL001327 | 100 | 2.60E-144 | WP_003244697.1 | MULTISPECIES: phage terminase small subunit [Bacillales] |
| BSLIN78GL001328 | 100 | 1.70E-254 | WP_003245584.1 | MULTISPECIES: PBSX family phage terminase large subunit [Bacillales] |
| BSLIN78GL001329 | 100 | 5.80E-286 | WP_003245427.1 | MULTISPECIES: phage portal protein [Bacillales] |
| BSLIN78GL001330 | 100 | 1.60E-152 | WP_003245836.1 | MULTISPECIES: XkdF-like putative serine protease domain-containing protein |
| BSLIN78GL001331 | 100 | 7.30E-170 | WP_003232690.1 | MULTISPECIES: phage major capsid protein [Bacillales] |
| BSLIN78GL001332 | 100 | 3.80E-64 | WP_014479552.1 | MULTISPECIES: DUF3199 family protein [Bacillus |
| BSLIN78GL001333 | 100 | 1.20E-64 | WP_009967053.1 | MULTISPECIES: YqbH/XkdH family protein [Bacillales] |
| BSLIN78GL001334 | 100 | 8.10E-88 | WP_003245226.1 | MULTISPECIES: HK97 gp10 family phage protein [Bacillales] |
| BSLIN78GL001335 | 100 | 2.60E-77 | WP_029726235.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL001336 | 100 | 6.30E-32 | WP_003232679.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL001337 | 100 | 3.90E-260 | WP_003245369.1 | MULTISPECIES: phage tail sheath family protein [Bacillales |
| BSLIN78GL001338 | 100 | 7.60E-77 | WP_003232677.1 | MULTISPECIES: phage tail tube protein [Bacillales] |
| BSLIN78GL001339 | 100 | 2.00E-77 | WP_015715734.1 | MULTISPECIES: phage portal protein [Bacillus] |
| BSLIN78GL001340 | 100 | 3.30E-18 | WP_072692631.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL001341 | 99.9 | 0.00E+00 | WP_046664098.1 | MULTISPECIES: transglycosylase SLT domain-containing protein [Bacillus |
| BSLIN78GL001342 | 99.4 | 3.00E-99 | AOA53896.1 | Phage-like element PBSX protein XkdP [Bacillus subtilis] |
| BSLIN78GL001343 | 100 | 9.30E-184 | EHA29935.1 | hypothetical protein BSSC8_30320 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001344 | 100 | 5.80E-40 | WP_015715735.1 | MULTISPECIES: DUF2577 family protein [Bacillus |
| BSLIN78GL001345 | 98.6 | 2.30E-73 | AGE63124.1 | hypothetical protein C663_1308 [Bacillus subtilis XF-1] |
| BSLIN78GL001346 | 100 | 6.90E-193 | WP_015715737.1 | MULTISPECIES: baseplate J/gp47 family protein [Bacillus] |
| BSLIN78GL001347 | 100 | 2.80E-100 | WP_015483131.1 | MULTISPECIES: YmfQ family protein [Bacillus] |
| BSLIN78GL001348 | 100 | 1.10E-41 | WP_015715738.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL001349 | 100 | 0.00E+00 | AIC97822.1 | terminase [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL001350 | 100 | 9.30E-56 | WP_029727046.1 | MULTISPECIES: XkdW family protein [Bacillus |
| BSLIN78GL001351 | 100 | 1.80E-23 | WP_014479563.1 | MULTISPECIES: XkdX family protein [Bacillus] |
| BSLIN78GL001352 | 100 | 3.20E-156 | WP_211197340.1 | phage-like element PBSX protein XepA [Bacillus subtilis] |
| BSLIN78GL001353 | 100 | 3.10E-41 | WP_015252265.1 | MULTISPECIES: hemolysin XhlA family protein [Bacillus |
| BSLIN78GL001354 | 100 | 1.20E-40 | WP_014479566.1 | MULTISPECIES: phage holin [Bacillus] |
| BSLIN78GL001355 | 99.3 | 2.60E-172 | BAI84879.2 | N-acetylmuramoyl-L-alanine amidase [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL001356 | 100 | 3.90E-16 | WP_119899277.1 | MULTISPECIES: three component toxin-antitoxin-antitoxin system antitoxin |
| BSLIN78GL001357 | 100 | 1.10E-23 | WP_003232646.1 | MULTISPECIES: three component toxin-antitoxin-antitoxin system antitoxin |
| BSLIN78GL001358 | 100 | 2.70E-132 | AGE63135.1 | two-component apoptosis factor [Bacillus subtilis XF-1] |
| BSLIN78GL001359 | 100 | 4.00E-182 | WP_003232642.1 | MULTISPECIES: inorganic phosphate transporter [Bacillales] |
| BSLIN78GL001360 | 100 | 5.30E-119 | AGE63137.1 | putative Pit accessory protein [Bacillus subtilis XF-1] |
| BSLIN78GL001361 | 100 | 1.20E-247 | WP_015252262.1 | MULTISPECIES: serine/threonine exchanger [Bacillus |
| BSLIN78GL001362 | 100 | 7.20E-181 | WP_003232637.1 | MULTISPECIES: VOC family protein [Bacillus] |
| BSLIN78GL001363 | 100 | 0.00E+00 | WP_029727043.1 | MULTISPECIES: glycosyltransferase family 39 protein [Bacillus |
| BSLIN78GL001364 | 99.7 | 5.60E-181 | WP_015715747.1 | MULTISPECIES: glycosyltransferase family 2 protein [Bacillus |

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| BSLIN78GL001365 | 100 | 6.40E-15 | AKE23161.1 | hypothetical protein BsLM_1362 [Bacillus sp. LM 4-2] |
| BSLIN78GL001366 | 100 | 8.50E-252 | QHF57246.1 | protease Do-like [Bacillus subtilis] |
| BSLIN78GL001367 | 100 | 1.40E-145 | WP_029727042.1 | MULTISPECIES: pyrroline-5-carboxylate reductase ProG [Bacillus |
| BSLIN78GL001368 | 90.7 | 4.60E-14 | KIL30620.1 | hypothetical protein B4067_1394 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL001369 | 100 | 3.00E-151 | WP_014479576.1 | MULTISPECIES: D-aminopeptidase DppA [Bacillus] |
| BSLIN78GL001370 | 100 | 6.90E-165 | WP_003245446.1 | MULTISPECIES: dipeptide ABC transporter permease DppB [Bacillales] |
| BSLIN78GL001371 | 100 | 6.00E-183 | AOA53924.1 | Dipeptide transport system permease protein DppC [Bacillus subtilis] |
| BSLIN78GL001372 | 100 | 8.90E-190 | WP_029727040.1 | MULTISPECIES: dipeptide ABC transporter ATP-binding subunit DppD [Bacillus |
| BSLIN78GL001373 | 100 | 0.00E+00 | WP_224912874.1 | dipeptide ABC transporter substrate-binding protein DppE [Bacillus subtilis] |
| BSLIN78GL001374 | 100 | 2.80E-17 | AKE23169.1 | hypothetical protein BsLM_1370 [Bacillus sp. LM 4-2] |
| BSLIN78GL001375 | 99.7 | 2.50E-167 | WP_106073858.1 | LD-carboxypeptidase [Bacillus subtilis] |
| BSLIN78GL001376 | 100 | 4.10E-204 | WP_038428839.1 | L-Ala-D/L-Glu epimerase [Bacillus subtilis] |
| BSLIN78GL001377 | 100 | 1.40E-170 | WP_038428840.1 | gamma-D-glutamyl-L-lysine dipeptidyl-peptidase [Bacillus subtilis |
| BSLIN78GL001378 | 100 | 3.10E-187 | WP_033884972.1 | MULTISPECIES: oligopeptide/dipeptide ABC transporter ATP-binding protein |
| BSLIN78GL001379 | 100 | 2.50E-203 | WP_069703536.1 | MULTISPECIES: 6-phosphogluconolactonase [Bacillus] |
| BSLIN78GL001380 | 100 | 3.70E-160 | WP_038428842.1 | MULTISPECIES: dimethylarginine dimethylaminohydrolase family protein [Bacillus |
| BSLIN78GL001381 | 100 | 2.50E-101 | AFI27965.1 | YkhA [Bacillus sp. JS] |
| BSLIN78GL001382 | 100 | 9.90E-228 | WP_003245238.1 | MULTISPECIES: NO-inducible flavohemoprotein [Bacillales] |
| BSLIN78GL001383 | 100 | 2.10E-34 | WP_009967080.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL001384 | 100 | 3.90E-131 | WP_003244848.1 | MULTISPECIES: DUF421 domain-containing protein [Bacillales] |
| BSLIN78GL001385 | 100 | 1.00E-93 | EHA29893.1 | hypothetical protein BSSC8_29900 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001386 | 100 | 2.70E-88 | AKE23181.1 | N-acetyltransferase [Bacillus sp. LM 4-2] |
| BSLIN78GL001387 | 100 | 2.50E-56 | WP_003232583.1 | MULTISPECIES: multidrug efflux SMR transporter subunit YkkC [Bacillales] |
| BSLIN78GL001388 | 100 | 1.30E-42 | EHA29890.1 | efflux transporter [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001389 | 100 | 9.20E-170 | WP_003245802.1 | MULTISPECIES: formyltetrahydrofolate deformylase [Bacillales |
| BSLIN78GL001390 | 100 | 1.20E-203 | WP_003244794.1 | MULTISPECIES: glutamate 5-kinase [Bacillales] |
| BSLIN78GL001391 | 100 | 2.90E-230 | WP_003245312.1 | MULTISPECIES: glutamate-5-semialdehyde dehydrogenase [Bacillales |
| BSLIN78GL001392 | 100 | 1.30E-70 | WP_003232574.1 | MULTISPECIES: organic hydroperoxide resistance protein [Bacillales |
| BSLIN78GL001393 | 100 | 7.10E-78 | AGE63165.1 | transcriptional regulator sensing organic peroxides [Bacillus subtilis XF-1] |
| BSLIN78GL001394 | 100 | 7.60E-71 | AGA22078.1 | Organic hydroperoxide resistance protein OhrB [Bacillus subtilis subsp. subtilis str. |
| BSLIN78GL001395 | 100 | 2.50E-18 | RAP06276.1 | hypothetical protein HS3_02967 [Bacillus subtilis] |
| BSLIN78GL001396 | 100 | 6.00E-91 | EHA29882.1 | guanine deaminase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001397 | 100 | 0.00E+00 | WP_038427612.1 | MULTISPECIES: 5-methyltetrahydropteroyltriglutamate--homocysteine S |
| BSLIN78GL001398 | 100 | 3.00E-168 | WP_014479598.1 | MULTISPECIES: serine protease Isp [Bacillus] |
| BSLIN78GL001399 | 100 | 1.30E-20 | RAP06271.1 | hypothetical protein HS3_02962 [Bacillus subtilis] |
| BSLIN78GL001400 | 100 | 1.50E-153 | WP_003232560.1 | MULTISPECIES: RsbT co-antagonist RsbRB [Bacillales] |
| BSLIN78GL001401 | 99.6 | 2.50E-133 | WP_029727027.1 | MULTISPECIES: HMP/thiamine ABC transporter permease ThiX [Bacillus] |
| BSLIN78GL001402 | 100 | 0.00E+00 | WP_163131011.1 | MULTISPECIES: ABC transporter ATP-binding protein [Bacillus] |
| BSLIN78GL001403 | 100 | 5.80E-104 | WP_003232554.1 | MULTISPECIES: ECF transporter S component [Bacillales] |
| BSLIN78GL001404 | 97.2 | 2.70E-115 | QHF57282.1 | hypothetical protein Bateq7PJ16_1476 [Bacillus subtilis] |
| BSLIN78GL001405 | 99.5 | 2.40E-119 | WP_046380970.1 | MULTISPECIES: two-component system response regulator YkoG [Bacillus |
| BSLIN78GL001406 | 100 | 1.60E-250 | WP_046380971.1 | MULTISPECIES: two-component system sensor histidine kinase YkoH [Bacillus |
| BSLIN78GL001407 | 100 | 5.60E-119 | WP_046160321.1 | MULTISPECIES: PepSY domain-containing protein [Bacillus] |
| BSLIN78GL001408 | 100 | 7.00E-90 | QHF57287.1 | membrane protein [Bacillus subtilis] |
| BSLIN78GL001409 | 100 | 1.10E-18 | WP_003218541.1 | MULTISPECIES: transcriptional regulator SplA domain-containing protein |
| BSLIN78GL001410 | 100 | 1.70E-247 | WP_003232543.1 | MULTISPECIES: magnesium transporter [Bacillales] |
| BSLIN78GL001411 | 100 | 6.20E-55 | WP_003232541.1 | MULTISPECIES: MerR family transcriptional regulator TnrA [Bacillales] |
| BSLIN78GL001412 | 100 | 5.60E-19 | WP_003232538.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL001413 | 100 | 1.20E-29 | AGE63184.1 | hypothetical protein C663_1372 [Bacillus subtilis XF-1] |
| BSLIN78GL001414 | 100 | 9.10E-81 | WP_003232536.1 | MULTISPECIES: MarR family transcriptional regulator [Bacillales] |
| BSLIN78GL001415 | 99.7 | 2.60E-211 | WP_038427614.1 | MULTISPECIES: glycosyl transferase [Bacillus |
| BSLIN78GL001416 | 99.6 | 3.60E-126 | EHA29862.1 | hypothetical protein BSSC8_29590 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001417 | 100 | 1.00E-148 | EHA29861.1 | hypothetical protein BSSC8_29580 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001418 | 100 | 0.00E+00 | WP_014479610.1 | MULTISPECIES: DUF6044 family protein [Bacillus |
| BSLIN78GL001419 | 100 | 5.80E-189 | WP_326253406.1 | glycosyltransferase family 2 protein [Bacillus subtilis |
| BSLIN78GL001420 | 100 | 0.00E+00 | WP_128737793.1 | DNA ligase D [Bacillus subtilis] |
| BSLIN78GL001421 | 100 | 4.40E-175 | WP_010886496.1 | MULTISPECIES: Ku protein [Bacillales] |
| BSLIN78GL001422 | 100 | 0.00E+00 | WP_119899286.1 | bifunctional diguanylate cyclase/phosphodiesterase [Bacillus subtilis |
| BSLIN78GL001423 | 100 | 3.20E-116 | AIX07108.1 | Inner membrane protein YqjA [Bacillus subtilis] |
| BSLIN78GL001424 | 100 | 1.30E-180 | WP_014479617.1 | MULTISPECIES: TerC family protein [Bacillus |
| BSLIN78GL001425 | 100 | 6.30E-129 | AGE63196.1 | sigmaI modulating factor [Bacillus subtilis XF-1] |
| BSLIN78GL001426 | 100 | 3.80E-221 | WP_029726985.1 | MULTISPECIES: anti-sigma-I factor RsgI [Bacillus |
| BSLIN78GL001427 | 100 | 1.80E-28 | AGE63198.1 | small acid-soluble spore protein (alpha/beta-type SASP) [Bacillus subtilis XF-1] |
| BSLIN78GL001428 | 100 | 1.70E-120 | BAI84953.2 | hypothetical protein BSNT_07835 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL001429 | 100 | 7.80E-161 | WP_029726986.1 | MULTISPECIES: protease HtpX [Bacillus] |
| BSLIN78GL001430 | 100 | 1.90E-251 | WP_003244672.1 | MULTISPECIES: Ktr system potassium transporter KtrD [Bacillales] |
| BSLIN78GL001431 | 100 | 1.40E-22 | WP_003232510.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL001432 | 100 | 5.10E-27 | WP_029317708.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001433 | 100 | 4.50E-200 | EHA29843.1 | hypothetical protein BSSC8_29400 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001434 | 100 | 0.00E+00 | WP_003232504.1 | MULTISPECIES: sporulation two-component system sensor histidine kinase KinE |
| BSLIN78GL001435 | 100 | 7.50E-89 | WP_029726987.1 | MULTISPECIES: methylated-DNA--protein-cysteine methyltransferase [Bacillus |
| BSLIN78GL001436 | 100 | 9.80E-14 | WP_003232500.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL001437 | 100 | 1.20E-197 | WP_029726988.1 | MULTISPECIES: S-methyl-5-thioribose-1-phosphate isomerase [Bacillus |
| BSLIN78GL001438 | 100 | 1.40E-229 | AGA22118.1 | Methylthioribose kinase [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL001439 | 100 | 3.50E-149 | WP_003232495.1 | MULTISPECIES: carbon-nitrogen family hydrolase [Bacillales |
| BSLIN78GL001440 | 100 | 3.60E-230 | WP_017695072.1 | MULTISPECIES: methionine-glutamine aminotransferase [Bacillus] |
| BSLIN78GL001441 | 99.8 | 1.70E-235 | AIC97901.1 | 2,3-diketo-5-methylthiopentyl-1-phosphate enolase [Bacillus subtilis subsp. subtilis |
| BSLIN78GL001442 | 100 | 2.30E-136 | WP_003232486.1 | MULTISPECIES: 2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphate phosphatase |
| BSLIN78GL001443 | 100 | 1.20E-115 | WP_029726989.1 | MULTISPECIES: methylthioribulose 1-phosphate dehydratase [Bacillus |
| BSLIN78GL001444 | 100 | 2.80E-97 | WP_003232483.1 | MULTISPECIES: acireductone dioxygenase [Bacillus |

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| BSLIN78GL001445 | 100 | 4.30E-53 | WP_014479630.1 | MULTISPECIES: YkvA family protein [Bacillus |
| BSLIN78GL001446 | 100 | 4.60E-42 | WP_003218598.1 | MULTISPECIES: aspartyl-phosphate phosphatase Spo0E [Bacillales |
| BSLIN78GL001447 | 100 | 4.10E-75 | WP_029726990.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL001448 | 100 | 1.00E-282 | WP_072557174.1 | MULTISPECIES: sporulation kinase KinD [Bacillus] |
| BSLIN78GL001449 | 100 | 3.30E-13 | TII14787.1 | hypothetical protein C6Y43_14195 [Bacillus subtilis] |
| BSLIN78GL001450 | 100 | 1.90E-75 | WP_003232475.1 | MULTISPECIES: MarR family transcriptional regulator MhqR [Bacillales] |
| BSLIN78GL001451 | 100 | 1.10E-142 | WP_128480781.1 | flagellar motor protein MotB [Bacillus subtilis] |
| BSLIN78GL001452 | 100 | 5.10E-143 | QJC88368.1 | Flagellar motor rotation protein MotA [Bacillus subtilis] |
| BSLIN78GL001453 | 100 | 0.00E+00 | WP_173614052.1 | ATP-dependent protease ATP-binding subunit ClpE [Bacillus subtilis] |
| BSLIN78GL001454 | 100 | 6.00E-189 | WP_021479408.1 | MULTISPECIES: membrane protein [Bacillus] |
| BSLIN78GL001455 | 100 | 3.30E-124 | WP_003232465.1 | MULTISPECIES: 7-cyano-7-deazaguanine synthase QueC [Bacillus |
| BSLIN78GL001456 | 100 | 7.20E-83 | WP_003232462.1 | MULTISPECIES: 6-carboxytetrahydropterin synthase QueD [Bacillales |
| BSLIN78GL001457 | 100 | 1.30E-137 | WP_003232460.1 | MULTISPECIES: 7-carboxy-7-deazaguanine synthase QueE [Bacillales |
| BSLIN78GL001458 | 100 | 3.70E-96 | AGE63226.1 | 7-cyano-7-deazaguanine reductase [Bacillus subtilis XF-1] |
| BSLIN78GL001459 | 100 | 7.20E-56 | WP_241495702.1 | winged helix-turn-helix transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL001460 | 100 | 1.10E-133 | WP_101172465.1 | glucose 1-dehydrogenase [Bacillus subtilis] |
| BSLIN78GL001461 | 89.5 | 1.20E-10 | AVX17170.1 | hypothetical protein C5I45_09895 [Bacillus sp. ZY-1-1] |
| BSLIN78GL001462 | 100 | 9.20E-234 | WP_089172532.1 | spore protein YkvP [Bacillus subtilis] |
| BSLIN78GL001463 | 100 | 9.70E-36 | WP_029726994.1 | MULTISPECIES: LysM peptidoglycan-binding domain-containing protein [Bacillus |
| BSLIN78GL001464 | 99.7 | 1.70E-179 | WP_029726995.1 | MULTISPECIES: glycosyl hydrolase family 18 protein [Bacillus |
| BSLIN78GL001465 | 100 | 2.20E-16 | KIL33953.1 | hypothetical protein B4067_1573 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL001466 | 100 | 9.50E-40 | WP_326253413.1 | YkvR family protein [Bacillus subtilis] |
| BSLIN78GL001467 | 100 | 9.40E-30 | AKE23265.1 | hypothetical protein BsLM_1466 [Bacillus sp. LM 4-2] |
| BSLIN78GL001468 | 100 | 5.70E-26 | WP_010328531.1 | MULTISPECIES: YkvS family protein [Bacillus |
| BSLIN78GL001469 | 98.7 | 2.90E-35 | QHF57345.1 | hypothetical protein Bateq7PJ16_1539 [Bacillus subtilis] |
| BSLIN78GL001470 | 100 | 7.20E-113 | WP_003232442.1 | MULTISPECIES: cell wall hydrolase [Bacillales |
| BSLIN78GL001471 | 100 | 3.00E-249 | WP_014476640.1 | MULTISPECIES: sporulation protein YkvU [Bacillus] |
| BSLIN78GL001472 | 100 | 1.80E-84 | WP_029726997.1 | MULTISPECIES: sporulation thiol-disulfide oxidoreductase StoA [Bacillus |
| BSLIN78GL001473 | 100 | 0.00E+00 | WP_029726998.1 | MULTISPECIES: metal-transporting ATPase PfeT [Bacillus] |
| BSLIN78GL001474 | 98.6 | 2.30E-31 | AGE63236.1 | hypothetical protein C663_1427 [Bacillus subtilis XF-1] |
| BSLIN78GL001475 | 100 | 2.70E-208 | WP_015715797.1 | MULTISPECIES: di/tri-peptidase [Bacillus] |
| BSLIN78GL001476 | 98.2 | 3.00E-185 | RPK10171.1 | hypothetical protein EH5_03009 [Bacillus subtilis] |
| BSLIN78GL001477 | 100 | 3.40E-161 | WP_003218635.1 | MULTISPECIES: ptsGHI operon transcription antiterminator GlcT [Bacillus |
| BSLIN78GL001478 | 100 | 0.00E+00 | WP_029727001.1 | MULTISPECIES: PTS glucose transporter subunit IIABC [Bacillus |
| BSLIN78GL001479 | 100 | 6.50E-42 | QHF57357.1 | hypothetical protein Bateq7PJ16_1551 [Bacillus subtilis] |
| BSLIN78GL001480 | 96.3 | 0.00E+00 | WP_326373203.1 | phosphoenolpyruvate--protein phosphotransferase [Bacillus amyloliquefaciens |
| BSLIN78GL001481 | 100 | 8.90E-40 | TDO11048.1 | transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL001482 | 100 | 1.00E-201 | WP_003245173.1 | MULTISPECIES: spore photoproduct lyase [Bacillales |
| BSLIN78GL001483 | 100 | 1.20E-129 | WP_029727002.1 | MULTISPECIES: GNAT family N-acetyltransferase [Bacillus |
| BSLIN78GL001484 | 100 | 0.00E+00 | WP_029727003.1 | MULTISPECIES: methyl-accepting chemotaxis protein McpC [Bacillus |
| BSLIN78GL001485 | 100 | 1.30E-160 | QHF57363.1 | oxidoreductase [Bacillus subtilis] |
| BSLIN78GL001486 | 100 | 1.70E-140 | WP_029727004.1 | MULTISPECIES: CAP domain-containing protein [Bacillus] |
| BSLIN78GL001487 | 100 | 0.00E+00 | WP_029727005.1 | MULTISPECIES: penicillin-binding protein 2 [Bacillus] |
| BSLIN78GL001488 | 100 | 0.00E+00 | QHF57367.1 | kinase A [Bacillus subtilis] |
| BSLIN78GL001489 | 100 | 2.10E-222 | WP_014476653.1 | MULTISPECIES: aminotransferase A [Bacillus] |
| BSLIN78GL001490 | 100 | 1.10E-17 | WP_003245246.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL001491 | 100 | 4.30E-164 | RAP06183.1 | hypothetical protein HS3_02873 [Bacillus subtilis] |
| BSLIN78GL001492 | 100 | 3.60E-85 | WP_003232406.1 | MULTISPECIES: YkyB family protein [Bacillales |
| BSLIN78GL001493 | 100 | 7.30E-245 | WP_029727007.1 | MULTISPECIES: MFS transporter [Bacillus] |
| BSLIN78GL001494 | 100 | 1.70E-85 | AEP90550.1 | spore protein YkuD [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL001495 | 100 | 8.50E-165 | WP_029727008.1 | MULTISPECIES: metallophosphoesterase [Bacillus] |
| BSLIN78GL001496 | 100 | 1.80E-142 | WP_029727009.1 | MULTISPECIES: 2,4-dienoyl-CoA reductase [Bacillus |
| BSLIN78GL001497 | 100 | 7.70E-236 | WP_029727010.1 | MULTISPECIES: EAL-associated domain-containing protein [Bacillus |
| BSLIN78GL001498 | 100 | 3.70E-35 | AKE23297.1 | hypothetical protein BsLM_1498 [Bacillus sp. LM 4-2] |
| BSLIN78GL001499 | 100 | 3.70E-35 | AGE63261.1 | hypothetical protein C663_1452 [Bacillus subtilis XF-1] |
| BSLIN78GL001500 | 100 | 3.10E-93 | WP_003232389.1 | MULTISPECIES: ribonuclease H-like YkuK family protein [Bacillales |
| BSLIN78GL001501 | 100 | 3.10E-27 | WP_003218673.1 | MULTISPECIES: AbrB antirepressor AbbA [Bacillus] |
| BSLIN78GL001502 | 100 | 1.70E-76 | WP_003218674.1 | MULTISPECIES: cyclic-di-AMP-binding protein CbpB [Bacillales |
| BSLIN78GL001503 | 100 | 2.40E-167 | WP_003232387.1 | MULTISPECIES: transcriptional regulator CcpC [Bacillales] |
| BSLIN78GL001504 | 100 | 8.80E-87 | WP_029727011.1 | MULTISPECIES: flavodoxin [Bacillus] |
| BSLIN78GL001505 | 100 | 5.50E-175 | WP_029727013.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL001506 | 100 | 1.40E-81 | WP_029727014.1 | MULTISPECIES: flavodoxin [Bacillus] |
| BSLIN78GL001507 | 100 | 4.90E-126 | WP_003218680.1 | MULTISPECIES: 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase |
| BSLIN78GL001508 | 100 | 1.80E-215 | WP_021479383.1 | MULTISPECIES: N-acetyldiaminopimelate deacetylase [Bacillus |
| BSLIN78GL001509 | 100 | 1.10E-37 | WP_003232382.1 | MULTISPECIES: YkuS family protein [Bacillales] |
| BSLIN78GL001510 | 100 | 4.70E-152 | EHA29765.1 | hypothetical protein BSSC8_28620 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001511 | 100 | 4.60E-100 | WP_003245371.1 | MULTISPECIES: biofilm-specific peroxidase AhpA [Bacillales |
| BSLIN78GL001512 | 100 | 1.50E-77 | WP_038428900.1 | thiol-disulfide oxidoreductase YkuV [Bacillus subtilis] |
| BSLIN78GL001513 | 100 | 6.30E-12 | KIL31776.1 | hypothetical protein B4067_1623 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL001514 | 100 | 1.40E-99 | WP_003232378.1 | MULTISPECIES: transcriptional regulator Rok [Bacillales] |
| BSLIN78GL001515 | 100 | 2.00E-178 | WP_029727015.1 | MULTISPECIES: spore protein Cse15 [Bacillus] |
| BSLIN78GL001516 | 100 | 6.00E-109 | WP_021479380.1 | MULTISPECIES: molybdenum cofactor guanylyltransferase [Bacillus |
| BSLIN78GL001517 | 100 | 1.50E-192 | WP_017696813.1 | MULTISPECIES: molybdopterin-synthase adenylyltransferase MoeB [Bacillus |
| BSLIN78GL001518 | 100 | 5.60E-245 | WP_038427631.1 | MULTISPECIES: gephyrin-like molybdotransferase Glp [Bacillus |
| BSLIN78GL001519 | 100 | 3.10E-93 | WP_029725925.1 | MULTISPECIES: molybdopterin-guanine dinucleotide biosynthesis protein B |
| BSLIN78GL001520 | 100 | 1.10E-84 | WP_015715811.1 | MULTISPECIES: molybdenum cofactor biosynthesis protein MoaE [Bacillus |
| BSLIN78GL001521 | 100 | 2.70E-33 | WP_014476678.1 | MULTISPECIES: molybdopterin converting factor subunit 1 [Bacillus |
| BSLIN78GL001522 | 99.3 | 0.00E+00 | AKE23321.1 | hypothetical protein BsLM_1522 [Bacillus sp. LM 4-2] |
| BSLIN78GL001523 | 100 | 0.00E+00 | WP_029725927.1 | MULTISPECIES: ABC transporter ATP-binding protein [Bacillus] |
| BSLIN78GL001524 | 100 | 9.40E-122 | WP_029725928.1 | MULTISPECIES: toxin SDP protection protein YknW [Bacillus] |

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| BSLIN78GL001525 | 99.5 | 9.80E-209 | AGA22987.1 | Hypothetical protein YknX [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL001526 | 100 | 7.60E-124 | WP_029725930.1 | MULTISPECIES: ABC transporter ATP-binding protein YknY [Bacillus] |
| BSLIN78GL001527 | 100 | 2.00E-217 | WP_015252177.1 | MULTISPECIES: sporulation-delaying-protein transporter subunit SkiZ [Bacillus] |
| BSLIN78GL001528 | 100 | 6.60E-137 | WP_014476685.1 | MULTISPECIES: DeoR/GlpR family DNA-binding transcription regulator [Bacillus] |
| BSLIN78GL001529 | 100 | 1.90E-167 | WP_003244923.1 | MULTISPECIES: 1-phosphofructokinase [Bacillales] |
| BSLIN78GL001530 | 100 | 0.00E+00 | WP_038427634.1 | PTS fructose transporter subunit IIABC [Bacillus subtilis] |
| BSLIN78GL001531 | 100 | 1.80E-105 | WP_003232348.1 | MULTISPECIES: signal peptidase I [Bacillales] |
| BSLIN78GL001532 | 100 | 1.40E-41 | WP_003232345.1 | MULTISPECIES: hypothetical protein [Bacillales] |
| BSLIN78GL001533 | 100 | 2.8e-310 | WP_029725931.1 | MULTISPECIES: ATP-binding cassette domain-containing protein [Bacillus] |
| BSLIN78GL001534 | 99.4 | 1.20E-172 | QHF57412.1 | oxidoreductase [Bacillus subtilis] |
| BSLIN78GL001535 | 99.8 | 1.80E-237 | WP_014476690.1 | aminopeptidase [Bacillus subtilis] |
| BSLIN78GL001536 | 100 | 1.50E-22 | AGE63297.1 | hypothetical protein C663_1489 [Bacillus subtilis XF-1] |
| BSLIN78GL001537 | 100 | 3.60E-186 | AIX07216.1 | Rod shape-determining protein MreB [Bacillus subtilis] |
| BSLIN78GL001538 | 100 | 1.50E-50 | AGE63299.1 | transcriptional regulator [Bacillus subtilis XF-1] |
| BSLIN78GL001539 | 100 | 3.10E-262 | AKE23338.1 | two-component sensor histidine kinase [Bacillus sp. LM 4-2] |
| BSLIN78GL001540 | 100 | 1.80E-159 | WP_003232330.1 | MULTISPECIES: gamma-glutamylcyclotransferase [Bacillus] |
| BSLIN78GL001541 | 100 | 1.10E-116 | WP_003222311.1 | MULTISPECIES: Ktr system potassium transporter KtrC [Bacillales] |
| BSLIN78GL001542 | 100 | 0.00E+00 | WP_032721495.1 | MULTISPECIES: adenine deaminase [Bacillus] |
| BSLIN78GL001543 | 99.8 | 0.00E+00 | EHA29733.1 | hypothetical protein BSSC8_28300 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001544 | 100 | 6.60E-31 | WP_003222303.1 | MULTISPECIES: RNA polymerase subunit omega 1 [Bacillales] |
| BSLIN78GL001545 | 100 | 4.00E-16 | AHA77473.1 | Hypothetical Protein U712_07640 [Bacillus subtilis PY79] |
| BSLIN78GL001546 | 100 | 3.20E-153 | EHA29730.1 | putative hydrolase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001547 | 100 | 8.80E-99 | WP_038427636.1 | MULTISPECIES: peptide deformylase [Bacillus] |
| BSLIN78GL001548 | 100 | 1.80E-25 | WP_003232317.1 | MULTISPECIES: YjcZ family sporulation protein [Bacillales] |
| BSLIN78GL001549 | 100 | 2.10E-106 | WP_009967146.1 | MULTISPECIES: YkyA family protein [Bacillales] |
| BSLIN78GL001550 | 100 | 8.60E-210 | WP_003222294.1 | MULTISPECIES: pyruvate dehydrogenase (acetyl-transferring) E1 component |
| BSLIN78GL001551 | 100 | 3.10E-179 | WP_014113660.1 | MULTISPECIES: pyruvate dehydrogenase complex E1 component subunit beta |
| BSLIN78GL001552 | 100 | 3.30E-248 | WP_003232311.1 | MULTISPECIES: pyruvate dehydrogenase complex dihydrolipoyllysine-residue |
| BSLIN78GL001553 | 100 | 4.50E-264 | WP_003232309.1 | MULTISPECIES: dihydrolipoyl dehydrogenase [Bacillales |
| BSLIN78GL001554 | 100 | 3.00E-60 | WP_003245672.1 | MULTISPECIES: peptidoglycan-associated lipoprotein Slp [Bacillales] |
| BSLIN78GL001555 | 100 | 3.10E-17 | WP_003232305.1 | MULTISPECIES: GapA-binding peptide SR1P [Bacillales] |
| BSLIN78GL001556 | 99.8 | 5.10E-282 | AGE63314.1 | arginine decarboxylase [Bacillus subtilis XF-1] |
| BSLIN78GL001557 | 100 | 2.10E-45 | AGA21181.1 | hypothetical protein YktA [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL001558 | 100 | 4.40E-118 | WP_038427637.1 | MULTISPECIES: YktB family protein [Bacillus] |
| BSLIN78GL001559 | 100 | 9.20E-40 | AEP86447.1 | conserved domain protein [Bacillus spizizenii TU-B-10] |
| BSLIN78GL001560 | 100 | 5.50E-150 | WP_003232297.1 | MULTISPECIES: inositol-1-monophosphatase [Bacillales] |
| BSLIN78GL001561 | 100 | 2.80E-85 | AIC98011.1 | hypothetical protein Q433_08415 [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL001562 | 98.7 | 6.60E-174 | EHA29714.1 | hypothetical protein BSSC8_28110 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001563 | 100 | 1.90E-14 | RAP06113.1 | hypothetical protein HS3_02802 [Bacillus subtilis] |
| BSLIN78GL001564 | 100 | 7.40E-300 | WP_003245026.1 | MULTISPECIES: neutral metalloprotease NprE [Bacillales] |
| BSLIN78GL001565 | 100 | 0.00E+00 | AOA54110.1 | uncharacterized protein BSHJ0_01538 [Bacillus subtilis] |
| BSLIN78GL001566 | 100 | 1.60E-45 | WP_003232287.1 | MULTISPECIES: hypothetical protein [Bacillales] |
| BSLIN78GL001567 | 100 | 1.80E-96 | RAP06109.1 | hypothetical protein HS3_02798 [Bacillus subtilis] |
| BSLIN78GL001568 | 100 | 3.40E-49 | WP_038427642.1 | anti-SigP sigma factor SigQ [Bacillus subtilis] |
| BSLIN78GL001569 | 100 | 8.90E-108 | WP_003232282.1 | MULTISPECIES: hypothetical protein [Bacillales] |
| BSLIN78GL001570 | 98.5 | 5.50E-27 | EHA29706.1 | hypothetical protein BSSC8_28030 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001571 | 92.3 | 0.00E+00 | WP_076789720.1 | translational GTPase TypA [Bacillus haynesii] |
| BSLIN78GL001572 | 100 | 7.40E-50 | WP_003232274.1 | MULTISPECIES: YlaH-like family protein [Bacillales] |
| BSLIN78GL001573 | 100 | 1.40E-33 | WP_003232271.1 | MULTISPECIES: YlaI family protein [Bacillales] |
| BSLIN78GL001574 | 100 | 7.20E-113 | WP_003232269.1 | MULTISPECIES: YhcN/YlaJ family sporulation lipoprotein [Bacillales] |
| BSLIN78GL001575 | 100 | 2.60E-245 | EHA29701.1 | hypothetical protein BSSC8_27980 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001576 | 100 | 2.00E-86 | WP_003232265.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL001577 | 100 | 4.50E-172 | WP_003232263.1 | MULTISPECIES: glutaminase A [Bacillus] |
| BSLIN78GL001578 | 100 | 3.70E-42 | WP_029726524.1 | MULTISPECIES: YlaN family protein [Bacillus] |
| BSLIN78GL001579 | 100 | 4.50E-13 | WGD76883.1 | hypothetical protein P5631_08910 [Bacillus subtilis] |
| BSLIN78GL001580 | 100 | 4.40E-195 | EHA29697.1 | cell wall shape-determining protein [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001581 | 98.4 | 0.00E+00 | WP_088679065.1 | pyruvate carboxylase [Bacillus spizizenii] |
| BSLIN78GL001582 | 100 | 1.30E-171 | WP_029726521.1 | MULTISPECIES: heme A synthase CtaA [Bacillus] |
| BSLIN78GL001583 | 100 | 2.20E-171 | WP_003232250.1 | MULTISPECIES: heme o synthase [Bacillales] |
| BSLIN78GL001584 | 100 | 2.80E-12 | AEP86471.1 | hypothetical protein GYO_1832 [Bacillus spizizenii TU-B-10] |
| BSLIN78GL001585 | 100 | 8.80E-204 | QHF57464.1 | oxidase [Bacillus subtilis] |
| BSLIN78GL001586 | 100 | 0.00E+00 | WP_003232245.1 | MULTISPECIES: cytochrome c oxidase subunit I [Bacillales] |
| BSLIN78GL001587 | 100 | 2.60E-115 | WP_003232244.1 | MULTISPECIES: cytochrome c oxidase subunit III [Bacillales] |
| BSLIN78GL001588 | 100 | 3.30E-56 | WP_003232242.1 | MULTISPECIES: cytochrome c oxidase subunit IVB [Bacillales] |
| BSLIN78GL001589 | 100 | 6.10E-143 | WP_038428915.1 | cytochrome c oxidase assembly factor CtaG [Bacillus subtilis] |
| BSLIN78GL001590 | 100 | 9.70E-62 | WP_003232238.1 | MULTISPECIES: YugN family protein [Bacillales] |
| BSLIN78GL001591 | 100 | 1.10E-75 | WP_326253424.1 | CBS domain-containing protein [Bacillus subtilis] |
| BSLIN78GL001592 | 99.7 | 4.90E-210 | QHM84151.1 | hypothetical protein DXY22_02223 [Bacillus subtilis] |
| BSLIN78GL001593 | 100 | 1.50E-71 | WP_003232233.1 | MULTISPECIES: YlbD family protein [Bacillales] |
| BSLIN78GL001594 | 100 | 3.80E-38 | WP_003232231.1 | MULTISPECIES: YlbE-like family protein [Bacillales] |
| BSLIN78GL001595 | 100 | 1.30E-79 | WP_003221370.1 | MULTISPECIES: regulatory iron-sulfur-containing complex subunit RicF [Bacillales] |
| BSLIN78GL001596 | 100 | 5.50E-40 | ASB93082.1 | UPF0298 protein [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL001597 | 100 | 8.70E-23 | AEP90652.1 | hypothetical protein I33_1685 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL001598 | 100 | 7.50E-80 | WP_029726518.1 | MULTISPECIES: 16S rRNA (guanine(966)-N(2))-methyltransferase RsmD |
| BSLIN78GL001599 | 100 | 1.40E-84 | WP_003245283.1 | MULTISPECIES: pantetheine-phosphate adenylyltransferase [Bacillales |
| BSLIN78GL001600 | 99.5 | 4.10E-232 | EHA29677.1 | hypothetical protein BSSC8_27740 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001601 | 100 | 1.90E-139 | WP_003232221.1 | MULTISPECIES: patatin family protein [Bacillales] |
| BSLIN78GL001602 | 100 | 5.00E-185 | WP_029726516.1 | protease DdcP [Bacillus subtilis] |
| BSLIN78GL001603 | 100 | 4.20E-237 | WP_029726515.1 | nucleotidyltransferase [Bacillus subtilis] |
| BSLIN78GL001604 | 100 | 1.30E-25 | WP_003232215.1 | MULTISPECIES: hypothetical protein [Bacillales] |

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|---|---|---|---|---|
| BSLIN78GL001605 | 100 | 3.10E-93 | WP_014479718.1 | MULTISPECIES: DUF177 domain-containing protein [Bacillus] |
| BSLIN78GL001606 | 100 | 2.60E-13 | AEP90661.1 | hypothetical protein I33_1694 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL001607 | 100 | 2.60E-101 | WP_015383592.1 | MULTISPECIES: sporulation specific transcriptional regulator GerR [Bacillus |
| BSLIN78GL001608 | 100 | 3.10E-107 | AGE63358.1 | hypothetical protein C663_1553 [Bacillus subtilis XF-1] |
| BSLIN78GL001609 | 100 | 7.70E-169 | WP_069703524.1 | 2-dehydropantoate 2-reductase [Bacillus subtilis] |
| BSLIN78GL001610 | 100 | 0.00E+00 | WP_113712981.1 | bacillithiol biosynthesis cysteine-adding enzyme BshC [Bacillus subtilis |
| BSLIN78GL001611 | 100 | 5.70E-80 | AEP86498.1 | MraZ protein [Bacillus spizizenii TU-B-10] |
| BSLIN78GL001612 | 100 | 1.10E-173 | WP_014479723.1 | MULTISPECIES: 16S rRNA (cytosine(1402)-N(4))-methyltransferase RsmH |
| BSLIN78GL001613 | 100 | 3.80E-55 | WP_003232200.1 | MULTISPECIES: cell division protein FtsL [Bacillales |
| BSLIN78GL001614 | 100 | 0.00E+00 | WP_072692621.1 | penicillin-binding protein 2B [Bacillus subtilis] |
| BSLIN78GL001615 | 100 | 0.00E+00 | EHA29662.1 | penicillin-binding protein [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001616 | 100 | 3.00E-282 | WP_046664176.1 | MULTISPECIES: UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6 |
| BSLIN78GL001617 | 100 | 9.90E-178 | WP_003232192.1 | MULTISPECIES: phospho-N-acetylmuramoyl-pentapeptide-transferase [Bacillales |
| BSLIN78GL001618 | 100 | 7.40E-256 | WP_029726512.1 | MULTISPECIES: UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase [Bacillus |
| BSLIN78GL001619 | 100 | 2.60E-206 | AGE63369.1 | factor for spore cortex peptidoglycan synthesis (stage V sporulation) [Bacillus subtilis |
| BSLIN78GL001620 | 100 | 5.00E-202 | WP_326253428.1 | undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase |
| BSLIN78GL001621 | 100 | 7.90E-169 | WP_003232182.1 | MULTISPECIES: UDP-N-acetylmuramate dehydrogenase [Bacillales |
| BSLIN78GL001622 | 100 | 4.90E-143 | WP_003232178.1 | MULTISPECIES: cell division protein DivIB [Bacillales |
| BSLIN78GL001623 | 100 | 4.10E-119 | WP_326224741.1 | DUF881 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL001624 | 100 | 2.50E-119 | WP_151262162.1 | DUF881 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL001625 | 99.1 | 9.10E-57 | WP_003238683.1 | MULTISPECIES: small basic family protein [Bacillales] |
| BSLIN78GL001626 | 100 | 5.20E-246 | AGA21115.1 | Cell division protein FtsA [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL001627 | 100 | 9.80E-209 | WP_003232167.1 | MULTISPECIES: cell division protein FtsZ [Bacillales |
| BSLIN78GL001628 | 99.8 | 0.00E+00 | WP_326224742.1 | bacillopeptidase F [Bacillus subtilis] |
| BSLIN78GL001629 | 99.7 | 2.00E-178 | AEP90684.1 | sigma-E processing putative peptidase SpoIIGA [Bacillus subtilis subsp. subtilis str. |
| BSLIN78GL001630 | 100 | 9.40E-119 | WP_268297965.1 | RNA polymerase sporulation sigma factor SigE [Bacillus inaquosorum] |
| BSLIN78GL001631 | 100 | 1.40E-128 | AGE63380.1 | sporulation sigma factor SigG [Bacillus subtilis XF-1] |
| BSLIN78GL001632 | 100 | 4.80E-146 | WP_326224744.1 | ABC transporter ATP-binding protein [Bacillus subtilis] |
| BSLIN78GL001633 | 100 | 1.20E-266 | RAP06043.1 | hypothetical protein HS3_02732 [Bacillus subtilis] |
| BSLIN78GL001634 | 100 | 2.50E-37 | WP_003232153.1 | MULTISPECIES: YlmC/YmxH family sporulation protein [Bacillales] |
| BSLIN78GL001635 | 100 | 4.60E-149 | WP_029726505.1 | MULTISPECIES: peptidoglycan editing factor PgeF [Bacillus |
| BSLIN78GL001636 | 100 | 2.40E-125 | WP_014479734.1 | MULTISPECIES: YggS family pyridoxal phosphate-dependent enzyme [Bacillus |
| BSLIN78GL001637 | 100 | 5.80E-80 | WP_014476753.1 | MULTISPECIES: cell division protein SepF [Bacillus |
| BSLIN78GL001638 | 100 | 7.50E-29 | WP_014479736.1 | MULTISPECIES: YggT family protein [Bacillus |
| BSLIN78GL001639 | 100 | 1.50E-139 | WP_003232140.1 | MULTISPECIES: RNA-binding protein [Bacillales] |
| BSLIN78GL001640 | 100 | 3.80E-85 | WP_003221468.1 | MULTISPECIES: septum site-determining protein DivIVA [Bacillales |
| BSLIN78GL001641 | 100 | 2.70E-17 | AEP90696.1 | hypothetical protein I33_1729 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL001642 | 100 | 1.80E-14 | AEP86530.1 | hypothetical protein GYO_1891 [Bacillus spizizenii TU-B-10 |
| BSLIN78GL001643 | 99.8 | 0.00E+00 | WP_021479325.1 | isoleucine--tRNA ligase [Bacillus subtilis] |
| BSLIN78GL001644 | 100 | 1.20E-55 | WP_029726503.1 | MULTISPECIES: sporulation-related RNA polymerase-binding protein YlyA |
| BSLIN78GL001645 | 100 | 1.40E-78 | WP_211197344.1 | signal peptidase II [Bacillus subtilis] |
| BSLIN78GL001646 | 100 | 2.10E-174 | WP_003245307.1 | MULTISPECIES: RluA family pseudouridine synthase [Bacillales |
| BSLIN78GL001647 | 100 | 1.00E-94 | WP_003232127.1 | MULTISPECIES: bifunctional pyrimidine operon transcriptional regulator/uracil |
| BSLIN78GL001648 | 100 | 3.40E-245 | RAP06028.1 | hypothetical protein HS3_02717 [Bacillus subtilis] |
| BSLIN78GL001649 | 100 | 5.10E-168 | WP_029726500.1 | MULTISPECIES: aspartate carbamoyltransferase catalytic subunit [Bacillus |
| BSLIN78GL001650 | 100 | 3.20E-248 | WP_003232117.1 | MULTISPECIES: dihydroorotase [Bacillus |
| BSLIN78GL001651 | 100 | 1.90E-209 | WP_003232115.1 | MULTISPECIES: carbamoyl phosphate synthase small subunit [Bacillales |
| BSLIN78GL001652 | 92.9 | 0.00E+00 | WP_327954194.1 | carbamoyl-phosphate synthase (glutamine-hydrolyzing) large subunit [Bacillus |
| BSLIN78GL001653 | 100 | 9.70E-144 | WP_014479746.1 | MULTISPECIES: dihydroorotate oxidase B electron transfer subunit [Bacillus |
| BSLIN78GL001654 | 99.7 | 1.40E-173 | WP_029726498.1 | MULTISPECIES: dihydroorotate dehydrogenase [Bacillus |
| BSLIN78GL001655 | 100 | 2.00E-127 | WP_003232107.1 | MULTISPECIES: orotidine-5'-phosphate decarboxylase [Bacillales |
| BSLIN78GL001656 | 99.5 | 1.80E-119 | WP_072557155.1 | MULTISPECIES: orotate phosphoribosyltransferase [Bacillus |
| BSLIN78GL001657 | 100 | 7.70E-140 | QHF57535.1 | phosphosulfate reductase [Bacillus subtilis] |
| BSLIN78GL001658 | 100 | 7.20E-190 | WP_015715862.1 | MULTISPECIES: sulfate permease [Bacillus] |
| BSLIN78GL001659 | 100 | 1.90E-223 | BAI85186.2 | sulfate adenylyltransferase [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL001660 | 100 | 1.30E-108 | WP_015715863.1 | MULTISPECIES: adenylyl-sulfate kinase [Bacillus |
| BSLIN78GL001661 | 100 | 2.00E-144 | WP_015715864.1 | MULTISPECIES: uroporphyrinogen-III C-methyltransferase [Bacillus |
| BSLIN78GL001662 | 100 | 1.10E-145 | WP_015715865.1 | MULTISPECIES: sirohydrochlorin chelatase [Bacillus |
| BSLIN78GL001663 | 100 | 2.10E-83 | WP_029726496.1 | MULTISPECIES: precorrin-2 dehydrogenase [Bacillus |
| BSLIN78GL001664 | 100 | 0.00E+00 | WP_029726495.1 | MULTISPECIES: tRNA modification protein RqcH [Bacillus] |
| BSLIN78GL001665 | 100 | 0.00E+00 | WP_021479314.1 | MULTISPECIES: calcium-translocating P-type ATPase, SERCA-type [Bacillus |
| BSLIN78GL001666 | 100 | 4.20E-156 | KIN33457.1 | hypothetical protein B4069_1627 [Bacillus subtilis] |
| BSLIN78GL001667 | 100 | 5.30E-41 | WP_003154355.1 | MULTISPECIES: extracellular matrix/biofilm regulator RemA [Bacteria] |
| BSLIN78GL001668 | 100 | 2.50E-110 | CAA74271.1 | putative Gmk protein [Bacillus subtilis subsp. subtilis str. 168] |
| BSLIN78GL001669 | 100 | 6.00E-29 | WP_003221520.1 | MULTISPECIES: DNA-directed RNA polymerase subunit omega [Bacillales |
| BSLIN78GL001670 | 100 | 4.00E-221 | RAP06006.1 | Phosphopantothenoylcysteine decarboxylase [Bacillus subtilis |
| BSLIN78GL001671 | 99.9 | 0.00E+00 | WP_046664189.1 | MULTISPECIES: primosomal protein N' [Bacillus] |
| BSLIN78GL001672 | 100 | 1.10E-84 | WP_029726494.1 | MULTISPECIES: peptide deformylase [Bacillus |
| BSLIN78GL001673 | 100 | 2.20E-177 | WP_326253434.1 | methionyl-tRNA formyltransferase [Bacillus subtilis] |
| BSLIN78GL001674 | 100 | 9.00E-254 | WP_225721989.1 | 16S rRNA (cytosine(967)-C(5))-methyltransferase RsmB [Bacillus subtilis] |
| BSLIN78GL001675 | 100 | 2.30E-207 | WP_015252110.1 | MULTISPECIES: 23S rRNA (adenine(2503)-C(2))-methyltransferase RlmN |
| BSLIN78GL001676 | 100 | 9.00E-142 | WP_014479762.1 | MULTISPECIES: protein-serine/threonine phosphatase PrpC [Bacillus |
| BSLIN78GL001677 | 100 | 0.00E+00 | WP_015252109.1 | MULTISPECIES: serine/threonine protein kinase PrkC [Bacillus] |
| BSLIN78GL001678 | 100 | 1.60E-169 | WP_015715871.1 | MULTISPECIES: ribosome small subunit-dependent GTPase A [Bacillus |
| BSLIN78GL001679 | 100 | 7.70E-118 | WP_029726492.1 | MULTISPECIES: ribulose-phosphate 3-epimerase [Bacillus |
| BSLIN78GL001680 | 100 | 7.30E-124 | BAI85207.2 | hypothetical protein BSNT_08092 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL001681 | 100 | 2.60E-14 | WP_003221548.1 | MULTISPECIES: 50S ribosomal protein L28 [Bacillales] |
| BSLIN78GL001682 | 100 | 9.10E-60 | WP_003232054.1 | MULTISPECIES: Asp23/Gls24 family envelope stress response protein [Bacillales |
| BSLIN78GL001683 | 100 | 4.50E-300 | BAI85210.2 | hypothetical protein BSNT_08095 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL001684 | 100 | 3.50E-118 | WP_003232050.1 | MULTISPECIES: L-serine ammonia-lyase, iron-sulfur-dependent subunit beta |

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| BSLIN78GL001685 | 100 | 9.20E-162 | WP_003232049.1 | MULTISPECIES: L-serine ammonia-lyase, iron-sulfur-dependent, subunit alpha |
| BSLIN78GL001686 | 100 | 0.00E+00 | WP_015715873.1 | MULTISPECIES: ATP-dependent DNA helicase RecG [Bacillus |
| BSLIN78GL001687 | 100 | 5.50E-96 | WP_003232044.1 | MULTISPECIES: transcription factor FapR [Bacillales] |
| BSLIN78GL001688 | 100 | 7.60E-178 | AGE63435.1 | putative glycerol-3-phosphate acyltransferase PlsX [Bacillus subtilis XF-1 |
| BSLIN78GL001689 | 100 | 6.70E-171 | WP_029726491.1 | MULTISPECIES: ACP S-malonyltransferase [Bacillus |
| BSLIN78GL001690 | 100 | 1.20E-130 | AIC98131.1 | 3-oxoacyl-ACP synthase [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL001691 | 100 | 7.10E-34 | WP_003154310.1 | MULTISPECIES: acyl carrier protein [Bacteria] |
| BSLIN78GL001692 | 100 | 1.20E-138 | WP_003232030.1 | MULTISPECIES: ribonuclease III [Bacillales |
| BSLIN78GL001693 | 100 | 0.00E+00 | WP_080529313.1 | chromosome segregation protein SMC [Bacillus subtilis] |
| BSLIN78GL001694 | 100 | 1.80E-179 | WP_003232026.1 | MULTISPECIES: signal recognition particle-docking protein FtsY [Bacillales |
| BSLIN78GL001695 | 100 | 1.00E-93 | EHA29582.1 | hypothetical protein BSSC8_26790 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001696 | 100 | 2.00E-37 | WP_202327685.1 | putative DNA-binding protein [Bacillus sp. RHFS10] |
| BSLIN78GL001697 | 99.1 | 4.90E-244 | WP_044428065.1 | signal recognition particle protein [Bacillus spizizenii] |
| BSLIN78GL001698 | 100 | 1.50E-43 | WP_003220815.1 | MULTISPECIES: 30S ribosomal protein S16 [Bacillales] |
| BSLIN78GL001699 | 100 | 3.30E-37 | WP_014476792.1 | MULTISPECIES: KH domain-containing protein [Bacillus] |
| BSLIN78GL001700 | 100 | 1.70E-64 | AKE23496.1 | hypothetical protein BsLM_1698 [Bacillus sp. LM 4-2] |
| BSLIN78GL001701 | 100 | 2.50E-95 | WP_003232013.1 | MULTISPECIES: ribosome maturation factor RimM [Bacillales] |
| BSLIN78GL001702 | 100 | 7.50E-138 | WP_003232011.1 | MULTISPECIES: tRNA (guanosine(37)-N1)-methyltransferase TrmD [Bacillales |
| BSLIN78GL001703 | 99.2 | 3.00E-64 | AFI28287.1 | 50S ribosomal protein L19 [Bacillus sp. JS] |
| BSLIN78GL001704 | 100 | 2.40E-156 | WP_015715878.1 | MULTISPECIES: ribosome biogenesis GTPase YlqF [Bacillus |
| BSLIN78GL001705 | 100 | 3.20E-139 | WP_029317794.1 | MULTISPECIES: ribonuclease HII [Bacillus |
| BSLIN78GL001706 | 100 | 0.00E+00 | WP_029726490.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL001707 | 100 | 1.10E-44 | WP_003232001.1 | MULTISPECIES: FlhB-like flagellar biosynthesis protein [Bacillales |
| BSLIN78GL001708 | 94 | 5.50E-202 | WP_020451378.1 | MULTISPECIES: ADP-forming succinate--CoA ligase subunit beta [Bacillus |
| BSLIN78GL001709 | 100 | 1.60E-169 | WP_003238566.1 | MULTISPECIES: succinate--CoA ligase subunit alpha [Bacillales |
| BSLIN78GL001710 | 99.6 | 2.10E-146 | WP_003245871.1 | MULTISPECIES: DNA-processing protein DprA [Bacillales] |
| BSLIN78GL001711 | 99.9 | 0.00E+00 | AEP90764.1 | DNA topoisomerase I [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL001712 | 100 | 7.20E-248 | WP_003244725.1 | MULTISPECIES: FADH(2)-oxidizing methylenetetrahydrofolate--tRNA-(uracil(54) |
| BSLIN78GL001713 | 100 | 3.80E-171 | WP_003231988.1 | MULTISPECIES: tyrosine recombinase XerC [Bacillales |
| BSLIN78GL001714 | 100 | 6.00E-83 | WP_268398640.1 | ATP-dependent protease subunit ClpQ [Bacillus inaquosorum] |
| BSLIN78GL001715 | 100 | 3.30E-259 | WP_003245556.1 | MULTISPECIES: HslU--HslV peptidase ATPase subunit [Bacillus] |
| BSLIN78GL001716 | 100 | 5.20E-137 | WP_003220850.1 | MULTISPECIES: GTP-sensing pleiotropic transcriptional regulator CodY |
| BSLIN78GL001717 | 99.2 | 5.40E-66 | AGE63463.1 | flagellar basal body rod protein FlgB [Bacillus subtilis XF-1] |
| BSLIN78GL001718 | 100 | 7.10E-78 | AGA24084.1 | Flagellar basal-body rod protein FlgC [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL001719 | 100 | 9.00E-51 | WP_003220856.1 | MULTISPECIES: flagellar hook-basal body complex protein FliE [Bacillus |
| BSLIN78GL001720 | 100 | 1.90E-298 | AHA77648.1 | Flagellar M-ring protein [Bacillus subtilis PY79] |
| BSLIN78GL001721 | 100 | 2.60E-181 | WP_003231981.1 | MULTISPECIES: flagellar motor switch protein FliG [Bacillales |
| BSLIN78GL001722 | 100 | 2.30E-134 | WP_003244804.1 | MULTISPECIES: flagellar assembly protein FliH [Bacillales |
| BSLIN78GL001723 | 100 | 2.80E-236 | WP_095843705.1 | flagellar protein export ATPase FliI [Bacillus subtilis] |
| BSLIN78GL001724 | 100 | 5.00E-76 | WP_003231977.1 | MULTISPECIES: flagellar export protein FliJ [Bacillales] |
| BSLIN78GL001725 | 100 | 1.30E-103 | WP_003231975.1 | MULTISPECIES: MotE family protein [Bacillales |
| BSLIN78GL001726 | 100 | 4.40E-270 | WP_015715887.1 | MULTISPECIES: flagellar hook-length control protein FliK [Bacillus |
| BSLIN78GL001727 | 100 | 7.50E-74 | WP_003231970.1 | MULTISPECIES: flagellar hook assembly protein FlgD [Bacillales |
| BSLIN78GL001728 | 100 | 3.40E-144 | WP_003231968.1 | MULTISPECIES: flagellar basal body rod protein FlgG [Bacillales |
| BSLIN78GL001729 | 100 | 4.70E-32 | WP_003231966.1 | MULTISPECIES: swarming motility protein SwrD [Bacillales] |
| BSLIN78GL001730 | 100 | 4.70E-68 | WP_003231964.1 | MULTISPECIES: flagellar basal body-associated protein FliL [Bacillales |
| BSLIN78GL001731 | 100 | 1.10E-184 | WP_003220879.1 | MULTISPECIES: flagellar motor switch protein FliM [Bacillales |
| BSLIN78GL001732 | 100 | 2.60E-206 | WP_014479788.1 | MULTISPECIES: flagellar motor switch phosphatase FliY [Bacillus] |
| BSLIN78GL001733 | 100 | 1.00E-58 | WP_014476812.1 | MULTISPECIES: chemotaxis protein CheY [Bacillus] |
| BSLIN78GL001734 | 100 | 1.30E-117 | WP_014479789.1 | MULTISPECIES: flagella biosynthesis regulatory protein FliZ [Bacillus |
| BSLIN78GL001735 | 100 | 1.90E-116 | AKE23531.1 | flagellar biosynthesis protein FliP [Bacillus sp. LM 4-2] |
| BSLIN78GL001736 | 100 | 1.80E-35 | AFI28321.1 | flagellar biosynthetic protein FliQ [Bacillus sp. JS] |
| BSLIN78GL001737 | 100 | 2.50E-139 | WP_003245510.1 | MULTISPECIES: flagellar biosynthetic protein FliR [Bacillales |
| BSLIN78GL001738 | 100 | 4.80E-197 | WP_003231949.1 | MULTISPECIES: flagellar biosynthesis protein FlhB [Bacillales |
| BSLIN78GL001739 | 100 | 0.00E+00 | WP_003231947.1 | MULTISPECIES: flagellar biosynthesis protein FlhA [Bacillales |
| BSLIN78GL001740 | 100 | 1.60E-203 | WP_003231945.1 | MULTISPECIES: flagellar biosynthesis protein FlhF [Bacillales |
| BSLIN78GL001741 | 100 | 6.30E-152 | WP_010886507.1 | MULTISPECIES: flagellum location/number ATPase FlhG [Bacillales |
| BSLIN78GL001742 | 99.7 | 2.30E-196 | EHA29533.1 | chemotaxis-specific methylesterase [Bacillus subtilis subsp. subtilis str. SC-8 |
| BSLIN78GL001743 | 100 | 0.00E+00 | WP_014476817.1 | MULTISPECIES: chemotaxis protein CheA [Bacillus] |
| BSLIN78GL001744 | 100 | 7.10E-81 | WP_003231938.1 | MULTISPECIES: chemotaxis protein CheW [Bacillales |
| BSLIN78GL001745 | 100 | 1.00E-111 | WP_003231935.1 | MULTISPECIES: CheY-P phosphatase CheC [Bacillales] |
| BSLIN78GL001746 | 100 | 4.60E-86 | WP_003244852.1 | MULTISPECIES: chemoreceptor glutamine deamidase CheD [Bacillales] |
| BSLIN78GL001747 | 100 | 8.40E-140 | WP_003220911.1 | MULTISPECIES: RNA polymerase sigma-28 factor SigD [Bacillales |
| BSLIN78GL001748 | 100 | 3.20E-87 | KIL29790.1 | hypothetical protein B4067_1858 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL001749 | 100 | 3.90E-134 | WP_003220918.1 | MULTISPECIES: 30S ribosomal protein S2 [Bacillales] |
| BSLIN78GL001750 | 100 | 2.50E-159 | WP_003231929.1 | MULTISPECIES: translation elongation factor Ts [Bacillales] |
| BSLIN78GL001751 | 100 | 2.00E-127 | WP_003220923.1 | MULTISPECIES: UMP kinase [Bacillales] |
| BSLIN78GL001752 | 100 | 4.60E-95 | WP_003231927.1 | MULTISPECIES: ribosome recycling factor [Bacillales |
| BSLIN78GL001753 | 100 | 8.90E-145 | WP_003231925.1 | MULTISPECIES: isoprenyl transferase [Bacillales |
| BSLIN78GL001754 | 99.6 | 3.70E-146 | WP_015252087.1 | MULTISPECIES: phosphatidate cytidylyltransferase [Bacillus |
| BSLIN78GL001755 | 100 | 5.80E-217 | AGA24047.1 | 1-deoxy-D-xylulose 5-phosphate reductoisomerase [Bacillus subtilis subsp. subtilis |
| BSLIN78GL001756 | 100 | 1.00E-235 | AHA77684.1 | Zinc metalloprotease rasP [Bacillus subtilis PY79] |
| BSLIN78GL001757 | 100 | 0.00E+00 | WP_003231918.1 | MULTISPECIES: proline--tRNA ligase [Bacillales |
| BSLIN78GL001758 | 99.9 | 0.00E+00 | BAI85288.2 | DNA polymerase III PolC [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL001759 | 100 | 7.10E-81 | WP_003231915.1 | MULTISPECIES: ribosome maturation factor RimP [Bacillales] |
| BSLIN78GL001760 | 100 | 2.20E-205 | WP_003231912.1 | MULTISPECIES: transcription termination factor NusA [Bacillales] |
| BSLIN78GL001761 | 100 | 7.70E-36 | EHA29514.1 | hypothetical protein BSSC8_26110 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001762 | 100 | 3.60E-36 | EHA29513.1 | hypothetical protein BSSC8_26100 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001763 | 99.9 | 0.00E+00 | WP_015649902.1 | MULTISPECIES: translation initiation factor IF-2 [Bacillales |
| BSLIN78GL001764 | 100 | 2.40E-44 | WP_003231905.1 | MULTISPECIES: DUF503 domain-containing protein [Bacillus] |

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| BSLIN78GL001765 | 100 | 1.50E-56 | AGA24037.1 | Ribosome-binding factor A [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL001766 | 100 | 3.70E-174 | WP_015252083.1 | MULTISPECIES: tRNA pseudouridine(55) synthase TruB [Bacillus |
| BSLIN78GL001767 | 100 | 1.10E-181 | WP_003231899.1 | MULTISPECIES: bifunctional riboflavin kinase/FAD synthetase [Bacillus |
| BSLIN78GL001768 | 100 | 0.00E+00 | WP_021479284.1 | MULTISPECIES: polyribonucleotide nucleotidyltransferase [Bacillus |
| BSLIN78GL001769 | 100 | 1.20E-183 | WP_003231894.1 | MULTISPECIES: polysaccharide deacetylase family protein [Bacillus |
| BSLIN78GL001770 | 100 | 1.10E-226 | AGE63515.1 | mitochondrial processing peptidase-like protein [Bacillus subtilis XF-1] |
| BSLIN78GL001771 | 100 | 1.30E-41 | AFQ57608.1 | YmxH [Bacillus subtilis QB928] |
| BSLIN78GL001772 | 100 | 7.00E-162 | WP_003231888.1 | MULTISPECIES: dipicolinic acid synthetase subunit A [Bacillales |
| BSLIN78GL001773 | 100 | 6.00E-109 | WP_003231884.1 | MULTISPECIES: dipicolinate synthase subunit B [Bacillus |
| BSLIN78GL001774 | 100 | 2.30E-193 | WP_003231882.1 | MULTISPECIES: aspartate-semialdehyde dehydrogenase [Bacillus |
| BSLIN78GL001775 | 100 | 3.20E-226 | AGA24026.1 | Aspartate kinase I [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL001776 | 100 | 1.10E-162 | EHA29499.1 | dihydrodipicolinate synthase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001777 | 99.8 | 6.4e-310 | WP_003231875.1 | MULTISPECIES: ribonuclease J2 [Bacillales] |
| BSLIN78GL001778 | 100 | 7.80E-135 | WP_003245712.1 | MULTISPECIES: translocation-enhancing protein TepA [Bacillales |
| BSLIN78GL001779 | 100 | 4.70E-32 | WP_003231871.1 | MULTISPECIES: TepA modulator TepJ [Bacteria] |
| BSLIN78GL001780 | 100 | 0.00E+00 | WP_003231869.1 | MULTISPECIES: DNA translocase SpoIIIE [Bacillus |
| BSLIN78GL001781 | 100 | 1.10E-133 | WP_003245732.1 | MULTISPECIES: GntR family transcriptional regulator [Bacillales |
| BSLIN78GL001782 | 100 | 2.10E-17 | AEP90836.1 | hypothetical protein I33_1870 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL001783 | 100 | 9.80E-231 | AEP90837.1 | multidrug resistance protein [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL001784 | 100 | 1.00E-238 | WP_015715896.1 | MULTISPECIES: pitrilysin family protein [Bacillus |
| BSLIN78GL001785 | 100 | 6.60E-246 | WP_003231858.1 | MULTISPECIES: pitrilysin family protein [Bacillus |
| BSLIN78GL001786 | 100 | 1.30E-137 | EHA29489.1 | 3-ketoacyl-(acyl-carrier-protein) reductase [Bacillus subtilis subsp. subtilis str. SC-8 |
| BSLIN78GL001787 | 100 | 4.00E-44 | AGE63530.1 | hypothetical protein C663_1732 [Bacillus subtilis XF-1] |
| BSLIN78GL001788 | 100 | 6.20E-149 | O31769.2 | RecName: Full=Uncharacterized protein YmfK [Bacillus subtilis subsp. subtilis str. |
| BSLIN78GL001789 | 100 | 1.20E-167 | AFQ57624.1 | YmfM [Bacillus subtilis QB928] |
| BSLIN78GL001790 | 100 | 1.50E-92 | AGE63533.1 | phosphatidylglycerophosphate synthase [Bacillus subtilis XF-1 |
| BSLIN78GL001791 | 100 | 6.00E-236 | WP_015715898.1 | MULTISPECIES: competence/damage-inducible protein A [Bacillus |
| BSLIN78GL001792 | 100 | 1.00E-185 | EHA29483.1 | recombinase A [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL001793 | 100 | 2.60E-225 | WP_029726484.1 | MULTISPECIES: serine hydrolase domain-containing protein [Bacillus |
| BSLIN78GL001794 | 99.8 | 5.50E-287 | WP_103748761.1 | ribonuclease Y [Bacillus sp. MBGLi79] |
| BSLIN78GL001795 | 99.6 | 2.80E-157 | AFQ57630.1 | Putative hydrolase involved in biofilm formation [Bacillus subtilis QB928] |
| BSLIN78GL001796 | 100 | 4.10E-38 | WP_003154135.1 | MULTISPECIES: stage V sporulation protein SpoVS [Bacteria] |
| BSLIN78GL001797 | 100 | 1.50E-195 | WP_029726482.1 | MULTISPECIES: L-threonine 3-dehydrogenase [Bacillus |
| BSLIN78GL001798 | 100 | 2.20E-219 | WP_014664025.1 | MULTISPECIES: glycine C-acetyltransferase [Bacillus |
| BSLIN78GL001799 | 100 | 1.90E-303 | BAI85331.2 | hypothetical protein BSNT_08215 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL001800 | 100 | 5.50E-72 | WP_003231834.1 | MULTISPECIES: regulatory iron-sulfur-containing complex subunit RicA |
| BSLIN78GL001801 | 100 | 9.30E-101 | WP_003231833.1 | MULTISPECIES: outer spore coat protein CotE [Bacillales] |
| BSLIN78GL001802 | 100 | 0.00E+00 | WP_029726481.1 | MULTISPECIES: DNA mismatch repair protein MutS [Bacillus] |
| BSLIN78GL001803 | 100 | 0.00E+00 | WP_211197337.1 | DNA mismatch repair endonuclease MutL [Bacillus subtilis] |
| BSLIN78GL001804 | 100 | 6.60E-76 | WP_015252068.1 | MULTISPECIES: regulatory YrvL family protein [Bacillus |
| BSLIN78GL001805 | 100 | 6.50E-111 | RAP05870.1 | hypothetical protein HS3_02559 [Bacillus subtilis] |
| BSLIN78GL001806 | 100 | 6.60E-111 | WP_029317807.1 | MULTISPECIES: TetR/AcrR family transcriptional regulator [Bacillus |
| BSLIN78GL001807 | 99.5 | 1.00E-125 | WP_029726478.1 | MULTISPECIES: MBL fold metallo-hydrolase [Bacillus |
| BSLIN78GL001808 | 100 | 4.00E-162 | WP_029317809.1 | MULTISPECIES: ACP S-malonyltransferase [Bacillus |
| BSLIN78GL001809 | 100 | 9.90E-17 | AOA54351.1 | hypothetical protein BSHJ0_01779 [Bacillus subtilis] |
| BSLIN78GL001810 | 100 | 9.00E-15 | AMR47185.1 | hypothetical protein KHRBS_12500 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL001811 | 100 | 4.90E-185 | WP_029726475.1 | MULTISPECIES: acyltransferase domain-containing protein [Bacillus |
| BSLIN78GL001812 | 100 | 0.00E+00 | WP_225721993.1 | ACP S-malonyltransferase [Bacillus subtilis] |
| BSLIN78GL001813 | 100 | 5.00E-28 | AGE63553.1 | acyl carrier protein [Bacillus subtilis XF-1] |
| BSLIN78GL001814 | 99.8 | 7.40E-231 | WP_161476980.1 | polyketide biosynthesis malonyl-ACP decarboxylase PksF [Bacillus subtilis |
| BSLIN78GL001815 | 100 | 3.50E-244 | WP_003231805.1 | MULTISPECIES: polyketide biosynthesis 3-hydroxy-3-methylglutaryl-ACP synthas |
| BSLIN78GL001816 | 100 | 2.30E-145 | WP_072692616.1 | MULTISPECIES: enoyl-CoA hydratase/isomerase [Bacillus |
| BSLIN78GL001817 | 100 | 6.50E-137 | WP_029726471.1 | MULTISPECIES: polyketide synthase [Bacillus |
| BSLIN78GL001818 | 100 | 0.00E+00 | WP_326253447.1 | polyketide synthase PksJ [Bacillus subtilis] |
| BSLIN78GL001819 | 99.9 | 0.00E+00 | WP_326253449.1 | polyketide synthase PksL [Bacillus subtilis |
| BSLIN78GL001820 | 100 | 0.00E+00 | WP_038427661.1 | polyketide synthase PksM [Bacillus subtilis] |
| BSLIN78GL001821 | 100 | 0.00E+00 | CAF1730451.1 | Polyketide synthase PksN [Bacillus subtilis] |
| BSLIN78GL001822 | 100 | 0.00E+00 | WP_326224793.1 | beta-ketoacyl synthase N-terminal-like domain-containing protein [Bacillus subtilis |
| BSLIN78GL001823 | 100 | 1.60E-233 | WP_029726465.1 | MULTISPECIES: cytochrome P450 [Bacillus |
| BSLIN78GL001824 | 100 | 3.60E-61 | WP_029726464.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL001825 | 100 | 2.00E-132 | RAP05851.1 | hypothetical protein HS3_02540 [Bacillus subtilis] |
| BSLIN78GL001826 | 99.8 | 3.90E-232 | WP_029726462.1 | MULTISPECIES: serine protease AprX [Bacillus] |
| BSLIN78GL001827 | 100 | 1.90E-30 | AGE63568.1 | hypothetical protein C663_1776 [Bacillus subtilis XF-1] |
| BSLIN78GL001828 | 100 | 1.40E-116 | QHF57694.1 | hypothetical protein Bateq7PJ16_1888 [Bacillus subtilis] |
| BSLIN78GL001829 | 100 | 1.30E-79 | WP_003245175.1 | MULTISPECIES: OsmC family protein [Bacillales |
| BSLIN78GL001830 | 99.2 | 1.70E-58 | BAI85352.2 | multidrug resistance protein [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL001831 | 100 | 5.10E-41 | AHA77759.1 | Multidrug resistance protein EbrA [Bacillus subtilis PY79] |
| BSLIN78GL001832 | 100 | 2.40E-71 | AGA23965.1 | Hypothetical protein YmaG [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL001833 | 100 | 5.30E-80 | WP_003231769.1 | MULTISPECIES: YmaF family protein [Bacillales |
| BSLIN78GL001834 | 100 | 2.00E-175 | WP_029726461.1 | MULTISPECIES: tRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA |
| BSLIN78GL001835 | 100 | 2.30E-33 | WP_003221097.1 | MULTISPECIES: RNA chaperone Hfq [Bacillales] |
| BSLIN78GL001836 | 100 | 2.10E-45 | WP_014479841.1 | MULTISPECIES: YmzC family protein [Bacillus |
| BSLIN78GL001837 | 100 | 1.50E-46 | AEP90893.1 | conserved domain protein [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL001838 | 100 | 6.30E-67 | WP_003231758.1 | MULTISPECIES: class Ib ribonucleoside-diphosphate reductase assembly |
| BSLIN78GL001839 | 100 | 0.00E+00 | QHF57705.1 | reductase subunit alpha [Bacillus subtilis] |
| BSLIN78GL001840 | 100 | 5.10E-190 | WP_003231754.1 | MULTISPECIES: class 1b ribonucleoside-diphosphate reductase subunit beta |
| BSLIN78GL001841 | 100 | 1.50E-110 | WP_003245105.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL001842 | 100 | 2.10E-138 | WP_088325922.1 | sporulation-specific N-acetylmuramoyl-L-alanine amidase [Bacillus subtilis |
| BSLIN78GL001843 | 100 | 6.10E-21 | AEP90899.1 | hypothetical protein I33_1933 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL001844 | 100 | 5.10E-114 | AOA54385.1 | Stage V sporulation protein [Bacillus subtilis] |

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| BSLIN78GL001845 | 100 | 7.60E-49 | WP_250636519.1 | hypothetical protein, partial [Bacillus subtilis] |
| BSLIN78GL001846 | 100 | 4.90E-94 | WP_003230849.1 | MULTISPECIES: N-acetyltransferase [Bacillus |
| BSLIN78GL001847 | 99.7 | 2.80E-166 | WP_128474005.1 | endonuclease YokF [Bacillus subtilis] |
| BSLIN78GL001848 | 100 | 6.10E-39 | WP_061891062.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001849 | 100 | 7.80E-100 | WP_061891063.1 | SMI1/KNR4 family protein [Bacillus subtilis] |
| BSLIN78GL001850 | 100 | 5.90E-194 | WP_250629512.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001851 | 100 | 0.00E+00 | WP_128474003.1 | T7SS effector LXG polymorphic toxin [Bacillus subtilis |
| BSLIN78GL001852 | 100 | 3.90E-84 | WP_071581355.1 | MULTISPECIES: YrhA family protein [Bacillus subtilis group] |
| BSLIN78GL001853 | 99.7 | 1.70E-185 | WP_068947491.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001854 | 100 | 2.60E-49 | WP_041336419.1 | MULTISPECIES: YolD-like family protein [Bacillus |
| BSLIN78GL001855 | 100 | 1.30E-238 | WP_072692677.1 | UV damage repair protein UvrX [Bacillus subtilis] |
| BSLIN78GL001856 | 100 | 2.30E-24 | WP_068947493.1 | aspartate phosphatase [Bacillus subtilis] |
| BSLIN78GL001857 | 99.7 | 1.10E-217 | WP_068947494.1 | MULTISPECIES: Rap family tetratricopeptide repeat protein [Bacillus |
| BSLIN78GL001858 | 100 | 1.40E-38 | WP_017696899.1 | MULTISPECIES: phage holin [Bacillus] |
| BSLIN78GL001859 | 100 | 9.10E-201 | WP_213417508.1 | N-acetylmuramoyl-L-alanine amidase family protein [Bacillus subtilis |
| BSLIN78GL001860 | 100 | 0.00E+00 | WP_113712853.1 | tail fiber domain-containing protein [Bacillus subtilis] |
| BSLIN78GL001861 | 100 | 3.60E-160 | RAP10641.1 | hypothetical protein HS3_01060 [Bacillus subtilis] |
| BSLIN78GL001862 | 100 | 0.00E+00 | WP_113712854.1 | phage tail protein [Bacillus subtilis] |
| BSLIN78GL001863 | 100 | 9.60E-144 | WP_113712855.1 | distal tail protein Dit [Bacillus subtilis] |
| BSLIN78GL001864 | 100 | 0.00E+00 | WP_113712856.1 | transglycosylase CwlP [Bacillus subtilis] |
| BSLIN78GL001865 | 100 | 3.10E-125 | WP_033885312.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001866 | 100 | 1.10E-156 | WP_003230937.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001867 | 100 | 4.40E-71 | WP_032677187.1 | hypothetical protein [Bacillus] |
| BSLIN78GL001868 | 100 | 1.00E-193 | WP_033885229.1 | site-specific integrase [Bacillus subtilis] |
| BSLIN78GL001869 | 100 | 4.80E-73 | WP_086343984.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001870 | 100 | 2.40E-87 | WP_086343983.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001871 | 100 | 1.30E-19 | WP_080332259.1 | XkdX family protein [Bacillus subtilis] |
| BSLIN78GL001872 | 100 | 3.50E-71 | WP_042976260.1 | MULTISPECIES: hypothetical protein [Bacillus subtilis group |
| BSLIN78GL001873 | 100 | 5.80E-175 | WP_128473995.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001874 | 99.2 | 3.50E-59 | CAF1772433.1 | hypothetical protein NRS6103_03877 [Bacillus subtilis] |
| BSLIN78GL001875 | 100 | 1.10E-36 | WP_086352603.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001876 | 100 | 5.00E-88 | WP_032721622.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL001877 | 100 | 1.60E-146 | WP_113712859.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001878 | 100 | 7.80E-132 | WP_003230954.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL001879 | 100 | 7.40E-46 | WP_041054454.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001880 | 100 | 3.10E-122 | CAF1916542.1 | hypothetical protein NRS6206_03863 [Bacillus subtilis] |
| BSLIN78GL001881 | 100 | 4.00E-69 | WP_068947513.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001882 | 100 | 4.40E-83 | WP_019712890.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL001883 | 100 | 4.20E-187 | WP_041337005.1 | MULTISPECIES: hypothetical protein [Bacillus subtilis group |
| BSLIN78GL001884 | 100 | 2.20E-94 | WP_010328108.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL001885 | 100 | 1.70E-274 | WP_121572574.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001886 | 100 | 1.40E-295 | WP_113712862.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001887 | 100 | 0.00E+00 | WP_003230970.1 | MULTISPECIES: terminase large subunit [Bacillales] |
| BSLIN78GL001888 | 100 | 3.30E-141 | WP_041352112.1 | MULTISPECIES: hypothetical protein [Bacillus subtilis group |
| BSLIN78GL001890 | 100 | 2.20E-88 | WP_113712863.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001891 | 98.2 | 4.30E-56 | QHF58121.1 | hypothetical protein Bateq7PJ16_2315 [Bacillus subtilis] |
| BSLIN78GL001892 | 100 | 2.60E-77 | WP_072692662.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001893 | 100 | 6.00E-233 | WP_072692661.1 | metallophosphoesterase family protein [Bacillus subtilis] |
| BSLIN78GL001894 | 100 | 3.10E-44 | QHM05551.1 | hypothetical protein C7M27_01488 [Bacillus subtilis] |
| BSLIN78GL001895 | 98 | 5.10E-21 | KIN51924.1 | hypothetical protein B4146_2252 [Bacillus subtilis] |
| BSLIN78GL001896 | 100 | 3.50E-43 | WP_042976245.1 | MULTISPECIES: HU family DNA-binding protein [Bacillus |
| BSLIN78GL001897 | 100 | 0.00E+00 | WP_213417509.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001898 | 100 | 6.50E-27 | WP_064814709.1 | MULTISPECIES: hypothetical protein [Bacteria |
| BSLIN78GL001899 | 100 | 6.30E-24 | WP_162985140.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001900 | 100 | 4.10E-23 | CAF1916652.1 | hypothetical protein NRS6206_03883 [Bacillus subtilis] |
| BSLIN78GL001901 | 100 | 1.40E-59 | AYK63071.1 | hypothetical protein D9C14_17685 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL001902 | 100 | 1.80E-20 | WP_121572579.1 | MULTISPECIES: hypothetical protein [Bacillus subtilis group |
| BSLIN78GL001903 | 100 | 3.10E-237 | WP_121572580.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001904 | 100 | 0.00E+00 | AYK63076.1 | OmpH family outer membrane protein [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL001905 | 100 | 0.00E+00 | WP_121572582.1 | DUF4942 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL001906 | 100 | 5.80E-17 | WP_014721229.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL001907 | 98.5 | 2.40E-33 | WP_144461684.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001908 | 100 | 1.20E-25 | WP_064814716.1 | MULTISPECIES: hypothetical protein [Bacteria |
| BSLIN78GL001909 | 100 | 2.50E-27 | WP_121572583.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001910 | 100 | 6.70E-14 | WP_121572653.1 | helix-turn-helix transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL001911 | 100 | 9.10E-139 | WP_121572584.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001912 | 100 | 3.60E-54 | WP_121572585.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001913 | 98.3 | 6.30E-28 | WP_003231000.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL001914 | 100 | 1.40E-38 | WP_068947530.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001915 | 100 | 7.30E-33 | WP_061891111.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001916 | 100 | 1.10E-18 | WP_042976227.1 | MULTISPECIES: hypothetical protein [Bacillus subtilis group |
| BSLIN78GL001917 | 100 | 6.40E-134 | WP_121572586.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001918 | 100 | 3.70E-126 | WP_121572587.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001919 | 100 | 5.10E-57 | WP_059293806.1 | MULTISPECIES: hypothetical protein [Bacillus subtilis group |
| BSLIN78GL001920 | 100 | 7.00E-223 | WP_059293807.1 | MULTISPECIES: AimR family lysis-lysogeny pheromone receptor [Bacillus subtilis |
| BSLIN78GL001921 | 100 | 5.10E-20 | WP_162983478.1 | MULTISPECIES: hypothetical protein [Bacillus subtilis group |
| BSLIN78GL001922 | 100 | 2.70E-32 | WP_041338583.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL001923 | 100 | 6.40E-41 | WP_061187761.1 | MULTISPECIES: hypothetical protein [Bacillus subtilis group |
| BSLIN78GL001924 | 100 | 3.80E-15 | KXJ35313.1 | hypothetical protein AX282_06205 [Bacillus spizizenii] |
| BSLIN78GL001925 | 99.7 | 2.60E-203 | WP_061187763.1 | tyrosine-type recombinase/integrase [Bacillus subtilis |

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| BSLIN78GL001926 | 100 | 2.20E-252 | WP_041338574.1 | MULTISPECIES: DNA sulfur modification protein DndB [Bacillus subtilis group] |
| BSLIN78GL001927 | 100 | 2.30E-182 | WP_129137732.1 | integrase [Bacillus subtilis] |
| BSLIN78GL001928 | 100 | 5.00E-48 | WP_041338565.1 | MULTISPECIES: hypothetical protein [Bacillus subtilis group] |
| BSLIN78GL001929 | 100 | 2.40E-37 | WP_041338559.1 | MULTISPECIES: hypothetical protein [Bacillus subtilis group] |
| BSLIN78GL001930 | 100 | 1.40E-63 | WP_032721693.1 | hypothetical protein [Bacillus] |
| BSLIN78GL001931 | 100 | 5.00E-40 | WP_032721694.1 | hypothetical protein [Bacillus] |
| BSLIN78GL001932 | 100 | 4.50E-28 | WP_032721695.1 | hypothetical protein [Bacillus] |
| BSLIN78GL001933 | 100 | 6.60E-69 | WP_121572590.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001934 | 100 | 4.10E-53 | CAF1916843.1 | hypothetical protein NRS6206_03917 [Bacillus subtilis] |
| BSLIN78GL001935 | 100 | 6.50E-60 | WP_017697051.1 | hypothetical protein [Bacillus] |
| BSLIN78GL001936 | 100 | 5.60E-71 | CAF1844037.1 | hypothetical protein NRS6127_03882 [Bacillus subtilis] |
| BSLIN78GL001937 | 100 | 1.10E-145 | WP_017697053.1 | hypothetical protein [Bacillus] |
| BSLIN78GL001938 | 100 | 1.00E-23 | WP_004399423.1 | MULTISPECIES: hypothetical protein [Bacillales] |
| BSLIN78GL001939 | 100 | 4.80E-34 | WP_009967498.1 | MULTISPECIES: hypothetical protein [Bacillales] |
| BSLIN78GL001940 | 99.5 | 1.30E-120 | WP_153912254.1 | DUF3920 family protein [Bacillus subtilis] |
| BSLIN78GL001941 | 97.8 | 9.20E-21 | WP_041335828.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL001942 | 100 | 1.00E-30 | WP_124058394.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001943 | 98.4 | 8.80E-27 | QHF58064.1 | prophage-derived uncharacterized protein [Bacillus subtilis] |
| BSLIN78GL001944 | 100 | 1.40E-26 | WP_271259402.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001945 | 100 | 1.60E-94 | WP_121572594.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001946 | 100 | 4.10E-53 | WP_032721720.1 | hypothetical protein [Bacillus] |
| BSLIN78GL001947 | 100 | 3.20E-40 | WP_121572595.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001948 | 100 | 8.10E-45 | WP_286239070.1 | hypothetical protein [Bacillus halotolerans] |
| BSLIN78GL001949 | 100 | 6.40E-58 | WP_121572596.1 | DUF2513 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL001950 | 98 | 2.10E-21 | WP_326211834.1 | hypothetical protein [Bacillus halotolerans] |
| BSLIN78GL001951 | 100 | 1.40E-150 | WP_213417511.1 | RNA ligase family protein [Bacillus subtilis] |
| BSLIN78GL001952 | 100 | 4.10E-130 | WP_213417512.1 | SOS response-associated peptidase [Bacillus subtilis] |
| BSLIN78GL001953 | 100 | 2.80E-35 | CAF1916953.1 | hypothetical protein NRS6206_03937 [Bacillus subtilis] |
| BSLIN78GL001954 | 99.1 | 1.60E-55 | WP_144483931.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001955 | 100 | 1.90E-150 | WP_213417513.1 | poly-gamma-glutamate hydrolase family protein [Bacillus subtilis] |
| BSLIN78GL001956 | 100 | 0.00E+00 | WP_213417514.1 | right-handed parallel beta-helix repeat-containing protein [Bacillus subtilis] |
| BSLIN78GL001957 | 100 | 1.90E-47 | WP_213417515.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001958 | 100 | 1.00E-66 | WP_121572600.1 | MULTISPECIES: hypothetical protein [Bacillus subtilis group] |
| BSLIN78GL001959 | 100 | 3.80E-114 | WP_229762343.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL001960 | 100 | 1.50E-172 | WP_041338504.1 | MULTISPECIES: hypothetical protein [Bacillus subtilis group] |
| BSLIN78GL001961 | 100 | 4.30E-181 | WP_004399537.1 | MULTISPECIES: ATP-binding protein [Bacillales] |
| BSLIN78GL001962 | 100 | 4.10E-47 | KIN27543.1 | hypothetical protein B4069_2094 [Bacillus subtilis] |
| BSLIN78GL001963 | 100 | 1.40E-262 | WP_198879079.1 | replicative DNA helicase [Bacillus subtilis] |
| BSLIN78GL001964 | 100 | 1.60E-224 | WP_198879078.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001965 | 99.8 | 0.00E+00 | WP_213417516.1 | single-stranded-DNA-specific exonuclease RecJ [Bacillus subtilis] |
| BSLIN78GL001966 | 100 | 0.00E+00 | WP_213417517.1 | DNA polymerase III subunit alpha [Bacillus subtilis] |
| BSLIN78GL001967 | 100 | 5.90E-118 | WP_153912240.1 | 3D domain-containing protein [Bacillus subtilis] |
| BSLIN78GL001968 | 100 | 1.20E-21 | WP_121572605.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL001969 | 100 | 4.80E-88 | WP_069322666.1 | deoxynucleoside kinase [Bacillus subtilis] |
| BSLIN78GL001970 | 100 | 1.00E-145 | KIN27532.1 | Adenine-specific methyltransferase [Bacillus subtilis] |
| BSLIN78GL001971 | 100 | 2.70E-32 | WP_041353160.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001972 | 100 | 3.00E-63 | WP_153256824.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001973 | 100 | 1.70E-35 | WP_153912238.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001974 | 98.4 | 1.50E-29 | AYK63141.1 | hypothetical protein D9C14_18075 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL001975 | 100 | 3.30E-43 | WP_061891143.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001976 | 100 | 8.80E-43 | WP_068947565.1 | metallophosphoesterase [Bacillus subtilis] |
| BSLIN78GL001977 | 100 | 7.40E-23 | WP_155117805.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001978 | 100 | 1.10E-77 | WP_032721791.1 | hypothetical protein [Bacillus] |
| BSLIN78GL001979 | 100 | 2.00E-56 | WP_032721793.1 | hypothetical protein [Bacillus] |
| BSLIN78GL001980 | 100 | 1.80E-15 | TDO89209.1 | hypothetical protein BDW29_2296 [Bacillus sp. AtDRG31] |
| BSLIN78GL001981 | 100 | 3.60E-39 | WP_041353147.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001982 | 100 | 1.50E-62 | WP_162105511.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001983 | 100 | 5.00E-38 | WP_268475121.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001984 | 100 | 5.20E-60 | WP_114523506.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001985 | 100 | 1.30E-67 | WP_142743348.1 | class Ib ribonucleoside-diphosphate reductase assembly flavoprotein NrdI [Bacillus |
| BSLIN78GL001986 | 97.5 | 4.80E-205 | WP_163136355.1 | class 1b ribonucleoside-diphosphate reductase subunit alpha [Bacillus subtilis] |
| BSLIN78GL001987 | 100 | 5.60E-178 | CAF1917174.1 | Ribonucleoside-diphosphate reductase 2 subunit alpha [Bacillus subtilis] |
| BSLIN78GL001988 | 100 | 2.00E-74 | WP_213417519.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001989 | 100 | 3.80E-111 | CAF1917183.1 | Ribonucleoside-diphosphate reductase subunit beta [Bacillus subtilis] |
| BSLIN78GL001990 | 99.4 | 1.60E-97 | AFQ57948.1 | SPbeta phage endodeoxyribonuclease [Bacillus subtilis QB928] |
| BSLIN78GL001991 | 100 | 3.60E-45 | CAF1917193.1 | Ribonucleoside-diphosphate reductase subunit beta [Bacillus subtilis] |
| BSLIN78GL001992 | 100 | 6.50E-28 | WP_151262253.1 | glutaredoxin domain-containing protein [Bacillus subtilis] |
| BSLIN78GL001993 | 100 | 7.40E-77 | WP_144500600.1 | dUTP diphosphatase DutA [Bacillus subtilis] |
| BSLIN78GL001994 | 100 | 8.20E-120 | WP_321836465.1 | VanZ family protein [Bacillus subtilis] |
| BSLIN78GL001995 | 97.6 | 6.30E-16 | KIN51205.1 | hypothetical protein B4073_1729 [Bacillus subtilis] |
| BSLIN78GL001996 | 100 | 2.70E-49 | WP_144500602.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001997 | 100 | 8.20E-24 | WP_151262256.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL001998 | 100 | 8.30E-165 | WP_153912229.1 | thymidylate synthase [Bacillus subtilis] |
| BSLIN78GL002000 | 100 | 2.80E-58 | WP_068947575.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002001 | 100 | 4.90E-137 | WP_068947576.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002002 | 98 | 5.80E-21 | WP_068947577.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002003 | 100 | 2.90E-24 | WP_041351976.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002004 | 98.7 | 1.00E-32 | AFQ57939.1 | Small acid-soluble spore protein (alpha/beta-typeSASP) [Bacillus subtilis QB928] |
| BSLIN78GL002005 | 100 | 1.10E-27 | WP_213417506.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002006 | 98.9 | 4.00E-44 | RJS58598.1 | hypothetical protein CJ481_17220 [Bacillus subtilis] |

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| BSLIN78GL002007 | 100 | 1.20E-100 | WP_147797684.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002008 | 100 | 5.00E-24 | WP_061891169.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002009 | 100 | 1.40E-78 | WP_213417507.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002010 | 100 | 3.40E-18 | AFQ57929.1 | YotK [Bacillus subtilis QB928] |
| BSLIN78GL002011 | 100 | 5.90E-39 | WP_080481958.1 | helix-turn-helix transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL002012 | 100 | 1.70E-111 | WP_068947582.1 | Holliday junction resolvase RecU [Bacillus subtilis] |
| BSLIN78GL002013 | 100 | 1.10E-19 | WP_155117806.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002014 | 100 | 0.00E+00 | WP_068947583.1 | MULTISPECIES: recombinase family protein [Bacillus] |
| BSLIN78GL002015 | 100 | 3.20E-69 | GLI88634.1 | stage V sporulation protein K [Bacillus subtilis] |
| BSLIN78GL002016 | 99.6 | 3.10E-257 | AGE63584.1 | putative GTP-binding protein [Bacillus subtilis XF-1] |
| BSLIN78GL002017 | 100 | 8.80E-243 | WP_029726458.1 | aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme [Bacillus |
| BSLIN78GL002018 | 100 | 2.90E-70 | WP_003238341.1 | MULTISPECIES: transcriptional repressor GlnR [Bacillales] |
| BSLIN78GL002019 | 100 | 2.40E-259 | WP_015252037.1 | MULTISPECIES: type I glutamate--ammonia ligase [Bacillus] |
| BSLIN78GL002020 | 100 | 2.50E-220 | WP_068947584.1 | site-specific integrase [Bacillus subtilis] |
| BSLIN78GL002021 | 99.7 | 1.30E-227 | AOA54557.1 | hypothetical protein BSHJ0_01985 [Bacillus subtilis] |
| BSLIN78GL002023 | 100 | 5.50E-69 | WP_038427668.1 | MULTISPECIES: helix-turn-helix transcriptional regulator [Bacillus subtilis group] |
| BSLIN78GL002024 | 100 | 1.10E-30 | AIC98285.1 | hypothetical protein Q433_09955 [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL002025 | 100 | 1.10E-116 | WP_038427672.1 | MULTISPECIES: hypothetical protein [Bacillus subtilis group] |
| BSLIN78GL002026 | 100 | 5.70E-161 | WP_068947586.1 | phage replisome organizer N-terminal domain-containing protein [Bacillus subtilis] |
| BSLIN78GL002027 | 100 | 8.50E-154 | WP_038427675.1 | ATP-binding protein [Bacillus subtilis] |
| BSLIN78GL002028 | 100 | 2.80E-17 | WP_196219456.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002029 | 100 | 2.10E-100 | WP_038427676.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002030 | 100 | 1.90E-23 | AOA54570.1 | hypothetical protein BSHJ0_01998 [Bacillus subtilis] |
| BSLIN78GL002031 | 97.4 | 5.90E-13 | WP_154230816.1 | BH0509 family protein [Bacillus subtilis] |
| BSLIN78GL002032 | 100 | 6.40E-23 | WP_014480890.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL002033 | 100 | 4.20E-33 | AOA54573.1 | uncharacterized protein BSHJ0_02001 [Bacillus subtilis] |
| BSLIN78GL002034 | 100 | 1.20E-53 | WP_038427678.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002035 | 100 | 2.20E-39 | WP_038427680.1 | MULTISPECIES: hypothetical protein [Bacillus subtilis group] |
| BSLIN78GL002036 | 100 | 3.60E-219 | WP_038427681.1 | DUF3578 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL002037 | 100 | 1.90E-122 | WP_038427682.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002039 | 100 | 2.70E-77 | WP_068947588.1 | ArpU family phage packaging/lysis transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL002040 | 100 | 3.30E-98 | WP_038427685.1 | MULTISPECIES: tyrosine-type recombinase/integrase [Bacillus subtilis group] |
| BSLIN78GL002042 | 100 | 6.20E-82 | WP_068947589.1 | DUF4145 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL002043 | 100 | 7.00E-81 | WP_068947590.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002044 | 100 | 5.80E-272 | WP_068947591.1 | metal-binding protein [Bacillus subtilis] |
| BSLIN78GL002046 | 100 | 1.40E-34 | AOA54584.1 | hypothetical protein BSHJ0_02012 [Bacillus subtilis] |
| BSLIN78GL002047 | 100 | 6.30E-91 | WP_038427692.1 | MULTISPECIES: phage terminase small subunit P27 family [Bacillus] |
| BSLIN78GL002048 | 100 | 0.00E+00 | WP_068947593.1 | terminase TerL endonuclease subunit [Bacillus subtilis] |
| BSLIN78GL002049 | 100 | 9.00E-31 | WP_214287137.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002050 | 100 | 7.00E-248 | WP_068947594.1 | phage portal protein [Bacillus subtilis] |
| BSLIN78GL002051 | 100 | 1.10E-113 | WP_068947595.1 | HK97 family phage prohead protease [Bacillus subtilis] |
| BSLIN78GL002052 | 99.8 | 2.90E-241 | WP_032725456.1 | MULTISPECIES: phage major capsid protein [Bacillus] |
| BSLIN78GL002053 | 99.3 | 1.10E-83 | WP_019260073.1 | MULTISPECIES: collagen-like protein [Bacillus subtilis group] |
| BSLIN78GL002054 | 100 | 7.80E-49 | WP_041057207.1 | head-tail connector protein [Bacillus subtilis] |
| BSLIN78GL002055 | 100 | 1.90E-53 | WP_041057204.1 | MULTISPECIES: phage head closure protein [Bacillus] |
| BSLIN78GL002056 | 100 | 1.20E-68 | WP_032725460.1 | MULTISPECIES: HK97-gp10 family putative phage morphogenesis protein |
| BSLIN78GL002057 | 100 | 1.50E-62 | WP_041057199.1 | DUF3168 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL002058 | 100 | 5.90E-112 | WP_059335732.1 | MULTISPECIES: major tail protein [Bacillus] |
| BSLIN78GL002059 | 100 | 1.60E-62 | WP_068947597.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002060 | 100 | 0.00E+00 | WP_068947598.1 | phage tail tape measure protein [Bacillus subtilis] |
| BSLIN78GL002061 | 100 | 7.30E-161 | WP_213417501.1 | phage tail family protein [Bacillus subtilis] |
| BSLIN78GL002062 | 100 | 0.00E+00 | WP_068947599.1 | MULTISPECIES: phage tail spike protein [Bacillus] |
| BSLIN78GL002063 | 100 | 0.00E+00 | WP_326223313.1 | teichoic acid biosynthesis protein [Bacillus subtilis] |
| BSLIN78GL002064 | 100 | 2.40E-53 | WP_038427704.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002065 | 100 | 5.90E-25 | WP_164906782.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL002066 | 100 | 7.00E-306 | WP_068947601.1 | phage baseplate upper protein [Bacillus subtilis] |
| BSLIN78GL002067 | 99 | 2.60E-49 | WP_038427706.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002068 | 100 | 5.30E-26 | WP_080282461.1 | XkdX family protein [Bacillus subtilis] |
| BSLIN78GL002069 | 97.6 | 4.00E-15 | AWM23192.1 | hypothetical protein DJ572_09130 [Bacillus subtilis] |
| BSLIN78GL002070 | 100 | 1.70E-70 | WP_038427709.1 | phage holin family protein [Bacillus subtilis] |
| BSLIN78GL002071 | 100 | 1.20E-183 | WP_038427711.1 | N-acetylmuramoyl-L-alanine amidase [Bacillus subtilis] |
| BSLIN78GL002072 | 100 | 9.10E-50 | WP_038427712.1 | contact-dependent growth inhibition system immunity protein [Bacillus subtilis] |
| BSLIN78GL002073 | 100 | 0.00E+00 | WP_068947602.1 | T7SS effector LXG polymorphic toxin [Bacillus subtilis] |
| BSLIN78GL002074 | 100 | 8.70E-90 | AIC98327.1 | hypothetical protein Q433_10245 [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL002075 | 100 | 1.90E-18 | RAP05810.1 | hypothetical protein HS3_02498 [Bacillus subtilis] |
| BSLIN78GL002076 | 100 | 1.20E-16 | QHF57727.1 | hypothetical protein Bateq7PJ16_1921 [Bacillus subtilis] |
| BSLIN78GL002077 | 89.1 | 0.00E+00 | WP_257182380.1 | NTTRR-F1 domain [Bacillus subtilis] |
| BSLIN78GL002078 | 100 | 1.20E-129 | WP_029726887.1 | MULTISPECIES: glycosyltransferase family protein [Bacillus |
| BSLIN78GL002079 | 100 | 4.90E-134 | WP_029726888.1 | MULTISPECIES: class I SAM-dependent methyltransferase [Bacillus |
| BSLIN78GL002080 | 100 | 5.60E-214 | WP_029726889.1 | glycosyltransferase [Bacillus subtilis] |
| BSLIN78GL002081 | 100 | 2.70E-266 | WP_236822287.1 | glycosyltransferase [Bacillus subtilis] |
| BSLIN78GL002082 | 100 | 7.90E-25 | RAP04121.1 | hypothetical protein HS3_04224 [Bacillus subtilis] |
| BSLIN78GL002083 | 99.4 | 1.30E-102 | WP_029726893.1 | GNAT family protein [Bacillus subtilis] |
| BSLIN78GL002084 | 100 | 7.30E-167 | WP_151262270.1 | CPBP family intramembrane glutamic endopeptidase [Bacillus subtilis] |
| BSLIN78GL002085 | 92.9 | 2.40E-06 | WP_267461664.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002086 | 100 | 1.50E-36 | WP_151262271.1 | helix-turn-helix transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL002087 | 100 | 1.30E-122 | WP_029726896.1 | DUF3885 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL002088 | 100 | 3.10E-14 | ADV92649.1 | hypothetical protein BSn5_00065 [Bacillus subtilis BSn5] |
| BSLIN78GL002089 | 100 | 7.50E-22 | WP_003231681.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL002090 | 100 | 4.00E-84 | WP_029726897.1 | hypothetical protein [Bacillus subtilis] |

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| BSLIN78GL002091 | 100 | 8.20E-94 | WP_029726898.1 | N-acetyltransferase [Bacillus subtilis] |
| BSLIN78GL002092 | 100 | 2.60E-14 | ADV92653.1 | hypothetical protein BSn5_00085 [Bacillus subtilis BSn5] |
| BSLIN78GL002093 | 100 | 1.40E-262 | WP_017697653.1 | MULTISPECIES: MFS transporter [Bacillus] |
| BSLIN78GL002094 | 100 | 0.00E+00 | WP_029726899.1 | MULTISPECIES: xylan 1,4-beta-xylosidase [Bacillus |
| BSLIN78GL002095 | 100 | 2.10E-219 | AKN13906.1 | Xylose-responsive transcription regulator, ROK family [Bacillus subtilis |
| BSLIN78GL002096 | 100 | 4.00E-262 | WP_003231664.1 | MULTISPECIES: xylose isomerase [Bacillus |
| BSLIN78GL002097 | 99.8 | 3.50E-291 | WP_038427718.1 | xylulokinase [Bacillus subtilis] |
| BSLIN78GL002098 | 100 | 4.10E-116 | WP_033885087.1 | endonuclease YncB [Bacillus subtilis] |
| BSLIN78GL002099 | 99.8 | 4.90E-241 | WP_048654892.1 | sugar porter family MFS transporter [Bacillus subtilis] |
| BSLIN78GL002100 | 100 | 3.40E-220 | WP_033884592.1 | MULTISPECIES: alanine racemase [Bacillus] |
| BSLIN78GL002101 | 100 | 3.80E-31 | WP_125121356.1 | DUF2691 family protein [Bacillus subtilis] |
| BSLIN78GL002102 | 100 | 3.70E-76 | WP_003231650.1 | MULTISPECIES: dUTP diphosphatase DutA [Bacillus] |
| BSLIN78GL002103 | 97.4 | 9.80E-76 | AIC98353.1 | hypothetical protein Q433_10420 [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL002104 | 100 | 1.70E-12 | AHA77800.1 | Hypothetical Protein U712_09285 [Bacillus subtilis PY79] |
| BSLIN78GL002105 | 100 | 2.30E-23 | WP_003231643.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002106 | 100 | 8.30E-165 | WP_029317846.1 | thymidylate synthase [Bacillus subtilis |
| BSLIN78GL002107 | 98.8 | 2.50E-136 | AOA54646.1 | uncharacterized protein BSHJ0_02074 [Bacillus subtilis] |
| BSLIN78GL002108 | 78 | 8.50E-10 | AGI29086.1 | hypothetical protein I653_09170 [Bacillus subtilis subsp. subtilis str. BAB-1] |
| BSLIN78GL002109 | 100 | 3.80E-16 | EHA30429.1 | hypothetical protein BSSC8_24880 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002110 | 100 | 3.80E-36 | WP_024573164.1 | MULTISPECIES: spore coat protein CotC [Bacillus] |
| BSLIN78GL002111 | 100 | 6.20E-32 | AGE63614.1 | component of the twin-arginine pre-protein translocation pathway [Bacillus subtilis |
| BSLIN78GL002112 | 100 | 2.90E-37 | AHA77808.1 | Uncharacterized protein yndA [Bacillus subtilis PY79] |
| BSLIN78GL002113 | 100 | 2.10E-79 | WP_326253874.1 | SRPBCC domain-containing protein [Bacillus subtilis] |
| BSLIN78GL002114 | 100 | 2.00E-26 | AIX07556.1 | hypothetical protein OB04_01896 [Bacillus subtilis] |
| BSLIN78GL002115 | 100 | 5.80E-26 | WP_003231626.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002116 | 95.7 | 1.20E-43 | AID00399.1 | hypothetical protein Q433_10490 [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL002117 | 100 | 3.40E-130 | AOA54655.1 | Spore germination protein YndE [Bacillus subtilis] |
| BSLIN78GL002118 | 100 | 2.30E-60 | AOA54656.1 | Spore germination protein YndE [Bacillus subtilis] |
| BSLIN78GL002119 | 100 | 3.30E-220 | WP_128473939.1 | Ger(x)C family spore germination protein [Bacillus subtilis] |
| BSLIN78GL002120 | 100 | 1.20E-155 | WP_029726668.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002121 | 100 | 1.60E-13 | EHA30419.1 | hypothetical protein BSSC8_24780 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002122 | 100 | 1.50E-68 | KIO55662.1 | hypothetical protein B4143_0953 [Bacillus subtilis] |
| BSLIN78GL002123 | 100 | 0.00E+00 | WP_029726670.1 | MULTISPECIES: YndJ family protein [Bacillus] |
| BSLIN78GL002124 | 100 | 2.80E-61 | ADV92682.1 | putative phage/plasmid replication protein [Bacillus subtilis BSn5] |
| BSLIN78GL002125 | 100 | 7.10E-139 | WP_015714006.1 | MULTISPECIES: gamma-polyglutamate hydrolase PghL [Bacillus |
| BSLIN78GL002126 | 100 | 1.50E-95 | WP_003231606.1 | YndM family protein [Bacillus subtilis] |
| BSLIN78GL002127 | 100 | 1.60E-79 | WP_003231604.1 | MULTISPECIES: FosM family fosfomycin resistance protein [Bacillales |
| BSLIN78GL002128 | 100 | 7.90E-112 | AGA21291.1 | Repressor LexA [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL002129 | 100 | 3.90E-51 | WP_003231598.1 | MULTISPECIES: cell division suppressor protein YneA [Bacillales |
| BSLIN78GL002130 | 100 | 2.70E-115 | WP_015714011.1 | MULTISPECIES: recombinase family protein [Bacillus] |
| BSLIN78GL002131 | 100 | 1.90E-34 | WP_003231595.1 | MULTISPECIES: DUF896 domain-containing protein [Bacillales] |
| BSLIN78GL002132 | 100 | 0.00E+00 | WP_014476936.1 | MULTISPECIES: transketolase [Bacillus] |
| BSLIN78GL002133 | 100 | 1.60E-82 | WP_003231591.1 | MULTISPECIES: sporulation inhibitor of replication protein SirA [Bacillales] |
| BSLIN78GL002134 | 100 | 6.40E-28 | AGE63632.1 | hypothetical protein C663_1844 [Bacillus subtilis XF-1] |
| BSLIN78GL002135 | 100 | 1.50E-26 | WP_003231588.1 | MULTISPECIES: aspartyl-phosphate phosphatase YnzD [Bacillus] |
| BSLIN78GL002136 | 100 | 5.10E-131 | WP_003231585.1 | MULTISPECIES: cytochrome c-type biogenesis protein CcdA [Bacillales |
| BSLIN78GL002137 | 100 | 2.80E-52 | WP_003245707.1 | MULTISPECIES: response regulator [Bacillales] |
| BSLIN78GL002138 | 100 | 1.50E-81 | WP_003231582.1 | CcdC family protein [Bacillus subtilis] |
| BSLIN78GL002139 | 100 | 4.30E-77 | WP_003231580.1 | MULTISPECIES: DynA interaction protein YneK [Bacillales |
| BSLIN78GL002140 | 100 | 3.90E-57 | WP_128992915.1 | outer spore coat protein CotM [Bacillus subtilis] |
| BSLIN78GL002141 | 100 | 1.10E-19 | AFI28499.1 | small, acid-soluble spore protein O [Bacillus sp. JS] |
| BSLIN78GL002142 | 99.9 | 0.00E+00 | WP_042975893.1 | aconitate hydratase AcnA [Bacillus subtilis] |
| BSLIN78GL002143 | 100 | 1.10E-92 | WP_029726674.1 | MULTISPECIES: redoxin domain-containing protein [Bacillus] |
| BSLIN78GL002144 | 100 | 4.10E-27 | ADV92704.1 | hypothetical protein BSn5_00340 [Bacillus subtilis BSn5] |
| BSLIN78GL002145 | 100 | 7.40E-21 | WP_003231569.1 | MULTISPECIES: acid-soluble spore protein SspN [Bacillales |
| BSLIN78GL002146 | 100 | 3.60E-39 | WP_003231568.1 | MULTISPECIES: small acid-soluble spore protein Tlp [Bacillales] |
| BSLIN78GL002147 | 100 | 2.70E-76 | WP_088467228.1 | YbgC/FadM family acyl-CoA thioesterase [Bacillus subtilis |
| BSLIN78GL002148 | 100 | 6.80E-53 | WP_029726676.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002149 | 100 | 4.40E-49 | WP_003231562.1 | MULTISPECIES: HesB/YadR/YfhF family protein [Bacillales |
| BSLIN78GL002150 | 100 | 2.60E-101 | WP_003231560.1 | MULTISPECIES: glycerol-3-phosphate 1-O-acyltransferase PlsY [Bacillales |
| BSLIN78GL002151 | 100 | 1.60E-24 | AGI29127.1 | hypothetical protein I653_09375 [Bacillus subtilis subsp. subtilis str. BAB-1] |
| BSLIN78GL002152 | 100 | 1.20E-68 | WP_014479943.1 | MULTISPECIES: CoA-binding protein [Bacillus |
| BSLIN78GL002153 | 100 | 8.80E-15 | AHA77847.1 | Hypothetical Protein U712_09520 [Bacillus subtilis PY79] |
| BSLIN78GL002154 | 99.8 | 0.00E+00 | WP_153529777.1 | DNA topoisomerase IV subunit B [Bacillus sp. TYF-B5-5] |
| BSLIN78GL002155 | 93.3 | 0.00E+00 | WP_242555906.1 | DNA topoisomerase IV subunit A [Bacillus sp. HU-1818] |
| BSLIN78GL002156 | 100 | 8.80E-15 | WP_003231548.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002157 | 100 | 1.20E-71 | Q45067.1 | RecName: Full=Uncharacterized protein YnfC [Bacillus subtilis subsp. subtilis str. |
| BSLIN78GL002158 | 100 | 3.80E-263 | WP_021479777.1 | MULTISPECIES: alanine/glycine:cation symporter family protein [Bacillus |
| BSLIN78GL002159 | 100 | 6.60E-298 | AKE23721.1 | alkali tolerable cellulase [Bacillus sp. LM 4-2] |
| BSLIN78GL002160 | 100 | 3.00E-44 | WP_033884057.1 | MULTISPECIES: YnfE family protein [Bacillus |
| BSLIN78GL002161 | 100 | 1.00E-240 | WP_046381056.1 | MULTISPECIES: glucuronoarabinoxylan endo-1,4-beta-xylanase XynC [Bacillus |
| BSLIN78GL002162 | 99.8 | 2.90E-301 | AKE23724.1 | endo-1,4-beta-xylanase [Bacillus sp. LM 4-2] |
| BSLIN78GL002163 | 100 | 1.10E-80 | WP_046381058.1 | MULTISPECIES: GtrA family protein [Bacillus |
| BSLIN78GL002164 | 100 | 1.30E-163 | WP_014479952.1 | MULTISPECIES: UTP--glucose-1-phosphate uridylyltransferase GalU [Bacillus |
| BSLIN78GL002165 | 100 | 1.10E-107 | WP_003231529.1 | MULTISPECIES: DedA family protein [Bacillales |
| BSLIN78GL002166 | 99.7 | 8.20E-227 | WP_046381059.1 | MULTISPECIES: oligoribonuclease NrnB [Bacillus] |
| BSLIN78GL002167 | 100 | 3.80E-293 | WP_080481021.1 | MULTISPECIES: acyl-CoA carboxylase subunit beta [Bacillus |
| BSLIN78GL002168 | 100 | 5.60E-139 | WP_046381061.1 | MULTISPECIES: enoyl-CoA hydratase [Bacillus |
| BSLIN78GL002169 | 100 | 5.60E-167 | WP_046381062.1 | MULTISPECIES: hydroxymethylglutaryl-CoA lyase [Bacillus |
| BSLIN78GL002170 | 100 | 3.50E-29 | WP_046381063.1 | MULTISPECIES: acetyl-CoA carboxylase biotin carboxyl carrier protein subunit |

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| BSLIN78GL002171 | 99.8 | 7.10E-251 | WP_072175930.1 | acetyl-CoA carboxylase biotin carboxylase subunit [Bacillus subtilis |
| BSLIN78GL002172 | 100 | 0.00E+00 | WP_046381065.1 | MULTISPECIES: AMP-binding protein [Bacillus] |
| BSLIN78GL002173 | 100 | 3.30E-220 | WP_202926446.1 | acyl-CoA dehydrogenase [Bacillus subtilis |
| BSLIN78GL002174 | 100 | 5.10E-54 | ADV92734.1 | hypothetical protein BSn5_00490 [Bacillus subtilis BSn5] |
| BSLIN78GL002175 | 100 | 7.20E-308 | WP_326253876.1 | glycoside hydrolase family 10 protein [Bacillus subtilis |
| BSLIN78GL002176 | 100 | 1.30E-67 | WP_014476970.1 | MULTISPECIES: DUF1360 domain-containing protein [Bacillus] |
| BSLIN78GL002177 | 100 | 0.00E+00 | WP_147797790.1 | plipastatin non-ribosomal peptide synthetase PpsE [Bacillus subtilis] |
| BSLIN78GL002178 | 100 | 0.00E+00 | WP_068947604.1 | MULTISPECIES: plipastatin non-ribosomal peptide synthetase PpsD [Bacillus] |
| BSLIN78GL002179 | 100 | 0.00E+00 | WP_046663264.1 | MULTISPECIES: plipastatin non-ribosomal peptide synthetase PpsC [Bacillus |
| BSLIN78GL002180 | 100 | 0.00E+00 | WP_326253880.1 | plipastatin non-ribosomal peptide synthetase PpsB [Bacillus subtilis] |
| BSLIN78GL002181 | 100 | 0.00E+00 | WP_068947606.1 | plipastatin non-ribosomal peptide synthetase PpsA [Bacillus subtilis] |
| BSLIN78GL002182 | 98.8 | 1.90E-281 | BAI85522.1 | penicillin-binding protein [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL002183 | 100 | 3.20E-192 | WP_038427744.1 | aldose 1-epimerase [Bacillus subtilis] |
| BSLIN78GL002184 | 100 | 9.80E-245 | WP_038427746.1 | MATE family efflux transporter [Bacillus subtilis] |
| BSLIN78GL002185 | 100 | 5.10E-99 | WP_004399558.1 | MULTISPECIES: DL-endopeptidase inhibitor IseA [Bacillales |
| BSLIN78GL002186 | 100 | 4.80E-97 | WP_003231473.1 | MULTISPECIES: site-specific integrase [Bacillales |
| BSLIN78GL002187 | 100 | 2.20E-35 | WP_029727237.1 | MULTISPECIES: excisionase family DNA-binding protein [Bacillus |
| BSLIN78GL002188 | 100 | 0.00E+00 | WP_029727236.1 | MULTISPECIES: gamma-glutamyltransferase [Bacillus] |
| BSLIN78GL002189 | 100 | 3.70E-12 | RAP10937.1 | hypothetical protein HS3_01358 [Bacillus subtilis] |
| BSLIN78GL002190 | 100 | 2.00E-158 | WP_029727235.1 | MULTISPECIES: LysR family transcriptional regulator YofA [Bacillus |
| BSLIN78GL002191 | 99.7 | 6.30E-191 | AGE63687.1 | putative oxidoreductase [Bacillus subtilis XF-1] |
| BSLIN78GL002192 | 100 | 2.70E-291 | WP_014479972.1 | MULTISPECIES: glutamate synthase small subunit [Bacillus] |
| BSLIN78GL002193 | 100 | 0.00E+00 | WP_029727234.1 | MULTISPECIES: glutamate synthase large subunit [Bacillus] |
| BSLIN78GL002194 | 100 | 2.80E-166 | WP_004399246.1 | MULTISPECIES: glutamate biosynthesis transcriptional regulator GltC [Bacillales |
| BSLIN78GL002195 | 100 | 2.00E-206 | WP_015714042.1 | MULTISPECIES: glutamate 5-kinase [Bacillus] |
| BSLIN78GL002196 | 100 | 3.60E-155 | WP_080282470.1 | MULTISPECIES: pyrroline-5-carboxylate reductase [Bacillus |
| BSLIN78GL002197 | 95.2 | 6.30E-16 | KZD95200.1 | hypothetical protein B4122_0172 [Bacillus subtilis] |
| BSLIN78GL002198 | 99.2 | 1.60E-65 | EHA30520.1 | replication terminator protein [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002199 | 100 | 3.50E-127 | BAI85542.2 | 3-ketoacyl-(acyl-carrier-protein) reductase [Bacillus subtilis subsp. natto BEST195 |
| BSLIN78GL002200 | 100 | 2.10E-47 | WP_029727232.1 | DUF948 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL002201 | 100 | 1.20E-141 | AIC98433.1 | hypothetical protein Q433_10940 [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL002202 | 100 | 9.80E-95 | WP_029727230.1 | GNAT family protein [Bacillus subtilis] |
| BSLIN78GL002203 | 100 | 0.00E+00 | AOA54736.1 | Triacylglycerol lipase [Bacillus subtilis] |
| BSLIN78GL002204 | 100 | 8.50E-162 | WP_029318086.1 | lipase family protein [Bacillus subtilis] |
| BSLIN78GL002205 | 100 | 8.60E-243 | WP_029727228.1 | MFS transporter [Bacillus subtilis] |
| BSLIN78GL002206 | 100 | 5.00E-282 | WP_029727227.1 | FGGY-family carbohydrate kinase [Bacillus subtilis |
| BSLIN78GL002207 | 100 | 1.70E-196 | WP_029727226.1 | MULTISPECIES: 2-hydroxyacid dehydrogenase [Bacillus |
| BSLIN78GL002208 | 100 | 0.00E+00 | WP_029727225.1 | MULTISPECIES: molybdopterin oxidoreductase family protein [Bacillus |
| BSLIN78GL002209 | 100 | 4.50E-49 | WP_015251960.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002210 | 100 | 5.30E-34 | WP_033883954.1 | UPF0715 family protein [Bacillus subtilis] |
| BSLIN78GL002211 | 100 | 5.00E-26 | WP_236822279.1 | UPF0715 family protein [Bacillus subtilis] |
| BSLIN78GL002212 | 100 | 4.40E-17 | QHF57857.1 | hypothetical protein Bateq7PJ16_2051 [Bacillus subtilis] |
| BSLIN78GL002213 | 100 | 1.20E-49 | WP_014477001.1 | MULTISPECIES: YozQ family protein [Bacillus] |
| BSLIN78GL002214 | 99.8 | 1.00E-302 | WP_029727224.1 | MULTISPECIES: methyl-accepting chemotaxis protein [Bacillus |
| BSLIN78GL002215 | 100 | 4.10E-14 | AKN14020.1 | hypothetical protein ABU16_2944 [Bacillus subtilis] |
| BSLIN78GL002216 | 100 | 7.10E-281 | WP_029727223.1 | MULTISPECIES: 4-hydroxyphenylacetate 3-monooxygenase, oxygenase component |
| BSLIN78GL002217 | 100 | 2.00E-132 | WP_003231419.1 | MULTISPECIES: expansin ExlX [Bacillales] |
| BSLIN78GL002218 | 100 | 9.90E-107 | EHA30504.1 | hypothetical protein BSSC8_23830 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002219 | 99.7 | 3.80E-207 | EHA30503.1 | pectate lyase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002220 | 100 | 4.00E-133 | WAE50279.1 | SOS response-associated peptidase [Bacillus subtilis] |
| BSLIN78GL002221 | 100 | 2.90E-232 | WP_029727221.1 | MULTISPECIES: oxalate decarboxylase [Bacillus] |
| BSLIN78GL002222 | 100 | 6.70E-90 | WP_029727220.1 | MULTISPECIES: DUF4944 domain-containing protein [Bacillus] |
| BSLIN78GL002223 | 100 | 2.70E-146 | WP_029727219.1 | MULTISPECIES: N-acetyltransferase [Bacillus |
| BSLIN78GL002224 | 98.4 | 6.50E-69 | EHA30497.1 | hypothetical protein BSSC8_23760 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002225 | 100 | 4.40E-89 | WP_029727217.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002226 | 100 | 9.90E-172 | WP_038829975.1 | VanW family protein [Bacillus subtilis] |
| BSLIN78GL002227 | 100 | 2.50E-66 | AYA43095.1 | DUF2975 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL002228 | 100 | 3.80E-32 | AEP91061.1 | transcription regulator, Cro/CI family -related protein [Bacillus subtilis subsp. subtilis |
| BSLIN78GL002229 | 98.5 | 1.10E-153 | EHA30492.1 | hypothetical protein BSSC8_23710 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002230 | 100 | 3.20E-159 | WP_015714065.1 | MULTISPECIES: LysR family transcriptional regulator [Bacillus |
| BSLIN78GL002231 | 100 | 5.10E-165 | WP_069703923.1 | DMT family transporter [Bacillus subtilis] |
| BSLIN78GL002232 | 100 | 3.60E-76 | WP_015714067.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002233 | 100 | 2.20E-117 | WP_015714068.1 | type 1 glutamine amidotransferase family protein [Bacillus subtilis] |
| BSLIN78GL002234 | 99.7 | 4.00E-162 | ADV92788.1 | beta-lactamase precursor [Bacillus subtilis BSn5] |
| BSLIN78GL002235 | 99.1 | 9.60E-56 | WP_015714070.1 | DUF3221 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL002236 | 100 | 2.30E-31 | WP_250540527.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002237 | 95 | 7.70E-13 | RPK12209.1 | hypothetical protein EH5_02375 [Bacillus subtilis] |
| BSLIN78GL002238 | 100 | 0.00E+00 | WP_015714072.1 | phosphoenolpyruvate synthase [Bacillus subtilis |
| BSLIN78GL002239 | 100 | 9.90E-126 | WP_015714073.1 | endo-1,4-beta-xylanase XynA [Bacillus subtilis |
| BSLIN78GL002240 | 100 | 4.90E-28 | AIC98469.1 | hypothetical protein Q433_11150 [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL002241 | 100 | 2.20E-38 | WP_029727213.1 | TM2 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL002242 | 100 | 3.70E-48 | RAP10890.1 | hypothetical protein HS3_01309 [Bacillus subtilis] |
| BSLIN78GL002243 | 100 | 1.60E-68 | AOA54776.1 | uncharacterized protein BSHJ0_02205 [Bacillus subtilis] |
| BSLIN78GL002245 | 100 | 3.80E-17 | WP_284929345.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002246 | 100 | 1.30E-31 | WP_211197294.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002247 | 100 | 1.40E-38 | WP_029727209.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002248 | 100 | 3.10E-176 | WP_029727208.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002249 | 100 | 1.30E-13 | RAP10884.1 | hypothetical protein HS3_01303 [Bacillus subtilis] |
| BSLIN78GL002250 | 100 | 1.30E-37 | WP_144500565.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002251 | 100 | 3.90E-99 | WP_029727204.1 | hypothetical protein [Bacillus subtilis] |

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| BSLIN78GL002252 | 100 | 1.40E-50 | WP_029727203.1 | DUF3775 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL002253 | 100 | 3.50E-152 | WP_032679227.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002254 | 100 | 4.10E-181 | WP_154230817.1 | nucleotidyltransferase [Bacillus subtilis] |
| BSLIN78GL002255 | 100 | 2.50E-95 | WP_029727200.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002256 | 100 | 7.60E-18 | WP_153912182.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002257 | 98.4 | 4.00E-30 | WP_032679225.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002258 | 100 | 1.60E-32 | AOA54794.1 | SPBc2 prophage-derived uncharacterized protein YorC [Bacillus subtilis] |
| BSLIN78GL002259 | 100 | 1.00E-15 | WP_257182224.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002260 | 95.5 | 1.50E-15 | QHF58157.1 | hypothetical protein Bateq7PJ16_2351 [Bacillus subtilis] |
| BSLIN78GL002261 | 100 | 9.20E-212 | WP_029727197.1 | response regulator aspartate phosphatase RapK [Bacillus subtilis] |
| BSLIN78GL002262 | 100 | 1.10E-12 | WP_004399440.1 | MULTISPECIES: phosphatase RapK inhibitor PhrK [Bacillales] |
| BSLIN78GL002263 | 100 | 6.80E-162 | AIC98487.1 | DNA repair protein [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL002264 | 100 | 1.20E-39 | RAP10872.1 | hypothetical protein HS3_01291 [Bacillus subtilis] |
| BSLIN78GL002265 | 100 | 6.20E-55 | WP_029727195.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002266 | 100 | 3.70E-137 | RAP10868.1 | hypothetical protein HS3_01287 [Bacillus subtilis] |
| BSLIN78GL002267 | 100 | 1.40E-273 | AIC98491.1 | amine oxidase [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL002268 | 100 | 4.40E-17 | RAP10866.1 | hypothetical protein HS3_01285 [Bacillus subtilis] |
| BSLIN78GL002269 | 96.8 | 1.60E-59 | EHA30755.1 | molecular chaperone [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002270 | 100 | 4.10E-136 | AIC98493.1 | AraC family transcriptional regulator [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL002271 | 100 | 5.10E-142 | WP_029726833.1 | MULTISPECIES: GNAT family N-acetyltransferase [Bacillus |
| BSLIN78GL002272 | 99.5 | 6.50E-100 | KIU11194.1 | metal-dependent hydrolase [Bacillus subtilis] |
| BSLIN78GL002273 | 100 | 2.20E-131 | WP_017697554.1 | MULTISPECIES: MBL fold metallo-hydrolase [Bacillus |
| BSLIN78GL002274 | 100 | 2.10E-88 | WP_029726832.1 | GyrI-like domain-containing protein [Bacillus subtilis] |
| BSLIN78GL002275 | 100 | 8.70E-179 | WP_029726831.1 | YafY family protein [Bacillus subtilis] |
| BSLIN78GL002276 | 100 | 1.70E-91 | WP_029726830.1 | MULTISPECIES: mother cell-specific sporulation protein Csk22 [Bacillus |
| BSLIN78GL002277 | 100 | 9.60E-53 | WP_003231284.1 | MULTISPECIES: Zn(II)-responsive metalloregulatory transcriptional repressor CzrA |
| BSLIN78GL002278 | 100 | 2.00E-124 | WP_014480011.1 | MULTISPECIES: lysozyme family protein [Bacillus |
| BSLIN78GL002279 | 100 | 5.20E-96 | WP_003231280.1 | MULTISPECIES: DUF420 domain-containing protein [Bacillales] |
| BSLIN78GL002280 | 99.3 | 1.40E-156 | EHA30743.1 | hypothetical protein BSSC8_23280 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002281 | 99.5 | 9.90E-109 | BAI85580.2 | hypothetical protein BSNT_08476 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL002282 | 100 | 2.40E-187 | WP_029726829.1 | MULTISPECIES: LD-carboxypeptidase [Bacillus |
| BSLIN78GL002283 | 100 | 3.20E-206 | WP_029726828.1 | MULTISPECIES: fatty acid desaturase DesE [Bacillus |
| BSLIN78GL002284 | 100 | 2.60E-206 | WP_015251908.1 | MULTISPECIES: two-component sensor histidine kinase DesK [Bacillus |
| BSLIN78GL002285 | 100 | 2.00E-107 | AGE63750.1 | two-component response regulator [Bacillus subtilis XF-1] |
| BSLIN78GL002286 | 100 | 9.50E-25 | RAP10848.1 | hypothetical protein HS3_01267 [Bacillus subtilis] |
| BSLIN78GL002287 | 100 | 2.50E-156 | WP_003231267.1 | MULTISPECIES: 3D domain-containing protein [Bacillales] |
| BSLIN78GL002288 | 100 | 0.00E+00 | WP_029726826.1 | MULTISPECIES: DNA helicase RecQ [Bacillus] |
| BSLIN78GL002289 | 100 | 1.30E-24 | AEP91116.1 | hypothetical protein I33_2158 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL002290 | 100 | 5.00E-114 | WP_003231260.1 | MULTISPECIES: FMN-dependent NADH-azoreductase AzoJ [Bacillales |
| BSLIN78GL002291 | 100 | 2.10E-97 | AAB84477.1 | dnaK suppressor homolog [Bacillus subtilis] |
| BSLIN78GL002292 | 100 | 3.30E-56 | WP_003231257.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002293 | 100 | 1.80E-34 | WP_015383862.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002294 | 100 | 2.70E-88 | WP_003231255.1 | MULTISPECIES: salt stress-responsive protein YocM [Bacillales |
| BSLIN78GL002295 | 100 | 1.40E-34 | WP_004399338.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002296 | 100 | 7.60E-36 | WP_029726825.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002297 | 100 | 1.70E-64 | AFQ57869.1 | YozO [Bacillus subtilis QB928] |
| BSLIN78GL002298 | 100 | 5.80E-32 | WP_101172399.1 | DUF6501 family protein [Bacillus subtilis] |
| BSLIN78GL002299 | 100 | 5.70E-286 | AGA23419.1 | Aldehyde dehydrogenase [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL002300 | 100 | 0.00E+00 | WP_029726823.1 | sporulenol synthase [Bacillus subtilis] |
| BSLIN78GL002301 | 100 | 4.00E-167 | WP_015714097.1 | MULTISPECIES: superoxide dismutase [Bacillus] |
| BSLIN78GL002302 | 100 | 1.80E-246 | WP_326253599.1 | sodium-dependent transporter [Bacillus subtilis] |
| BSLIN78GL002303 | 100 | 1.60E-175 | WP_029726822.1 | MULTISPECIES: bile acid:sodium symporter family protein [Bacillus |
| BSLIN78GL002304 | 100 | 4.20E-229 | WP_014480026.1 | MULTISPECIES: 2-oxoglutarate dehydrogenase complex dihydrolipoyllysine-residue |
| BSLIN78GL002305 | 100 | 0.00E+00 | WP_069703916.1 | 2-oxoglutarate dehydrogenase E1 component [Bacillus subtilis] |
| BSLIN78GL002306 | 100 | 0.00E+00 | WP_069703915.1 | nitric oxide reductase activation protein NorD [Bacillus subtilis] |
| BSLIN78GL002307 | 99.7 | 5.50E-156 | WP_213385664.1 | MoxR family ATPase [Bacillus subtilis] |
| BSLIN78GL002308 | 100 | 2.40E-110 | WP_015251895.1 | MULTISPECIES: superoxide dismutase family protein [Bacillus |
| BSLIN78GL002309 | 100 | 3.60E-233 | WP_004399265.1 | MULTISPECIES: D-gamma-glutamyl-meso-diaminopimelic acid endopeptidase |
| BSLIN78GL002310 | 100 | 1.80E-232 | WP_004399256.1 | MULTISPECIES: macrolide family glycosyltransferase [Bacillales |
| BSLIN78GL002311 | 100 | 1.10E-116 | QHF57968.1 | cyclase [Bacillus subtilis] |
| BSLIN78GL002312 | 100 | 2.00E-253 | WP_069703913.1 | MATE family efflux transporter [Bacillus subtilis] |
| BSLIN78GL002313 | 100 | 2.50E-153 | WP_014480032.1 | MULTISPECIES: RsbT co-antagonist RsbRC [Bacillus] |
| BSLIN78GL002314 | 100 | 2.30E-125 | WP_003231215.1 | MULTISPECIES: bacillithiol biosynthesis deacetylase BshB2 [Bacillales |
| BSLIN78GL002315 | 100 | 1.10E-59 | WP_003231213.1 | MULTISPECIES: YojF family protein [Bacillales |
| BSLIN78GL002316 | 100 | 1.80E-44 | WP_029726817.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002317 | 100 | 1.60E-166 | WP_029726816.1 | MULTISPECIES: EamA family transporter RarD [Bacillus] |
| BSLIN78GL002318 | 100 | 6.00E-88 | WP_046663369.1 | MULTISPECIES: spore germination protein GerT [Bacillus] |
| BSLIN78GL002319 | 100 | 1.60E-27 | EHA30705.1 | hypothetical protein BSSC8_22900 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002320 | 100 | 2.20E-244 | WP_029726814.1 | MULTISPECIES: gluconate:H+ symporter [Bacillus |
| BSLIN78GL002321 | 100 | 3.10E-66 | WP_021481482.1 | MULTISPECIES: tautomerase family protein [Bacillus |
| BSLIN78GL002322 | 100 | 2.10E-52 | EHA30702.1 | hypothetical protein BSSC8_22870 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002323 | 100 | 4.00E-108 | WP_014477092.1 | MULTISPECIES: nitroreductase family protein [Bacillus |
| BSLIN78GL002324 | 100 | 7.60E-112 | WP_029318030.1 | MULTISPECIES: alpha/beta hydrolase [Bacillus] |
| BSLIN78GL002325 | 100 | 5.60E-175 | WP_029318029.1 | MULTISPECIES: ring-cleaving dioxygenase [Bacillus |
| BSLIN78GL002326 | 100 | 3.10E-30 | WP_003231189.1 | MULTISPECIES: DUF3311 domain-containing protein [Bacillales] |
| BSLIN78GL002327 | 100 | 4.00E-279 | WP_029726813.1 | MULTISPECIES: sodium:solute symporter [Bacillus |
| BSLIN78GL002328 | 100 | 6.70E-260 | WP_015714111.1 | MULTISPECIES: carboxy-terminal processing protease CtpA [Bacillus |
| BSLIN78GL002329 | 100 | 4.30E-127 | WP_015251882.1 | MULTISPECIES: class I SAM-dependent methyltransferase [Bacillus |
| BSLIN78GL002330 | 100 | 4.80E-44 | WP_003231182.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002331 | 100 | 9.30E-153 | WP_014480046.1 | MULTISPECIES: LD-carboxypeptidase LdcB [Bacillus |

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| BSLIN78GL002332 | 100 | 7.50E-127 | WP_003231176.1 | MULTISPECIES: purine-nucleoside phosphorylase [Bacillales |
| BSLIN78GL002333 | 100 | 8.00E-16 | WP_003231174.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002334 | 100 | 9.20E-53 | AIY93285.1 | hypothetical protein QU35_10820 [Bacillus subtilis subsp. subtilis str. 168] |
| BSLIN78GL002335 | 99.5 | 1.70E-114 | QHF57993.1 | phosphate phosphatase delta [Bacillus subtilis] |
| BSLIN78GL002336 | 100 | 6.00E-25 | WP_003231166.1 | MULTISPECIES: YozD family protein [Bacillales |
| BSLIN78GL002337 | 100 | 4.00E-19 | WP_003231164.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002338 | 100 | 1.50E-127 | WP_014477102.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002339 | 100 | 1.00E-37 | AFQ57911.1 | YozE [Bacillus subtilis QB928] |
| BSLIN78GL002340 | 100 | 2.30E-47 | AFQ57912.1 | YokU [Bacillus subtilis QB928] |
| BSLIN78GL002341 | 100 | 9.10E-281 | WP_004399420.1 | MULTISPECIES: lysine 2,3-aminomutase [Bacillales] |
| BSLIN78GL002342 | 100 | 3.90E-148 | AKN14146.1 | Beta-lysine acetyltransferase [Bacillus subtilis |
| BSLIN78GL002343 | 100 | 4.20E-256 | WP_010886532.1 | MULTISPECIES: peptidase [Bacillales] |
| BSLIN78GL002344 | 100 | 2.20E-117 | WP_004399417.1 | MULTISPECIES: 3-oxoacid CoA-transferase subunit B [Bacillales |
| BSLIN78GL002345 | 100 | 2.40E-125 | WP_003230839.1 | MULTISPECIES: CoA transferase subunit A [Bacillales] |
| BSLIN78GL002346 | 100 | 1.20E-250 | WP_003230836.1 | MULTISPECIES: aspartate aminotransferase family protein [Bacillales] |
| BSLIN78GL002347 | 100 | 2.40E-22 | WP_003230835.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002348 | 100 | 1.30E-20 | ADV92886.1 | hypothetical protein BSn5_01260 [Bacillus subtilis BSn5] |
| BSLIN78GL002349 | 100 | 2.10E-146 | WP_326253594.1 | spore maturation N-acetyltransferase CgeE [Bacillus subtilis] |
| BSLIN78GL002350 | 100 | 3.50E-255 | WP_326253593.1 | spore maturation glycosyltransferase CgeD [Bacillus subtilis] |
| BSLIN78GL002351 | 100 | 5.10E-48 | WP_014477111.1 | MULTISPECIES: spore maturation protein CgeC [Bacillus] |
| BSLIN78GL002352 | 100 | 1.90E-66 | WP_017697128.1 | MULTISPECIES: spore crust protein CgeA [Bacillus] |
| BSLIN78GL002353 | 100 | 9.00E-167 | WP_326253591.1 | spore maturation protein CgeB [Bacillus subtilis] |
| BSLIN78GL002354 | 100 | 1.20E-222 | WP_326253589.1 | phytase [Bacillus subtilis] |
| BSLIN78GL002355 | 100 | 1.10E-192 | WP_029726803.1 | MULTISPECIES: nucleoside-diphosphate sugar epimerase/dehydratase [Bacillus |
| BSLIN78GL002356 | 100 | 1.70E-81 | WP_014480061.1 | MULTISPECIES: peptide-methionine (R)-S-oxide reductase MsrB [Bacillus |
| BSLIN78GL002357 | 100 | 1.70E-102 | WP_029726802.1 | MULTISPECIES: peptide-methionine (S)-S-oxide reductase MsrA [Bacillus |
| BSLIN78GL002358 | 100 | 2.70E-68 | QHF58191.1 | HTH-type transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL002359 | 99.1 | 1.70E-255 | AFQ58117.1 | Damage inducible, Na+ driven multidrug effluxpump [Bacillus subtilis QB928] |
| BSLIN78GL002360 | 100 | 6.80E-30 | AFQ58118.1 | YpmT [Bacillus subtilis QB928] |
| BSLIN78GL002361 | 100 | 2.80E-100 | WP_003230807.1 | MULTISPECIES: YpmS family protein [Bacillales] |
| BSLIN78GL002362 | 100 | 1.70E-140 | WP_003245956.1 | MULTISPECIES: SGNH/GDSL hydrolase family protein [Bacillales |
| BSLIN78GL002363 | 100 | 1.20E-109 | AGE63825.1 | hypothetical protein C663_2048 [Bacillus subtilis XF-1] |
| BSLIN78GL002364 | 100 | 8.40E-54 | AFQ58122.1 | YpmP [Bacillus subtilis QB928] |
| BSLIN78GL002365 | 100 | 1.10E-242 | WP_019712861.1 | threonine ammonia-lyase IlvA [Bacillus subtilis] |
| BSLIN78GL002366 | 100 | 5.00E-185 | WP_004399025.1 | MULTISPECIES: sigma-54-dependent transcriptional regulator [Bacillales] |
| BSLIN78GL002367 | 100 | 1.30E-117 | AFQ58125.1 | Putative membrane hydrolase [Bacillus subtilis QB928] |
| BSLIN78GL002368 | 100 | 1.30E-108 | EHA31647.1 | hypothetical protein BSSC8_20900 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002369 | 100 | 5.40E-95 | WP_003230799.1 | MULTISPECIES: dihydrofolate reductase DfrA [Bacillales |
| BSLIN78GL002370 | 99.6 | 5.20E-156 | KIN38703.1 | Thymidylate synthase [Bacillus subtilis |
| BSLIN78GL002371 | 100 | 4.10E-96 | AFQ58129.1 | Putative phosphatidylglycerophosphatase [Bacillus subtilis QB928] |
| BSLIN78GL002372 | 100 | 3.70E-111 | QJD04476.1 | YpjP [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL002373 | 100 | 1.10E-144 | WP_069703905.1 | class I SAM-dependent methyltransferase [Bacillus subtilis] |
| BSLIN78GL002374 | 100 | 4.90E-76 | WP_003230794.1 | MULTISPECIES: bacilliredoxin BrxA [Bacillales] |
| BSLIN78GL002375 | 100 | 0.00E+00 | WP_144530223.1 | dihydroxy-acid dehydratase [Bacillus subtilis |
| BSLIN78GL002376 | 100 | 5.50E-212 | WP_015714132.1 | conserved virulence factor C family protein [Bacillus subtilis] |
| BSLIN78GL002377 | 100 | 1.10E-110 | WP_015714133.1 | Mn(2+)-dependent (deoxy)ribonucleoside pyrophosphohydrolase [Bacillus subtilis |
| BSLIN78GL002378 | 100 | 7.30E-89 | WP_015383916.1 | glutathione peroxidase [Bacillus subtilis] |
| BSLIN78GL002379 | 99.7 | 8.60E-190 | QHF58212.1 | O-succinyltransferase [Bacillus subtilis] |
| BSLIN78GL002380 | 100 | 3.30E-17 | AEP91208.1 | hypothetical protein I33_2250 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL002381 | 100 | 3.80E-213 | AKN14184.1 | diglucosyldiacylglycerol synthase [Bacillus subtilis |
| BSLIN78GL002382 | 100 | 6.30E-31 | WP_003230776.1 | MULTISPECIES: cold-shock protein CspD [Bacteria] |
| BSLIN78GL002383 | 100 | 2.80E-25 | WP_003230774.1 | MULTISPECIES: transcriptional regulator DegR [Bacillales] |
| BSLIN78GL002384 | 100 | 6.50E-45 | WP_031600611.1 | MULTISPECIES: DUF2564 family protein [Bacillus |
| BSLIN78GL002385 | 100 | 1.00E-30 | AFQ58142.1 | YpeQ [Bacillus subtilis QB928] |
| BSLIN78GL002386 | 100 | 7.20E-130 | QHJ94865.1 | hypothetical protein C7M16_01909 [Bacillus subtilis] |
| BSLIN78GL002387 | 100 | 2.40E-125 | WP_014477139.1 | MULTISPECIES: queuosine precursor transporter [Bacillus] |
| BSLIN78GL002388 | 100 | 1.50E-68 | WP_015714135.1 | MULTISPECIES: reverse transcriptase-like protein [Bacillus] |
| BSLIN78GL002389 | 100 | 2.20E-16 | WP_003218255.1 | MULTISPECIES: small, acid-soluble spore protein L [Bacillales] |
| BSLIN78GL002390 | 100 | 1.00E-165 | AFQ58147.1 | 5'3'-exonuclease [Bacillus subtilis QB928] |
| BSLIN78GL002391 | 100 | 8.20E-20 | AFQ58148.1 | YpzF [Bacillus subtilis QB928] |
| BSLIN78GL002392 | 100 | 7.40E-40 | WP_014477141.1 | YpbS family protein [Bacillus subtilis] |
| BSLIN78GL002393 | 100 | 0.00E+00 | WP_128474014.1 | dynamin GTPase [Bacillus subtilis] |
| BSLIN78GL002394 | 100 | 1.20E-89 | WP_004398552.1 | MULTISPECIES: alkylpyrone methyltransferase [Bacillales |
| BSLIN78GL002395 | 100 | 7.90E-208 | WP_003230750.1 | MULTISPECIES: type III polyketide synthase BpsA [Bacillales |
| BSLIN78GL002396 | 100 | 3.60E-239 | WP_003230748.1 | MULTISPECIES: xanthine permease [Bacillales] |
| BSLIN78GL002397 | 100 | 6.50E-100 | WP_015714142.1 | MULTISPECIES: xanthine phosphoribosyltransferase [Bacillus |
| BSLIN78GL002398 | 99.8 | 4.80E-296 | AGA23512.1 | putative metalloprotease YpwA [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL002399 | 100 | 2.20E-180 | WP_015714144.1 | MULTISPECIES: 2-keto-3-deoxygluconate transporter [Bacillus |
| BSLIN78GL002400 | 100 | 1.20E-104 | WP_029726795.1 | MULTISPECIES: bifunctional 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3-deoxy |
| BSLIN78GL002401 | 100 | 1.70E-185 | WP_015251846.1 | MULTISPECIES: 2-dehydro-3-deoxygluconokinase [Bacillus |
| BSLIN78GL002402 | 100 | 1.10E-187 | WP_029726794.1 | MULTISPECIES: pectin utilization transcriptional regulator KdgR [Bacillus] |
| BSLIN78GL002403 | 100 | 4.30E-158 | WP_029726793.1 | MULTISPECIES: 5-dehydro-4-deoxy-D-glucuronate isomerase [Bacillus |
| BSLIN78GL002404 | 100 | 3.80E-140 | WP_029726792.1 | MULTISPECIES: 2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase KduD [Bacillus |
| BSLIN78GL002405 | 100 | 0.00E+00 | WP_015251842.1 | MULTISPECIES: ATP-dependent DNA helicase [Bacillus |
| BSLIN78GL002406 | 100 | 5.70E-33 | WP_009967570.1 | hypothetical protein [Lactobacillus paragasseri] |
| BSLIN78GL002407 | 100 | 1.20E-222 | WP_009967571.1 | MULTISPECIES: class I SAM-dependent RNA methyltransferase [Bacillales |
| BSLIN78GL002408 | 100 | 3.50E-49 | AFQ58166.1 | Cell division protein [Bacillus subtilis QB928] |
| BSLIN78GL002409 | 100 | 2.20E-117 | AYK63509.1 | DUF1273 domain-containing protein [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL002410 | 100 | 2.40E-15 | WP_003230707.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002411 | 100 | 8.90E-240 | WP_029726790.1 | metal-dependent exonucleaseMrfB [Bacillus subtilis] |

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| BSLIN78GL002412 | 100 | 0.00E+00 | WP_029726789.1 | ATP-dependent helicase MrfA [Bacillus subtilis] |
| BSLIN78GL002413 | 100 | 2.20E-97 | ARV99124.1 | Protein-N(pi)-phosphohistidine--sugar phosphotransferase [Bacillus subtilis subsp. |
| BSLIN78GL002414 | 98.6 | 2.20E-73 | AGE63873.1 | hypothetical protein C663_2097 [Bacillus subtilis XF-1] |
| BSLIN78GL002415 | 100 | 1.10E-62 | WP_015251832.1 | MULTISPECIES: YppG family protein [Bacillus |
| BSLIN78GL002416 | 100 | 1.10E-27 | WP_003230690.1 | MULTISPECIES: YppF family protein [Bacillales |
| BSLIN78GL002417 | 100 | 1.30E-58 | WP_029726786.1 | MULTISPECIES: YppE family protein [Bacillus] |
| BSLIN78GL002418 | 100 | 3.90E-31 | EHA31597.1 | hypothetical protein BSSC8_20400 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002419 | 100 | 1.00E-16 | AEP87076.1 | small, acid-soluble spore protein M [Bacillus spizizenii TU-B-10] |
| BSLIN78GL002420 | 100 | 9.40E-189 | WP_029726785.1 | MULTISPECIES: DUF2515 domain-containing protein [Bacillus] |
| BSLIN78GL002421 | 100 | 3.00E-96 | WP_042976356.1 | Holliday junction resolvase RecU [Bacillus subtilis] |
| BSLIN78GL002422 | 99.8 | 0.00E+00 | WP_129092493.1 | PBP1A family penicillin-binding protein [Bacillus subtilis] |
| BSLIN78GL002423 | 100 | 2.50E-92 | WP_009967579.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002424 | 100 | 2.50E-101 | EHA31591.1 | endonuclease III [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002425 | 100 | 5.90E-132 | AFQ58183.1 | DNA-remodelling primosomal protein [Bacillus subtilis QB928] |
| BSLIN78GL002426 | 100 | 3.10E-251 | AFQ58184.1 | Asparaginyl-tRNA synthetase [Bacillus subtilis QB928] |
| BSLIN78GL002427 | 100 | 1.20E-222 | WP_003230667.1 | MULTISPECIES: aspartate transaminase AspB [Bacillus] |
| BSLIN78GL002428 | 100 | 6.00E-83 | WP_014477164.1 | MULTISPECIES: cell wall elongation/penicillin-binding protein regulator TseB |
| BSLIN78GL002429 | 98.9 | 6.90E-44 | QHM15173.1 | hypothetical protein C7M29_02876 [Bacillus subtilis] |
| BSLIN78GL002430 | 100 | 0.00E+00 | WP_326253576.1 | ATP-dependent DNA helicase DinG [Bacillus subtilis] |
| BSLIN78GL002431 | 100 | 9.90E-62 | AFQ58189.1 | Aspartate 1-decarboxylase [Bacillus subtilis QB928] |
| BSLIN78GL002432 | 100 | 5.00E-157 | WP_029726778.1 | pantoate--beta-alanine ligase [Bacillus subtilis] |
| BSLIN78GL002433 | 100 | 6.10E-152 | WP_015714158.1 | MULTISPECIES: 3-methyl-2-oxobutanoate hydroxymethyltransferase [Bacillus |
| BSLIN78GL002434 | 99.7 | 2.50E-184 | QHF58303.1 | ligase/repressor [Bacillus subtilis] |
| BSLIN78GL002435 | 100 | 2.10E-222 | WP_014480110.1 | MULTISPECIES: CCA tRNA nucleotidyltransferase [Bacillus |
| BSLIN78GL002436 | 100 | 1.40E-210 | WP_042976368.1 | N-acetyl-alpha-D-glucosaminyl L-malate synthase BshA [Bacillus subtilis |
| BSLIN78GL002437 | 100 | 2.10E-129 | WP_015383958.1 | MULTISPECIES: bacillithiol biosynthesis deacetylase BshB1 [Bacillus |
| BSLIN78GL002438 | 100 | 1.30E-70 | WP_014477171.1 | MULTISPECIES: methylglyoxal synthase [Bacillus |
| BSLIN78GL002439 | 100 | 1.50E-147 | WP_003230638.1 | MULTISPECIES: 4-hydroxy-tetrahydrodipicolinate reductase [Bacillus |
| BSLIN78GL002440 | 100 | 3.90E-57 | WP_004398044.1 | MULTISPECIES: nucleotide pyrophosphohydrolase [Bacillus |
| BSLIN78GL002441 | 100 | 1.40E-159 | WP_003230635.1 | MULTISPECIES: YitT family protein [Bacillales |
| BSLIN78GL002442 | 100 | 4.00E-145 | WP_015251822.1 | MULTISPECIES: sporulation protein YpjB [Bacillus] |
| BSLIN78GL002443 | 100 | 3.20E-110 | WP_326253572.1 | DUF1405 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL002444 | 100 | 1.60E-146 | WP_004398051.1 | MULTISPECIES: menaquinol-cytochrome c reductase cytochrome b/c subunit |
| BSLIN78GL002445 | 100 | 3.80E-128 | WP_003225560.1 | MULTISPECIES: menaquinol-cytochrome c reductase cytochrome b subunit |
| BSLIN78GL002446 | 100 | 6.40E-96 | WP_003230627.1 | MULTISPECIES: ubiquinol-cytochrome c reductase iron-sulfur subunit [Bacillales |
| BSLIN78GL002447 | 100 | 2.00E-77 | WP_041337728.1 | MULTISPECIES: YpiF family protein [Bacillus |
| BSLIN78GL002448 | 100 | 2.30E-99 | WP_003225551.1 | MULTISPECIES: ReoY family proteolytic degradation factor [Bacillus |
| BSLIN78GL002449 | 100 | 1.30E-238 | WP_076458057.1 | tetratricopeptide repeat protein [Bacillus subtilis] |
| BSLIN78GL002450 | 100 | 1.00E-241 | QJD04552.1 | 5-Enolpyruvylshikimate-3-phosphate synthase / 3-phosphoshikimate 1- |
| BSLIN78GL002451 | 100 | 7.30E-209 | WP_003230615.1 | MULTISPECIES: prephenate dehydrogenase [Bacillales |
| BSLIN78GL002452 | 100 | 4.80E-205 | BAI85760.2 | histidinol-phosphate aminotransferase [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL002453 | 100 | 3.50E-144 | WP_003230608.1 | MULTISPECIES: tryptophan synthase subunit alpha [Bacillales |
| BSLIN78GL002454 | 100 | 8.10E-230 | WP_029317985.1 | MULTISPECIES: tryptophan synthase subunit beta [Bacillus |
| BSLIN78GL002455 | 100 | 2.00E-118 | WP_326253570.1 | phosphoribosylanthranilate isomerase [Bacillus subtilis] |
| BSLIN78GL002456 | 100 | 4.90E-132 | WP_014480123.1 | MULTISPECIES: indole-3-glycerol phosphate synthase TrpC [Bacillus |
| BSLIN78GL002457 | 99.7 | 1.70E-180 | WP_029726770.1 | anthranilate phosphoribosyltransferase [Bacillus subtilis] |
| BSLIN78GL002458 | 99.8 | 3.50E-283 | WP_029726769.1 | anthranilate synthase component I [Bacillus subtilis] |
| BSLIN78GL002459 | 100 | 2.30E-19 | EHA31557.1 | hypothetical protein BSSC8_19990 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002460 | 100 | 4.10E-69 | EHA31555.1 | chorismate mutase (isozymes 1 and 2) [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002461 | 100 | 3.70E-205 | WP_029726768.1 | 3-dehydroquinate synthase [Bacillus subtilis] |
| BSLIN78GL002462 | 99.7 | 9.50E-223 | EHA31553.1 | chorismate synthase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002463 | 99.3 | 9.40E-170 | CAF1836395.1 | Chemotaxis protein methyltransferase [Bacillus subtilis] |
| BSLIN78GL002464 | 100 | 1.80E-14 | ADV93002.1 | hypothetical protein BSn5_01840 [Bacillus subtilis BSn5] |
| BSLIN78GL002465 | 100 | 7.80E-58 | WP_003225522.1 | MULTISPECIES: nucleoside-diphosphate kinase [Bacillus |
| BSLIN78GL002466 | 100 | 3.10E-179 | EHA31549.1 | heptaprenyl diphosphate synthase component II [Bacillus subtilis subsp. subtilis str. |
| BSLIN78GL002467 | 100 | 8.30E-134 | WP_029726765.1 | MULTISPECIES: demethylmenaquinone methyltransferase [Bacillus |
| BSLIN78GL002468 | 100 | 4.90E-140 | AGA23583.1 | Spore germination protein C1 [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL002469 | 100 | 3.10E-34 | WP_003230576.1 | MULTISPECIES: trp RNA-binding attenuation protein MtrB [Bacillales] |
| BSLIN78GL002470 | 100 | 2.30E-102 | WP_003225516.1 | MULTISPECIES: GTP cyclohydrolase I FolE [Bacillales |
| BSLIN78GL002471 | 100 | 9.60E-53 | AGE63927.1 | non-specific DNA-binding protein HBsu; signal recognition particle-like (SRP) |
| BSLIN78GL002472 | 100 | 2.00E-278 | WP_003230572.1 | MULTISPECIES: stage IV sporulation protein A [Bacillales] |
| BSLIN78GL002473 | 100 | 2.90E-137 | WP_015714176.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002474 | 100 | 2.50E-19 | QHF58343.1 | hypothetical protein Bateq7PJ16_2537 [Bacillus subtilis] |
| BSLIN78GL002475 | 100 | 6.80E-193 | WP_029726764.1 | MULTISPECIES: NAD(P)H-dependent glycerol-3-phosphate dehydrogenase |
| BSLIN78GL002476 | 100 | 1.60E-247 | WP_003230565.1 | MULTISPECIES: ribosome-associated GTPase EngA [Bacillales |
| BSLIN78GL002477 | 100 | 6.40E-28 | WP_038427784.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002478 | 100 | 3.70E-163 | WP_003230562.1 | MULTISPECIES: YIEGIA family protein [Bacillales |
| BSLIN78GL002479 | 100 | 5.40E-110 | WP_014480136.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002480 | 100 | 4.60E-17 | C0H446.1 | RecName: Full=Uncharacterized protein YpzI [Bacillus subtilis subsp. subtilis str. |
| BSLIN78GL002481 | 99.7 | 1.50E-181 | WP_038428154.1 | type 2 isopentenyl-diphosphate Delta-isomerase [Bacillus subtilis |
| BSLIN78GL002482 | 100 | 2.30E-210 | WP_014477197.1 | MULTISPECIES: 30S ribosomal protein S1 [Bacillus] |
| BSLIN78GL002483 | 100 | 3.40E-116 | WP_024572170.1 | MULTISPECIES: (d)CMP kinase [Bacillus] |
| BSLIN78GL002484 | 100 | 6.00E-25 | WP_003230553.1 | MULTISPECIES: YpfB family protein [Bacillales |
| BSLIN78GL002485 | 100 | 3.60E-115 | WP_038427785.1 | MULTISPECIES: cyclic di-GMP receptor DgrA [Bacillus |
| BSLIN78GL002486 | 100 | 1.10E-256 | WP_029726759.1 | MULTISPECIES: germination protein YpeB [Bacillus] |
| BSLIN78GL002487 | 100 | 8.70E-176 | WP_014480142.1 | MULTISPECIES: spore cortex-lytic enzyme [Bacillus |
| BSLIN78GL002488 | 100 | 1.50E-121 | WP_003230542.1 | MULTISPECIES: glutamic-type intramembrane protease PrsW [Bacillales] |
| BSLIN78GL002489 | 100 | 2.60E-186 | WP_029317974.1 | MULTISPECIES: YpdA family putative bacillithiol disulfide reductase [Bacillus |
| BSLIN78GL002490 | 100 | 2.10E-244 | WP_003230536.1 | MULTISPECIES: NAD-specific glutamate dehydrogenase [Bacillales |
| BSLIN78GL002491 | 100 | 7.90E-106 | WP_003230533.1 | MULTISPECIES: genetic competence negative regulator [Bacillales |

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| BSLIN78GL002492 | 99.6 | 1.50E-144 | WP_029726758.1 | MULTISPECIES: metallophosphoesterase [Bacillus] |
| BSLIN78GL002493 | 100 | 5.50E-83 | WP_014480147.1 | MULTISPECIES: YpbF family protein [Bacillus |
| BSLIN78GL002494 | 100 | 1.50E-130 | AIC98697.1 | hypothetical protein Q433_12545 [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL002495 | 100 | 2.50E-110 | AKE24045.1 | hypothetical protein BsLM_2247 [Bacillus sp. LM 4-2] |
| BSLIN78GL002496 | 100 | 3.40E-286 | WP_015251799.1 | MULTISPECIES: ATP-dependent DNA helicase RecQ [Bacillus |
| BSLIN78GL002497 | 100 | 2.70E-197 | WP_029726756.1 | helix-turn-helix domain-containing protein [Bacillus subtilis] |
| BSLIN78GL002498 | 100 | 2.90E-41 | WP_003225461.1 | MULTISPECIES: ferredoxin [Bacillales] |
| BSLIN78GL002499 | 100 | 2.70E-98 | WP_029726755.1 | riboflavin transporter FmnP [Bacillus subtilis] |
| BSLIN78GL002500 | 100 | 2.80E-24 | AFQ58256.1 | YpzE [Bacillus subtilis QB928] |
| BSLIN78GL002501 | 100 | 8.10E-291 | EHA31513.1 | D-3-phosphoglycerate dehydrogenase [Bacillus subtilis subsp. subtilis str. SC-8 |
| BSLIN78GL002502 | 100 | 3.00E-137 | WP_015251797.1 | type I 3-dehydroquinate dehydratase [Bacillus subtilis |
| BSLIN78GL002503 | 99.7 | 3.60E-197 | AIX07923.1 | Sigma-X negative effector [Bacillus subtilis] |
| BSLIN78GL002504 | 100 | 1.40E-105 | WP_003230521.1 | MULTISPECIES: RNA polymerase sigma factor SigX [Bacteria] |
| BSLIN78GL002505 | 100 | 0.00E+00 | WP_029726754.1 | sensor histidine kinase ResE [Bacillus subtilis] |
| BSLIN78GL002506 | 100 | 9.20E-139 | AGE63962.1 | two-component response regulator [Bacillus subtilis XF-1] |
| BSLIN78GL002507 | 100 | 3.80E-224 | WP_015714189.1 | MULTISPECIES: cytochrome c biogenesis protein ResC [Bacillus |
| BSLIN78GL002508 | 100 | 0.00E+00 | WP_015251793.1 | MULTISPECIES: cytochrome c biogenesis protein ResB [Bacillus |
| BSLIN78GL002509 | 100 | 6.60E-99 | WP_014480156.1 | MULTISPECIES: thiol-disulfide oxidoreductase ResA [Bacillus |
| BSLIN78GL002510 | 100 | 7.90E-135 | AGE63966.1 | ribosomal large subunit pseudouridine synthase B [Bacillus subtilis XF-1] |
| BSLIN78GL002511 | 100 | 1.90E-90 | WP_003230509.1 | MULTISPECIES: spore maturation protein SpmB [Bacillales] |
| BSLIN78GL002512 | 100 | 3.10E-99 | AGE63968.1 | spore maturation protein [Bacillus subtilis XF-1] |
| BSLIN78GL002513 | 100 | 5.70E-217 | WP_015251792.1 | D-alanyl-D-alanine carboxypeptidase DacB [Bacillus subtilis] |
| BSLIN78GL002514 | 100 | 1.90E-98 | WP_014477219.1 | MULTISPECIES: YpuI family protein [Bacillus |
| BSLIN78GL002515 | 100 | 8.90E-105 | WP_003223904.1 | MULTISPECIES: SMC-Scp complex subunit ScpB [Bacillales |
| BSLIN78GL002516 | 99.6 | 1.10E-139 | QHF58386.1 | segregation and condensation protein A [Bacillus subtilis] |
| BSLIN78GL002517 | 100 | 1.80E-96 | WP_015251790.1 | DUF309 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL002518 | 100 | 5.70E-65 | WP_003223910.1 | MULTISPECIES: GNAT family N-acetyltransferase RibT [Bacillales |
| BSLIN78GL002519 | 100 | 1.20E-80 | WP_208555803.1 | 6,7-dimethyl-8-ribityllumazine synthase [Bacillus subtilis |
| BSLIN78GL002520 | 100 | 1.80E-229 | WP_003230496.1 | MULTISPECIES: bifunctional 3,4-dihydroxy-2-butanone-4-phosphate synthase/GTP |
| BSLIN78GL002521 | 100 | 5.90E-118 | API42502.1 | riboflavin synthase subunit alpha [Bacillus subtilis] |
| BSLIN78GL002522 | 99.7 | 5.30E-204 | WP_004398763.1 | MULTISPECIES: bifunctional diaminohydroxyphosphoribosylaminopyrimidine deaminase/5-amino-6-(5-phosphoribosylamino)uracil reductase RibD [Bacillales] |
| BSLIN78GL002523 | 100 | 3.40E-56 | WP_003230488.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002524 | 98.4 | 6.80E-102 | EHA31490.1 | type I signal peptidase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002525 | 100 | 4.10E-33 | WP_003230483.1 | MULTISPECIES: zinc ribbon domain-containing protein [Bacillus] |
| BSLIN78GL002526 | 97.8 | 1.90E-18 | WP_231940261.1 | MULTISPECIES: phosphatase PAP2 family protein [Bacillus] |
| BSLIN78GL002527 | 100 | 8.70E-93 | QHM84830.1 | hypothetical protein DXY22_02903 [Bacillus subtilis] |
| BSLIN78GL002528 | 100 | 4.70E-32 | WP_003230479.1 | MULTISPECIES: spore germination protein [Bacillales] |
| BSLIN78GL002529 | 100 | 2.50E-86 | AFI28883.1 | PpiB [Bacillus sp. JS] |
| BSLIN78GL002530 | 100 | 4.70E-169 | AKE24084.1 | hypothetical protein BsLM_2286 [Bacillus sp. LM 4-2] |
| BSLIN78GL002531 | 99.8 | 6.10E-255 | CAF1767642.1 | Diaminopimelate decarboxylase [Bacillus subtilis] |
| BSLIN78GL002532 | 100 | 2.30E-279 | WP_003230471.1 | MULTISPECIES: spore germination protein SpoVAF [Bacillales |
| BSLIN78GL002533 | 100 | 1.50E-110 | WP_003230469.1 | MULTISPECIES: stage V sporulation protein SpoVABEA [Bacillales] |
| BSLIN78GL002534 | 100 | 3.30E-59 | WP_003230467.1 | MULTISPECIES: stage V sporulation protein AE [Bacillales] |
| BSLIN78GL002535 | 100 | 1.50E-192 | WP_003230465.1 | MULTISPECIES: stage V sporulation protein AD [Bacillales] |
| BSLIN78GL002536 | 100 | 2.90E-79 | WP_003223947.1 | MULTISPECIES: stage V sporulation protein AC [Bacillales] |
| BSLIN78GL002537 | 100 | 5.40E-72 | WP_003230463.1 | MULTISPECIES: stage V sporulation protein SpoVAB [Bacillales] |
| BSLIN78GL002538 | 100 | 9.30E-113 | AHA78220.1 | Stage V sporulation protein AA [Bacillus subtilis PY79] |
| BSLIN78GL002539 | 100 | 1.60E-138 | WP_003230458.1 | MULTISPECIES: RNA polymerase sporulation sigma factor SigF [Bacillales |
| BSLIN78GL002540 | 100 | 8.40E-76 | WP_003230452.1 | MULTISPECIES: anti-sigma F factor [Bacillales] |
| BSLIN78GL002541 | 100 | 2.90E-58 | AAA22789.1 | sporulation protein ORF1 (put.); putative [Bacillus subtilis] |
| BSLIN78GL002542 | 100 | 8.80E-246 | EHA31472.1 | penicilin binding protein (putative D-alanyl-D-alanine carboxypeptidase) [Bacillus |
| BSLIN78GL002543 | 100 | 2.40E-148 | WP_080529504.1 | purine nucleoside phosphorylase I, inosine and guanosine-specific [Bacillus subtilis |
| BSLIN78GL002544 | 100 | 3.00E-229 | WP_032722059.1 | phosphopentomutase [Bacillus subtilis] |
| BSLIN78GL002545 | 100 | 1.20E-158 | WP_032722060.1 | site-specific tyrosine recombinase XerD [Bacillus subtilis] |
| BSLIN78GL002546 | 100 | 1.80E-37 | WP_003230440.1 | MULTISPECIES: YqzK family protein [Bacillales |
| BSLIN78GL002547 | 99.4 | 5.70E-86 | AGE64001.1 | FUR family transcriptional regulator [Bacillus subtilis XF-1] |
| BSLIN78GL002548 | 100 | 3.00E-114 | WP_004398593.1 | MULTISPECIES: stage II sporulation protein M [Bacillales] |
| BSLIN78GL002549 | 100 | 1.50E-33 | WP_003246030.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002550 | 100 | 4.80E-244 | WP_004398731.1 | MULTISPECIES: NAD-dependent malic enzyme [Bacillales |
| BSLIN78GL002551 | 100 | 6.10E-261 | WP_003230432.1 | MULTISPECIES: malate-H+/Na+-lactate antiporter MleN [Bacillales] |
| BSLIN78GL002552 | 99.6 | 8.90E-268 | WP_187953649.1 | aspartate ammonia-lyase [Bacillus subtilis] |
| BSLIN78GL002553 | 100 | 5.00E-185 | WP_004399032.1 | MULTISPECIES: asparaginase [Bacillales] |
| BSLIN78GL002554 | 100 | 4.40E-62 | AGE64008.1 | transcriptional regulator of ansAB (Xre family) [Bacillus subtilis XF-1] |
| BSLIN78GL002555 | 100 | 1.70E-221 | WP_003246128.1 | MULTISPECIES: TIGR00375 family protein [Bacillales |
| BSLIN78GL002556 | 100 | 2.60E-104 | EHA31458.1 | ADP-ribose pyrophosphatase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002557 | 100 | 2.30E-26 | BAO93450.1 | hypothetical protein BSNT_08784 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL002558 | 99.7 | 4.70E-169 | WP_015714213.1 | MULTISPECIES: aldo/keto reductase [Bacillus] |
| BSLIN78GL002559 | 100 | 2.00E-43 | AIC40815.1 | hypothetical protein BSUA_02536 [Bacillus subtilis subsp. subtilis str. JH642 substr. |
| BSLIN78GL002560 | 100 | 1.00E-176 | WP_004398519.1 | MULTISPECIES: alpha/beta hydrolase [Bacillales |
| BSLIN78GL002561 | 100 | 3.40E-39 | WP_003230411.1 | MULTISPECIES: YqkC family protein [Bacillales |
| BSLIN78GL002562 | 100 | 1.00E-51 | KIN52180.1 | hypothetical protein B4146_2518 [Bacillus subtilis] |
| BSLIN78GL002563 | 100 | 1.60E-197 | WP_004398771.1 | MULTISPECIES: bifunctional GNAT family N-acetyltransferase/GrpB family protein |
| BSLIN78GL002564 | 100 | 1.70E-60 | WP_003245961.1 | MULTISPECIES: antibiotic biosynthesis monooxygenase [Bacillales |
| BSLIN78GL002565 | 100 | 5.60E-86 | WP_004398668.1 | MULTISPECIES: GNAT family N-acetyltransferase [Bacillales |
| BSLIN78GL002566 | 100 | 3.20E-59 | WP_004398477.1 | MULTISPECIES: YolD-like family protein [Bacillales |
| BSLIN78GL002567 | 99.8 | 3.20E-245 | QHF58440.1 | polymerase IV 2 [Bacillus subtilis] |
| BSLIN78GL002568 | 97.8 | 5.30E-44 | QHF58441.1 | hypothetical protein Bateq7PJ16_2635 [Bacillus subtilis] |
| BSLIN78GL002569 | 100 | 1.80E-47 | WP_015251765.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002570 | 99.5 | 1.70E-230 | WP_257437722.1 | MFS transporter [Bacillus subtilis] |

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| BSLIN78GL002571 | 100 | 4.10E-27 | AGE64024.1 | hypothetical protein C663_2254 [Bacillus subtilis XF-1] |
| BSLIN78GL002572 | 100 | 4.90E-72 | WP_004398989.1 | MULTISPECIES: VOC family protein [Bacillales] |
| BSLIN78GL002573 | 99.7 | 3.00E-179 | WP_003245966.1 | MULTISPECIES: type I pantothenate kinase [Bacillales] |
| BSLIN78GL002574 | 100 | 1.40E-262 | WP_015251762.1 | MULTISPECIES: D-serine ammonia-lyase [Bacillus] |
| BSLIN78GL002575 | 99.6 | 5.80E-144 | AGE64028.1 | putative metabolite dehydrogenase, NAD-binding protein [Bacillus subtilis XF-1] |
| BSLIN78GL002576 | 100 | 6.10E-180 | WP_195727821.1 | MBL fold metallo-hydrolase [Bacillus subtilis] |
| BSLIN78GL002577 | 100 | 5.70E-150 | WP_123373113.1 | pyrroline-5-carboxylate reductase [Bacillus subtilis] |
| BSLIN78GL002578 | 100 | 0.00E+00 | WP_015251758.1 | MULTISPECIES: M20/M25/M40 family metallo-hydrolase [Bacillus] |
| BSLIN78GL002579 | 100 | 4.30E-192 | WP_015251757.1 | MULTISPECIES: NADPH dehydrogenase NamA [Bacillus] |
| BSLIN78GL002580 | 100 | 1.30E-145 | WP_003230373.1 | MULTISPECIES: alpha/beta hydrolase [Bacillales] |
| BSLIN78GL002581 | 100 | 4.20E-22 | AGE64034.1 | 50S ribosomal protein [Bacillus subtilis XF-1] |
| BSLIN78GL002582 | 100 | 3.50E-172 | WP_004398681.1 | MULTISPECIES: ribonuclease Z [Bacillales] |
| BSLIN78GL002583 | 100 | 3.20E-289 | WP_003246151.1 | MULTISPECIES: glucose-6-phosphate dehydrogenase [Bacillales] |
| BSLIN78GL002584 | 99.8 | 2.80E-266 | WP_041849996.1 | MULTISPECIES: NADP-dependent phosphogluconate dehydrogenase [Bacillus] |
| BSLIN78GL002585 | 99.8 | 7.30E-245 | EHA31428.1 | DNA polymerase IV [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002586 | 100 | 5.90E-49 | ADV93128.1 | hypothetical protein BSn5_02470 [Bacillus subtilis BSn5] |
| BSLIN78GL002587 | 100 | 1.30E-149 | WP_151262320.1 | membrane protein insertase YidC [Bacillus subtilis] |
| BSLIN78GL002588 | 98 | 1.60E-52 | WP_208944654.1 | DUF2071 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL002589 | 100 | 1.30E-63 | WP_217024278.1 | MULTISPECIES: DUF2071 domain-containing protein [Bacillus] |
| BSLIN78GL002590 | 100 | 1.70E-205 | WP_003230352.1 | MULTISPECIES: tripeptidase T [Bacillales] |
| BSLIN78GL002591 | 99.8 | 2.20E-288 | WP_122894954.1 | acyl-CoA carboxylase subunit beta [Bacillus subtilis] |
| BSLIN78GL002592 | 100 | 1.50E-74 | EHA31421.1 | hypothetical protein BSSC8_18640 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002593 | 100 | 1.10E-101 | AGE64045.1 | hypothetical protein C663_2275 [Bacillus subtilis XF-1] |
| BSLIN78GL002594 | 99.7 | 1.10E-181 | EHA31419.1 | hypothetical protein BSSC8_18620 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002595 | 100 | 2.00E-130 | WP_004398740.1 | MULTISPECIES: arginine ABC transporter ATP-binding protein ArtR [Bacillales] |
| BSLIN78GL002596 | 100 | 1.10E-114 | WP_003230340.1 | MULTISPECIES: arginine ABC transporter permease ArtQ [Bacillales] |
| BSLIN78GL002597 | 100 | 1.40E-139 | WP_004398706.1 | MULTISPECIES: arginine ABC transporter substrate-binding protein ArtP |
| BSLIN78GL002598 | 100 | 3.70E-76 | WP_003226477.1 | MULTISPECIES: bacilliredoxin BrxB [Bacillales] |
| BSLIN78GL002599 | 99.7 | 4.20E-198 | AGE64051.1 | hypothetical protein C663_2280 [Bacillus subtilis XF-1] |
| BSLIN78GL002600 | 100 | 4.20E-215 | WP_015251751.1 | MULTISPECIES: multidrug efflux MFS transporter Bmr [Bacillus] |
| BSLIN78GL002601 | 100 | 1.00E-154 | WP_015251750.1 | MULTISPECIES: multidrug efflux transcriptional regulator BmrR [Bacillus] |
| BSLIN78GL002602 | 100 | 1.90E-237 | WP_029726741.1 | MULTISPECIES: branched-chain alpha-keto dehydrogenase complex dihydrolipoyllysine-residue (2-methylpropanoyl)transferase [Bacillus |
| BSLIN78GL002603 | 100 | 1.10E-181 | WP_004398638.1 | MULTISPECIES: 3-methyl-2-oxobutanoate dehydrogenase subunit beta [Bacillales] |
| BSLIN78GL002604 | 100 | 4.80E-174 | WP_015251748.1 | MULTISPECIES: 3-methyl-2-oxobutanoate dehydrogenase subunit alpha [Bacillus] |
| BSLIN78GL002605 | 99.8 | 5.20E-268 | WP_029726740.1 | MULTISPECIES: dihydrolipoyl dehydrogenase [Bacillus |
| BSLIN78GL002606 | 100 | 1.50E-203 | WP_029726739.1 | MULTISPECIES: butyrate kinase [Bacillus] |
| BSLIN78GL002607 | 100 | 1.30E-207 | WP_003230309.1 | MULTISPECIES: branched-chain amino acid dehydrogenase [Bacillales] |
| BSLIN78GL002608 | 100 | 2.50E-159 | WP_017696446.1 | MULTISPECIES: phosphate butyryltransferase [Bacillus] |
| BSLIN78GL002609 | 100 | 0.00E+00 | WP_004398669.1 | MULTISPECIES: sigma-54-dependent Fis family transcriptional regulator |
| BSLIN78GL002610 | 100 | 1.30E-35 | WP_003230304.1 | MULTISPECIES: DUF2627 domain-containing protein [Bacillales] |
| BSLIN78GL002611 | 100 | 5.20E-165 | WP_038427795.1 | methylisocitrate lyase [Bacillus subtilis] |
| BSLIN78GL002612 | 99.6 | 1.70E-279 | EXF54045.1 | 2-methylcitrate dehydratase [Bacillus subtilis QH-1] |
| BSLIN78GL002613 | 100 | 2.10E-211 | WP_029726736.1 | MULTISPECIES: citrate synthase [Bacillus] |
| BSLIN78GL002614 | 92.4 | 6.20E-192 | WP_268449547.1 | acyl-CoA dehydrogenase [Bacillus mojavensis] |
| BSLIN78GL002615 | 100 | 1.60E-158 | WP_029726734.1 | MULTISPECIES: 3-hydroxybutyryl-CoA dehydrogenase [Bacillus |
| BSLIN78GL002616 | 100 | 8.80E-221 | WP_003230291.1 | MULTISPECIES: acetyl-CoA C-acetyltransferase [Bacillales |
| BSLIN78GL002617 | 100 | 5.60E-133 | WP_015714234.1 | MULTISPECIES: glycerophosphodiester phosphodiesterase [Bacillus] |
| BSLIN78GL002618 | 100 | 8.10E-106 | RAP10350.1 | N-acetylmuramoyl-L-alanine amidase AmiC precursor [Bacillus subtilis] |
| BSLIN78GL002619 | 100 | 3.80E-48 | WP_014480225.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL002620 | 100 | 6.50E-20 | WP_014480226.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL002621 | 100 | 2.50E-220 | RAP10347.1 | hypothetical protein HS3_00760 [Bacillus subtilis] |
| BSLIN78GL002622 | 100 | 1.40E-23 | EHA31390.1 | hypothetical protein BSSC8_18330 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002623 | 100 | 4.30E-153 | AID00479.1 | CheY [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL002624 | 100 | 4.10E-240 | WP_004398697.1 | MULTISPECIES: SpoIVB peptidase [Bacillales] |
| BSLIN78GL002625 | 100 | 0.00E+00 | WP_029726732.1 | MULTISPECIES: DNA repair protein RecN [Bacillus] |
| BSLIN78GL002626 | 100 | 1.40E-78 | WP_003230265.1 | MULTISPECIES: arginine repressor ArgR [Bacillales] |
| BSLIN78GL002627 | 100 | 1.40E-156 | WP_003230264.1 | MULTISPECIES: TlyA family RNA methyltransferase [Bacillales |
| BSLIN78GL002628 | 100 | 0.00E+00 | WP_003245985.1 | MULTISPECIES: 1-deoxy-D-xylulose-5-phosphate synthase [Bacillales |
| BSLIN78GL002629 | 98 | 4.60E-22 | KZD91679.1 | hypothetical protein B4122_2321 [Bacillus subtilis] |
| BSLIN78GL002630 | 100 | 1.10E-162 | WP_003230262.1 | MULTISPECIES: farnesyl diphosphate synthase [Bacillales] |
| BSLIN78GL002631 | 100 | 1.90E-40 | WP_029726731.1 | MULTISPECIES: exodeoxyribonuclease VII small subunit [Bacillus] |
| BSLIN78GL002632 | 100 | 1.90E-259 | RAP10336.1 | Exodeoxyribonuclease VII large subunit [Bacillus subtilis] |
| BSLIN78GL002633 | 100 | 1.40E-156 | WP_003230259.1 | MULTISPECIES: bifunctional methylenetetrahydrofolate |
| BSLIN78GL002634 | 100 | 4.10E-66 | WP_003230256.1 | MULTISPECIES: transcription antitermination factor NusB [Bacillales] |
| BSLIN78GL002635 | 100 | 2.70E-68 | WP_003230254.1 | MULTISPECIES: fatty acid biosynthesis protein YqhY [Bacillales] |
| BSLIN78GL002636 | 100 | 4.30E-256 | WP_003230253.1 | MULTISPECIES: acetyl-CoA carboxylase biotin carboxylase subunit [Bacillales |
| BSLIN78GL002637 | 100 | 3.80E-82 | WP_003230252.1 | MULTISPECIES: acetyl-CoA carboxylase biotin carboxyl carrier protein [Bacillales |
| BSLIN78GL002638 | 100 | 6.80E-114 | WP_015251732.1 | MULTISPECIES: stage III sporulation ratchet engulfment protein SpoIIIAH |
| BSLIN78GL002639 | 100 | 1.70E-123 | RAP10329.1 | hypothetical protein HS3_00742 [Bacillus subtilis] |
| BSLIN78GL002640 | 100 | 4.00E-108 | WP_015251730.1 | MULTISPECIES: stage III sporulation protein AF [Bacillus] |
| BSLIN78GL002641 | 100 | 1.80E-213 | WP_029317923.1 | MULTISPECIES: stage III sporulation protein AE [Bacillus] |
| BSLIN78GL002642 | 100 | 1.50E-63 | WP_003230228.1 | MULTISPECIES: stage III sporulation protein AD [Bacillales] |
| BSLIN78GL002643 | 100 | 5.50E-30 | WP_003153142.1 | MULTISPECIES: stage III sporulation protein AC [Bacillales] |
| BSLIN78GL002644 | 100 | 3.80E-88 | WP_014477309.1 | MULTISPECIES: stage III sporulation protein SpoIIIAB [Bacillus |
| BSLIN78GL002645 | 100 | 2.20E-171 | WP_015251728.1 | MULTISPECIES: stage III sporulation protein AA [Bacillus] |
| BSLIN78GL002646 | 100 | 7.30E-41 | WP_004398639.1 | MULTISPECIES: YqhV family protein [Bacillales] |
| BSLIN78GL002647 | 100 | 6.80E-99 | AFQ58396.1 | Elongation factor P [Bacillus subtilis QB928] |
| BSLIN78GL002648 | 100 | 1.50E-195 | WP_015251726.1 | MULTISPECIES: aminopeptidase PapA [Bacillus] |
| BSLIN78GL002649 | 100 | 2.00E-77 | WP_003230223.1 | MULTISPECIES: type II 3-dehydroquinate dehydratase [Bacillales |

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| BSLIN78GL002650 | 100 | 3.80E-108 | QHF58522.1 | hypothetical protein Bateq7PJ16_2716 [Bacillus subtilis] |
| BSLIN78GL002651 | 100 | 7.50E-178 | WP_029726729.1 | MULTISPECIES: DUF1385 domain-containing protein [Bacillus] |
| BSLIN78GL002652 | 100 | 1.20E-65 | AFQ58401.1 | YqhP [Bacillus subtilis QB928] |
| BSLIN78GL002653 | 100 | 1.60E-163 | WP_041850011.1 | MULTISPECIES: patatin-like phospholipase family protein [Bacillus |
| BSLIN78GL002654 | 100 | 6.90E-72 | WP_003236923.1 | MULTISPECIES: transcriptional regulator MntR [Bacillales] |
| BSLIN78GL002655 | 100 | 3.00E-159 | WP_014664579.1 | MULTISPECIES: octanoyltransferase LipM [Bacillus |
| BSLIN78GL002656 | 100 | 8.10E-64 | AGE64105.1 | hypothetical protein C663_2337 [Bacillus subtilis XF-1] |
| BSLIN78GL002657 | 100 | 1.30E-285 | WP_029726727.1 | MULTISPECIES: aminomethyl-transferring glycine dehydrogenase subunit GcvPB |
| BSLIN78GL002658 | 100 | 3.60E-255 | WP_029317920.1 | MULTISPECIES: aminomethyl-transferring glycine dehydrogenase subunit GcvPA |
| BSLIN78GL002659 | 100 | 9.60E-206 | WP_015714248.1 | MULTISPECIES: glycine cleavage system aminomethyltransferase GcvT [Bacillus |
| BSLIN78GL002660 | 100 | 0.00E+00 | WP_029726726.1 | MULTISPECIES: SNF2-related protein [Bacillus |
| BSLIN78GL002661 | 100 | 4.50E-152 | WP_015714249.1 | MULTISPECIES: YqhG family protein [Bacillus |
| BSLIN78GL002662 | 100 | 3.40E-25 | WP_003230187.1 | MULTISPECIES: anti-repressor SinI family protein [Bacillales |
| BSLIN78GL002663 | 99.2 | 7.50E-62 | EIF13893.1 | SinR [Bacillus sp. 5B6] |
| BSLIN78GL002664 | 100 | 1.40E-145 | WP_014664586.1 | MULTISPECIES: biofilm matrix protein TasA [Bacillus] |
| BSLIN78GL002665 | 99.4 | 3.20E-93 | WP_072692741.1 | MULTISPECIES: signal peptidase I [Bacillus] |
| BSLIN78GL002666 | 100 | 1.50E-144 | WP_029726724.1 | MULTISPECIES: amyloid fiber anchoring/assembly protein TapA [Bacillus |
| BSLIN78GL002667 | 100 | 2.60E-65 | AFQ58416.1 | Putative exported protein [Bacillus subtilis QB928] |
| BSLIN78GL002668 | 100 | 8.50E-27 | WP_029726723.1 | MULTISPECIES: YqzE family protein [Bacillus] |
| BSLIN78GL002669 | 100 | 1.40E-63 | WP_029726722.1 | MULTISPECIES: ComG operon protein ComGG [Bacillus |
| BSLIN78GL002670 | 100 | 8.10E-67 | WP_029726721.1 | MULTISPECIES: ComG operon protein ComGF [Bacillus |
| BSLIN78GL002671 | 100 | 3.90E-60 | WP_014480255.1 | MULTISPECIES: ComG operon protein 5 [Bacillus] |
| BSLIN78GL002672 | 100 | 1.10E-72 | WP_029726720.1 | MULTISPECIES: comG operon protein ComGD [Bacillus] |
| BSLIN78GL002673 | 100 | 2.90E-48 | WP_029726719.1 | MULTISPECIES: comG operon protein ComGC [Bacillus] |
| BSLIN78GL002674 | 100 | 2.60E-192 | WP_029726718.1 | MULTISPECIES: comG operon protein ComGB [Bacillus] |
| BSLIN78GL002675 | 100 | 1.30E-205 | AFQ58424.1 | Membrane associated ATPase for DNA competence [Bacillus subtilis QB928] |
| BSLIN78GL002676 | 100 | 1.10E-23 | AOA55203.1 | hypothetical protein BSHJ0_02632 [Bacillus subtilis] |
| BSLIN78GL002677 | 100 | 7.60E-18 | WGD72511.1 | hypothetical protein P5645_08875 [Bacillus subtilis] |
| BSLIN78GL002678 | 99.7 | 5.20E-187 | AFQ58425.1 | Putative CorA-type Mg(2+) transporter [Bacillus subtilis QB928] |
| BSLIN78GL002679 | 100 | 4.70E-247 | WP_029726716.1 | MULTISPECIES: hemolysin family protein [Bacillus |
| BSLIN78GL002680 | 100 | 1.50E-153 | WP_003230149.1 | MULTISPECIES: RsbT co-antagonist protein RsbRD [Bacillus] |
| BSLIN78GL002681 | 100 | 2.60E-65 | AFQ58428.1 | Transcriptional regulator of stress [Bacillus subtilis QB928] |
| BSLIN78GL002682 | 100 | 3.20E-40 | AFQ58429.1 | YqgY [Bacillus subtilis QB928] |
| BSLIN78GL002683 | 99.1 | 5.90E-132 | QHF58554.1 | metallo-hydrolase [Bacillus subtilis] |
| BSLIN78GL002684 | 100 | 2.90E-24 | WP_003230141.1 | MULTISPECIES: DUF2759 family protein [Bacillales |
| BSLIN78GL002685 | 100 | 1.50E-50 | WP_003230139.1 | MULTISPECIES: MTH1187 family thiamine-binding protein [Bacillales |
| BSLIN78GL002686 | 100 | 9.70E-203 | WP_015251709.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002687 | 100 | 3.10E-223 | EHA31327.1 | gamma-D-glutamyl-L-diamino acid endopeptidase [Bacillus subtilis subsp. subtilis |
| BSLIN78GL002688 | 100 | 0.00E+00 | WP_015251707.1 | MULTISPECIES: LTA synthase family protein [Bacillus |
| BSLIN78GL002689 | 99.7 | 4.20E-184 | AFQ58436.1 | Glucose kinase [Bacillus subtilis QB928] |
| BSLIN78GL002690 | 100 | 7.40E-36 | AFQ58437.1 | Putative single strand nucleic acid bindingtranscription [Bacillus subtilis QB928] |
| BSLIN78GL002691 | 100 | 3.50E-286 | WP_003230128.1 | MULTISPECIES: rhomboid protease YqgP [Bacillales] |
| BSLIN78GL002692 | 100 | 1.10E-23 | WP_003230126.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002693 | 100 | 3.20E-104 | WP_029726712.1 | MULTISPECIES: 5-formyltetrahydrofolate cyclo-ligase [Bacillus |
| BSLIN78GL002694 | 100 | 7.10E-14 | AEP91523.1 | hypothetical protein I33_2572 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL002695 | 100 | 1.50E-203 | WP_029726711.1 | MULTISPECIES: glycosyltransferase family 4 protein [Bacillus |
| BSLIN78GL002696 | 100 | 7.30E-59 | AHA78376.1 | Uncharacterized protein yqgL [Bacillus subtilis PY79] |
| BSLIN78GL002697 | 100 | 1.20E-17 | AEP91526.1 | hypothetical protein I33_2575 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL002698 | 100 | 1.10E-54 | WP_014477348.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002699 | 100 | 3.30E-78 | WP_014480272.1 | MULTISPECIES: endolytic transglycosylase MltG [Bacillus |
| BSLIN78GL002700 | 100 | 4.40E-141 | WP_014480273.1 | MULTISPECIES: phosphate ABC transporter ATP-binding protein PstB [Bacillus] |
| BSLIN78GL002701 | 100 | 5.80E-161 | AFQ58447.1 | Phosphate ABC transporter (ATP-binding protein) [Bacillus subtilis QB928] |
| BSLIN78GL002702 | 100 | 7.70E-161 | WP_003230103.1 | MULTISPECIES: phosphate ABC transporter permease PstA [Bacillales] |
| BSLIN78GL002703 | 100 | 2.20E-166 | WP_015714268.1 | MULTISPECIES: phosphate ABC transporter permease subunit PstC [Bacillus] |
| BSLIN78GL002704 | 100 | 1.20E-164 | AOA55230.1 | Phosphate-binding protein PstS [Bacillus subtilis] |
| BSLIN78GL002705 | 99 | 0.00E+00 | QHF58576.1 | hypothetical protein Bateq7PJ16_2770 [Bacillus subtilis] |
| BSLIN78GL002706 | 100 | 1.00E-238 | WP_003230095.1 | MULTISPECIES: MFS transporter [Bacillales] |
| BSLIN78GL002707 | 100 | 3.90E-93 | AGE64151.1 | superoxide dismutase [Bacillus subtilis XF-1] |
| BSLIN78GL002708 | 100 | 1.30E-85 | AFQ58454.1 | Putative integral inner membrane protein [Bacillus subtilis QB928] |
| BSLIN78GL002709 | 100 | 2.10E-135 | WP_015384107.1 | MULTISPECIES: DUF1189 domain-containing protein [Bacillus] |
| BSLIN78GL002710 | 100 | 1.30E-48 | WP_029317899.1 | MULTISPECIES: LysM domain-containing protein [Bacillus subtilis group |
| BSLIN78GL002711 | 100 | 1.30E-197 | AGE64155.1 | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase [Bacillus subtilis XF-1 |
| BSLIN78GL002712 | 100 | 1.20E-83 | AFQ58459.1 | YqfX [Bacillus subtilis QB928] |
| BSLIN78GL002713 | 100 | 6.90E-110 | WP_003246215.1 | MULTISPECIES: nucleotidase [Bacillales |
| BSLIN78GL002714 | 100 | 1.70E-81 | WP_003230079.1 | MULTISPECIES: zinc uptake transcriptional repressor Zur [Bacillus] |
| BSLIN78GL002715 | 100 | 1.20E-161 | WP_003230077.1 | MULTISPECIES: YitT family protein [Bacillales |
| BSLIN78GL002716 | 100 | 1.50E-37 | WP_003230076.1 | MULTISPECIES: DUF2624 domain-containing protein [Bacillales] |
| BSLIN78GL002717 | 100 | 4.70E-163 | AHA78397.1 | putative endonuclease 4 [Bacillus subtilis PY79] |
| BSLIN78GL002718 | 100 | 1.30E-255 | AKN14528.1 | DEAD-box ATP-dependent RNA helicase CshB [Bacillus subtilis] |
| BSLIN78GL002719 | 100 | 5.80E-124 | WP_003246095.1 | MULTISPECIES: YqfQ family protein [Bacillales |
| BSLIN78GL002720 | 100 | 1.60E-177 | WP_003246170.1 | MULTISPECIES: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase [Bacillales |
| BSLIN78GL002721 | 100 | 1.90E-212 | WP_029726707.1 | MULTISPECIES: Nif3-like dinuclear metal center hexameric protein [Bacillus |
| BSLIN78GL002722 | 100 | 5.70E-130 | P54471.2 | RecName: Full=tRNA (adenine(22)-N(1))-methyltransferase; AltName: Full=TrMet(m1A22); AltName: Full=tRNA(m1A22)-methyltransferase; |
| BSLIN78GL002723 | 100 | 1.90E-62 | WP_003230068.1 | MULTISPECIES: cytochrome c-550 [Bacillales |
| BSLIN78GL002724 | 100 | 7.20E-26 | AHA78404.1 | Hypothetical Protein U712_12315 [Bacillus subtilis PY79] |
| BSLIN78GL002725 | 100 | 2.60E-206 | WP_003226225.1 | MULTISPECIES: RNA polymerase sigma factor RpoD [Bacillales] |
| BSLIN78GL002726 | 100 | 0.00E+00 | WP_003230066.1 | MULTISPECIES: DNA primase [Bacillales] |
| BSLIN78GL002727 | 100 | 3.70E-88 | AGA23845.1 | Hypothetical protein A7A1_3227 [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL002728 | 100 | 1.10E-148 | WP_003230064.1 | MULTISPECIES: pyruvate, water dikinase regulatory protein [Bacillales |

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| BSLIN78GL002729 | 100 | 1.20E-112 | WP_003237058.1 | MULTISPECIES: transcriptional regulator CcpN [Bacillales] |
| BSLIN78GL002730 | 99.6 | 0.00E+00 | WP_217024292.1 | glycine--tRNA ligase subunit beta [Bacillus subtilis] |
| BSLIN78GL002731 | 100 | 1.80E-181 | AGE64174.1 | glycyl-tRNA synthetase subunit alpha [Bacillus subtilis XF-1 |
| BSLIN78GL002732 | 100 | 7.40E-144 | AFQ58479.1 | DNA double strand break repair and homologous recombination [Bacillus subtilis |
| BSLIN78GL002733 | 100 | 1.80E-19 | WP_003230053.1 | MULTISPECIES: YqzL family protein [Bacillales |
| BSLIN78GL002734 | 100 | 3.30E-167 | WP_003230051.1 | MULTISPECIES: GTPase Era [Bacillales] |
| BSLIN78GL002735 | 100 | 4.40E-71 | WP_003230049.1 | MULTISPECIES: cytidine deaminase [Bacilli |
| BSLIN78GL002736 | 100 | 1.40E-14 | AHA78416.1 | Hypothetical Protein U712_12375 [Bacillus subtilis PY79] |
| BSLIN78GL002737 | 100 | 8.10E-64 | WP_004398824.1 | MULTISPECIES: diacylglycerol kinase family protein [Bacillales |
| BSLIN78GL002738 | 100 | 1.10E-81 | WP_003230039.1 | MULTISPECIES: rRNA maturation RNase YbeY [Bacillales] |
| BSLIN78GL002739 | 100 | 0.00E+00 | EHA31274.1 | hypothetical protein BSSC8_17170 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002740 | 100 | 2.70E-175 | WP_003230035.1 | MULTISPECIES: PhoH family protein [Bacillales |
| BSLIN78GL002741 | 100 | 8.30E-227 | WP_003230033.1 | MULTISPECIES: sporulation protein YqfD [Bacillales] |
| BSLIN78GL002742 | 100 | 6.70E-41 | WP_003226191.1 | MULTISPECIES: sporulation protein YqfC [Bacillales] |
| BSLIN78GL002743 | 100 | 5.90E-71 | WP_003230029.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002744 | 100 | 5.00E-177 | WP_029726705.1 | MULTISPECIES: flotillin-like protein FloA [Bacillus |
| BSLIN78GL002745 | 100 | 6.70E-238 | WP_029726704.1 | MULTISPECIES: nodulation protein NfeD [Bacillus] |
| BSLIN78GL002746 | 100 | 2.00E-72 | WP_003230022.1 | MULTISPECIES: GatB/YqeY domain-containing protein [Bacillales] |
| BSLIN78GL002747 | 100 | 9.40E-23 | WP_003152957.1 | MULTISPECIES: 30S ribosomal protein S21 [Bacteria] |
| BSLIN78GL002748 | 100 | 4.80E-166 | AIC40997.1 | Na+/anion cotransporter [Bacillus subtilis subsp. subtilis str. JH642 substr. AG174] |
| BSLIN78GL002749 | 100 | 5.00E-260 | WP_003230017.1 | MULTISPECIES: tRNA (N(6)-L-threonylcarbamoyladenosine(37)-C(2)) |
| BSLIN78GL002750 | 100 | 6.90E-142 | WP_003230015.1 | MULTISPECIES: 16S rRNA (uracil(1498)-N(3))-methyltransferase [Bacillales |
| BSLIN78GL002751 | 100 | 5.80E-175 | WP_004398884.1 | MULTISPECIES: 50S ribosomal protein L11 methyltransferase [Bacillales |
| BSLIN78GL002752 | 100 | 4.00E-223 | WP_003230010.1 | MULTISPECIES: molecular chaperone DnaJ [Bacillales] |
| BSLIN78GL002753 | 99 | 0.00E+00 | WP_254500986.1 | molecular chaperone DnaK [Bacillus halotolerans] |
| BSLIN78GL002754 | 100 | 7.00E-99 | BAO93464.1 | hypothetical protein BSNT_08992 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL002755 | 99.7 | 7.00E-176 | WP_326243290.1 | heat-inducible transcriptional repressor HrcA [Bacillus subtilis] |
| BSLIN78GL002756 | 100 | 1.50E-220 | EHA31257.1 | coproporphyrinogen III oxidase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002757 | 98 | 0.00E+00 | WP_325084431.1 | translation elongation factor 4 [Bacillus amyloliquefaciens] |
| BSLIN78GL002758 | 100 | 2.10E-58 | EHA31255.1 | hypothetical protein BSSC8_16980 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002759 | 100 | 5.40E-226 | WP_003229993.1 | MULTISPECIES: spore autolysin SpoIIP [Bacillales |
| BSLIN78GL002760 | 100 | 2.80E-205 | WP_003229991.1 | MULTISPECIES: GPR endopeptidase [Bacillales |
| BSLIN78GL002761 | 100 | 1.00E-39 | AGA21492.1 | 30S ribosomal protein S20 [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL002762 | 100 | 8.90E-193 | WP_003229987.1 | MULTISPECIES: DNA polymerase III subunit delta [Bacillales |
| BSLIN78GL002763 | 100 | 9.20E-19 | WP_003229985.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002764 | 100 | 3.80E-16 | WP_003229983.1 | MULTISPECIES: YqzM family protein [Bacillales |
| BSLIN78GL002765 | 100 | 0.00E+00 | AHA78445.1 | ComE operon protein 3 [Bacillus subtilis PY79] |
| BSLIN78GL002766 | 100 | 3.80E-105 | WP_003229978.1 | MULTISPECIES: ComE operon protein 2 [Bacillales] |
| BSLIN78GL002767 | 100 | 5.20E-108 | WP_004398514.1 | MULTISPECIES: competence protein ComEA [Bacillales] |
| BSLIN78GL002768 | 100 | 8.00E-166 | EHA31245.1 | late competence protein ComER [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002769 | 100 | 2.40E-139 | WP_003229973.1 | MULTISPECIES: class I SAM-dependent methyltransferase [Bacillales |
| BSLIN78GL002770 | 100 | 2.80E-61 | WP_003229971.1 | MULTISPECIES: ribosome silencing factor [Bacillales] |
| BSLIN78GL002771 | 100 | 5.50E-104 | AGA21484.1 | Hypothetical protein YqeK [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL002772 | 100 | 1.70E-108 | AGA21483.1 | Nicotinate-nucleotide adenylyltransferase [Bacillus subtilis subsp. subtilis str. BSP1 |
| BSLIN78GL002773 | 100 | 1.30E-45 | WP_003226133.1 | MULTISPECIES: ribosome assembly RNA-binding protein YhbY [Bacillales |
| BSLIN78GL002774 | 100 | 1.60E-155 | WP_003229967.1 | MULTISPECIES: shikimate dehydrogenase [Bacillales |
| BSLIN78GL002775 | 100 | 5.30E-212 | WP_003229966.1 | MULTISPECIES: ribosome biogenesis GTPase YqeH [Bacillales |
| BSLIN78GL002776 | 100 | 5.40E-110 | AGE64217.1 | putative hydrolase [Bacillus subtilis XF-1] |
| BSLIN78GL002777 | 100 | 1.80E-16 | WP_010886571.1 | sporulation histidine kinase inhibitor Sda [Bacillus subtilis] |
| BSLIN78GL002778 | 100 | 4.70E-140 | WP_029726702.1 | MULTISPECIES: SGNH/GDSL hydrolase family protein [Bacillus |
| BSLIN78GL002779 | 100 | 2.70E-21 | EME06359.1 | hypothetical protein BS732_3098 [Bacillus subtilis MB73/2] |
| BSLIN78GL002780 | 100 | 2.70E-146 | WP_029726701.1 | MULTISPECIES: N-acetylmuramoyl-L-alanine amidase CwlH [Bacillus |
| BSLIN78GL002781 | 100 | 2.00E-110 | WP_038427798.1 | MULTISPECIES: TVP38/TMEM64 family protein [Bacillus |
| BSLIN78GL002782 | 100 | 8.50E-148 | AID00484.1 | hypothetical protein Q433_14085 [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL002783 | 100 | 4.50E-135 | WP_010886572.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002784 | 100 | 4.70E-76 | EHA31229.1 | nuclease [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002785 | 100 | 7.40E-267 | AHA78464.1 | Putative DNA recombinase [Bacillus subtilis PY79] |
| BSLIN78GL002786 | 99.3 | 6.00E-79 | AKE24336.1 | arsenate reductase [Bacillus sp. LM 4-2] |
| BSLIN78GL002787 | 100 | 4.90E-160 | EHA31226.1 | membrane-associated protein [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002788 | 100 | 3.00E-81 | WP_003229954.1 | MULTISPECIES: ArsI/CadI family heavy metal resistance metalloenzyme |
| BSLIN78GL002789 | 100 | 4.50E-55 | WP_004399122.1 | MULTISPECIES: arsenical resistance operon transcriptional regulator ArsR |
| BSLIN78GL002790 | 100 | 5.10E-153 | AHA78469.1 | Uncharacterized protein yqcI [Bacillus subtilis PY79] |
| BSLIN78GL002791 | 100 | 2.00E-52 | RAP10179.1 | hypothetical protein HS3_00588 [Bacillus subtilis] |
| BSLIN78GL002792 | 100 | 5.90E-166 | AOA55319.1 | Assimilatory sulfite reductase (NADPH) [Bacillus subtilis] |
| BSLIN78GL002793 | 100 | 6.60E-108 | WP_015714302.1 | MULTISPECIES: TetR/AcrR family transcriptional regulator [Bacillus |
| BSLIN78GL002794 | 100 | 2.30E-185 | WP_015714303.1 | MULTISPECIES: acryloyl-CoA reductase [Bacillus |
| BSLIN78GL002795 | 100 | 1.90E-21 | WP_231940260.1 | MULTISPECIES: DUF255 domain-containing protein [Bacillus] |
| BSLIN78GL002796 | 92.1 | 1.20E-152 | WP_136654237.1 | collagen-like protein [Bacillus subtilis] |
| BSLIN78GL002797 | 100 | 2.70E-29 | WP_015714305.1 | MULTISPECIES: S-Ena type endospore appendage [Bacillus |
| BSLIN78GL002798 | 100 | 1.20E-126 | WP_133516484.1 | CotZ-related putative spore coat protein [Bacillus subtilis] |
| BSLIN78GL002799 | 99.7 | 2.00E-214 | WP_015714307.1 | MULTISPECIES: response regulator aspartate phosphatase RapE [Bacillus] |
| BSLIN78GL002800 | 100 | 8.60E-78 | EHA31222.1 | hypothetical protein BSSC8_16650 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002801 | 100 | 5.80E-308 | EHA31221.1 | putative phage DNA manipulating enzyme [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002802 | 100 | 3.00E-12 | AHA78474.1 | Hypothetical Protein U712_12665 [Bacillus subtilis PY79] |
| BSLIN78GL002803 | 100 | 6.90E-37 | AHA78475.1 | Uncharacterized protein yqcF [Bacillus subtilis PY79] |
| BSLIN78GL002804 | 100 | 7.40E-62 | WP_003229947.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002805 | 100 | 5.50E-81 | WP_004399085.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002806 | 100 | 7.50E-141 | WP_213391230.1 | N-acetylmuramoyl-L-alanine amidase [Bacillus subtilis] |
| BSLIN78GL002807 | 100 | 1.70E-70 | WP_003246208.1 | MULTISPECIES: holin family protein [Bacillales |
| BSLIN78GL002808 | 100 | 1.80E-165 | WP_003246010.1 | MULTISPECIES: hypothetical protein [Bacillales |

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| BSLIN78GL002809 | 100 | 1.00E-23 | WP_003229944.1 | MULTISPECIES: XkdX family protein [Bacillales] |
| BSLIN78GL002810 | 100 | 4.60E-224 | WP_003229943.1 | MULTISPECIES: pyocin knob domain-containing protein [Bacillales |
| BSLIN78GL002811 | 100 | 3.20E-41 | WP_003229942.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002812 | 100 | 3.60E-103 | WP_003229941.1 | MULTISPECIES: YmfQ family protein [Bacillales |
| BSLIN78GL002813 | 100 | 2.00E-192 | WP_003229940.1 | MULTISPECIES: baseplate J/gp47 family protein [Bacillales] |
| BSLIN78GL002814 | 100 | 3.50E-74 | EHA31210.1 | hypothetical protein BSSC8_16530 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002815 | 100 | 8.30E-39 | WP_003229938.1 | MULTISPECIES: DUF2577 family protein [Bacillales |
| BSLIN78GL002816 | 100 | 3.50E-183 | WP_004398524.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002817 | 100 | 7.30E-124 | WP_004398548.1 | MULTISPECIES: LysM peptidoglycan-binding domain-containing protein |
| BSLIN78GL002818 | 99.9 | 0.00E+00 | WP_326253542.1 | phage tail tape measure protein [Bacillus subtilis] |
| BSLIN78GL002819 | 100 | 3.60E-17 | WP_003229934.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002820 | 100 | 3.70E-78 | WP_003229933.1 | MULTISPECIES: phage portal protein [Bacillales] |
| BSLIN78GL002821 | 95.6 | 3.60E-17 | EHA31202.1 | hypothetical protein BSSC8_16450 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002822 | 100 | 5.90E-77 | WP_015714312.1 | MULTISPECIES: phage tail tube protein [Bacillus] |
| BSLIN78GL002823 | 100 | 5.10E-260 | WP_015714313.1 | MULTISPECIES: phage tail sheath family protein [Bacillus |
| BSLIN78GL002824 | 100 | 8.90E-27 | WP_032679171.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002825 | 100 | 2.00E-77 | WP_015714315.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002826 | 100 | 2.30E-93 | WP_015714316.1 | MULTISPECIES: HK97 gp10 family phage protein [Bacillus] |
| BSLIN78GL002827 | 98.9 | 1.80E-47 | WP_015714317.1 | MULTISPECIES: YqbH/XkdH family protein [Bacillus] |
| BSLIN78GL002828 | 100 | 1.40E-66 | WP_015714318.1 | MULTISPECIES: DUF3199 family protein [Bacillus |
| BSLIN78GL002829 | 100 | 2.70E-52 | WP_015714319.1 | MULTISPECIES: YqbF domain-containing protein [Bacillus] |
| BSLIN78GL002830 | 100 | 3.60E-169 | WP_015714320.1 | MULTISPECIES: phage major capsid protein [Bacillus] |
| BSLIN78GL002831 | 100 | 2.40E-179 | WP_015714321.1 | MULTISPECIES: XkdF-like putative serine protease domain-containing protein |
| BSLIN78GL002832 | 100 | 2.10E-98 | WP_015714322.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002833 | 100 | 3.80E-171 | WP_015714323.1 | MULTISPECIES: phage minor head protein [Bacillus] |
| BSLIN78GL002834 | 100 | 1.10E-295 | WP_015714324.1 | MULTISPECIES: phage portal protein [Bacillus] |
| BSLIN78GL002835 | 100 | 6.60E-254 | WP_015714325.1 | MULTISPECIES: PBSX family phage terminase large subunit [Bacillus] |
| BSLIN78GL002836 | 97.9 | 2.10E-132 | WP_032722175.1 | MULTISPECIES: phage terminase small subunit [Bacillus] |
| BSLIN78GL002837 | 100 | 4.10E-139 | WP_068947621.1 | DNA-directed RNA polymerase [Bacillus subtilis] |
| BSLIN78GL002838 | 100 | 2.70E-80 | WP_017697601.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002839 | 100 | 4.30E-81 | WP_017697600.1 | MULTISPECIES: sigma factor-like helix-turn-helix DNA-binding protein [Bacillus |
| BSLIN78GL002840 | 100 | 4.90E-140 | WP_017697599.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002841 | 100 | 4.60E-32 | WP_017697597.1 | MULTISPECIES: XtrA/YqaO family protein [Bacillus subtilis group] |
| BSLIN78GL002842 | 100 | 1.30E-38 | KIN30606.1 | hypothetical protein B4070_2591 [Bacillus subtilis] |
| BSLIN78GL002843 | 100 | 4.40E-18 | WP_072692702.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002844 | 100 | 8.90E-139 | KIN30608.1 | hypothetical protein B4070_2593 [Bacillus subtilis] |
| BSLIN78GL002845 | 100 | 6.60E-131 | KIN30609.1 | hypothetical protein B4070_2594 [Bacillus subtilis] |
| BSLIN78GL002846 | 100 | 5.30E-159 | WP_017697591.1 | MULTISPECIES: recombinase RecT [Bacillus] |
| BSLIN78GL002847 | 100 | 3.20E-181 | WP_068947622.1 | MULTISPECIES: YqaJ viral recombinase family protein [Bacillus] |
| BSLIN78GL002848 | 100 | 2.30E-30 | WP_068947623.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002849 | 98.7 | 4.30E-34 | EHA31175.1 | hypothetical protein BSSC8_16180 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002850 | 100 | 2.20E-42 | WP_174616763.1 | helix-turn-helix transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL002851 | 100 | 4.70E-17 | WP_003229902.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002852 | 100 | 1.10E-57 | WP_021480133.1 | MULTISPECIES: helix-turn-helix domain-containing protein [Bacillus |
| BSLIN78GL002853 | 100 | 8.30E-23 | WP_021480134.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002854 | 100 | 2.70E-100 | WP_128480820.1 | MULTISPECIES: AAA family ATPase [Bacillus |
| BSLIN78GL002855 | 100 | 3.70E-99 | WP_068947627.1 | MULTISPECIES: ImmA/IrrE family metallo-endopeptidase [Bacillus |
| BSLIN78GL002856 | 100 | 5.40E-63 | AIC98962.1 | RNA polymerase sigma 70 [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL002857 | 100 | 2.20E-12 | WP_003229898.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL002858 | 100 | 2.20E-73 | AFQ58484.1 | Phosphate starvation inducible protein [Bacillus subtilis QB928] |
| BSLIN78GL002859 | 100 | 1.60E-233 | AFQ58485.1 | Two-component sensor histidine kinase [YrkP] [Bacillus subtilis QB928] |
| BSLIN78GL002860 | 100 | 2.50E-127 | WP_003229895.1 | MULTISPECIES: two-component response regulator YrkP [Bacillales] |
| BSLIN78GL002861 | 100 | 1.60E-230 | WP_003229894.1 | MULTISPECIES: DUF418 domain-containing protein [Bacillales] |
| BSLIN78GL002862 | 100 | 1.20E-18 | AGE64230.1 | hypothetical protein C663_2467 [Bacillus subtilis XF-1] |
| BSLIN78GL002863 | 100 | 9.90E-106 | WP_029318133.1 | MULTISPECIES: GNAT family N-acetyltransferase [Bacillus |
| BSLIN78GL002864 | 100 | 1.00E-96 | WP_003246192.1 | MULTISPECIES: NAD(P)H-dependent oxidoreductase [Bacillales] |
| BSLIN78GL002865 | 100 | 1.30E-52 | WP_124072928.1 | HXXEE domain-containing protein [Bacillus subtilis] |
| BSLIN78GL002866 | 100 | 2.60E-136 | WP_032726225.1 | sulfite exporter TauE/SafE family protein [Bacillus subtilis] |
| BSLIN78GL002867 | 100 | 5.70E-36 | WP_003229888.1 | MULTISPECIES: sulfurtransferase TusA family protein [Bacillales |
| BSLIN78GL002868 | 100 | 8.70E-218 | AII36411.1 | hypothetical protein M036_13025 [Bacillus subtilis TO-A] |
| BSLIN78GL002869 | 100 | 4.80E-91 | AII36412.1 | hypothetical protein M036_13035 [Bacillus subtilis TO-A] |
| BSLIN78GL002870 | 100 | 4.90E-85 | WP_003229885.1 | MULTISPECIES: DsrE/DsrF/DrsH-like family protein [Bacillales |
| BSLIN78GL002871 | 100 | 2.20E-12 | WGD61981.1 | metal-sensitive transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL002872 | 100 | 1.00E-15 | AHA78541.1 | Hypothetical Protein U712_13005 [Bacillus subtilis PY79] |
| BSLIN78GL002873 | 100 | 1.10E-95 | WP_120363475.1 | cupin domain-containing protein [Bacillus subtilis] |
| BSLIN78GL002874 | 100 | 3.20E-153 | WP_014480349.1 | MULTISPECIES: multidrug efflux transcriptional regulator BltR [Bacillus] |
| BSLIN78GL002875 | 100 | 4.40E-220 | WP_113712829.1 | multidrug efflux MFS transporter Blt [Bacillus subtilis] |
| BSLIN78GL002876 | 100 | 8.70E-84 | WP_113712828.1 | spermine/spermidine acetyltransferase [Bacillus subtilis] |
| BSLIN78GL002877 | 100 | 4.10E-243 | WP_113712827.1 | hemolysin family protein [Bacillus subtilis] |
| BSLIN78GL002878 | 100 | 1.70E-17 | WP_014477437.1 | MULTISPECIES: YrzO family protein [Bacillus] |
| BSLIN78GL002879 | 98.2 | 1.10E-187 | AFQ58504.1 | Putative efflux transporter [Bacillus subtilis QB928] |
| BSLIN78GL002880 | 100 | 2.20E-160 | WP_029727177.1 | MULTISPECIES: LysR family transcriptional regulator CzcR [Bacillus |
| BSLIN78GL002881 | 100 | 1.90E-198 | WP_029727176.1 | MULTISPECIES: NAD(P)/FAD-dependent oxidoreductase [Bacillus |
| BSLIN78GL002882 | 97.4 | 5.50E-190 | AFQ58507.1 | Potassium/proton-divalent cation antiporter [Bacillus subtilis QB928] |
| BSLIN78GL002883 | 99.1 | 5.20E-57 | WP_004398711.1 | MULTISPECIES: tautomerase family protein [Bacillales] |
| BSLIN78GL002884 | 100 | 4.20E-116 | WP_029727174.1 | MULTISPECIES: glutamate biosynthesis transcriptional regulator GltR [Bacillus |
| BSLIN78GL002885 | 99.3 | 1.50E-71 | AOA55410.1 | Sulfite oxidase [Bacillus subtilis] |
| BSLIN78GL002886 | 100 | 2.70E-242 | WP_029727173.1 | MULTISPECIES: branched-chain amino acid transport system II carrier protein |
| BSLIN78GL002887 | 100 | 1.40E-51 | WP_003245988.1 | MULTISPECIES: branched-chain amino acid transporter AzlD [Bacillales] |
| BSLIN78GL002888 | 100 | 1.70E-131 | WP_015251618.1 | MULTISPECIES: azaleucine resistance protein AzlC [Bacillus |

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| BSLIN78GL002889 | 100 | 3.50E-80 | WP_015251617.1 | MULTISPECIES: azlBCD operon transcriptional regulator AzlB [Bacillus] |
| BSLIN78GL002890 | 100 | 7.80E-20 | ADV93429.1 | putative ribonuclease inhibitor [Bacillus subtilis BSn5] |
| BSLIN78GL002891 | 100 | 3.60E-233 | WP_038427806.1 | MULTISPECIES: cytochrome P450 [Bacillus |
| BSLIN78GL002892 | 98.5 | 3.20E-30 | WP_251233087.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002893 | 98 | 1.10E-19 | WP_069322790.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002894 | 100 | 1.00E-102 | WP_015251614.1 | MULTISPECIES: cysteine hydrolase family protein [Bacillus |
| BSLIN78GL002895 | 100 | 1.90E-92 | WP_015251612.1 | MULTISPECIES: DinB family protein [Bacillus |
| BSLIN78GL002896 | 100 | 2.40E-167 | WP_015714371.1 | MULTISPECIES: aminoglycoside 6-adenylyltransferase AadK [Bacillus |
| BSLIN78GL002897 | 99.4 | 2.50E-195 | WP_326253530.1 | nitronate monooxygenase [Bacillus subtilis] |
| BSLIN78GL002898 | 100 | 1.10E-23 | QAT46656.1 | hypothetical protein EQZ01_13765 [Bacillus subtilis] |
| BSLIN78GL002899 | 99.6 | 2.50E-147 | WP_015714374.1 | MULTISPECIES: glutamate racemase [Bacillus] |
| BSLIN78GL002900 | 100 | 2.10E-129 | AGE64275.1 | putative lipoprotein [Bacillus subtilis XF-1] |
| BSLIN78GL002901 | 100 | 9.90E-127 | WP_029727166.1 | MULTISPECIES: FadR/GntR family transcriptional regulator [Bacillus |
| BSLIN78GL002902 | 100 | 2.10E-25 | WP_231940258.1 | MULTISPECIES: GapA-binding peptide SR1P [Bacillus |
| BSLIN78GL002903 | 100 | 1.90E-256 | WP_029727165.1 | MFS transporter [Bacillus subtilis] |
| BSLIN78GL002904 | 99.6 | 1.70E-129 | WP_029727164.1 | MULTISPECIES: 3-oxoacyl-ACP reductase family protein [Bacillus |
| BSLIN78GL002905 | 100 | 9.70E-178 | WP_029727163.1 | MULTISPECIES: transketolase C-terminal domain-containing protein [Bacillus] |
| BSLIN78GL002906 | 100 | 6.70E-162 | WP_029727162.1 | transketolase [Bacillus subtilis] |
| BSLIN78GL002907 | 100 | 7.10E-107 | WP_015714381.1 | MULTISPECIES: flavin reductase family protein [Bacillus |
| BSLIN78GL002908 | 100 | 4.20E-164 | WP_015714382.1 | MULTISPECIES: MerR family DNA-binding transcriptional regulator [Bacillus |
| BSLIN78GL002909 | 100 | 2.90E-69 | WP_326253529.1 | MmcQ/YjbR family DNA-binding protein [Bacillus subtilis] |
| BSLIN78GL002910 | 100 | 8.80E-14 | RAP10060.1 | hypothetical protein HS3_00468 [Bacillus subtilis] |
| BSLIN78GL002911 | 100 | 2.30E-31 | AID00406.1 | hypothetical protein Q433_14415 [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL002912 | 100 | 3.70E-16 | WP_015714385.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002913 | 100 | 1.70E-146 | WP_029727159.1 | MULTISPECIES: metal-binding protein ZinT [Bacillus] |
| BSLIN78GL002914 | 100 | 1.50E-95 | WP_029727158.1 | MULTISPECIES: RNA polymerase sigma factor SigZ [Bacillus |
| BSLIN78GL002915 | 99.7 | 7.90E-180 | AAB80886.1 | YrpG [Bacillus subtilis subsp. subtilis str. 168] |
| BSLIN78GL002916 | 99.3 | 3.10E-246 | AFQ58527.1 | Putative citrate transporter [Bacillus subtilis QB928] |
| BSLIN78GL002917 | 100 | 4.60E-169 | EHA31126.1 | hypothetical protein BSSC8_15690 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002918 | 98.5 | 3.00E-28 | AHA78575.1 | Hypothetical Protein U712_13185 [Bacillus subtilis PY79] |
| BSLIN78GL002919 | 100 | 2.70E-183 | WP_326253526.1 | 2-methylaconitate cis-trans isomerase PrpF family protein [Bacillus subtilis] |
| BSLIN78GL002920 | 100 | 2.80E-157 | WP_029727156.1 | MULTISPECIES: chitosanase [Bacillus] |
| BSLIN78GL002921 | 100 | 3.60E-42 | WP_003229850.1 | MULTISPECIES: CD3324 family protein [Bacillales |
| BSLIN78GL002922 | 99.6 | 4.80E-140 | WP_029727155.1 | MULTISPECIES: alpha/beta hydrolase [Bacillus] |
| BSLIN78GL002923 | 100 | 1.30E-63 | AAB80879.1 | YraJ [Bacillus subtilis subsp. subtilis str. 168] |
| BSLIN78GL002924 | 100 | 6.40E-57 | WP_009967867.1 | MULTISPECIES: SH3 domain-containing protein [Bacillus] |
| BSLIN78GL002925 | 100 | 1.40E-47 | WP_249848042.1 | VOC family protein [Bacillus subtilis] |
| BSLIN78GL002926 | 100 | 8.60E-38 | WP_003229845.1 | MULTISPECIES: spore coat protein F-like protein YraG [Bacillales |
| BSLIN78GL002927 | 100 | 3.20E-40 | AGE64286.1 | putative spore coat protein [Bacillus subtilis XF-1] |
| BSLIN78GL002928 | 100 | 5.90E-222 | WP_003229843.1 | MULTISPECIES: zinc-dependent alcohol dehydrogenase [Bacillales |
| BSLIN78GL002929 | 100 | 1.10E-27 | WP_014480384.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL002930 | 100 | 7.00E-50 | WP_003246006.1 | MULTISPECIES: spore coat protein [Bacillales] |
| BSLIN78GL002931 | 98.6 | 1.50E-75 | AGE64290.1 | hypothetical protein C663_2533 [Bacillus subtilis XF-1] |
| BSLIN78GL002932 | 98.6 | 8.30E-202 | RPK21587.1 | alcohol dehydrogenase [Bacillus subtilis] |
| BSLIN78GL002933 | 100 | 1.50E-95 | AGE64293.1 | general stress protein [Bacillus subtilis XF-1] |
| BSLIN78GL002934 | 100 | 0.00E+00 | RAP10034.1 | Sucrose-6-phosphate hydrolase [Bacillus subtilis] |
| BSLIN78GL002935 | 100 | 9.90E-158 | QHF58700.1 | permease IID component [Bacillus subtilis] |
| BSLIN78GL002936 | 100 | 2.50E-142 | WP_003229833.1 | MULTISPECIES: PTS fructose transporter subunit IIC [Bacillales |
| BSLIN78GL002937 | 100 | 7.90E-83 | AGA20965.1 | Fructose-specific phosphotransferase enzyme IIB component [Bacillus subtilis subsp. |
| BSLIN78GL002938 | 100 | 1.10E-75 | WP_128992282.1 | PTS fructose transporter subunit IIA [Bacillus subtilis] |
| BSLIN78GL002939 | 100 | 0.00E+00 | WP_029727152.1 | MULTISPECIES: transcriptional regulator LevR [Bacillus |
| BSLIN78GL002940 | 100 | 1.10E-248 | WP_029727151.1 | MULTISPECIES: amino acid permease [Bacillus] |
| BSLIN78GL002941 | 100 | 2.30E-111 | WP_003229828.1 | MULTISPECIES: LysE family transporter [Bacillales |
| BSLIN78GL002942 | 99 | 5.50E-170 | QHF58707.1 | sugar sensing transcriptional regulator TrmBL1 [Bacillus subtilis] |
| BSLIN78GL002943 | 100 | 2.40E-87 | WP_015251591.1 | MULTISPECIES: RNA polymerase sigma factor SigV [Bacillus] |
| BSLIN78GL002944 | 100 | 5.50E-156 | WP_003229823.1 | MULTISPECIES: anti-sigma-V factor RsiV [Bacillus] |
| BSLIN78GL002945 | 100 | 0.00E+00 | WP_038429383.1 | MULTISPECIES: peptidoglycan O-acetyltransferase OatA [Bacillus |
| BSLIN78GL002946 | 100 | 3.60E-35 | AKE24466.1 | hypothetical protein BsLM_2668 [Bacillus sp. LM 4-2] |
| BSLIN78GL002947 | 100 | 1.30E-24 | AKE24467.1 | hypothetical protein BsLM_2669 [Bacillus sp. LM 4-2] |
| BSLIN78GL002948 | 100 | 1.60E-191 | AKE24468.1 | hypothetical protein BsLM_2670 [Bacillus sp. LM 4-2] |
| BSLIN78GL002949 | 100 | 2.10E-103 | WP_046381222.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL002950 | 100 | 1.10E-223 | WP_015714407.1 | MULTISPECIES: Gfo/Idh/MocA family oxidoreductase [Bacillus |
| BSLIN78GL002951 | 100 | 3.40E-239 | WP_015714408.1 | MULTISPECIES: ArgE/DapE family deacylase [Bacillus |
| BSLIN78GL002952 | 100 | 4.80E-241 | PKF91172.1 | hypothetical protein CWT11_12075 [Bacillus subtilis] |
| BSLIN78GL002953 | 100 | 1.60E-302 | WP_046381224.1 | MULTISPECIES: phenylalanine aminomutase (D-beta-phenylalanine forming) |
| BSLIN78GL002954 | 100 | 2.00E-164 | WP_015714411.1 | MULTISPECIES: NAD(P)-dependent oxidoreductase [Bacillus |
| BSLIN78GL002955 | 100 | 0.00E+00 | WP_015714412.1 | MULTISPECIES: amino acid adenylation domain-containing protein [Bacillus] |
| BSLIN78GL002956 | 100 | 3.10E-148 | WP_015714413.1 | MULTISPECIES: ABC-2 family transporter protein [Bacillus |
| BSLIN78GL002957 | 100 | 7.00E-139 | WP_128753637.1 | ABC-2 family transporter protein [Bacillus subtilis] |
| BSLIN78GL002958 | 100 | 9.50E-187 | WP_015714415.1 | MULTISPECIES: ATP-binding cassette domain-containing protein [Bacillus |
| BSLIN78GL002959 | 100 | 1.20E-186 | WP_015714416.1 | MULTISPECIES: SDR family oxidoreductase [Bacillus |
| BSLIN78GL002960 | 100 | 3.30E-267 | WP_015714417.1 | MULTISPECIES: nucleotide sugar dehydrogenase [Bacillus |
| BSLIN78GL002961 | 100 | 0.00E+00 | WP_163130518.1 | MULTISPECIES: bifunctional cytochrome P450/NADPH--P450 reductase CypB |
| BSLIN78GL002962 | 100 | 3.70E-88 | WP_046381225.1 | MULTISPECIES: transcriptional regulator FatR [Bacillus] |
| BSLIN78GL002963 | 100 | 2.00E-80 | WP_015251586.1 | methyltransferase domain-containing protein [Bacillus subtilis] |
| BSLIN78GL002964 | 100 | 3.50E-17 | AGE64309.1 | hypothetical protein C663_2553 [Bacillus subtilis XF-1] |
| BSLIN78GL002965 | 100 | 3.10E-25 | RJS56634.1 | hypothetical protein CJ481_12415 [Bacillus subtilis] |
| BSLIN78GL002966 | 98.1 | 5.20E-20 | EHA31090.1 | hypothetical protein BSSC8_15330 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002967 | 100 | 6.30E-146 | WP_003229815.1 | MULTISPECIES: formate/nitrite transporter family protein [Bacillales] |
| BSLIN78GL002968 | 100 | 8.30E-61 | WP_003229814.1 | MULTISPECIES: DUF2294 domain-containing protein [Bacillus] |

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| BSLIN78GL002969 | 100 | 0.00E+00 | EHA31087.1 | oxidoreductase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002970 | 100 | 1.60E-80 | WP_014477490.1 | MULTISPECIES: DUF1641 domain-containing protein [Bacillus] |
| BSLIN78GL002971 | 100 | 7.10E-37 | EHA31085.1 | hypothetical protein BSSC8_15280 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL002972 | 98.7 | 5.70E-209 | WP_101169771.1 | bifunctional cystathionine gamma-lyase/homocysteine desulfhydrase [Bacillus sp. |
| BSLIN78GL002973 | 100 | 1.00E-171 | WP_046381226.1 | MULTISPECIES: O-acetylserine dependent cystathionine beta-synthase [Bacillus |
| BSLIN78GL002974 | 100 | 9.10E-125 | WP_009967881.1 | MULTISPECIES: 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase |
| BSLIN78GL002975 | 100 | 5.30E-119 | WP_015714425.1 | MULTISPECIES: class I SAM-dependent methyltransferase [Bacillus |
| BSLIN78GL002976 | 100 | 5.10E-28 | WP_014477495.1 | MULTISPECIES: YrzA family protein [Bacillus] |
| BSLIN78GL002977 | 100 | 4.40E-127 | WP_326253513.1 | YrrS family protein [Bacillus subtilis] |
| BSLIN78GL002978 | 100 | 0.00E+00 | WP_046381228.1 | MULTISPECIES: penicillin-binding protein 2 [Bacillus] |
| BSLIN78GL002979 | 100 | 1.90E-75 | AGE64325.1 | transcription elongation factor [Bacillus subtilis XF-1] |
| BSLIN78GL002980 | 100 | 9.20E-116 | WP_003225916.1 | MULTISPECIES: uridine kinase [Bacillales] |
| BSLIN78GL002981 | 100 | 8.50E-246 | WP_003229802.1 | MULTISPECIES: U32 family peptidase [Bacillales] |
| BSLIN78GL002982 | 100 | 3.60E-177 | AGA20995.1 | Hypothetical protein YrrN [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL002983 | 100 | 6.30E-120 | WP_015714429.1 | MULTISPECIES: O-methyltransferase [Bacillus] |
| BSLIN78GL002984 | 100 | 2.20E-202 | WP_029727142.1 | MULTISPECIES: endolytic transglycosylase MltG [Bacillus |
| BSLIN78GL002985 | 100 | 3.40E-49 | AGA20998.1 | Hypothetical protein YrzB [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL002986 | 100 | 2.90E-70 | WEY91118.1 | Holliday junction resolvase RuvX [Bacillus subtilis] |
| BSLIN78GL002987 | 100 | 1.60E-42 | WP_003225903.1 | MULTISPECIES: IreB family regulatory phosphoprotein [Bacillales] |
| BSLIN78GL002988 | 99.9 | 0.00E+00 | WP_326243518.1 | alanine--tRNA ligase [Bacillus subtilis] |
| BSLIN78GL002989 | 100 | 5.90E-200 | WP_029727140.1 | MULTISPECIES: AI-2E family transporter [Bacillus] |
| BSLIN78GL002990 | 99.2 | 1.40E-131 | QHF58743.1 | transport ATP-binding protein [Bacillus subtilis] |
| BSLIN78GL002991 | 100 | 2.00E-147 | WP_003245954.1 | MULTISPECIES: glutamine ABC transporter substrate-binding protein GlnH |
| BSLIN78GL002992 | 100 | 6.70E-114 | AGA21005.1 | Glutamine ABC transporter (Integral membrane protein) [Bacillus subtilis subsp. |
| BSLIN78GL002993 | 100 | 2.20E-112 | WP_003229784.1 | MULTISPECIES: amino acid ABC transporter permease [Bacillales] |
| BSLIN78GL002994 | 100 | 4.20E-15 | WP_003229780.1 | MULTISPECIES: YrzQ family protein [Bacillales] |
| BSLIN78GL002995 | 100 | 5.10E-30 | WP_003225893.1 | MULTISPECIES: hypothetical protein [Bacillales] |
| BSLIN78GL002996 | 99.1 | 5.20E-54 | OIR62389.1 | hypothetical protein BLL41_06205 [Bacillus sp. FMQ74] |
| BSLIN78GL002997 | 100 | 0.00E+00 | WP_014477509.1 | MULTISPECIES: ATP-dependent RecD-like DNA helicase [Bacillus] |
| BSLIN78GL002998 | 100 | 2.20E-117 | AIC99068.1 | hypothetical protein Q433_14810 [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL002999 | 100 | 9.30E-220 | BAM53183.1 | tRNA-specific 2-thiouridylase MnmA [Bacillus subtilis BEST7613] |
| BSLIN78GL003000 | 100 | 3.80E-213 | WP_003229769.1 | MULTISPECIES: cysteine desulfurase family protein [Bacillus |
| BSLIN78GL003001 | 100 | 2.00E-77 | AGE64347.1 | transcriptional regulator of cysteine biosynthesis [Bacillus subtilis XF-1] |
| BSLIN78GL003002 | 100 | 1.00E-238 | WP_015714437.1 | MULTISPECIES: replication-associated recombination protein A [Bacillus] |
| BSLIN78GL003003 | 100 | 4.60E-138 | WP_014480428.1 | MULTISPECIES: tRNA threonylcarbamoyladenosine dehydratase [Bacillus |
| BSLIN78GL003004 | 100 | 1.90E-33 | AEP91745.1 | hypothetical protein I33_2800 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL003005 | 100 | 0.00E+00 | WP_003229758.1 | MULTISPECIES: aspartate--tRNA ligase [Bacillales] |
| BSLIN78GL003006 | 100 | 4.70E-244 | WP_003229755.1 | MULTISPECIES: histidine--tRNA ligase [Bacillales] |
| BSLIN78GL003007 | 100 | 3.80E-27 | AGE64353.1 | hypothetical protein C663_2598 [Bacillus subtilis XF-1] |
| BSLIN78GL003008 | 100 | 0.00E+00 | KIO60084.1 | N-acetylmuramoyl-L-alanine amidase [Bacillus subtilis] |
| BSLIN78GL003009 | 100 | 1.40E-75 | WP_004398689.1 | MULTISPECIES: D-aminoacyl-tRNA deacylase [Bacillus] |
| BSLIN78GL003010 | 100 | 0.00E+00 | WP_003229747.1 | MULTISPECIES: GTP diphosphokinase [Bacillales] |
| BSLIN78GL003011 | 100 | 1.10E-90 | WP_029727134.1 | MULTISPECIES: adenine phosphoribosyltransferase [Bacillus] |
| BSLIN78GL003012 | 100 | 0.00E+00 | WP_029727133.1 | MULTISPECIES: single-stranded-DNA-specific exonuclease RecJ [Bacillus |
| BSLIN78GL003013 | 100 | 1.40E-54 | AGA21023.1 | Hypothetical protein YrvD [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003014 | 100 | 8.30E-88 | WP_029727132.1 | MULTISPECIES: cation:proton antiporter regulatory subunit [Bacillus] |
| BSLIN78GL003015 | 100 | 0.00E+00 | WP_015714442.1 | MULTISPECIES: protein translocase subunit SecDF [Bacillus] |
| BSLIN78GL003016 | 100 | 9.10E-50 | WP_003229735.1 | MULTISPECIES: post-transcriptional regulator ComN [Bacillus] |
| BSLIN78GL003017 | 100 | 9.00E-282 | WP_003229733.1 | MULTISPECIES: stage V sporulation protein B [Bacillus] |
| BSLIN78GL003018 | 100 | 2.30E-117 | AGE64364.1 | hypothetical protein C663_2608 [Bacillus subtilis XF-1] |
| BSLIN78GL003019 | 100 | 2.70E-77 | AOA55526.1 | putative membrane protein YrzE [Bacillus subtilis] |
| BSLIN78GL003020 | 100 | 4.90E-42 | AGA21030.1 | Membrane protein YrbF [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003021 | 100 | 4.00E-226 | WP_003229725.1 | MULTISPECIES: tRNA guanosine(34) transglycosylase Tgt [Bacillales] |
| BSLIN78GL003022 | 100 | 1.40E-193 | WP_003229723.1 | MULTISPECIES: tRNA preQ1(34) S-adenosylmethionine ribosyltransferase- |
| BSLIN78GL003023 | 100 | 1.70E-28 | WP_003222669.1 | MULTISPECIES: DUF2905 domain-containing protein [Bacillales] |
| BSLIN78GL003024 | 100 | 3.50E-186 | AGA21033.1 | Holliday junction ATP-dependent DNA helicase RuvB [Bacillus subtilis subsp. |
| BSLIN78GL003025 | 100 | 8.80E-108 | WP_003229717.1 | MULTISPECIES: Holliday junction branch migration protein RuvA [Bacillales] |
| BSLIN78GL003026 | 100 | 8.80E-93 | WP_003229715.1 | MULTISPECIES: sporulation cell-cell signaling protein BofC [Bacillales] |
| BSLIN78GL003027 | 100 | 8.20E-260 | EHA31029.1 | sigma-B-transcription [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003028 | 99.4 | 1.10E-195 | BAI86263.2 | hypothetical protein BSNT_09178 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL003029 | 99.5 | 2.20E-120 | EHA31027.1 | yrzF [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003030 | 100 | 1.10E-14 | WP_003229707.1 | MULTISPECIES: hypothetical protein [Bacillales] |
| BSLIN78GL003031 | 100 | 6.10E-82 | AOL26523.1 | hypothetical protein BGM23_08035 [Bacillus sp. FJAT-14266] |
| BSLIN78GL003032 | 100 | 2.20E-16 | WP_029727127.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL003033 | 100 | 6.10E-272 | WP_038427814.1 | alanine/glycine:cation symporter family protein [Bacillus subtilis] |
| BSLIN78GL003034 | 100 | 3.50E-138 | EHA31022.1 | hypothetical protein BSSC8_14650 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003035 | 99.5 | 3.50E-103 | WP_169057994.1 | spore germination protein SgpA [Bacillus subtilis] |
| BSLIN78GL003036 | 100 | 6.60E-245 | WP_029727124.1 | MULTISPECIES: spore coat assembly protein SafA [Bacillus] |
| BSLIN78GL003037 | 100 | 3.70E-213 | WP_038427815.1 | quinolinate synthase NadA [Bacillus subtilis] |
| BSLIN78GL003038 | 100 | 9.80E-161 | WP_029318181.1 | MULTISPECIES: carboxylating nicotinate-nucleotide diphosphorylase [Bacillus |
| BSLIN78GL003039 | 100 | 6.40E-307 | WP_326253509.1 | L-aspartate oxidase [Bacillus subtilis] |
| BSLIN78GL003040 | 99 | 2.10E-230 | QJD05091.1 | Cysteine desulfurase [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL003041 | 100 | 2.90E-91 | EHA31015.1 | transcriptional repressor of de novo NAD biosynthesis [Bacillus subtilis subsp. |
| BSLIN78GL003042 | 99.7 | 2.10E-166 | AOA55549.1 | Prephenate dehydratase [Bacillus subtilis] |
| BSLIN78GL003043 | 100 | 3.50E-86 | AGE64387.1 | hypothetical protein C663_2632 [Bacillus subtilis XF-1] |
| BSLIN78GL003044 | 100 | 1.70E-246 | WP_029727119.1 | MULTISPECIES: GTPase ObgE [Bacillus] |
| BSLIN78GL003045 | 100 | 1.20E-109 | EHA31011.1 | sporulation initiation phosphotransferase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003046 | 100 | 3.90E-15 | WP_003229671.1 | MULTISPECIES: hypothetical protein [Bacillales] |
| BSLIN78GL003047 | 100 | 3.40E-46 | AGA21053.1 | 50S ribosomal protein L27 [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003048 | 100 | 2.50E-56 | WP_003229669.1 | MULTISPECIES: ribosomal-processing cysteine protease Prp [Bacillales] |

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| BSLIN78GL003049 | 100 | 1.90E-50 | WP_003229668.1 | MULTISPECIES: 50S ribosomal protein L21 [Bacillales] |
| BSLIN78GL003050 | 100 | 4.40E-158 | EHA31006.1 | membrane metalloprotease [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003051 | 99.6 | 1.20E-149 | BAI86286.2 | stage IV sporulation protein [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL003052 | 92.5 | 1.40E-12 | EHA31004.1 | hypothetical protein BSSC8_14470 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003053 | 100 | 6.00E-118 | WP_004398624.1 | MULTISPECIES: septum site-determining protein MinD [Bacillales] |
| BSLIN78GL003054 | 100 | 2.00E-124 | AGE64397.1 | septum formation inhibitor [Bacillus subtilis XF-1] |
| BSLIN78GL003055 | 100 | 2.20E-85 | WP_004398811.1 | MULTISPECIES: rod shape-determining protein MreD [Bacillales] |
| BSLIN78GL003056 | 100 | 3.90E-151 | WP_003222609.1 | MULTISPECIES: rod shape-determining protein MreC [Bacillus] |
| BSLIN78GL003057 | 100 | 2.30E-185 | WP_003229650.1 | MULTISPECIES: cell shape-determining protein MreB [Bacillales] |
| BSLIN78GL003058 | 100 | 3.80E-117 | WP_015251546.1 | MULTISPECIES: DNA repair protein RadC [Bacillus] |
| BSLIN78GL003059 | 100 | 3.30E-104 | AGA21064.1 | Septum formation protein Maf [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003060 | 100 | 1.50E-181 | WP_038427816.1 | MULTISPECIES: stage II sporulation protein SpoIIB [Bacillus] |
| BSLIN78GL003061 | 99.2 | 4.80E-135 | AGA21066.1 | Type 4 prepilin-like proteins leader peptide-processing enzyme [Bacillus subtilis |
| BSLIN78GL003062 | 100 | 1.00E-15 | RAP09921.1 | hypothetical protein HS3_00327 [Bacillus subtilis] |
| BSLIN78GL003063 | 100 | 4.60E-247 | WP_029727116.1 | MULTISPECIES: folylpolyglutamate synthase/dihydrofolate synthase family proteir |
| BSLIN78GL003064 | 99.2 | 0.00E+00 | WP_268397832.1 | valine--tRNA ligase [Bacillus sp. C28GYM-DRY-1] |
| BSLIN78GL003065 | 100 | 1.10E-27 | WP_003222590.1 | MULTISPECIES: hypothetical protein [Bacillales] |
| BSLIN78GL003066 | 99.7 | 8.60E-204 | AGE64408.1 | spore coat protein [Bacillus subtilis XF-1] |
| BSLIN78GL003067 | 99.8 | 0.00E+00 | WP_326253505.1 | spore coat morphogenetic protein SpoVID [Bacillus subtilis] |
| BSLIN78GL003068 | 94.4 | 1.90E-232 | WP_016938771.1 | glutamate-1-semialdehyde 2,1-aminomutase [Bacillus siamensis] |
| BSLIN78GL003069 | 100 | 1.70E-182 | WP_029727112.1 | MULTISPECIES: porphobilinogen synthase [Bacillus] |
| BSLIN78GL003070 | 100 | 1.40E-145 | AKE24589.1 | uroporphyrinogen-III synthase [Bacillus sp. LM 4-2] |
| BSLIN78GL003071 | 100 | 4.00E-165 | WP_072692716.1 | MULTISPECIES: hydroxymethylbilane synthase [Bacillus |
| BSLIN78GL003072 | 100 | 6.50E-154 | WP_003222575.1 | MULTISPECIES: cytochrome c biogenesis protein [Bacillales] |
| BSLIN78GL003073 | 100 | 1.30E-247 | AGE64414.1 | glutamyl-tRNA reductase [Bacillus subtilis XF-1] |
| BSLIN78GL003074 | 100 | 1.60E-103 | BAI86308.2 | hypothetical protein BSNT_09223 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL003075 | 100 | 6.10E-106 | WP_003229621.1 | MULTISPECIES: ribosome biogenesis GTP-binding protein YihA/YsxC [Bacillales] |
| BSLIN78GL003076 | 97.5 | 0.00E+00 | KAF1679415.1 | endopeptidase La [Bacillus sp. SKDU12] |
| BSLIN78GL003077 | 100 | 0.00E+00 | WP_029726366.1 | ATP-dependent protease LonB [Bacillus subtilis] |
| BSLIN78GL003078 | 100 | 4.30E-234 | WP_003229613.1 | MULTISPECIES: ATP-dependent protease ATP-binding subunit ClpX [Bacillales] |
| BSLIN78GL003079 | 100 | 6.80E-235 | WP_015714466.1 | MULTISPECIES: trigger factor [Bacillus] |
| BSLIN78GL003080 | 100 | 8.90E-190 | WP_029726367.1 | MULTISPECIES: DNA damage checkpoint antagonist DdcA [Bacillus] |
| BSLIN78GL003081 | 100 | 1.70E-16 | AHA78725.1 | Hypothetical Protein U712_13935 [Bacillus subtilis PY79] |
| BSLIN78GL003082 | 100 | 1.10E-113 | WP_029726368.1 | MULTISPECIES: 3-isopropylmalate dehydratase small subunit [Bacillus] |
| BSLIN78GL003083 | 99.8 | 4.40E-275 | WP_326148367.1 | 3-isopropylmalate dehydratase large subunit [Bacillus subtilis] |
| BSLIN78GL003084 | 99.7 | 5.60E-198 | WP_029726369.1 | MULTISPECIES: 3-isopropylmalate dehydrogenase [Bacillus] |
| BSLIN78GL003085 | 99.8 | 7.40E-281 | WP_029726370.1 | MULTISPECIES: 2-isopropylmalate synthase [Bacillus] |
| BSLIN78GL003086 | 100 | 3.40E-192 | WP_029726371.1 | MULTISPECIES: ketol-acid reductoisomerase [Bacillus] |
| BSLIN78GL003087 | 100 | 1.80E-82 | EHA30970.1 | acetolactate synthase 3 regulatory subunit [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003088 | 100 | 0.00E+00 | EHA30969.1 | acetolactate synthase catalytic subunit [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003089 | 100 | 3.30E-14 | AGE64429.1 | hypothetical protein C663_2675 [Bacillus subtilis XF-1] |
| BSLIN78GL003090 | 98.3 | 5.40E-65 | EHA30968.1 | hypothetical protein BSSC8_14110 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003091 | 99.3 | 7.50E-74 | WP_080529633.1 | GNAT family N-acetyltransferase [Bacillus subtilis] |
| BSLIN78GL003092 | 100 | 1.00E-23 | AMK73247.1 | hypothetical protein AWV81_14440 [Bacillus subtilis subsp. natto] |
| BSLIN78GL003093 | 100 | 1.30E-151 | WP_029726375.1 | MULTISPECIES: YsnF/AvaK domain-containing protein [Bacillus] |
| BSLIN78GL003094 | 100 | 2.20E-91 | WP_029726376.1 | MULTISPECIES: metallophosphoesterase [Bacillus] |
| BSLIN78GL003095 | 100 | 2.60E-104 | ADV93629.1 | nucleoside-triphosphatase [Bacillus subtilis BSn5] |
| BSLIN78GL003096 | 100 | 1.90E-133 | WP_019712911.1 | MULTISPECIES: ribonuclease PH [Bacillus] |
| BSLIN78GL003097 | 100 | 1.30E-202 | WP_003229578.1 | MULTISPECIES: spore germination protein GerM [Bacillales] |
| BSLIN78GL003098 | 100 | 1.20E-152 | AHA78742.1 | Glutamate racemase 1 [Bacillus subtilis PY79] |
| BSLIN78GL003099 | 100 | 4.90E-76 | BAM58918.1 | MarR family transcriptional regulator [Bacillus subtilis BEST7003] |
| BSLIN78GL003100 | 100 | 2.60E-13 | AEP91838.1 | hypothetical protein I33_2894 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL003101 | 100 | 8.40E-32 | WP_003184172.1 | MULTISPECIES: spore germination transcription factor GerE [Bacillales] |
| BSLIN78GL003102 | 100 | 1.10E-78 | WP_003229571.1 | MULTISPECIES: thioesterase family protein [Bacillus] |
| BSLIN78GL003103 | 100 | 1.60E-146 | WP_003229569.1 | MULTISPECIES: succinate dehydrogenase iron-sulfur subunit [Bacillales] |
| BSLIN78GL003104 | 100 | 0.00E+00 | WP_003229567.1 | MULTISPECIES: succinate dehydrogenase flavoprotein subunit [Bacillales] |
| BSLIN78GL003105 | 100 | 6.70E-102 | QHF58856.1 | dehydrogenase cytochrome b558 subunit [Bacillus subtilis] |
| BSLIN78GL003106 | 100 | 9.70E-80 | WP_003222508.1 | MULTISPECIES: YslB family protein [Bacillales] |
| BSLIN78GL003107 | 100 | 7.00E-221 | WP_024572581.1 | MULTISPECIES: aspartate kinase [Bacillus] |
| BSLIN78GL003108 | 100 | 9.90E-17 | AIC99164.1 | aspartate kinase [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL003109 | 95.1 | 0.00E+00 | WP_003325185.1 | excinuclease ABC subunit UvrC [Bacillus atrophaeus] |
| BSLIN78GL003110 | 100 | 3.50E-52 | WP_003222500.1 | MULTISPECIES: thioredoxin [Bacillales] |
| BSLIN78GL003111 | 100 | 5.90E-26 | WP_003229558.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL003112 | 100 | 3.50E-307 | QJD05156.1 | Exo-alpha-L-arabinofuranosidase [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL003113 | 100 | 1.00E-177 | WP_003229553.1 | MULTISPECIES: electron transfer flavoprotein subunit alpha [Bacillus] |
| BSLIN78GL003114 | 100 | 1.20E-141 | EHA30945.1 | electron transfer flavoprotein subunit beta [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003115 | 100 | 1.60E-138 | WP_029318207.1 | enoyl-CoA hydratase [Bacillus subtilis] |
| BSLIN78GL003116 | 100 | 3.20E-96 | WP_003229547.1 | MULTISPECIES: fatty acid metabolism transcriptional regulator FadR [Bacillales] |
| BSLIN78GL003117 | 100 | 0.00E+00 | WP_029726378.1 | long-chain-fatty-acid--CoA ligase LcfA [Bacillus subtilis] |
| BSLIN78GL003118 | 100 | 4.90E-70 | AGA23808.1 | Hypothetical protein YshE [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003119 | 100 | 0.00E+00 | WP_029726379.1 | MULTISPECIES: endonuclease MutS2 [Bacillus] |
| BSLIN78GL003120 | 100 | 0.00E+00 | WP_003229538.1 | MULTISPECIES: DNA polymerase/3'-5' exonuclease PolX [Bacillales |
| BSLIN78GL003121 | 100 | 1.30E-91 | WP_003229537.1 | MULTISPECIES: CvpA family protein [Bacillales] |
| BSLIN78GL003122 | 100 | 3.90E-41 | WP_003229534.1 | MULTISPECIES: cell division protein ZapA [Bacillales] |
| BSLIN78GL003123 | 100 | 2.20E-188 | WP_211197298.1 | ribonuclease HIII [Bacillus subtilis] |
| BSLIN78GL003124 | 99.9 | 0.00E+00 | WP_069322805.1 | phenylalanine--tRNA ligase subunit beta [Bacillus subtilis] |
| BSLIN78GL003125 | 100 | 3.50E-197 | WP_004398818.1 | MULTISPECIES: phenylalanine--tRNA ligase subunit alpha [Bacillales] |
| BSLIN78GL003126 | 100 | 3.50E-32 | WP_004398812.1 | MULTISPECIES: hypothetical protein [Bacillales] |
| BSLIN78GL003127 | 100 | 4.70E-135 | WP_015714484.1 | MULTISPECIES: RNA methyltransferase [Bacillus] |
| BSLIN78GL003128 | 100 | 2.10E-32 | WP_021480275.1 | MULTISPECIES: small acid-soluble spore protein SspI [Bacillus] |

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| BSLIN78GL003129 | 99.7 | 1.60E-211 | EHA30931.1 | hypothetical protein BSSC8_13740 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003130 | 99.4 | 5.60E-281 | EHA30930.1 | hypothetical protein BSSC8_13730 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003131 | 100 | 1.70E-257 | WP_017696691.1 | MULTISPECIES: (Fe-S)-binding protein [Bacillus |
| BSLIN78GL003132 | 100 | 1.80E-63 | AOL98718.1 | Lactoylglutathione lyase [Bacillus subtilis |
| BSLIN78GL003133 | 100 | 0.00E+00 | WP_014477607.1 | MULTISPECIES: carbon starvation protein CstA [Bacillus] |
| BSLIN78GL003134 | 100 | 4.90E-301 | EHA30926.1 | alpha-L-arabinofuranosidase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003135 | 100 | 4.00E-145 | QHF58885.1 | transport system permease protein [Bacillus subtilis] |
| BSLIN78GL003136 | 100 | 4.00E-176 | WP_087961011.1 | sugar ABC transporter permease [Bacillus subtilis] |
| BSLIN78GL003137 | 99.5 | 6.50E-257 | EHA30923.1 | sugar-binding protein [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003138 | 100 | 5.00E-224 | WP_015251502.1 | MULTISPECIES: sn-glycerol-1-phosphate dehydrogenase [Bacillus |
| BSLIN78GL003139 | 100 | 2.90E-146 | AKE24655.1 | arabinose operon protein L [Bacillus sp. LM 4-2] |
| BSLIN78GL003140 | 100 | 5.80E-132 | WP_015251500.1 | MULTISPECIES: L-ribulose-5-phosphate 4-epimerase [Bacillus |
| BSLIN78GL003141 | 100 | 0.00E+00 | WP_015251499.1 | MULTISPECIES: ribulokinase [Bacillus] |
| BSLIN78GL003142 | 100 | 2.90E-293 | WP_015251498.1 | L-arabinose isomerase [Bacillus subtilis] |
| BSLIN78GL003143 | 100 | 1.90E-192 | WP_015251497.1 | MULTISPECIES: arabinan endo-1,5-alpha-L-arabinosidase AbnA [Bacillus] |
| BSLIN78GL003144 | 100 | 3.10E-204 | WP_015251496.1 | MULTISPECIES: M42 family metallopeptidase [Bacillus |
| BSLIN78GL003145 | 100 | 6.10E-70 | WP_003229493.1 | MULTISPECIES: sigma W pathway protein YsdB [Bacillales] |
| BSLIN78GL003146 | 100 | 1.00E-44 | WP_003229490.1 | MULTISPECIES: DUF1294 domain-containing protein [Bacillales] |
| BSLIN78GL003147 | 100 | 2.10E-18 | WP_014114727.1 | MULTISPECIES: 50S ribosomal protein L20 [Bacillus] |
| BSLIN78GL003148 | 100 | 5.90E-29 | WP_003222418.1 | MULTISPECIES: 50S ribosomal protein L35 [Bacillales] |
| BSLIN78GL003149 | 100 | 1.90E-87 | WP_003222413.1 | MULTISPECIES: translation initiation factor IF-3 [Bacillus |
| BSLIN78GL003150 | 100 | 1.30E-117 | WP_015714496.1 | hypothetical protein [Bacillus] |
| BSLIN78GL003151 | 100 | 2.50E-122 | WP_003229482.1 | MULTISPECIES: antiholin-like protein LrgB [Bacillales |
| BSLIN78GL003152 | 100 | 5.20E-73 | AGA23774.1 | Antiholin-like protein LrgA [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003153 | 100 | 8.70E-131 | AGE64490.1 | two-component response regulator [Bacillus subtilis XF-1] |
| BSLIN78GL003154 | 100 | 0.00E+00 | WP_015251492.1 | MULTISPECIES: two-component system sensor histidine kinase LytS [Bacillus |
| BSLIN78GL003155 | 100 | 1.80E-156 | AGE64492.1 | hypothetical protein C663_2739 [Bacillus subtilis XF-1] |
| BSLIN78GL003156 | 100 | 0.00E+00 | WP_014480529.1 | MULTISPECIES: threonine--tRNA ligase [Bacillus |
| BSLIN78GL003157 | 100 | 1.40E-159 | WP_003229471.1 | MULTISPECIES: putative sporulation protein YtxC [Bacillales] |
| BSLIN78GL003158 | 100 | 6.00E-115 | AII36649.1 | TVP38/TMEM64 family membrane protein ytxB [Bacillus subtilis TO-A] |
| BSLIN78GL003159 | 100 | 5.20E-176 | WP_015251490.1 | MULTISPECIES: primosomal protein DnaI [Bacillus] |
| BSLIN78GL003160 | 100 | 2.90E-271 | WP_015251489.1 | MULTISPECIES: replication initiation membrane attachment protein DnaB |
| BSLIN78GL003161 | 100 | 1.40E-69 | AGE64498.1 | transcriptional regulator [Bacillus subtilis XF-1] |
| BSLIN78GL003162 | 100 | 1.80E-66 | AAC00356.1 | YtcF [Bacillus subtilis] |
| BSLIN78GL003163 | 100 | 4.40E-192 | WP_003229459.1 | MULTISPECIES: glyceraldehyde-3-phosphate dehydrogenase [Bacillales |
| BSLIN78GL003164 | 100 | 4.00E-66 | WP_003229458.1 | MULTISPECIES: winged helix-turn-helix transcriptional regulator [Bacillales |
| BSLIN78GL003165 | 100 | 6.10E-214 | WP_326253494.1 | MFS transporter [Bacillus subtilis] |
| BSLIN78GL003166 | 100 | 4.30E-161 | AGA21394.1 | Morphine dehydrogenase YtbE [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003167 | 99.5 | 4.20E-102 | QHF58918.1 | kinase [Bacillus subtilis] |
| BSLIN78GL003168 | 100 | 2.30E-111 | WP_003229449.1 | MULTISPECIES: sporulation membrane protein YtaF [Bacillus] |
| BSLIN78GL003169 | 100 | 4.40E-158 | WP_032678849.1 | MULTISPECIES: DNA-formamidopyrimidine glycosylase [Bacillus |
| BSLIN78GL003170 | 100 | 0.00E+00 | WP_014480537.1 | MULTISPECIES: DNA polymerase I [Bacillus |
| BSLIN78GL003171 | 99.8 | 0.00E+00 | WP_029726381.1 | MULTISPECIES: sensory box histidine kinase PhoR [Bacillus |
| BSLIN78GL003172 | 100 | 3.00E-131 | KDE23519.1 | chemotaxis protein CheY [Bacillus subtilis] |
| BSLIN78GL003173 | 100 | 2.40E-15 | AWM21882.1 | hypothetical protein DJ572_14285 [Bacillus subtilis] |
| BSLIN78GL003174 | 100 | 3.30E-170 | WP_003237775.1 | MULTISPECIES: malate dehydrogenase [Bacillus] |
| BSLIN78GL003175 | 100 | 5.70E-242 | WP_003229433.1 | MULTISPECIES: NADP-dependent isocitrate dehydrogenase [Bacillales |
| BSLIN78GL003176 | 100 | 8.40E-213 | EHA30884.1 | methylcitrate synthase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003177 | 100 | 8.90E-76 | WP_014480542.1 | MULTISPECIES: DUF441 family protein [Bacillus] |
| BSLIN78GL003178 | 100 | 4.50E-192 | WP_326352908.1 | sporulation integral membrane protein YtvI [Bacillus subtilis] |
| BSLIN78GL003179 | 99.2 | 2.00E-68 | QHF58930.1 | hypothetical protein Bateq7PJ16_3124 [Bacillus subtilis] |
| BSLIN78GL003180 | 99.8 | 0.00E+00 | AGA21381.1 | Pyruvate kinase [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003181 | 100 | 3.00E-179 | WP_003229420.1 | MULTISPECIES: 6-phosphofructokinase [Bacillales] |
| BSLIN78GL003182 | 100 | 7.50E-13 | AEP91921.1 | hypothetical protein I33_2978 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL003183 | 100 | 4.20E-184 | WP_003229417.1 | MULTISPECIES: acetyl-CoA carboxylase carboxyl transferase subunit alpha |
| BSLIN78GL003184 | 100 | 9.00E-173 | AGE64518.1 | acetyl-CoA carboxylase subunit beta [Bacillus subtilis XF-1 |
| BSLIN78GL003185 | 100 | 7.80E-228 | WP_029726397.1 | NADP-dependent malic enzyme [Bacillus subtilis] |
| BSLIN78GL003186 | 100 | 0.00E+00 | WP_029726398.1 | DNA polymerase III subunit alpha [Bacillus subtilis] |
| BSLIN78GL003187 | 100 | 2.00E-56 | WP_003229410.1 | MULTISPECIES: sporulation membrane protein YtrH [Bacillales] |
| BSLIN78GL003188 | 100 | 5.20E-90 | ASB62014.1 | sporulation protein [Bacillus sp. MD-5] |
| BSLIN78GL003189 | 100 | 1.60E-28 | WP_003229407.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL003190 | 99.7 | 5.50E-167 | WP_029726399.1 | bifunctional oligoribonuclease/PAP phosphatase NrnA [Bacillus subtilis] |
| BSLIN78GL003191 | 100 | 4.40E-13 | AEP91930.1 | hypothetical protein I33_2987 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL003192 | 100 | 1.60E-49 | WP_003229401.1 | MULTISPECIES: YtpI family protein [Bacillales |
| BSLIN78GL003193 | 100 | 1.20E-245 | AGA21371.1 | Hypothetical protein YtoI [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003194 | 100 | 5.20E-165 | WP_015714506.1 | MULTISPECIES: sulfite exporter TauE/SafE family protein [Bacillus |
| BSLIN78GL003195 | 100 | 7.60E-239 | WP_029726400.1 | S-alkyl-N-acetyl-metabolite deacetylase SndA [Bacillus subtilis |
| BSLIN78GL003196 | 100 | 3.00E-128 | WP_029318236.1 | MULTISPECIES: RNA-binding riboflavin kinase RibR [Bacillus] |
| BSLIN78GL003197 | 99.3 | 1.90E-256 | WP_019712898.1 | MULTISPECIES: LLM class flavin-dependent oxidoreductase [Bacillus |
| BSLIN78GL003198 | 100 | 5.20E-47 | WP_029726402.1 | glutaredoxin family protein [Bacillus subtilis] |
| BSLIN78GL003199 | 100 | 1.70E-185 | WP_029726403.1 | LLM class flavin-dependent oxidoreductase [Bacillus subtilis] |
| BSLIN78GL003200 | 100 | 2.20E-143 | WP_003229383.1 | MULTISPECIES: sulfur-containing amino-acid ABC transporter ATP-binding |
| BSLIN78GL003201 | 100 | 9.20E-125 | WP_019712895.1 | MULTISPECIES: sulfur-containing amino acid ABC transporter permease TcyM |
| BSLIN78GL003202 | 100 | 2.40E-131 | KIN55473.1 | hypothetical protein B4146_2952 [Bacillus subtilis] |
| BSLIN78GL003203 | 100 | 1.90E-150 | WP_029726404.1 | MULTISPECIES: sulfur-containing amino acid ABC transporter substrate-binding |
| BSLIN78GL003204 | 100 | 5.90E-152 | WP_029726405.1 | MULTISPECIES: sulfur-containing amino acid ABC transporter substrate-binding |
| BSLIN78GL003205 | 99.4 | 2.70E-100 | AGE64538.1 | putative N-acetyltransferase [Bacillus subtilis XF-1] |
| BSLIN78GL003206 | 100 | 7.00E-173 | WP_029726406.1 | MULTISPECIES: LysR family transcriptional regulator YtlI [Bacillus |
| BSLIN78GL003207 | 100 | 3.20E-130 | AGA21357.1 | Metal-dependent hydrolase YtkL [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003208 | 100 | 2.60E-141 | WP_004398521.1 | MULTISPECIES: SDR family oxidoreductase [Bacillales |

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| BSLIN78GL003209 | 100 | 6.40E-20 | AYK58019.1 | hypothetical protein D9C10_13035 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL003210 | 96.7 | 8.10E-258 | KAF1681547.1 | argininosuccinate lyase [Bacillus sp. SKDU12] |
| BSLIN78GL003211 | 99.8 | 5.60E-231 | WP_101502180.1 | argininosuccinate synthase [Bacillus subtilis] |
| BSLIN78GL003212 | 100 | 2.20E-88 | QHF58963.1 | cofactor biosynthesis protein B [Bacillus subtilis] |
| BSLIN78GL003213 | 100 | 3.00E-221 | RPK05741.1 | Acetate kinase [Bacillus subtilis] |
| BSLIN78GL003214 | 100 | 1.20E-17 | WP_119899691.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL003215 | 100 | 1.30E-185 | WP_003229346.1 | MULTISPECIES: N-6 DNA methylase [Bacillales |
| BSLIN78GL003216 | 100 | 2.00E-95 | AGE64548.1 | putative peroxiredoxin [Bacillus subtilis XF-1] |
| BSLIN78GL003217 | 99.4 | 5.80E-86 | EHA30843.1 | hypothetical protein BSSC8_12860 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003218 | 100 | 8.30E-126 | CAF1823503.1 | hypothetical protein NRS6137_02066 [Bacillus subtilis] |
| BSLIN78GL003219 | 100 | 6.70E-90 | WP_014480553.1 | MULTISPECIES: RDD family protein [Bacillus |
| BSLIN78GL003220 | 100 | 3.60E-183 | WP_015714516.1 | MULTISPECIES: signal peptide peptidase SppA [Bacillus |
| BSLIN78GL003221 | 100 | 1.00E-154 | AKE24736.1 | inorganic polyphosphate/ATP-NAD kinase [Bacillus sp. LM 4-2] |
| BSLIN78GL003222 | 99.8 | 7.2e-311 | WP_151262373.1 | amidohydrolase [Bacillus subtilis] |
| BSLIN78GL003223 | 100 | 0.00E+00 | WP_192857916.1 | acyl--CoA ligase [Bacillus subtilis] |
| BSLIN78GL003224 | 100 | 3.60E-17 | WGD68631.1 | alpha type acid-soluble spore protein SspA [Bacillus subtilis] |
| BSLIN78GL003225 | 100 | 1.30E-227 | WP_003229326.1 | MULTISPECIES: tRNA uracil 4-sulfurtransferase ThiI [Bacillales |
| BSLIN78GL003226 | 99.4 | 1.10E-198 | WP_029726412.1 | cysteine desulfurase family protein [Bacillus subtilis |
| BSLIN78GL003227 | 100 | 1.20E-245 | WP_017695726.1 | MULTISPECIES: branched-chain amino acid transport system II carrier protein |
| BSLIN78GL003228 | 100 | 0.00E+00 | WP_029726413.1 | septation ring formation regulator EzrA [Bacillus subtilis] |
| BSLIN78GL003229 | 99.6 | 1.30E-154 | AGA22329.1 | Histidinol-phosphatase (HolPase) [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003230 | 100 | 3.50E-112 | WP_014477663.1 | MULTISPECIES: transcriptional regulator RefZ [Bacillus] |
| BSLIN78GL003231 | 100 | 2.80E-88 | WP_014477664.1 | MULTISPECIES: GAF domain-containing protein [Bacillus |
| BSLIN78GL003232 | 100 | 0.00E+00 | WP_029726414.1 | diguanylate cyclase [Bacillus subtilis |
| BSLIN78GL003233 | 100 | 2.30E-27 | AEP91961.1 | hypothetical protein I33_3018 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL003234 | 100 | 2.70E-109 | WP_003229304.1 | MULTISPECIES: 30S ribosomal protein S4 [Bacillales] |
| BSLIN78GL003235 | 100 | 6.40E-15 | WP_015714524.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL003236 | 100 | 7.00E-240 | WP_029726415.1 | tyrosine--tRNA ligase [Bacillus subtilis] |
| BSLIN78GL003237 | 99.8 | 0.00E+00 | AKE24752.1 | acetyl-CoA synthetase [Bacillus sp. LM 4-2 |
| BSLIN78GL003238 | 100 | 2.50E-121 | WP_029726417.1 | acetoin utilization protein acetyltransferase AcuA [Bacillus subtilis |
| BSLIN78GL003239 | 100 | 3.80E-117 | WP_003229294.1 | MULTISPECIES: acetoin utilization AcuB family protein [Bacillales |
| BSLIN78GL003240 | 100 | 9.80E-236 | ASB94514.1 | Acetoin utilization protein AcuC [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL003241 | 100 | 2.00E-130 | WP_080529668.1 | flagellar motor protein MotS [Bacillus subtilis] |
| BSLIN78GL003242 | 99.3 | 2.50E-153 | AGE64571.1 | flagellar motor protein [Bacillus subtilis XF-1] |
| BSLIN78GL003243 | 100 | 2.10E-183 | WP_003229285.1 | MULTISPECIES: catabolite control protein A [Bacillales] |
| BSLIN78GL003244 | 100 | 3.00E-199 | BAI86482.2 | bifunctional 3-deoxy-7-phosphoheptulonate synthase/chorismate mutase [Bacillus |
| BSLIN78GL003245 | 100 | 1.20E-55 | WP_014480571.1 | MULTISPECIES: bacillithiol system redox-active protein YtxJ [Bacillus |
| BSLIN78GL003246 | 100 | 1.30E-76 | AAB40045.1 | similar to plant water stress proteins; ORF2 [Bacillus subtilis subsp. subtilis str. 168] |
| BSLIN78GL003247 | 100 | 9.50E-69 | WP_003229276.1 | MULTISPECIES: DUF948 domain-containing protein [Bacillales] |
| BSLIN78GL003248 | 100 | 3.30E-253 | WP_003229274.1 | MULTISPECIES: UDP-N-acetylmuramate--L-alanine ligase [Bacillales |
| BSLIN78GL003249 | 100 | 0.00E+00 | WP_029726418.1 | DNA translocase SftA [Bacillus subtilis] |
| BSLIN78GL003250 | 100 | 7.90E-109 | WP_003229269.1 | MULTISPECIES: DUF4479 family protein [Bacillales |
| BSLIN78GL003251 | 100 | 3.00E-148 | WP_029726419.1 | DUF1444 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL003252 | 100 | 2.90E-57 | WP_003229265.1 | MULTISPECIES: thioredoxin family protein [Bacillales |
| BSLIN78GL003253 | 100 | 3.70E-15 | AFI29520.1 | hypothetical protein MY9_2987 [Bacillus sp. JS] |
| BSLIN78GL003254 | 100 | 4.10E-78 | WP_003229263.1 | MULTISPECIES: YtoQ family protein [Bacillales |
| BSLIN78GL003255 | 100 | 1.00E-204 | WP_014480574.1 | MULTISPECIES: M42 family metallopeptidase [Bacillus |
| BSLIN78GL003256 | 100 | 1.10E-14 | AEP91983.1 | hypothetical protein I33_3042 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL003257 | 100 | 4.70E-52 | WP_014480575.1 | MULTISPECIES: PepSY domain-containing protein [Bacillus] |
| BSLIN78GL003258 | 100 | 0.00E+00 | WP_128471895.1 | NAD-dependent malic enzyme [Bacillus subtilis] |
| BSLIN78GL003259 | 99.3 | 3.70E-168 | AGE64586.1 | hypothetical protein C663_2836 [Bacillus subtilis XF-1] |
| BSLIN78GL003260 | 100 | 7.30E-121 | AKE24774.1 | tRNA (guanine-N(7)-)-methyltransferase [Bacillus sp. LM 4-2] |
| BSLIN78GL003261 | 100 | 3.30E-46 | WP_003237926.1 | MULTISPECIES: YtzH-like family protein [Bacillales |
| BSLIN78GL003262 | 100 | 8.00E-157 | C0SPC1.2 | RecName: Full=Cell cycle regulator CcrZ; AltName: Full=Cell cycle regulator protein interacting with FtsZ [Bacillus subtilis subsp. subtilis str. 168] |
| BSLIN78GL003263 | 100 | 0.00E+00 | WP_225722088.1 | type I pullulanase [Bacillus subtilis] |
| BSLIN78GL003264 | 100 | 3.80E-179 | WP_003229243.1 | MULTISPECIES: diacylglycerol kinase family lipid kinase [Bacillales |
| BSLIN78GL003265 | 100 | 1.10E-170 | WP_003229241.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL003266 | 99.5 | 9.60E-121 | QHF59016.1 | 2',3'-cyclic phosphodiesterase [Bacillus subtilis |
| BSLIN78GL003267 | 100 | 6.40E-174 | AGA22296.1 | Cysteine synthase [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003268 | 99.4 | 6.30E-274 | BAI86506.2 | dipeptidase PepV [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL003269 | 100 | 9.60E-237 | WP_069964255.1 | hypoxanthine/guanine permease PbuO [Bacillus subtilis] |
| BSLIN78GL003270 | 100 | 1.50E-217 | WP_041339776.1 | ABC transporter permease [Bacillus subtilis] |
| BSLIN78GL003271 | 100 | 1.70E-131 | WP_041339774.1 | ABC transporter ATP-binding protein [Bacillus subtilis] |
| BSLIN78GL003272 | 100 | 2.20E-24 | WP_003152337.1 | MULTISPECIES: DeoR family transcriptional regulator [Bacillales |
| BSLIN78GL003273 | 100 | 1.00E-131 | WP_017695479.1 | MULTISPECIES: pseudouridine synthase [Bacillus |
| BSLIN78GL003274 | 100 | 8.80E-304 | WP_088467337.1 | lipid II flippase MurJ [Bacillus subtilis] |
| BSLIN78GL003275 | 100 | 2.40E-240 | WP_029946380.1 | MULTISPECIES: NAD(P)/FAD-dependent oxidoreductase [Bacillus |
| BSLIN78GL003276 | 100 | 1.10E-292 | WP_015384403.1 | MULTISPECIES: glycine betaine transporter OpuD [Bacillus |
| BSLIN78GL003277 | 100 | 4.30E-26 | WP_003223398.1 | MULTISPECIES: sporulation protein Cse60 [Bacillales] |
| BSLIN78GL003278 | 97.8 | 5.70E-127 | QHF59028.1 | hypothetical protein Bateq7PJ16_3222 [Bacillus subtilis] |
| BSLIN78GL003279 | 100 | 4.40E-247 | WP_064911649.1 | Gfo/Idh/MocA family oxidoreductase [Bacillus subtilis |
| BSLIN78GL003280 | 99.4 | 2.90E-82 | WP_172480856.1 | rhamnogalaturonan transport/degradation protein RmgS [Bacillus subtilis] |
| BSLIN78GL003281 | 100 | 1.10E-223 | WP_157678514.1 | unsaturated rhamnogalacturonyl hydrolase [Bacillus subtilis] |
| BSLIN78GL003282 | 100 | 8.90E-179 | WP_003229209.1 | MULTISPECIES: polygalacturonan/rhamnogalacturonan ABC transporter permease |
| BSLIN78GL003283 | 100 | 0.00E+00 | WP_003229207.1 | MULTISPECIES: helix-turn-helix domain-containing protein [Bacillus |
| BSLIN78GL003284 | 100 | 4.60E-291 | WP_003229205.1 | MULTISPECIES: extracellular solute-binding protein [Bacillus |
| BSLIN78GL003285 | 100 | 2.50E-159 | ADV93813.1 | putative ABC transporter permease [Bacillus subtilis BSn5] |
| BSLIN78GL003286 | 99.2 | 7.70E-139 | AGE64613.1 | hypothetical protein C663_2863 [Bacillus subtilis XF-1] |
| BSLIN78GL003287 | 99.3 | 3.60E-233 | WP_051673219.1 | biotin biosynthesis cytochrome P450 [Bacillus subtilis] |

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| BSLIN78GL003288 | 100 | 3.70E-191 | EHA30774.1 | biotin synthase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003289 | 100 | 8.90E-125 | WAE47409.1 | dethiobiotin synthase [Bacillus subtilis] |
| BSLIN78GL003290 | 100 | 3.20E-212 | WP_147797521.1 | 8-amino-7-oxononanoate synthase [Bacillus subtilis] |
| BSLIN78GL003291 | 100 | 1.30E-260 | WP_088467342.1 | adenosylmethionine--8-amino-7-oxononanoate transaminase [Bacillus subtilis] |
| BSLIN78GL003292 | 100 | 4.10E-150 | WP_029726434.1 | 6-carboxyhexanoate--CoA ligase [Bacillus subtilis] |
| BSLIN78GL003293 | 100 | 2.60E-172 | WP_038427848.1 | MULTISPECIES: alpha/beta hydrolase [Bacillus] |
| BSLIN78GL003294 | 100 | 9.80E-192 | WP_038427849.1 | MULTISPECIES: LacI family DNA-binding transcriptional regulator [Bacillus |
| BSLIN78GL003295 | 100 | 5.40E-248 | WP_038427850.1 | ABC transporter substrate-binding protein [Bacillus subtilis] |
| BSLIN78GL003296 | 100 | 1.30E-157 | WP_015251409.1 | MULTISPECIES: sugar ABC transporter permease [Bacillus] |
| BSLIN78GL003297 | 100 | 7.50E-150 | WP_014480612.1 | MULTISPECIES: carbohydrate ABC transporter permease [Bacillus] |
| BSLIN78GL003298 | 100 | 2.10E-252 | WP_038427852.1 | alpha-galactosidase MelA [Bacillus subtilis] |
| BSLIN78GL003299 | 99.1 | 2.50E-53 | AGE64627.1 | hypothetical protein C663_2878 [Bacillus subtilis XF-1] |
| BSLIN78GL003300 | 99.1 | 0.00E+00 | WP_326154529.1 | leucine--tRNA ligase [Bacillus subtilis] |
| BSLIN78GL003301 | 100 | 3.40E-56 | AGE64629.1 | hypothetical protein C663_2880 [Bacillus subtilis XF-1] |
| BSLIN78GL003302 | 100 | 2.90E-143 | WP_119899714.1 | blue-light photoreceptor [Bacillus subtilis] |
| BSLIN78GL003303 | 99.7 | 7.50E-220 | WP_119899716.1 | MFS transporter [Bacillus subtilis] |
| BSLIN78GL003304 | 100 | 2.50E-136 | WP_014480618.1 | MULTISPECIES: LMBR1 domain-containing protein [Bacillus] |
| BSLIN78GL003305 | 100 | 0.00E+00 | WP_088326787.1 | bacitracin ABC transporter permease BceB [Bacillus subtilis] |
| BSLIN78GL003306 | 100 | 7.10E-139 | WP_003229137.1 | MULTISPECIES: bacitracin ABC transporter ATP-binding protein BceA [Bacillales |
| BSLIN78GL003307 | 100 | 4.40E-189 | WP_088326789.1 | two-component sensor histidine kinase BceS [Bacillus subtilis] |
| BSLIN78GL003308 | 100 | 1.60E-129 | WP_003229133.1 | MULTISPECIES: two-component response regulator BceR [Bacillus |
| BSLIN78GL003309 | 100 | 3.70E-244 | WP_038427856.1 | MULTISPECIES: ABC transporter permease YtrF [Bacillus] |
| BSLIN78GL003310 | 100 | 2.80E-126 | WP_003229129.1 | MULTISPECIES: ABC transporter ATP-binding protein YtrE [Bacillales] |
| BSLIN78GL003311 | 100 | 5.80E-186 | WP_029726913.1 | MULTISPECIES: ABC transporter permease YtrD [Bacillus] |
| BSLIN78GL003312 | 99.7 | 2.80E-177 | WP_029726914.1 | MULTISPECIES: ABC transporter permease YtrC [Bacillus] |
| BSLIN78GL003313 | 100 | 6.90E-162 | WP_003229123.1 | MULTISPECIES: ABC transporter ATP-binding protein YtrB [Bacillus |
| BSLIN78GL003314 | 100 | 3.10E-66 | WP_003229121.1 | MULTISPECIES: GntR family transcriptional regulator YtrA [Bacillales |
| BSLIN78GL003315 | 100 | 9.40E-18 | AFQ58889.1 | Hypothetical protein B657_30465 [Bacillus subtilis QB928] |
| BSLIN78GL003316 | 100 | 1.30E-35 | WP_003229117.1 | MULTISPECIES: YtzC family protein [Bacillales |
| BSLIN78GL003317 | 100 | 1.50E-189 | WP_024572829.1 | MULTISPECIES: TIGR01212 family radical SAM protein [Bacillus |
| BSLIN78GL003318 | 100 | 6.70E-105 | WP_003229113.1 | MULTISPECIES: class I SAM-dependent methyltransferase [Bacillus |
| BSLIN78GL003319 | 100 | 1.50E-217 | AHA78968.1 | Uncharacterized protein ytpB [Bacillus subtilis PY79] |
| BSLIN78GL003320 | 100 | 1.10E-147 | WP_004398545.1 | MULTISPECIES: phospholipase YtpA [Bacillales] |
| BSLIN78GL003321 | 100 | 6.80E-93 | WP_029726915.1 | gamma carbonic anhydrase family protein [Bacillus subtilis] |
| BSLIN78GL003322 | 99.6 | 9.90E-264 | WP_131227870.1 | alanine permease AlaP [Bacillus subtilis] |
| BSLIN78GL003323 | 100 | 0.00E+00 | WP_326253479.1 | asparagine synthase (glutamine-hydrolyzing) [Bacillus subtilis |
| BSLIN78GL003324 | 100 | 8.40E-227 | WP_003229102.1 | MULTISPECIES: methionine adenosyltransferase [Bacillales |
| BSLIN78GL003325 | 100 | 0.00E+00 | WP_029726916.1 | MULTISPECIES: phosphoenolpyruvate carboxykinase (ATP) [Bacillus |
| BSLIN78GL003326 | 100 | 4.10E-37 | WP_004398611.1 | MULTISPECIES: DUF2584 domain-containing protein [Bacillales] |
| BSLIN78GL003327 | 100 | 1.30E-148 | WP_326253478.1 | prolyl oligopeptidase family serine peptidase [Bacillus subtilis |
| BSLIN78GL003328 | 99.7 | 1.50E-195 | AIX08687.1 | NMT1/THI5 like protein [Bacillus subtilis] |
| BSLIN78GL003329 | 100 | 3.40E-144 | WP_003229092.1 | MULTISPECIES: ABC transporter ATP-binding protein [Bacillales |
| BSLIN78GL003330 | 100 | 6.20E-149 | WP_014477740.1 | MULTISPECIES: ABC transporter permease [Bacillus] |
| BSLIN78GL003331 | 100 | 1.80E-87 | WP_003229087.1 | MULTISPECIES: nucleoside triphosphatase YtkD [Bacillales] |
| BSLIN78GL003332 | 100 | 4.20E-66 | WP_015714569.1 | MULTISPECIES: holin family protein [Bacillus |
| BSLIN78GL003333 | 100 | 1.50E-22 | AEP92062.1 | hypothetical protein I33_3121 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL003334 | 100 | 1.50E-77 | WP_003229083.1 | MULTISPECIES: Dps family protein [Bacillales] |
| BSLIN78GL003335 | 100 | 9.60E-18 | AGE64660.1 | hypothetical protein C663_2914 [Bacillus subtilis XF-1] |
| BSLIN78GL003336 | 100 | 1.30E-76 | WP_029727098.1 | FixH family protein [Bacillus subtilis] |
| BSLIN78GL003337 | 100 | 1.90E-86 | WP_029318295.1 | S-ribosylhomocysteine lyase [Bacillus subtilis |
| BSLIN78GL003338 | 100 | 5.50E-39 | WP_003229076.1 | MULTISPECIES: membrane protein insertion efficiency factor YidD [Bacillales |
| BSLIN78GL003339 | 100 | 1.80E-102 | WP_003229074.1 | MULTISPECIES: carbonic anhydrase [Bacillales |
| BSLIN78GL003340 | 100 | 9.90E-42 | WP_003219346.1 | MULTISPECIES: type B 50S ribosomal protein L31 [Bacillales |
| BSLIN78GL003341 | 100 | 6.80E-254 | WP_029318296.1 | MULTISPECIES: cytochrome ubiquinol oxidase subunit I [Bacillus |
| BSLIN78GL003342 | 100 | 1.10E-193 | UBZ19951.1 | Putative cytochrome bd menaquinol oxidase subunit II [Bacillus subtilis] |
| BSLIN78GL003343 | 100 | 2.00E-24 | WP_003229069.1 | MULTISPECIES: DUF1540 domain-containing protein [Bacillales] |
| BSLIN78GL003344 | 100 | 7.20E-159 | WP_029727099.1 | MULTISPECIES: manganese ABC transporter permease MntD [Bacillus] |
| BSLIN78GL003345 | 100 | 2.00E-242 | WP_029727100.1 | manganese ABC transporter permease MntC [Bacillus subtilis] |
| BSLIN78GL003346 | 99.6 | 2.40E-139 | QHF59095.1 | transport system ATP-binding protein [Bacillus subtilis] |
| BSLIN78GL003347 | 99.4 | 1.70E-174 | BAI86590.2 | manganese ABC transporter, membrane protein [Bacillus subtilis subsp. natto |
| BSLIN78GL003348 | 100 | 3.70E-213 | WP_003229057.1 | MULTISPECIES: o-succinylbenzoate synthase [Bacillus |
| BSLIN78GL003349 | 100 | 1.10E-278 | WP_029727102.1 | o-succinylbenzoate--CoA ligase [Bacillus subtilis |
| BSLIN78GL003350 | 100 | 3.40E-155 | WP_003229054.1 | MULTISPECIES: 1,4-dihydroxy-2-naphthoyl-CoA synthase [Bacillales |
| BSLIN78GL003351 | 100 | 1.10E-153 | WP_326147265.1 | 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Bacillus subtilis |
| BSLIN78GL003352 | 100 | 0.00E+00 | WP_326147266.1 | 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthas |
| BSLIN78GL003353 | 100 | 2.90E-285 | BAI86597.2 | menaquinone-specific isochorismate synthase [Bacillus subtilis subsp. natto |
| BSLIN78GL003354 | 97.6 | 9.40E-17 | ADV93881.1 | hypothetical protein BSn5_06265 [Bacillus subtilis BSn5] |
| BSLIN78GL003355 | 100 | 8.20E-137 | WP_029727104.1 | yteA family sporulation protein [Bacillus subtilis] |
| BSLIN78GL003356 | 100 | 3.50E-152 | WP_003229044.1 | MULTISPECIES: UTP--glucose-1-phosphate uridylyltransferase [Bacillales |
| BSLIN78GL003357 | 100 | 1.10E-240 | EHA31690.1 | hypothetical protein BSSC8_11480 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003358 | 100 | 1.80E-179 | WP_029318306.1 | MULTISPECIES: NAD-dependent epimerase/dehydratase family protein [Bacillus |
| BSLIN78GL003359 | 100 | 5.50E-234 | WP_003229035.1 | MULTISPECIES: glycosyltransferase family 4 protein [Bacillales |
| BSLIN78GL003360 | 100 | 3.70E-76 | WP_004399071.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL003361 | 100 | 6.50E-207 | WP_003229031.1 | MULTISPECIES: spore coat protein CotS [Bacillales] |
| BSLIN78GL003362 | 100 | 8.70E-218 | WP_038427868.1 | spore coat protein CotSA [Bacillus subtilis] |
| BSLIN78GL003363 | 100 | 2.10E-205 | WP_072692952.1 | spore coat kinase CotI [Bacillus subtilis] |
| BSLIN78GL003364 | 100 | 9.20E-81 | WP_003229024.1 | MULTISPECIES: TspO/MBR family protein [Bacillales |
| BSLIN78GL003365 | 99.4 | 0.00E+00 | AGE64687.1 | glycogen phosphorylase [Bacillus subtilis XF-1 |
| BSLIN78GL003366 | 99.8 | 1.40E-284 | WP_038427871.1 | glycogen synthase GlgA [Bacillus subtilis |
| BSLIN78GL003367 | 100 | 3.80E-196 | WP_032679196.1 | glucose-1-phosphate adenylyltransferase subunit GlgD [Bacillus subtilis |

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| BSLIN78GL003368 | 100 | 8.50E-221 | WP_003229018.1 | MULTISPECIES: glucose-1-phosphate adenylyltransferase [Bacillus |
| BSLIN78GL003369 | 100 | 0.00E+00 | WP_068947633.1 | 1,4-alpha-glucan branching enzyme [Bacillus subtilis] |
| BSLIN78GL003370 | 100 | 1.30E-16 | AGE64691.1 | hypothetical protein C663_2948 [Bacillus subtilis XF-1] |
| BSLIN78GL003371 | 99.4 | 1.40E-84 | AKE21963.1 | hypothetical protein BsLM_0164 [Bacillus sp. LM 4-2] |
| BSLIN78GL003372 | 100 | 1.40E-99 | WP_003228966.1 | MULTISPECIES: energy-coupled thiamine transporter ThiT [Bacillales |
| BSLIN78GL003373 | 100 | 6.20E-94 | WP_003228963.1 | MULTISPECIES: GNAT family N-acetyltransferase [Bacillales |
| BSLIN78GL003374 | 100 | 2.50E-276 | WP_003228960.1 | MULTISPECIES: flotillin lipid rafts scaffold protein FloT [Bacillales |
| BSLIN78GL003375 | 100 | 3.70E-100 | ADV93901.1 | putative membreane integrity integral inner membrane protein [Bacillus subtilis |
| BSLIN78GL003376 | 100 | 6.80E-96 | AGE64697.1 | hypothetical protein C663_2954 [Bacillus subtilis XF-1] |
| BSLIN78GL003377 | 100 | 4.60E-106 | WP_003243361.1 | MULTISPECIES: MOSC domain-containing protein [Bacillales] |
| BSLIN78GL003378 | 100 | 8.70E-232 | AGA22833.1 | Alcohol dehydrogenase [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003379 | 100 | 1.90E-292 | EHA32871.1 | glycine betaine aldehyde dehydrogenase [Bacillus subtilis subsp. subtilis str. SC-8 |
| BSLIN78GL003380 | 100 | 3.70E-97 | WP_003244320.1 | MULTISPECIES: transcriptional regulator GbsR [Bacillales] |
| BSLIN78GL003381 | 99.5 | 3.10E-108 | BAI86623.2 | hypothetical protein BSNT_09558 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL003382 | 100 | 5.30E-122 | WP_003228942.1 | MULTISPECIES: potassium uptake protein KtrA [Bacillus] |
| BSLIN78GL003383 | 100 | 2.40E-246 | WP_003228940.1 | MULTISPECIES: Ktr system potassium transporter KtrB [Bacillus] |
| BSLIN78GL003384 | 100 | 8.90E-41 | WP_121591084.1 | YiaA/YiaB family protein [Bacillus subtilis] |
| BSLIN78GL003385 | 100 | 4.20E-156 | QHK00957.1 | Exo-glucosaminidase LytG [Bacillus subtilis] |
| BSLIN78GL003386 | 99.8 | 1.90E-287 | WP_326224829.1 | MFS transporter [Bacillus subtilis] |
| BSLIN78GL003387 | 100 | 2.50E-25 | ASK25096.1 | putative membrane protein [Bacillus subtilis] |
| BSLIN78GL003388 | 100 | 4.00E-87 | WP_029726532.1 | MULTISPECIES: cysteine dioxygenase [Bacillus |
| BSLIN78GL003389 | 100 | 1.60E-17 | AHA79033.1 | Hypothetical Protein U712_15475 [Bacillus subtilis PY79] |
| BSLIN78GL003390 | 100 | 4.80E-152 | AGA22844.1 | Undecaprenyl-diphosphatase [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003391 | 99.7 | 2.30E-216 | WP_198421544.1 | MULTISPECIES: AI-2E family transporter [Bacillus |
| BSLIN78GL003392 | 100 | 1.10E-184 | ANY33165.1 | oxidoreductase [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL003393 | 100 | 1.10E-250 | WP_017695497.1 | MULTISPECIES: L-rhamnose isomerase [Bacillus] |
| BSLIN78GL003394 | 100 | 6.90E-56 | WP_015714599.1 | MULTISPECIES: L-rhamnose mutarotase [Bacillus] |
| BSLIN78GL003395 | 100 | 1.40E-281 | WP_147797753.1 | rhamnulokinase [Bacillus subtilis] |
| BSLIN78GL003396 | 100 | 4.00E-137 | WP_147797754.1 | rhamnose catabolism operon transcriptional regulator RhaR [Bacillus subtilis] |
| BSLIN78GL003397 | 100 | 0.00E+00 | BAI86637.2 | short chain dehydrogenase [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL003398 | 100 | 1.30E-27 | AMK73522.1 | hypothetical protein AWV81_16030 [Bacillus subtilis subsp. natto] |
| BSLIN78GL003399 | 100 | 0.00E+00 | WP_015714602.1 | MULTISPECIES: methyl-accepting chemotaxis protein TlpB [Bacillus |
| BSLIN78GL003400 | 100 | 0.00E+00 | WP_029318506.1 | methyl-accepting chemotaxis protein [Bacillus subtilis] |
| BSLIN78GL003401 | 100 | 0.00E+00 | WP_086344247.1 | methyl-accepting chemotaxis protein TlpA [Bacillus subtilis] |
| BSLIN78GL003402 | 100 | 0.00E+00 | WP_015714604.1 | MULTISPECIES: methyl-accepting chemotaxis protein McpB [Bacillus |
| BSLIN78GL003403 | 100 | 2.40E-139 | WP_003228904.1 | MULTISPECIES: protein-glutamine gamma-glutamyltransferase [Bacillus] |
| BSLIN78GL003404 | 98.9 | 1.70E-44 | QHF59223.1 | hypothetical protein Bateq7PJ16_3417 [Bacillus subtilis] |
| BSLIN78GL003405 | 98 | 1.40E-19 | KIN27349.1 | hypothetical protein B4069_3352 [Bacillus subtilis] |
| BSLIN78GL003406 | 100 | 1.50E-77 | EHA32845.1 | hypothetical protein BSSC8_11020 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003407 | 100 | 0.00E+00 | WP_147797755.1 | alpha-glucosidase [Bacillus subtilis] |
| BSLIN78GL003408 | 100 | 2.70E-239 | KIN34757.1 | hypothetical protein B4068_3139 [Bacillus subtilis] |
| BSLIN78GL003409 | 100 | 2.50E-119 | WP_003228889.1 | MULTISPECIES: zinc metallopeptidase [Bacillales] |
| BSLIN78GL003410 | 98.9 | 7.50E-43 | AGE64728.1 | hypothetical protein C663_2989 [Bacillus subtilis XF-1] |
| BSLIN78GL003411 | 100 | 8.00E-55 | WP_003228886.1 | MULTISPECIES: biofilm formation protein MstX [Bacillales] |
| BSLIN78GL003412 | 100 | 1.20E-183 | WP_015384493.1 | MULTISPECIES: potassium channel protein KbfO [Bacillus] |
| BSLIN78GL003413 | 100 | 2.00E-71 | WP_021480481.1 | YugN-like family protein [Bacillus subtilis] |
| BSLIN78GL003414 | 100 | 2.90E-73 | AIX08764.1 | hypothetical protein OB04_03145 [Bacillus subtilis] |
| BSLIN78GL003415 | 99.6 | 1.90E-259 | WP_003220778.1 | glucose-6-phosphate isomerase [Bacillus spizizenii] |
| BSLIN78GL003416 | 100 | 3.70E-227 | WP_326253848.1 | iron-containing alcohol dehydrogenase [Bacillus subtilis] |
| BSLIN78GL003417 | 100 | 9.90E-225 | WP_195727740.1 | iron-containing alcohol dehydrogenase [Bacillus subtilis] |
| BSLIN78GL003418 | 100 | 1.00E-35 | WP_003220771.1 | MULTISPECIES: DUF378 domain-containing protein [Bacillales] |
| BSLIN78GL003419 | 100 | 1.60E-65 | WP_003228864.1 | MULTISPECIES: S1 domain-containing post-transcriptional regulator GSP13 |
| BSLIN78GL003420 | 100 | 1.30E-216 | WP_003228862.1 | MULTISPECIES: aminotransferase [Bacillus] |
| BSLIN78GL003421 | 100 | 3.80E-88 | AGE64739.1 | putative transcriptional regulator (Lrp/AsnC family) [Bacillus subtilis XF-1] |
| BSLIN78GL003422 | 100 | 9.90E-155 | WP_080529726.1 | alpha/beta hydrolase [Bacillus subtilis] |
| BSLIN78GL003423 | 100 | 4.70E-42 | WP_101172172.1 | YugE family protein [Bacillus subtilis] |
| BSLIN78GL003424 | 100 | 6.90E-226 | WP_326253850.1 | cystathionine beta-lyase PatB [Bacillus subtilis] |
| BSLIN78GL003425 | 100 | 1.20E-239 | WP_095010587.1 | sporulation sensor histidine kinase KinB [Bacillus subtilis] |
| BSLIN78GL003426 | 100 | 1.00E-69 | WP_122894651.1 | MULTISPECIES: kinase-associated lipoprotein KapB [Bacillus] |
| BSLIN78GL003427 | 100 | 1.20E-115 | WP_014480688.1 | MULTISPECIES: 3'-5' exonuclease KapD [Bacillus |
| BSLIN78GL003428 | 100 | 2.40E-30 | WP_128471905.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL003429 | 100 | 1.90E-212 | WP_122894652.1 | multidrug efflux MFS transporter [Bacillus subtilis] |
| BSLIN78GL003430 | 99.8 | 0.00E+00 | WP_003244316.1 | MULTISPECIES: transglycosylase domain-containing protein [Bacillus |
| BSLIN78GL003431 | 100 | 5.60E-74 | WP_122894653.1 | thiol-disulfide oxidoreductase DCC family protein [Bacillus subtilis] |
| BSLIN78GL003432 | 100 | 3.20E-96 | WP_003228837.1 | MULTISPECIES: YufK family protein [Bacillales |
| BSLIN78GL003433 | 100 | 1.10E-298 | WP_003228835.1 | MULTISPECIES: two-component system sensor histidine kinase MaeL [Bacillales |
| BSLIN78GL003434 | 100 | 8.50E-120 | AGE64752.1 | two-component response regulator [Bacillus subtilis XF-1] |
| BSLIN78GL003435 | 100 | 7.10E-201 | WP_015384509.1 | MULTISPECIES: guanosine ABC transporter substrate-binding protein NupN |
| BSLIN78GL003436 | 99.6 | 7.80E-286 | WP_125121161.1 | guanosine ABC transporter ATP-binding protein NupO [Bacillus subtilis] |
| BSLIN78GL003437 | 99.7 | 9.40E-187 | WP_046160790.1 | MULTISPECIES: guanosine ABC transporter permease NupP [Bacillus] |
| BSLIN78GL003438 | 100 | 3.50E-175 | WP_014480697.1 | MULTISPECIES: guanosine ABC transporter permease NupQ [Bacillus] |
| BSLIN78GL003439 | 99.8 | 5.90E-253 | AGE64757.1 | Na+/malate symporter [Bacillus subtilis XF-1] |
| BSLIN78GL003440 | 100 | 1.20E-21 | WP_206695941.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL003441 | 100 | 0.00E+00 | WP_326253855.1 | Na+/H+ antiporter subunit A [Bacillus subtilis] |
| BSLIN78GL003442 | 100 | 4.20E-72 | WP_003228819.1 | MULTISPECIES: Na(+)/H(+) antiporter subunit B [Bacillales] |
| BSLIN78GL003443 | 100 | 5.40E-54 | WP_003220730.1 | MULTISPECIES: Na(+)/H(+) antiporter subunit C [Bacillales] |
| BSLIN78GL003444 | 99.8 | 7.80E-275 | KIO58225.1 | hypothetical protein B4143_4236 [Bacillus subtilis] |
| BSLIN78GL003445 | 100 | 1.00E-82 | WP_003228815.1 | MULTISPECIES: Na+/H+ antiporter subunit E [Bacillus] |
| BSLIN78GL003446 | 100 | 1.10E-41 | AKE24957.1 | putative monovalent cation/H+ antiporter subunit F [Bacillus sp. LM 4-2] |
| BSLIN78GL003447 | 100 | 3.40E-62 | WP_326253858.1 | monovalent cation/H(+) antiporter subunit G [Bacillus subtilis] |

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| BSLIN78GL003448 | 98.4 | 3.40E-65 | CAF1754827.1 | Putative esterase HI_1161 [Bacillus subtilis] |
| BSLIN78GL003449 | 100 | 1.90E-113 | QHF59268.1 | regulatory protein [Bacillus subtilis] |
| BSLIN78GL003450 | 100 | 0.00E+00 | WP_032722435.1 | MULTISPECIES: histidine kinase [Bacillus] |
| BSLIN78GL003451 | 100 | 1.40E-34 | WP_014480704.1 | MULTISPECIES: competence pheromone ComX [Bacillus] |
| BSLIN78GL003452 | 100 | 3.80E-157 | D4G0R4.2 | RecName: Full=Tryptophan prenyltransferase ComQ; AltName: Full=ComX-tryptophan prenyltransferase [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL003453 | 100 | 1.60E-18 | AGE64770.1 | pleiotropic regulator [Bacillus subtilis XF-1] |
| BSLIN78GL003454 | 100 | 4.40E-18 | AKE24965.1 | hypothetical protein BsLM_3168 [Bacillus sp. LM 4-2] |
| BSLIN78GL003455 | 99.2 | 5.80E-62 | WP_046381300.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL003456 | 100 | 1.40E-232 | WP_046381301.1 | MULTISPECIES: cyclic di-GMP phosphodiesterase [Bacillus] |
| BSLIN78GL003457 | 100 | 2.40E-284 | WP_003228788.1 | MULTISPECIES: nicotinate phosphoribosyltransferase [Bacillales] |
| BSLIN78GL003458 | 99.5 | 2.70E-106 | AGA22906.1 | Hypothetical protein YueJ [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003459 | 100 | 2.00E-68 | WP_015251331.1 | MULTISPECIES: YueI family protein [Bacillus] |
| BSLIN78GL003460 | 100 | 6.00E-39 | WP_021480501.1 | MULTISPECIES: YueH family protein [Bacillus] |
| BSLIN78GL003461 | 100 | 3.40E-33 | WP_014477839.1 | MULTISPECIES: spore germination protein [Bacillus] |
| BSLIN78GL003462 | 100 | 1.30E-202 | WP_015483636.1 | MULTISPECIES: AI-2E family transporter [Bacillus] |
| BSLIN78GL003463 | 95.6 | 4.00E-72 | EHA32787.1 | hypothetical protein BSSC8_10440 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003464 | 98.1 | 6.10E-21 | QHF59283.1 | hypothetical protein Bateq7PJ16_3477 [Bacillus subtilis] |
| BSLIN78GL003466 | 100 | 8.00E-97 | WP_003244444.1 | MULTISPECIES: HD domain-containing protein [Bacillales] |
| BSLIN78GL003467 | 100 | 2.80E-132 | WP_038429544.1 | (S)-benzoin forming benzil reductase [Bacillus subtilis] |
| BSLIN78GL003468 | 100 | 2.20E-82 | ADV93990.1 | hypothetical protein BSn5_06820 [Bacillus subtilis BSn5] |
| BSLIN78GL003469 | 100 | 0.00E+00 | WP_114523642.1 | type VII secretion protein EsaA [Bacillus subtilis] |
| BSLIN78GL003470 | 99.3 | 0.00E+00 | TDY58500.1 | S-DNA-T family DNA segregation ATPase FtsK/SpoIIIE [Bacillus subtilis] |
| BSLIN78GL003471 | 100 | 9.70E-256 | WP_134982796.1 | type VII secretion protein EssB [Bacillus subtilis] |
| BSLIN78GL003472 | 100 | 1.20E-39 | WP_003228763.1 | MULTISPECIES: ESX secretion system protein YukD [Bacillales] |
| BSLIN78GL003473 | 100 | 3.50E-46 | WP_003220661.1 | MULTISPECIES: WXG100 family type VII secretion target [Bacillales |
| BSLIN78GL003474 | 98.5 | 9.20E-30 | API43297.1 | hypothetical protein BSR08_12710 [Bacillus subtilis] |
| BSLIN78GL003475 | 100 | 2.80E-230 | POD88043.1 | Transcriptional activator AdeR [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL003476 | 100 | 2.20E-227 | AGE64789.1 | L-alanine dehydrogenase [Bacillus subtilis XF-1] |
| BSLIN78GL003477 | 100 | 2.80E-131 | WP_003228755.1 | MULTISPECIES: YukJ family protein [Bacillus] |
| BSLIN78GL003478 | 100 | 1.30E-34 | WP_003243183.1 | MULTISPECIES: MbtH family protein [Bacillales] |
| BSLIN78GL003479 | 99.6 | 0.00E+00 | WP_247470728.1 | non-ribosomal peptide synthetase DhbF [Bacillus subtilis] |
| BSLIN78GL003480 | 100 | 1.20E-177 | WP_019712935.1 | isochorismatase [Bacillus subtilis] |
| BSLIN78GL003481 | 100 | 0.00E+00 | WP_076457638.1 | (2,3-dihydroxybenzoyl)adenylate synthase [Bacillus subtilis |
| BSLIN78GL003482 | 100 | 1.70E-227 | WP_119899735.1 | isochorismate synthase DhbC [Bacillus subtilis] |
| BSLIN78GL003483 | 100 | 1.20E-141 | WP_014480725.1 | MULTISPECIES: 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase [Bacillus |
| BSLIN78GL003484 | 100 | 3.50E-166 | WP_032722448.1 | ferri-bacillibactin esterase BesA [Bacillus subtilis] |
| BSLIN78GL003485 | 100 | 5.80E-120 | WP_003228739.1 | MULTISPECIES: sulfite oxidase-like oxidoreductase [Bacillales] |
| BSLIN78GL003486 | 100 | 3.30E-107 | WP_038427890.1 | biotin transporter BioY [Bacillus subtilis] |
| BSLIN78GL003487 | 100 | 3.90E-241 | WP_003228736.1 | MULTISPECIES: Na+/H+ antiporter family protein [Bacillales] |
| BSLIN78GL003488 | 100 | 1.90E-284 | WP_015251314.1 | MULTISPECIES: leucyl aminopeptidase [Bacillus] |
| BSLIN78GL003489 | 100 | 1.10E-90 | AGE64802.1 | putative integral inner membrane protein [Bacillus subtilis XF-1] |
| BSLIN78GL003490 | 100 | 4.80E-120 | AOA55969.1 | uncharacterized protein BSHJ0_03425 [Bacillus subtilis] |
| BSLIN78GL003491 | 100 | 1.20E-20 | RPJ99217.1 | hypothetical protein BSBH6_04048 [Bacillus subtilis] |
| BSLIN78GL003492 | 100 | 9.80E-50 | WP_003228728.1 | MULTISPECIES: YuiB family protein [Bacillus] |
| BSLIN78GL003493 | 100 | 9.60E-242 | AHA79136.1 | NADH dehydrogenase-like protein yumB [Bacillus subtilis PY79] |
| BSLIN78GL003494 | 100 | 1.20E-186 | WP_222141964.1 | ferredoxin--NADP reductase 2 [Bacillus sp. SPARC3] |
| BSLIN78GL003495 | 100 | 1.40E-16 | WP_003228723.1 | MULTISPECIES: hypothetical protein [Bacillales] |
| BSLIN78GL003496 | 99.7 | 1.70E-186 | AGA22943.1 | GMP reductase [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003497 | 100 | 4.70E-120 | BAI86739.2 | transcriptional regulator [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL003498 | 100 | 1.20E-92 | WP_029318471.1 | MULTISPECIES: spermidine/spermine N(1)-acetyltransferase [Bacillus] |
| BSLIN78GL003499 | 100 | 4.70E-64 | AEP92231.1 | hypothetical protein yadR [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL003500 | 100 | 8.20E-157 | WP_167568494.1 | diaminopimelate epimerase [Bacillus subtilis] |
| BSLIN78GL003501 | 100 | 2.20E-219 | WP_003228710.1 | MULTISPECIES: NupC/NupG family nucleoside CNT transporter [Bacillus] |
| BSLIN78GL003502 | 100 | 2.80E-38 | WP_003222913.1 | MULTISPECIES: YuzB family protein [Bacillales] |
| BSLIN78GL003503 | 100 | 4.70E-205 | WP_003228707.1 | MULTISPECIES: NAD(P)/FAD-dependent oxidoreductase [Bacillus] |
| BSLIN78GL003504 | 100 | 2.20E-57 | WP_015714646.1 | MULTISPECIES: YuzD family protein [Bacillus] |
| BSLIN78GL003505 | 100 | 2.60E-40 | WP_223251887.1 | NifU family protein [Bacillus atrophaeus] |
| BSLIN78GL003506 | 100 | 0.00E+00 | WP_163138390.1 | S9 family peptidase [Bacillus subtilis] |
| BSLIN78GL003507 | 100 | 4.50E-172 | WP_032730335.1 | MULTISPECIES: homoserine kinase [Bacillus] |
| BSLIN78GL003508 | 100 | 1.90E-198 | WP_003228697.1 | MULTISPECIES: threonine synthase [Bacillales] |
| BSLIN78GL003509 | 100 | 1.50E-242 | WP_003228694.1 | MULTISPECIES: homoserine dehydrogenase [Bacillales] |
| BSLIN78GL003510 | 100 | 1.10E-200 | WP_014480751.1 | MULTISPECIES: spore coat-associated protein CotNH [Bacillus] |
| BSLIN78GL003511 | 100 | 1.50E-13 | AEP92243.1 | hypothetical protein I33_3327 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL003512 | 100 | 2.90E-88 | AGA22952.1 | Hypothetical protein YutG [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003513 | 100 | 1.20E-141 | WP_116972580.1 | 5' nucleotidase NucF [Bacillus subtilis] |
| BSLIN78GL003514 | 100 | 1.40E-75 | WP_003228684.1 | MULTISPECIES: DUF86 domain-containing protein [Bacillales] |
| BSLIN78GL003515 | 100 | 2.30E-47 | AGE64826.1 | hypothetical protein C663_3089 [Bacillus subtilis XF-1] |
| BSLIN78GL003516 | 100 | 3.10E-116 | WP_038429562.1 | YhcN/YlaJ family sporulation lipoprotein [Bacillus subtilis] |
| BSLIN78GL003517 | 100 | 1.20E-169 | WP_003222888.1 | MULTISPECIES: lipoyl synthase [Bacteria] |
| BSLIN78GL003518 | 100 | 5.50E-200 | AGA22958.1 | L-Ala--D-Glu endopeptidase [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003519 | 100 | 3.40E-127 | EHA32734.1 | hypothetical protein BSSC8_09910 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003520 | 100 | 1.30E-48 | WP_038429565.1 | MULTISPECIES: YunC family protein [Bacillus] |
| BSLIN78GL003521 | 99.8 | 1.40E-273 | EHA32732.1 | hypothetical protein BSSC8_09890 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003522 | 100 | 1.20E-147 | AFQ59083.1 | Putative integral inner membrane protein [Bacillus subtilis QB928] |
| BSLIN78GL003523 | 100 | 7.90E-171 | WP_003228668.1 | MULTISPECIES: DUF72 domain-containing protein [Bacillus] |
| BSLIN78GL003524 | 100 | 6.40E-63 | WP_015714653.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL003525 | 100 | 3.50E-258 | WP_038429567.1 | allantoinase [Bacillus subtilis] |
| BSLIN78GL003526 | 100 | 1.10E-303 | WP_038429568.1 | purine catabolism transcriptional regulator PucR [Bacillus subtilis] |
| BSLIN78GL003527 | 100 | 6.90E-246 | WP_088467374.1 | uric acid permease PucJ [Bacillus subtilis] |

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| BSLIN78GL003528 | 100 | 8.10E-236 | WP_088467375.1 | uric acid permease PucK [Bacillus subtilis] |
| BSLIN78GL003529 | 100 | 4.90E-285 | WP_088467376.1 | urate oxidase [Bacillus subtilis] |
| BSLIN78GL003530 | 100 | 1.20E-62 | AGA23078.1 | Transthyretin-like protein PucM [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003531 | 100 | 5.60E-19 | AHA79175.1 | Hypothetical Protein U712_16190 [Bacillus subtilis PY79] |
| BSLIN78GL003532 | 100 | 2.70E-97 | WP_088467378.1 | xanthine dehydrogenase subunit E [Bacillus subtilis] |
| BSLIN78GL003533 | 100 | 0.00E+00 | WP_046160818.1 | MULTISPECIES: xanthine dehydrogenase subunit D [Bacillus |
| BSLIN78GL003534 | 100 | 1.20E-152 | WP_046160819.1 | MULTISPECIES: xanthine dehydrogenase subunit C [Bacillus |
| BSLIN78GL003535 | 100 | 1.30E-111 | WP_038427899.1 | MULTISPECIES: xanthine dehydrogenase accessory protein PucB [Bacillus |
| BSLIN78GL003536 | 100 | 3.40E-186 | WP_038427900.1 | MULTISPECIES: XdhC family protein [Bacillus |
| BSLIN78GL003537 | 100 | 1.50E-239 | AFQ59098.1 | Aminotransferase acting on ureidoglycine andglyoxylate [Bacillus subtilis QB928 |
| BSLIN78GL003538 | 100 | 3.50E-236 | WP_046663932.1 | MULTISPECIES: allantoate deiminase [Bacillus] |
| BSLIN78GL003539 | 100 | 7.30E-172 | WP_046663933.1 | MULTISPECIES: endonuclease I family protein [Bacillus |
| BSLIN78GL003540 | 99.7 | 1.30E-205 | WP_160221802.1 | sn-glycerol-3-phosphate ABC transporter ATP-binding protein UgpC [Bacillus |
| BSLIN78GL003541 | 99.6 | 1.60E-135 | WP_014480777.1 | MULTISPECIES: transcriptional regulator FrlR [Bacillus] |
| BSLIN78GL003542 | 99.6 | 6.30E-160 | WP_046663934.1 | MULTISPECIES: fructosamine kinase FrlD [Bacillus] |
| BSLIN78GL003543 | 100 | 1.70E-171 | WP_014477909.1 | MULTISPECIES: carbohydrate ABC transporter permease [Bacillus] |
| BSLIN78GL003544 | 99.7 | 5.50E-170 | AGE64854.1 | putative fructose-amino acid permease [Bacillus subtilis XF-1] |
| BSLIN78GL003545 | 100 | 1.90E-242 | WP_046663935.1 | MULTISPECIES: ABC transporter substrate-binding protein [Bacillus] |
| BSLIN78GL003546 | 100 | 4.10E-187 | AGE64856.1 | fructoselysine-6-P-deglycase [Bacillus subtilis XF-1 |
| BSLIN78GL003547 | 100 | 4.60E-67 | WP_003228617.1 | MULTISPECIES: nucleotide excision repair endonuclease [Bacillales |
| BSLIN78GL003548 | 100 | 1.30E-210 | WP_046663936.1 | MULTISPECIES: FAD-binding oxidoreductase [Bacillus |
| BSLIN78GL003549 | 100 | 2.00E-18 | WP_003228613.1 | MULTISPECIES: acid-soluble spore protein SspG [Bacillales |
| BSLIN78GL003550 | 100 | 1.20E-43 | WP_003243521.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL003551 | 99.8 | 6.40E-271 | WP_041850559.1 | MULTISPECIES: Fe-S cluster assembly protein SufB [Bacillus |
| BSLIN78GL003552 | 100 | 5.30E-69 | AFQ59115.1 | Iron-sulfur cluster assembly scaffold protein [Bacillus subtilis QB928] |
| BSLIN78GL003553 | 100 | 5.50E-234 | WP_015251273.1 | MULTISPECIES: cysteine desulfurase SufS [Bacillus |
| BSLIN78GL003554 | 100 | 4.20E-248 | WP_003228602.1 | MULTISPECIES: Fe-S cluster assembly protein SufD [Bacillales |
| BSLIN78GL003555 | 100 | 6.40E-143 | WP_003151872.1 | MULTISPECIES: Fe-S cluster assembly ATPase SufC [Bacillales |
| BSLIN78GL003556 | 100 | 1.50E-29 | AEP92292.1 | hypothetical protein I33_3376 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL003557 | 100 | 3.60E-17 | AFQ59119.1 | YuzK [Bacillus subtilis QB928] |
| BSLIN78GL003558 | 100 | 4.30E-17 | WP_003228598.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL003559 | 100 | 8.80E-66 | WP_003228596.1 | MULTISPECIES: carboxymuconolactone decarboxylase family protein [Bacillales |
| BSLIN78GL003560 | 99.6 | 9.80E-147 | WP_003228595.1 | MULTISPECIES: methionine ABC transporter substrate-binding lipoprotein MetQ |
| BSLIN78GL003561 | 100 | 6.30E-115 | WP_015251270.1 | MULTISPECIES: methionine ABC transporter permease MetP [Bacillus] |
| BSLIN78GL003562 | 100 | 6.40E-191 | AGE64871.1 | methionine ABC transporter (ATP-binding protein) [Bacillus subtilis XF-1] |
| BSLIN78GL003563 | 100 | 3.10E-15 | AEP92299.1 | hypothetical protein I33_3383 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL003564 | 100 | 2.00E-56 | WP_015251269.1 | MULTISPECIES: SCP2 sterol-binding domain-containing protein [Bacillus] |
| BSLIN78GL003565 | 100 | 5.90E-55 | WP_015251268.1 | MULTISPECIES: thioredoxin family protein [Bacillus |
| BSLIN78GL003566 | 100 | 2.40E-75 | AGE64875.1 | putative ribonuclease [Bacillus subtilis XF-1] |
| BSLIN78GL003567 | 100 | 8.80E-40 | AFQ59127.1 | YusG [Bacillus subtilis QB928] |
| BSLIN78GL003568 | 100 | 2.00E-74 | BAI86828.2 | glycine cleavage system protein H [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL003569 | 100 | 1.30E-63 | WP_003222779.1 | MULTISPECIES: arsenate reductase family protein [Bacillales |
| BSLIN78GL003570 | 99.7 | 0.00E+00 | EHA32682.1 | acyl-CoA dehydrogenase [Bacillus subtilis subsp. subtilis str. SC-8 |
| BSLIN78GL003571 | 100 | 6.30E-219 | WP_003228574.1 | MULTISPECIES: acetyl-CoA C-acyltransferase [Bacillales |
| BSLIN78GL003572 | 100 | 0.00E+00 | ASC84786.1 | 3-hydroxyacyl-CoA dehydrogenase [Bacillus subtilis |
| BSLIN78GL003573 | 100 | 2.70E-21 | AGE64882.1 | hypothetical protein C663_3146 [Bacillus subtilis XF-1] |
| BSLIN78GL003574 | 100 | 5.60E-167 | WP_015714674.1 | MULTISPECIES: proline dehydrogenase [Bacillus |
| BSLIN78GL003575 | 100 | 8.60E-47 | AFQ59135.1 | YuzM [Bacillus subtilis QB928] |
| BSLIN78GL003576 | 100 | 1.30E-57 | WP_088467384.1 | spore coat protein [Bacillus subtilis] |
| BSLIN78GL003577 | 99.4 | 1.10E-78 | QHF59399.1 | HTH-type transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL003578 | 100 | 1.40E-301 | RPK18901.1 | hypothetical protein EH2_01543 [Bacillus subtilis] |
| BSLIN78GL003579 | 100 | 3.20E-50 | WP_088467385.1 | tautomerase family protein [Bacillus subtilis] |
| BSLIN78GL003580 | 96.9 | 6.80E-137 | AGE64889.1 | putative Short-chain dehydrogenase/reductase [Bacillus subtilis XF-1 |
| BSLIN78GL003581 | 99 | 2.80E-169 | AFQ59142.1 | Putative transcriptional regulator (LysR family) [Bacillus subtilis QB928] |
| BSLIN78GL003582 | 100 | 2.80E-48 | WP_003228549.1 | MULTISPECIES: YusU family protein [Bacillales |
| BSLIN78GL003583 | 100 | 2.30E-165 | KAF1340393.1 | putative siderophore transport system ATP-binding protein YusV [Bacillus subtilis] |
| BSLIN78GL003584 | 100 | 3.20E-75 | WP_014477935.1 | MULTISPECIES: YusW family protein [Bacillus |
| BSLIN78GL003585 | 99.7 | 0.00E+00 | QHF59407.1 | hypothetical protein Bateq7PJ16_3601 [Bacillus subtilis] |
| BSLIN78GL003586 | 100 | 3.00E-154 | WP_088467388.1 | oxidoreductase [Bacillus subtilis] |
| BSLIN78GL003587 | 100 | 8.20E-82 | WP_003228537.1 | MULTISPECIES: metalloregulation DNA-binding stress protein MgrA [Bacillales] |
| BSLIN78GL003588 | 100 | 2.90E-255 | WP_015251256.1 | MULTISPECIES: serine protease Do-like protein HtrB [Bacillus] |
| BSLIN78GL003589 | 100 | 1.00E-125 | WP_003228529.1 | MULTISPECIES: secretion stress-responsive two-component system response |
| BSLIN78GL003590 | 100 | 6.30E-255 | WP_003228527.1 | MULTISPECIES: secretion stress-responsive two-component system sensor histidine |
| BSLIN78GL003591 | 100 | 1.20E-32 | AFQ59151.1 | Regulator of SpxA degradation [Bacillus subtilis QB928] |
| BSLIN78GL003592 | 99.7 | 2.60E-161 | AGE64902.1 | putative transcriptional regulator [Bacillus subtilis XF-1] |
| BSLIN78GL003593 | 91.1 | 5.30E-241 | WP_276787245.1 | class II fumarate hydratase [Bacillus sp. (in: firmicutes)] |
| BSLIN78GL003594 | 100 | 3.30E-26 | WP_003228521.1 | MULTISPECIES: YvzF family protein [Bacillus |
| BSLIN78GL003595 | 100 | 9.00E-268 | WP_003243555.1 | MULTISPECIES: spore germination receptor protein GerAA [Bacillus |
| BSLIN78GL003596 | 100 | 2.00E-192 | WP_009968145.1 | MULTISPECIES: spore germination receptor protein GerAB [Bacillales |
| BSLIN78GL003597 | 100 | 7.20E-209 | WP_003243203.1 | MULTISPECIES: spore germination receptor protein GerAC [Bacillus |
| BSLIN78GL003598 | 99.5 | 1.50E-107 | WP_003243201.1 | MULTISPECIES: two-component system response regulator LiaR [Bacillales |
| BSLIN78GL003599 | 100 | 1.60E-197 | WP_003244464.1 | MULTISPECIES: two-component system sensor histidine kinase LiaS [Bacillales |
| BSLIN78GL003600 | 100 | 1.40E-131 | WP_015714682.1 | MULTISPECIES: LiaRS two-component regulatory system accessory protein LiaF |
| BSLIN78GL003601 | 100 | 2.10E-155 | WP_088467389.1 | MULTISPECIES: DUF4097 domain-containing protein [Bacillus] |
| BSLIN78GL003602 | 100 | 3.60E-118 | WP_015714684.1 | MULTISPECIES: PspA/IM30 family protein [Bacillus |
| BSLIN78GL003603 | 100 | 2.60E-65 | WP_003243447.1 | MULTISPECIES: cell envelope stress-induced membrane anchor protein LiaI |
| BSLIN78GL003604 | 100 | 8.80E-235 | WP_003244338.1 | MULTISPECIES: MFS transporter [Bacillales] |
| BSLIN78GL003605 | 100 | 5.30E-102 | AFQ59165.1 | ATP:cob(I)alamin adenosyltransferase [Bacillus subtilis QB928] |
| BSLIN78GL003606 | 100 | 7.80E-250 | AOL25997.1 | iron ABC transporter ATP-binding protein [Bacillus sp. FJAT-14266] |
| BSLIN78GL003607 | 100 | 2.90E-177 | RAP08314.1 | hypothetical protein HS3_02256 [Bacillus subtilis] |

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| BSLIN78GL003608 | 100 | 1.90E-173 | WP_015714689.1 | MULTISPECIES: ABC transporter substrate-binding protein [Bacillus] |
| BSLIN78GL003609 | 100 | 7.10E-19 | AKE25119.1 | hypothetical protein BsLM_3322 [Bacillus sp. LM 4-2] |
| BSLIN78GL003610 | 100 | 9.30E-142 | AGA23154.1 | Ketoreductase YvrD [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003611 | 100 | 5.30E-170 | WP_003228493.1 | MULTISPECIES: SMP-30/gluconolactonase/LRE family protein [Bacillales] |
| BSLIN78GL003612 | 100 | 0.00E+00 | WP_003243980.1 | MULTISPECIES: two-component system sensor histidine kinase YvrG [Bacillales] |
| BSLIN78GL003613 | 100 | 6.90E-26 | AKN11238.1 | hypothetical protein ABU16_0162 [Bacillus subtilis] |
| BSLIN78GL003614 | 100 | 3.90E-131 | WP_003243545.1 | MULTISPECIES: two-component system response regulator YvrH [Bacillales] |
| BSLIN78GL003615 | 100 | 7.60E-39 | WP_003228484.1 | MULTISPECIES: sigma-O factor regulator RsoA [Bacillales] |
| BSLIN78GL003616 | 100 | 2.60E-95 | ADV94132.1 | alternative sigma factor sigmaO [Bacillus subtilis BSn5] |
| BSLIN78GL003617 | 100 | 2.00E-26 | WP_010886612.1 | YvrJ family protein [Bacillus subtilis] |
| BSLIN78GL003618 | 100 | 7.80E-16 | AGE64927.1 | hypothetical protein C663_3191 [Bacillus subtilis XF-1] |
| BSLIN78GL003619 | 100 | 9.50E-228 | AFQ59176.1 | Oxalate decarboxylase [Bacillus subtilis QB928] |
| BSLIN78GL003620 | 100 | 9.30E-69 | WP_003243579.1 | MULTISPECIES: acid stress-sensitive anti sigma factor RsiO [Bacillales] |
| BSLIN78GL003621 | 100 | 1.40E-224 | WP_014480847.1 | MULTISPECIES: ABC transporter permease [Bacillus] |
| BSLIN78GL003622 | 100 | 1.70E-123 | WP_014480848.1 | MULTISPECIES: ABC transporter ATP-binding protein [Bacillus] |
| BSLIN78GL003623 | 100 | 1.60E-225 | WP_015714694.1 | MULTISPECIES: efflux RND transporter periplasmic adaptor subunit [Bacillus] |
| BSLIN78GL003624 | 100 | 1.40E-148 | WP_015714695.1 | MULTISPECIES: ABC transporter ATP-binding protein [Bacillus] |
| BSLIN78GL003625 | 100 | 1.10E-182 | WP_003228452.1 | MULTISPECIES: iron ABC transporter permease [Bacillus] |
| BSLIN78GL003626 | 100 | 9.50E-212 | EHA32627.1 | ferrichrome ABC transporter (permease) [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003627 | 100 | 1.20E-180 | WP_003228448.1 | MULTISPECIES: iron-hydroxamate ABC transporter substrate-binding protein |
| BSLIN78GL003628 | 100 | 3.20E-20 | EHA32625.1 | hypothetical protein BSSC8_08820 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003629 | 100 | 1.10E-262 | WP_003228445.1 | MULTISPECIES: amino acid permease [Bacillus] |
| BSLIN78GL003630 | 100 | 9.60E-18 | AFQ59186.1 | Small acid-soluble spore protein [Bacillus subtilis QB928] |
| BSLIN78GL003631 | 100 | 3.40E-86 | WP_003228444.1 | MULTISPECIES: metal-dependent hydrolase [Bacillales] |
| BSLIN78GL003632 | 100 | 0.00E+00 | WP_003228441.1 | MULTISPECIES: LTA synthase family protein [Bacillus] |
| BSLIN78GL003633 | 100 | 3.50E-172 | EHA32620.1 | putative molybdate binding regulator [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003634 | 99.6 | 2.30E-140 | WP_003228438.1 | MULTISPECIES: molybdate ABC transporter substrate-binding protein [Bacillus] |
| BSLIN78GL003635 | 100 | 4.90E-123 | AIC99641.1 | molybdenum ABC transporter permease [Bacillus subtilis subsp. subtilis str. OH |
| BSLIN78GL003636 | 100 | 4.00E-159 | AGE64944.1 | benzil reductase [Bacillus subtilis XF-1] |
| BSLIN78GL003637 | 100 | 3.00E-84 | AGE64945.1 | hypothetical protein C663_3210 [Bacillus subtilis XF-1] |
| BSLIN78GL003638 | 100 | 0.00E+00 | EHA32615.1 | Na+/H+ antiporter [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003639 | 100 | 0.00E+00 | WP_029725918.1 | MULTISPECIES: assimilatory sulfite reductase (NADPH) hemoprotein subunit |
| BSLIN78GL003640 | 100 | 0.00E+00 | WP_029725919.1 | MULTISPECIES: assimilatory sulfite reductase (NADPH) flavoprotein subunit |
| BSLIN78GL003641 | 99.1 | 0.00E+00 | EHA32612.1 | DNA 3'-5' helicase IV [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003642 | 100 | 2.70E-88 | EHA32611.1 | hypothetical protein BSSC8_08680 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003643 | 100 | 5.50E-110 | WP_003228419.1 | MULTISPECIES: trimeric intracellular cation channel family protein [Bacillus] |
| BSLIN78GL003644 | 100 | 7.40E-74 | WP_003228417.1 | MULTISPECIES: disulfide oxidoreductase [Bacillales] |
| BSLIN78GL003645 | 100 | 8.20E-123 | WP_003228414.1 | MULTISPECIES: disulfide bond formation protein BdbD [Bacillales] |
| BSLIN78GL003646 | 100 | 0.00E+00 | AIC99652.1 | cadmium transporter [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL003647 | 100 | 0.00E+00 | AGA23186.1 | Cation-transporting ATPase [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003648 | 100 | 1.10E-30 | WP_003228406.1 | MULTISPECIES: copper chaperone CopZ [Bacillus] |
| BSLIN78GL003649 | 100 | 2.50E-50 | WP_003228404.1 | MULTISPECIES: copper-sensing transcriptional repressor CsoR [Bacillales] |
| BSLIN78GL003650 | 99.7 | 1.20E-197 | AOA56122.1 | Scyllo-inositol 2-dehydrogenase (NADP(+)) [Bacillus subtilis] |
| BSLIN78GL003651 | 100 | 4.40E-118 | WP_003228400.1 | MULTISPECIES: FMN-dependent NADH-azoreductase AzoRB [Bacillus] |
| BSLIN78GL003652 | 100 | 0.00E+00 | WP_029725935.1 | MULTISPECIES: FUSC family protein [Bacillus] |
| BSLIN78GL003653 | 100 | 2.20E-72 | WP_003242541.1 | MULTISPECIES: YvaD family protein [Bacillales] |
| BSLIN78GL003654 | 100 | 4.50E-56 | WP_015384643.1 | multidrug efflux SMR transporter [Bacillus subtilis] |
| BSLIN78GL003655 | 100 | 8.90E-102 | WP_003228390.1 | MULTISPECIES: TetR/AcrR family transcriptional regulator [Bacillus] |
| BSLIN78GL003656 | 100 | 1.10E-142 | WP_029725936.1 | MULTISPECIES: SDR family oxidoreductase [Bacillus] |
| BSLIN78GL003657 | 100 | 8.10E-91 | AFQ59212.1 | TmRNA-binding protein [Bacillus subtilis QB928] |
| BSLIN78GL003658 | 99.9 | 0.00E+00 | WP_038829364.1 | ribonuclease R [Bacillus subtilis] |
| BSLIN78GL003659 | 100 | 2.00E-144 | AFQ59214.1 | Carboxylesterase [Bacillus subtilis QB928] |
| BSLIN78GL003660 | 100 | 9.50E-31 | WP_003220028.1 | MULTISPECIES: preprotein translocase subunit SecG [Bacillales] |
| BSLIN78GL003661 | 100 | 3.70E-151 | WP_038427911.1 | MULTISPECIES: alpha/beta hydrolase [Bacillus] |
| BSLIN78GL003662 | 100 | 5.10E-27 | AFI29945.1 | transcriptional regulator [Bacillus sp. JS] |
| BSLIN78GL003663 | 100 | 8.30E-70 | AFQ59218.1 | Transcriptional repressor [Bacillus subtilis QB928] |
| BSLIN78GL003664 | 100 | 1.00E-70 | WP_038427912.1 | MULTISPECIES: helix-turn-helix transcriptional regulator [Bacillus] |
| BSLIN78GL003665 | 100 | 1.40E-57 | EHA32587.1 | hypothetical protein BSSC8_08440 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003666 | 100 | 0.00E+00 | WP_038427913.1 | MULTISPECIES: methyl-accepting chemotaxis protein [Bacillus] |
| BSLIN78GL003667 | 100 | 2.80E-118 | WP_038427914.1 | MULTISPECIES: choline ABC transporter permease OpuBD [Bacillus] |
| BSLIN78GL003668 | 100 | 2.70E-169 | WP_038427915.1 | MULTISPECIES: choline ABC transporter substrate-binding lipoprotein OpuBC |
| BSLIN78GL003669 | 100 | 1.40E-114 | WP_003228370.1 | MULTISPECIES: choline ABC transporter permease OpuBB [Bacillales] |
| BSLIN78GL003670 | 99.2 | 9.30E-215 | AGA23210.1 | Choline transport ATP-binding protein OpuBA [Bacillus subtilis subsp. subtilis str. |
| BSLIN78GL003671 | 100 | 4.80E-97 | AGE64979.1 | hypothetical protein C663_3248 [Bacillus subtilis XF-1] |
| BSLIN78GL003672 | 100 | 4.00E-117 | WP_038427917.1 | glycine betaine/carnitine/choline/choline sulfate ABC transporter permease OpuCD |
| BSLIN78GL003673 | 99.7 | 8.30E-174 | AIC99679.1 | glycine/betaine ABC transporter substrate-binding protein [Bacillus subtilis subsp. |
| BSLIN78GL003674 | 100 | 2.10E-115 | WP_038427919.1 | glycine betaine/carnitine/choline/choline sulfate ABC transporter permease OpuCB |
| BSLIN78GL003675 | 100 | 6.00E-214 | AFQ59235.1 | Glycine betaine/carnitine/choline/choline sulfateABC [Bacillus subtilis QB928] |
| BSLIN78GL003676 | 100 | 2.40E-99 | WP_003228345.1 | MULTISPECIES: opuC operon transcriptional regulator OpcR [Bacillus] |
| BSLIN78GL003677 | 100 | 8.90E-111 | WP_080481002.1 | MULTISPECIES: NAAT family transporter [Bacillus] |
| BSLIN78GL003678 | 100 | 4.10E-113 | WP_326253780.1 | PH domain-containing protein [Bacillus subtilis] |
| BSLIN78GL003679 | 100 | 2.50E-130 | WP_038427921.1 | MULTISPECIES: zinc ribbon domain-containing protein [Bacillus] |
| BSLIN78GL003680 | 100 | 0.00E+00 | WP_038427922.1 | MULTISPECIES: zinc ribbon domain-containing protein [Bacillus] |
| BSLIN78GL003681 | 100 | 7.50E-83 | WP_072692768.1 | MULTISPECIES: GNAT family N-acetyltransferase [Bacillus] |
| BSLIN78GL003682 | 100 | 4.00E-243 | WP_003228333.1 | MULTISPECIES: phosphopyruvate hydratase [Bacillales] |
| BSLIN78GL003683 | 100 | 5.70E-297 | AFQ59243.1 | Phosphoglycerate mutase [Bacillus subtilis QB928] |
| BSLIN78GL003684 | 100 | 8.50E-140 | AFQ59244.1 | Triose phosphate isomerase [Bacillus subtilis QB928] |
| BSLIN78GL003685 | 100 | 2.10E-225 | AFQ59245.1 | Phosphoglycerate kinase [Bacillus subtilis QB928] |
| BSLIN78GL003686 | 99.7 | 1.30E-185 | WP_283010178.1 | type I glyceraldehyde-3-phosphate dehydrogenase [Bacillus subtilis |
| BSLIN78GL003687 | 99.7 | 1.10E-179 | WP_003228324.1 | MULTISPECIES: gapA transcriptional regulator CggR [Bacillus] |

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| BSLIN78GL003688 | 100 | 8.60E-249 | WP_003243899.1 | MULTISPECIES: arabinose-proton symporter AraE [Bacillales] |
| BSLIN78GL003689 | 100 | 1.50E-203 | QBJ84704.1 | GntR family transcriptional regulator [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL003690 | 100 | 7.60E-186 | QHF59534.1 | monooxygenase alpha chain [Bacillus subtilis] |
| BSLIN78GL003691 | 100 | 1.80E-75 | WP_029318390.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL003692 | 100 | 1.40E-159 | WP_029725944.1 | MULTISPECIES: LysR family transcriptional regulator [Bacillus |
| BSLIN78GL003693 | 100 | 2.40E-165 | WP_003228315.1 | MULTISPECIES: DMT family transporter [Bacillus |
| BSLIN78GL003694 | 100 | 4.90E-252 | WP_029725945.1 | amino acid permease [Bacillus subtilis] |
| BSLIN78GL003695 | 100 | 1.70E-199 | WP_029725946.1 | MULTISPECIES: glycoside hydrolase family 18 protein [Bacillus |
| BSLIN78GL003696 | 100 | 5.50E-133 | WP_029725947.1 | MULTISPECIES: lactate utilization protein LutC [Bacillus |
| BSLIN78GL003697 | 100 | 1.60E-277 | WP_014480926.1 | MULTISPECIES: lactate utilization iron-sulfur protein LutB [Bacillus |
| BSLIN78GL003698 | 99.2 | 1.20E-138 | EHA32551.1 | hypothetical protein BSSC8_08080 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003699 | 100 | 3.70E-106 | WP_014478018.1 | MULTISPECIES: two-component system response regulator YvfU [Bacillus |
| BSLIN78GL003700 | 100 | 9.90E-206 | WP_029725949.1 | MULTISPECIES: two-component system sensor histidine kinase YvfT [Bacillus |
| BSLIN78GL003701 | 100 | 6.40E-137 | WP_015714732.1 | MULTISPECIES: ABC transporter permease [Bacillus] |
| BSLIN78GL003702 | 100 | 7.50E-164 | WP_072692770.1 | MULTISPECIES: ABC transporter ATP-binding protein [Bacillus] |
| BSLIN78GL003703 | 100 | 1.60E-16 | AHA79346.1 | Hypothetical Protein U712_17060 [Bacillus subtilis PY79] |
| BSLIN78GL003704 | 100 | 5.20E-156 | WP_064911622.1 | MULTISPECIES: sigma factor SigB/phosphatase RsbP regulator RsbQ [Bacillus] |
| BSLIN78GL003705 | 100 | 1.60E-230 | WP_015714734.1 | MULTISPECIES: phosphoserine phosphatase RsbP [Bacillus] |
| BSLIN78GL003706 | 98.2 | 2.50E-256 | AHA79349.1 | Arabinogalactan endo-1,4-beta-galactosidase [Bacillus subtilis PY79] |
| BSLIN78GL003707 | 100 | 0.00E+00 | WP_088467398.1 | beta-galactosidase GanA [Bacillus subtilis] |
| BSLIN78GL003708 | 100 | 2.70E-155 | WP_015714737.1 | MULTISPECIES: arabinogalactan oligomer ABC transporter permease GanQ |
| BSLIN78GL003709 | 100 | 3.30E-242 | AGA23252.1 | Hypothetical protein YvfL [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003710 | 100 | 3.80E-238 | WP_003228280.1 | MULTISPECIES: arabinogalactan oligomer ABC transporter substrate-binding |
| BSLIN78GL003711 | 99.7 | 1.10E-187 | BAI87024.2 | LacI family transcription regulator [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL003712 | 100 | 1.70E-16 | RPK19041.1 | hypothetical protein EH2_01683 [Bacillus subtilis] |
| BSLIN78GL003713 | 100 | 2.90E-126 | WP_015714739.1 | MULTISPECIES: L-lactate utilization/bacilysin biosynthesis transcriptional regulator |
| BSLIN78GL003714 | 100 | 0.00E+00 | WP_015714740.1 | MULTISPECIES: L-lactate permease LutP [Bacillus |
| BSLIN78GL003715 | 99.6 | 5.40E-251 | KIN29165.1 | hypothetical protein B4069_3531 [Bacillus subtilis] |
| BSLIN78GL003716 | 100 | 7.10E-14 | AEP88328.1 | hypothetical protein GYO_3755 [Bacillus spizizenii TU-B-10 |
| BSLIN78GL003717 | 100 | 1.60E-32 | WP_003219905.1 | MULTISPECIES: protein YvfG [Bacillales |
| BSLIN78GL003718 | 100 | 5.30E-184 | WP_029725952.1 | polysaccharide pyruvyl transferase family protein [Bacillus subtilis |
| BSLIN78GL003719 | 100 | 9.00E-215 | WP_029725953.1 | MULTISPECIES: aminotransferase class I/II-fold pyridoxal phosphate-dependent |
| BSLIN78GL003720 | 100 | 1.60E-115 | WP_029725954.1 | MULTISPECIES: acetyltransferase [Bacillus |
| BSLIN78GL003721 | 100 | 6.70E-99 | BAI87033.2 | hypothetical protein BSNT_10008 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL003722 | 100 | 1.00E-266 | WP_029725955.1 | MULTISPECIES: MATE family efflux transporter [Bacillus |
| BSLIN78GL003723 | 100 | 1.10E-198 | WP_015714746.1 | MULTISPECIES: glycosyltransferase [Bacillus |
| BSLIN78GL003724 | 100 | 1.90E-206 | WP_015714747.1 | MULTISPECIES: polysaccharide pyruvyl transferase family protein [Bacillus |
| BSLIN78GL003725 | 99.7 | 1.50E-200 | QHF59567.1 | glycosyltransferase [Bacillus subtilis] |
| BSLIN78GL003726 | 100 | 5.30E-212 | WP_015714749.1 | MULTISPECIES: biofilm exopolysaccharide biosynthesis protein EpsG [Bacillus |
| BSLIN78GL003727 | 100 | 6.80E-218 | AIX09062.1 | Putative glycosyltransferase EpsF [Bacillus subtilis |
| BSLIN78GL003728 | 100 | 5.70E-158 | WP_003228255.1 | MULTISPECIES: glycosyltransferase EpsE [Bacillus |
| BSLIN78GL003729 | 99.5 | 3.10E-223 | QHF59571.1 | L-malate synthase [Bacillus subtilis] |
| BSLIN78GL003730 | 100 | 0.00E+00 | WP_186302388.1 | MULTISPECIES: nucleoside-diphosphate sugar epimerase/dehydratase [Bacillus |
| BSLIN78GL003731 | 100 | 2.80E-118 | WP_003228249.1 | MULTISPECIES: protein tyrosine kinase EpsB [Bacillales |
| BSLIN78GL003732 | 100 | 1.40E-125 | WP_144453247.1 | YveK family protein [Bacillus subtilis] |
| BSLIN78GL003733 | 100 | 1.90E-78 | WP_003228245.1 | MULTISPECIES: transcriptional regulator SlrR [Bacillus] |
| BSLIN78GL003734 | 100 | 2.30E-287 | WP_015714751.1 | MULTISPECIES: para-nitrobenzyl esterase [Bacillus |
| BSLIN78GL003735 | 100 | 4.80E-28 | WP_015714752.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL003736 | 100 | 2.40E-92 | WP_003228238.1 | MULTISPECIES: phenolic acid decarboxylase [Bacillus |
| BSLIN78GL003737 | 100 | 7.60E-86 | WP_211197314.1 | DUF3237 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL003738 | 98.3 | 5.10E-128 | AAA22641.1 | amino acid racemase [Bacillus subtilis] |
| BSLIN78GL003739 | 100 | 2.50E-267 | EHA32512.1 | penicillin-binding protein 4* [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003740 | 100 | 1.40E-276 | WP_001022105.1 | MULTISPECIES: levansucrase [Bacteria] |
| BSLIN78GL003741 | 99.4 | 0.00E+00 | QHF59583.1 | levanase [Bacillus subtilis] |
| BSLIN78GL003742 | 100 | 1.80E-301 | WP_003228228.1 | MULTISPECIES: aspartate/proton symporter AspP [Bacillales] |
| BSLIN78GL003743 | 99.6 | 4.10E-125 | AYK63912.1 | TetR family transcriptional regulator [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL003744 | 100 | 5.80E-56 | BAI87058.2 | hypothetical protein BSNT_10035 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL003745 | 100 | 6.10E-52 | WP_003228222.1 | MULTISPECIES: QacE family quaternary ammonium compound efflux SMR |
| BSLIN78GL003746 | 100 | 3.60E-94 | WP_003243249.1 | MULTISPECIES: DUF3231 family protein [Bacillales |
| BSLIN78GL003747 | 100 | 3.70E-20 | WP_220562307.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL003748 | 100 | 1.90E-267 | WP_029725961.1 | MULTISPECIES: FAD-binding oxidoreductase [Bacillus |
| BSLIN78GL003749 | 100 | 3.30E-178 | WP_029725962.1 | sporulation hydrolase CotR [Bacillus subtilis] |
| BSLIN78GL003750 | 100 | 1.70E-103 | WP_003228214.1 | MULTISPECIES: ATP-dependent Clp endopeptidase proteolytic subunit ClpP |
| BSLIN78GL003751 | 100 | 5.80E-121 | WP_029725963.1 | beta-phosphoglucomutase [Bacillus subtilis] |
| BSLIN78GL003752 | 100 | 0.00E+00 | WP_029725964.1 | oligo-1,6-glucosidase [Bacillus subtilis] |
| BSLIN78GL003753 | 100 | 0.00E+00 | WP_029725965.1 | maltose phosphorylase [Bacillus subtilis] |
| BSLIN78GL003754 | 100 | 1.30E-163 | WP_029725966.1 | DUF1189 family protein [Bacillus subtilis] |
| BSLIN78GL003755 | 100 | 1.90E-153 | WP_029725967.1 | maltodextrin ABC transporter permease MdxG [Bacillus subtilis] |
| BSLIN78GL003756 | 100 | 1.50E-250 | WP_029725968.1 | maltodextrin ABC transporter permease MdxF [Bacillus subtilis] |
| BSLIN78GL003757 | 100 | 8.10E-241 | WP_015714763.1 | MULTISPECIES: maltodextrin ABC transporter substrate-binding protein MdxE |
| BSLIN78GL003758 | 100 | 0.00E+00 | WP_032678700.1 | MULTISPECIES: maltogenic alpha-amylase [Bacillus] |
| BSLIN78GL003759 | 99.7 | 1.30E-174 | AGA23301.1 | HTH-type transcriptional regulator YvdE [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003760 | 100 | 4.60E-106 | WP_003228180.1 | MULTISPECIES: TIGR00730 family Rossman fold protein [Bacillales |
| BSLIN78GL003761 | 100 | 5.20E-60 | AFQ59316.1 | Putative pyrophosphohydrolase [Bacillus subtilis QB928] |
| BSLIN78GL003762 | 100 | 1.20E-297 | WP_003228175.1 | MULTISPECIES: SulP family inorganic anion transporter [Bacillus] |
| BSLIN78GL003763 | 100 | 1.10E-107 | WP_010886620.1 | MULTISPECIES: carbonic anhydrase [Bacillales |
| BSLIN78GL003764 | 100 | 7.80E-183 | WP_029725971.1 | D-glycerate dehydrogenase [Bacillus subtilis |
| BSLIN78GL003765 | 99.8 | 0.00E+00 | WP_029725972.1 | MULTISPECIES: lantibiotic ABC transporter permease PsdB [Bacillus] |
| BSLIN78GL003766 | 100 | 1.60E-141 | WP_003228167.1 | MULTISPECIES: lantibiotic ABC transporter ATP-binding protein PsdA [Bacillales |
| BSLIN78GL003767 | 100 | 2.30E-199 | WP_029725973.1 | MULTISPECIES: two-component sensor histidine kinase PsdS [Bacillus |

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| BSLIN78GL003768 | 100 | 1.00E-131 | WP_003244535.1 | MULTISPECIES: two-component system response regulator PsdR [Bacillales |
| BSLIN78GL003769 | 100 | 6.50E-34 | AFQ59324.1 | Putative lipoprotein [Bacillus subtilis QB928] |
| BSLIN78GL003770 | 100 | 1.60E-146 | WP_072692779.1 | MULTISPECIES: arylamine N-acetyltransferase [Bacillus |
| BSLIN78GL003771 | 100 | 1.50E-37 | WP_003219835.1 | MULTISPECIES: HPr family phosphocarrier protein [Bacillales] |
| BSLIN78GL003772 | 100 | 1.20E-172 | WP_003243775.1 | MULTISPECIES: DNA-binding protein WhiA [Bacillales |
| BSLIN78GL003773 | 100 | 6.30E-177 | AFQ59328.1 | Gluconeogenesis morphogenetic factor [Bacillus subtilis QB928] |
| BSLIN78GL003774 | 100 | 1.40E-165 | WP_003243903.1 | MULTISPECIES: RNase adapter RapZ [Bacillales] |
| BSLIN78GL003775 | 100 | 2.10E-82 | AHA79415.1 | putative Nudix hydrolase yvcI [Bacillus subtilis PY79 |
| BSLIN78GL003776 | 100 | 9.80E-178 | AFQ59331.1 | Thioredoxin reductase [Bacillus subtilis QB928] |
| BSLIN78GL003777 | 100 | 2.00E-256 | WP_003228138.1 | MULTISPECIES: peptidoglycan DL-endopeptidase CwlO [Bacillus |
| BSLIN78GL003778 | 100 | 1.70E-282 | WP_003228135.1 | MULTISPECIES: tetratricopeptide repeat protein [Bacillus] |
| BSLIN78GL003779 | 99.8 | 0.00E+00 | WP_003228133.1 | MULTISPECIES: multidrug resistance ABC transporter ATP-binding |
| BSLIN78GL003780 | 100 | 2.90E-58 | WP_003228131.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL003781 | 100 | 0.00E+00 | WP_003242583.1 | MULTISPECIES: DUF6792 domain-containing protein [Bacillales] |
| BSLIN78GL003782 | 100 | 2.80E-137 | WP_003244157.1 | MULTISPECIES: lipoprotein [Bacillales] |
| BSLIN78GL003783 | 100 | 1.30E-114 | WP_003243045.1 | MULTISPECIES: bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl |
| BSLIN78GL003784 | 100 | 1.70E-137 | WP_015384749.1 | MULTISPECIES: imidazole glycerol phosphate synthase subunit HisF [Bacillus |
| BSLIN78GL003785 | 100 | 3.30E-133 | WP_015714778.1 | MULTISPECIES: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase |
| BSLIN78GL003786 | 100 | 7.10E-116 | WP_015714779.1 | MULTISPECIES: imidazole glycerol phosphate synthase subunit HisH [Bacillus |
| BSLIN78GL003787 | 100 | 9.40E-107 | WP_015714780.1 | MULTISPECIES: imidazoleglycerol-phosphate dehydratase HisB [Bacillus |
| BSLIN78GL003788 | 99.8 | 5.20E-235 | WP_029318339.1 | histidinol dehydrogenase [Bacillus subtilis] |
| BSLIN78GL003789 | 100 | 5.10E-111 | AGE65099.1 | ATP phosphoribosyltransferase catalytic subunit [Bacillus subtilis XF-1 |
| BSLIN78GL003790 | 100 | 3.00E-221 | WP_014481016.1 | MULTISPECIES: ATP phosphoribosyltransferase regulatory subunit [Bacillus |
| BSLIN78GL003791 | 100 | 1.20E-135 | WP_015714782.1 | MULTISPECIES: C39 family peptidase [Bacillus |
| BSLIN78GL003793 | 100 | 2.20E-117 | AEP92541.1 | pectate lyase [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL003794 | 100 | 2.30E-93 | WP_003228107.1 | MULTISPECIES: heptaprenylglyceryl phosphate O-acetyltransferase [Bacillus |
| BSLIN78GL003795 | 97 | 7.90E-29 | WP_231087479.1 | HAD-IA family hydrolase, partial [Staphylococcus aureus |
| BSLIN78GL003796 | 100 | 1.50E-86 | EHA32458.1 | pyrophosphatase PpaX [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003797 | 100 | 2.30E-171 | WP_017695286.1 | MULTISPECIES: nucleoside recognition domain-containing protein [Bacillus] |
| BSLIN78GL003798 | 100 | 3.90E-151 | WP_029725975.1 | MULTISPECIES: prolipoprotein diacylglyceryl transferase [Bacillus |
| BSLIN78GL003799 | 100 | 9.50E-170 | WP_003228097.1 | MULTISPECIES: HPr(Ser) kinase/phosphatase [Bacillales] |
| BSLIN78GL003800 | 100 | 8.00E-222 | WP_029725976.1 | MULTISPECIES: N-acetylglucosamine-6-phosphate deacetylase [Bacillus |
| BSLIN78GL003801 | 100 | 2.50E-133 | WP_029725977.1 | MULTISPECIES: glucosamine-6-phosphate deaminase [Bacillus] |
| BSLIN78GL003802 | 100 | 8.60E-134 | WP_029725978.1 | MULTISPECIES: N-acetylglucosamine utilization transcriptional regulator NagR |
| BSLIN78GL003803 | 100 | 1.20E-29 | RAP08129.1 | hypothetical protein HS3_02067 [Bacillus subtilis] |
| BSLIN78GL003804 | 100 | 0.00E+00 | WP_029725979.1 | MULTISPECIES: metallophosphoesterase [Bacillus] |
| BSLIN78GL003805 | 100 | 8.10E-85 | AFQ59357.1 | Putative transcriptional regulator [Bacillus subtilis QB928] |
| BSLIN78GL003806 | 100 | 7.40E-231 | WP_017695292.1 | MULTISPECIES: pulcherriminic acid synthase [Bacillus |
| BSLIN78GL003807 | 100 | 7.70E-138 | WP_029725980.1 | MULTISPECIES: cyclo(L-leucyl-L-leucyl) synthase [Bacillus |
| BSLIN78GL003808 | 97.3 | 6.10E-15 | AKE25312.1 | hypothetical protein BsLM_3515 [Bacillus sp. LM 4-2] |
| BSLIN78GL003809 | 100 | 1.50E-89 | WP_003228073.1 | MULTISPECIES: pulcherriminic acid biosynthesis transcriptional regulator PchR |
| BSLIN78GL003810 | 99.5 | 1.70E-222 | AFQ59361.1 | Putative efflux transporter [Bacillus subtilis QB928] |
| BSLIN78GL003811 | 100 | 2.70E-56 | WP_003228066.1 | MULTISPECIES: phage holin family protein [Bacillales |
| BSLIN78GL003812 | 100 | 3.80E-28 | WP_003228065.1 | MULTISPECIES: PspC domain-containing protein [Bacillales] |
| BSLIN78GL003813 | 100 | 3.70E-205 | WP_029725982.1 | MULTISPECIES: DUF4097 domain-containing protein [Bacillus] |
| BSLIN78GL003814 | 100 | 1.60E-55 | AGE65114.1 | hypothetical protein C663_3397 [Bacillus subtilis XF-1] |
| BSLIN78GL003815 | 100 | 8.30E-35 | WP_003228059.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL003816 | 100 | 5.70E-153 | QHF59646.1 | hypothetical protein Bateq7PJ16_3840 [Bacillus subtilis] |
| BSLIN78GL003817 | 97.8 | 0.00E+00 | WP_268449798.1 | excinuclease ABC subunit UvrA [Bacillus mojavensis] |
| BSLIN78GL003818 | 98 | 0.00E+00 | WP_148962650.1 | excinuclease ABC subunit UvrB [Bacillus subtilis] |
| BSLIN78GL003819 | 100 | 9.20E-34 | WP_003228053.1 | MULTISPECIES: CsbA family protein [Bacillales |
| BSLIN78GL003820 | 100 | 2.60E-13 | AHA79458.1 | Hypothetical Protein U712_17630 [Bacillus subtilis PY79] |
| BSLIN78GL003821 | 99.2 | 0.00E+00 | EHA32435.1 | putative phosphotransferase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003822 | 100 | 2.80E-94 | WP_326253759.1 | TetR/AcrR family transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL003823 | 100 | 1.70E-244 | WP_106073356.1 | MFS transporter [Bacillus subtilis] |
| BSLIN78GL003824 | 100 | 2.70E-225 | WP_003228042.1 | MULTISPECIES: cell division topological determinant MinJ [Bacillus |
| BSLIN78GL003825 | 100 | 8.70E-57 | ADM39488.1 | SwrA motility protein [Bacillus spizizenii str. W23] |
| BSLIN78GL003826 | 100 | 1.00E-271 | WP_003228041.1 | MULTISPECIES: carboxy-terminal processing protease CtpB [Bacillales |
| BSLIN78GL003827 | 100 | 4.90E-163 | AIC42002.1 | cell-division ABC transporter [Bacillus subtilis subsp. subtilis str. JH642 substr. |
| BSLIN78GL003828 | 100 | 5.80E-124 | WP_003228039.1 | MULTISPECIES: cell division ATP-binding protein FtsE [Bacillales |
| BSLIN78GL003829 | 100 | 5.40E-53 | AFQ59378.1 | Cytochrome c551 [Bacillus subtilis QB928] |
| BSLIN78GL003830 | 100 | 4.80E-180 | AFQ59379.1 | Putative integral inner membrane protein [Bacillus subtilis QB928] |
| BSLIN78GL003831 | 100 | 1.40E-187 | ADV94335.1 | peptide chain release factor 2 [Bacillus subtilis BSn5] |
| BSLIN78GL003832 | 99.9 | 0.00E+00 | WP_161986335.1 | preprotein translocase subunit SecA [Bacillus subtilis] |
| BSLIN78GL003833 | 100 | 4.70E-103 | WP_003228031.1 | MULTISPECIES: ribosome hibernation promotion factor [Bacillales] |
| BSLIN78GL003834 | 100 | 6.70E-69 | AFQ59383.1 | YvzG [Bacillus subtilis QB928] |
| BSLIN78GL003835 | 100 | 7.80E-49 | WP_003242603.1 | MULTISPECIES: flagella biosynthesis regulatory protein FliT [Bacillales |
| BSLIN78GL003836 | 100 | 2.40E-69 | WP_003243747.1 | MULTISPECIES: flagellar export chaperone FliS [Bacillales |
| BSLIN78GL003837 | 100 | 1.50E-278 | WP_326253758.1 | flagellar hook-associated protein 2 [Bacillus subtilis] |
| BSLIN78GL003838 | 100 | 2.90E-31 | EHA32418.1 | flagellar protein FlaG [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003839 | 100 | 3.50E-144 | WP_029725988.1 | MULTISPECIES: flagellin Hag [Bacillus] |
| BSLIN78GL003840 | 100 | 4.20E-31 | WP_029725989.1 | MULTISPECIES: carbon storage regulator CsrA [Bacillus] |
| BSLIN78GL003841 | 100 | 5.90E-74 | WP_029725990.1 | MULTISPECIES: flagellar assembly protein FliW [Bacillus |
| BSLIN78GL003842 | 100 | 7.30E-104 | WP_014481045.1 | MULTISPECIES: DUF6470 family protein [Bacillus |
| BSLIN78GL003843 | 100 | 2.70E-161 | WP_015714797.1 | MULTISPECIES: flagellar hook-associated protein FlgL [Bacillus |
| BSLIN78GL003844 | 100 | 1.20E-281 | WP_003228001.1 | MULTISPECIES: flagellar hook-associated protein FlgK [Bacillales |
| BSLIN78GL003845 | 100 | 3.30E-81 | WP_014481048.1 | MULTISPECIES: flagellar protein FlgN [Bacillus] |
| BSLIN78GL003846 | 100 | 4.80E-42 | WP_014478128.1 | MULTISPECIES: flagellar biosynthesis anti-sigma factor FlgM [Bacillus |
| BSLIN78GL003847 | 100 | 1.80E-75 | WP_003227995.1 | MULTISPECIES: TIGR03826 family flagellar region protein [Bacillales |

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| BSLIN78GL003848 | 100 | 1.50E-135 | WP_029725992.1 | MULTISPECIES: comF operon protein ComFC [Bacillus |
| BSLIN78GL003849 | 100 | 7.20E-47 | WP_015483764.1 | MULTISPECIES: late competence protein ComFB [Bacillus |
| BSLIN78GL003850 | 100 | 3.20E-270 | WP_029725993.1 | MULTISPECIES: ATP-dependent helicase ComFA [Bacillus |
| BSLIN78GL003851 | 100 | 2.40E-156 | WP_003227986.1 | MULTISPECIES: DegV family protein [Bacillus |
| BSLIN78GL003852 | 100 | 3.60E-126 | WP_003219701.1 | MULTISPECIES: two-component system response regulator DegU [Bacillales |
| BSLIN78GL003853 | 100 | 6.20E-211 | WP_003227983.1 | MULTISPECIES: two-component sensor histidine kinase DegS [Bacillales |
| BSLIN78GL003854 | 100 | 2.00E-121 | AFQ59403.1 | YvyE [Bacillus subtilis QB928] |
| BSLIN78GL003855 | 100 | 2.40E-218 | WP_029318786.1 | polyisoprenyl-teichoic acid--peptidoglycan teichoic acid transferase TagV [Bacillus |
| BSLIN78GL003856 | 100 | 1.60E-192 | WP_003227975.1 | MULTISPECIES: MraY family glycosyltransferase [Bacillales |
| BSLIN78GL003857 | 99.7 | 4.10E-234 | WP_214287104.1 | MULTISPECIES: glycosyltransferase family 1 protein [Bacillus |
| BSLIN78GL003858 | 100 | 6.00E-146 | AFQ59407.1 | Putative glycosyltransferase [Bacillus subtilis QB928 |
| BSLIN78GL003859 | 100 | 1.30E-106 | AGE65156.1 | putative hydrolase involved in teichuronic acid synthesis [Bacillus subtilis XF-1 |
| BSLIN78GL003860 | 100 | 5.90E-261 | WP_326253752.1 | teichuronic acid biosynthesis protein TuaE [Bacillus subtilis] |
| BSLIN78GL003861 | 99.8 | 6.00E-261 | WP_048655016.1 | UDP-glucose 6-dehydrogenase TuaD [Bacillus subtilis] |
| BSLIN78GL003862 | 100 | 7.60E-214 | WP_129137970.1 | MULTISPECIES: glycosyltransferase family 4 protein [Bacillus |
| BSLIN78GL003863 | 100 | 9.00E-268 | RAP08072.1 | hypothetical protein HS3_02008 [Bacillus subtilis] |
| BSLIN78GL003864 | 100 | 5.80E-121 | WP_003242561.1 | MULTISPECIES: sugar transferase [Bacillales] |
| BSLIN78GL003865 | 100 | 0.00E+00 | WP_198878460.1 | (poly)ribitol-phosphate teichoic acid beta-D-glucosyltransferase TarQ [Bacillus |
| BSLIN78GL003866 | 99.8 | 1.80E-263 | WP_038428159.1 | MULTISPECIES: N-acetylmuramoyl-L-alanine amidase [Bacillus |
| BSLIN78GL003867 | 100 | 0.00E+00 | WP_038427951.1 | MULTISPECIES: SpoIID/LytB domain-containing protein [Bacillus |
| BSLIN78GL003868 | 100 | 8.90E-51 | WP_038427952.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL003869 | 100 | 1.50E-172 | WP_015251104.1 | MULTISPECIES: transcription antiterminator LytR [Bacillus |
| BSLIN78GL003870 | 99.5 | 2.00E-217 | BBK74330.1 | UDP-N-acetylglucosamine 2-epimerase [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL003871 | 100 | 0.00E+00 | WP_038427954.1 | MULTISPECIES: glycosyltransferase [Bacillus |
| BSLIN78GL003872 | 100 | 4.50E-302 | WP_029726001.1 | MULTISPECIES: glycosyltransferase [Bacillus |
| BSLIN78GL003873 | 100 | 1.20E-266 | WP_029726002.1 | MULTISPECIES: alpha-glucosyltransferase N-terminal domain-containing protein |
| BSLIN78GL003874 | 100 | 1.40E-14 | AGE65170.1 | hypothetical protein C663_3456 [Bacillus subtilis XF-1] |
| BSLIN78GL003875 | 100 | 3.30E-164 | AGA21772.1 | UTP--glucose-1-phosphate uridylyltransferase [Bacillus subtilis subsp. subtilis str. |
| BSLIN78GL003876 | 100 | 2.10E-302 | WP_088327089.1 | teichoic acids export ABC transporter ATP-binding subunit TagH [Bacillus subtilis] |
| BSLIN78GL003877 | 100 | 3.10E-156 | WP_014665585.1 | MULTISPECIES: teichoic acids export ABC transporter permease subunit TagG |
| BSLIN78GL003878 | 99.8 | 0.00E+00 | WP_211197325.1 | DUF6270 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL003879 | 100 | 9.80E-152 | WP_029726005.1 | MULTISPECIES: DUF6270 domain-containing protein [Bacillus |
| BSLIN78GL003880 | 100 | 0.00E+00 | WP_029726006.1 | MULTISPECIES: CDP-glycerol glycerophosphotransferase family protein [Bacillus |
| BSLIN78GL003881 | 100 | 1.60E-258 | WP_029726007.1 | MULTISPECIES: glycosyltransferase family A protein [Bacillus |
| BSLIN78GL003882 | 100 | 2.00E-233 | WP_029726008.1 | MULTISPECIES: CDP-glycerol glycerophosphotransferase family protein [Bacillus |
| BSLIN78GL003883 | 100 | 7.90E-70 | WP_029318766.1 | MULTISPECIES: glycerol-3-phosphate cytidylyltransferase [Bacillus |
| BSLIN78GL003884 | 98.9 | 5.60E-147 | QHF59707.1 | acid transferase [Bacillus subtilis] |
| BSLIN78GL003885 | 99.7 | 4.40E-214 | WP_128473328.1 | CDP-glycerol glycerophosphotransferase family protein [Bacillus subtilis |
| BSLIN78GL003886 | 100 | 4.80E-129 | WP_015384812.1 | MULTISPECIES: 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase [Bacillus |
| BSLIN78GL003887 | 100 | 3.20E-195 | WP_003235523.1 | MULTISPECIES: ribitol-5-phosphate dehydrogenase [Bacillus |
| BSLIN78GL003888 | 100 | 9.60E-228 | WP_029726010.1 | MULTISPECIES: CDP-glycerol glycerophosphotransferase family protein [Bacillus |
| BSLIN78GL003889 | 100 | 0.00E+00 | WP_224913080.1 | MULTISPECIES: CDP-glycerol glycerophosphotransferase family protein [Bacillus |
| BSLIN78GL003890 | 100 | 0.00E+00 | WP_038427957.1 | beta-N-acetylglucosaminidase LytD [Bacillus subtilis |
| BSLIN78GL003891 | 100 | 8.70E-187 | WP_032722626.1 | MULTISPECIES: mannose-6-phosphate isomerase, class I [Bacillus |
| BSLIN78GL003892 | 100 | 6.90E-14 | AHA79525.1 | Hypothetical Protein U712_17970 [Bacillus subtilis PY79] |
| BSLIN78GL003893 | 100 | 2.50E-270 | WP_046663991.1 | MULTISPECIES: spore germination protein GerBA [Bacillus |
| BSLIN78GL003894 | 99.7 | 1.60E-208 | QHM82116.1 | Spore germination protein B2 [Bacillus subtilis] |
| BSLIN78GL003895 | 100 | 9.60E-217 | WP_029726014.1 | MULTISPECIES: spore germination protein GerBC [Bacillus |
| BSLIN78GL003896 | 100 | 1.50E-256 | WP_015251080.1 | MULTISPECIES: sugar porter family MFS transporter [Bacillus |
| BSLIN78GL003897 | 100 | 1.40E-176 | WP_015251079.1 | MULTISPECIES: polyisoprenyl-teichoic acid--peptidoglycan teichoic acid transferase |
| BSLIN78GL003898 | 100 | 2.40E-159 | WP_003244395.1 | MULTISPECIES: 5-amino-6-(5-phospho-D-ribitylamino)uracil phosphatase YwtE |
| BSLIN78GL003899 | 100 | 6.50E-246 | CAF1737192.1 | Gamma-DL-glutamyl hydrolase [Bacillus subtilis |
| BSLIN78GL003900 | 100 | 5.30E-23 | WP_015251077.1 | MULTISPECIES: extrachromosomal elements maintenance protein EdmS [Bacillus] |
| BSLIN78GL003901 | 100 | 6.10E-219 | AFQ59439.1 | Capsular polyglutamate synthetase [Bacillus subtilis QB928] |
| BSLIN78GL003902 | 100 | 1.20E-74 | WP_003227889.1 | MULTISPECIES: poly-gamma-glutamate biosynthesis protein PgsC [Bacillales |
| BSLIN78GL003903 | 100 | 2.90E-224 | WP_003227883.1 | MULTISPECIES: poly-gamma-glutamate synthase PgsB [Bacillales |
| BSLIN78GL003904 | 99.7 | 1.60E-189 | EHA32359.1 | LacI family transcriptional regulator [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL003905 | 100 | 1.10E-156 | WP_029318754.1 | ribokinase [Bacillus subtilis] |
| BSLIN78GL003906 | 100 | 9.20E-66 | WP_029318753.1 | MULTISPECIES: D-ribose pyranase [Bacillus |
| BSLIN78GL003907 | 100 | 2.40E-276 | WP_029726016.1 | ribose ABC transporter ATP-binding protein RbsA [Bacillus subtilis] |
| BSLIN78GL003908 | 100 | 2.10E-172 | WP_017696600.1 | MULTISPECIES: ribose ABC transporter permease RbsC [Bacillus |
| BSLIN78GL003909 | 99.7 | 3.80E-163 | WP_003242760.1 | MULTISPECIES: ribose ABC transporter substrate-binding protein RbsB [Bacillales |
| BSLIN78GL003910 | 100 | 1.80E-96 | WP_003243596.1 | MULTISPECIES: SH3 domain-containing protein [Bacillales] |
| BSLIN78GL003911 | 100 | 1.70E-48 | WP_003243460.1 | MULTISPECIES: DUF3892 domain-containing protein [Bacillales |
| BSLIN78GL003912 | 100 | 2.10E-97 | WP_003242788.1 | MULTISPECIES: NAD(P)H-dependent oxidoreductase [Bacillales |
| BSLIN78GL003913 | 99.6 | 1.10E-147 | AFQ59451.1 | Alpha-acetolactate decarboxylase [Bacillus subtilis QB928] |
| BSLIN78GL003914 | 99.8 | 0.00E+00 | AGA21734.1 | Acetolactate synthase [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL003915 | 100 | 2.70E-169 | WP_003227859.1 | MULTISPECIES: als operon DNA-binding transcriptional repressor AlsR [Bacillales |
| BSLIN78GL003916 | 100 | 2.20E-249 | WP_080529885.1 | MULTISPECIES: arsenic transporter [Bacillus] |
| BSLIN78GL003917 | 100 | 1.60E-126 | WP_003227857.1 | MULTISPECIES: DUF2642 domain-containing protein [Bacillus |
| BSLIN78GL003918 | 99.8 | 8.50E-227 | WP_326225157.1 | spore coat protein CotH [Bacillus subtilis] |
| BSLIN78GL003919 | 100 | 2.20E-210 | WP_015714831.1 | MULTISPECIES: spore coat protein CotH [Bacillus] |
| BSLIN78GL003920 | 100 | 2.50E-110 | WP_003227852.1 | MULTISPECIES: flavin reductase family protein [Bacillales |
| BSLIN78GL003921 | 100 | 7.80E-58 | WP_021480762.1 | MULTISPECIES: DUF4181 domain-containing protein [Bacillus |
| BSLIN78GL003922 | 100 | 3.70E-307 | WP_046381376.1 | MULTISPECIES: gamma-glutamyltransferase [Bacillus |
| BSLIN78GL003923 | 100 | 2.40E-84 | AGE65218.1 | hypothetical protein C663_3506 [Bacillus subtilis XF-1] |
| BSLIN78GL003924 | 100 | 1.60E-106 | WP_015251064.1 | MULTISPECIES: chromate efflux transporter subunit ChrB [Bacillus] |
| BSLIN78GL003925 | 100 | 1.40E-93 | WP_014665634.1 | MULTISPECIES: chromate resistance efflux protein ChrA [Bacillus |
| BSLIN78GL003926 | 100 | 1.70E-32 | WP_032722655.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL003927 | 98.5 | 2.70E-106 | AFQ59466.1 | Putative oxidoreductase [Bacillus subtilis QB928] |

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| BSLIN78GL003928 | 100 | 3.70E-163 | WP_014481127.1 | MULTISPECIES: LysR family transcriptional regulator [Bacillus |
| BSLIN78GL003929 | 99.4 | 7.40E-98 | WP_046381377.1 | MULTISPECIES: endonuclease V [Bacillus] |
| BSLIN78GL003930 | 100 | 2.40E-14 | KIO57734.1 | hypothetical protein B4143_3744 [Bacillus subtilis] |
| BSLIN78GL003931 | 100 | 3.20E-184 | AKE25431.1 | putative transposase or phage integrase [Bacillus sp. LM 4-2] |
| BSLIN78GL003932 | 100 | 1.50E-14 | WP_234939187.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL003933 | 100 | 6.10E-73 | WP_202926373.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL003934 | 100 | 0.00E+00 | WP_046381378.1 | MULTISPECIES: T7SS effector LXG polymorphic toxin [Bacillus |
| BSLIN78GL003935 | 100 | 7.50E-40 | WP_046381379.1 | MULTISPECIES: YwqI/YxiC family protein [Bacillus |
| BSLIN78GL003936 | 100 | 6.40E-73 | WP_010332155.1 | MULTISPECIES: DUF5082 family protein [Bacillus |
| BSLIN78GL003937 | 100 | 1.00E-24 | AKE25437.1 | hypothetical protein BsLM_3640 [Bacillus sp. LM 4-2] |
| BSLIN78GL003938 | 100 | 1.20E-154 | WP_033885053.1 | MULTISPECIES: YwqG family protein [Bacillus |
| BSLIN78GL003939 | 99.3 | 1.90E-259 | BAI87270.2 | hypothetical protein BSNT_10270 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL003940 | 100 | 1.20E-141 | WP_033885052.1 | MULTISPECIES: tyrosine-protein phosphatase [Bacillus |
| BSLIN78GL003941 | 100 | 7.10E-122 | WP_015483794.1 | tyrosine-protein kinase PtkA [Bacillus subtilis] |
| BSLIN78GL003942 | 100 | 6.50E-129 | AFQ59477.1 | Modulator of YwqD protein tyrosine kinaseactivity [Bacillus subtilis QB928] |
| BSLIN78GL003943 | 100 | 1.50E-22 | AFQ59478.1 | YwzD [Bacillus subtilis QB928] |
| BSLIN78GL003944 | 100 | 0.00E+00 | WP_038427968.1 | MULTISPECIES: SWIM zinc finger family protein [Bacillus |
| BSLIN78GL003945 | 100 | 0.00E+00 | WP_069322953.1 | DEAD/DEAH box helicase [Bacillus subtilis] |
| BSLIN78GL003946 | 100 | 2.00E-158 | WP_273797260.1 | phosphatase YwpJ [Bacillus subtilis] |
| BSLIN78GL003947 | 100 | 9.10E-145 | WP_003227799.1 | MULTISPECIES: transcriptional regulator GlcR [Bacillus] |
| BSLIN78GL003948 | 100 | 2.30E-57 | WP_014478203.1 | MULTISPECIES: single-stranded DNA-binding protein SsbB [Bacillus |
| BSLIN78GL003949 | 100 | 7.30E-68 | WP_014478204.1 | MULTISPECIES: DynA interaction protein YwpG [Bacillus |
| BSLIN78GL003950 | 100 | 4.60E-68 | WP_003227794.1 | MULTISPECIES: YwpF-like family protein [Bacillales |
| BSLIN78GL003951 | 100 | 2.20E-51 | WP_166668891.1 | class A sortase [Bacillus subtilis] |
| BSLIN78GL003952 | 100 | 8.00E-21 | WP_175407070.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL003953 | 99 | 1.10E-159 | WP_252348816.1 | histidine kinase [Bacillus subtilis] |
| BSLIN78GL003954 | 100 | 1.50E-72 | ADV94443.1 | large-conductance mechanosensitive channel [Bacillus subtilis BSn5] |
| BSLIN78GL003955 | 100 | 4.40E-83 | AFQ59489.1 | (3R)-hydroxymyristoyl-[acyl carrier protein]dehydratase [Bacillus subtilis QB928 |
| BSLIN78GL003956 | 100 | 1.10E-203 | WP_108029072.1 | MULTISPECIES: aspartate phosphatase RapD [Bacillus] |
| BSLIN78GL003957 | 100 | 9.10E-145 | WP_108029073.1 | MULTISPECIES: flagellar hook-basal body complex protein FlhP [Bacillus |
| BSLIN78GL003958 | 99.6 | 5.20E-151 | AGE65245.1 | putative flagellar basal-body rod protein [Bacillus subtilis XF-1] |
| BSLIN78GL003959 | 100 | 1.50E-181 | WP_003227776.1 | MULTISPECIES: cell shape-determining protein Mbl [Bacillales] |
| BSLIN78GL003960 | 100 | 1.30E-35 | AGE65247.1 | transcriptional regulator [Bacillus subtilis XF-1] |
| BSLIN78GL003961 | 100 | 3.10E-72 | WP_003227771.1 | MULTISPECIES: MarR family transcriptional regulator [Bacillales] |
| BSLIN78GL003962 | 100 | 1.70E-219 | WP_072175614.1 | MFS transporter [Bacillus subtilis] |
| BSLIN78GL003963 | 99.8 | 6.90E-273 | KAF1339979.1 | putative protein YwoF [Bacillus subtilis] |
| BSLIN78GL003964 | 100 | 5.70E-286 | WP_014481153.1 | MULTISPECIES: allantoin permease [Bacillus] |
| BSLIN78GL003965 | 100 | 7.90E-250 | WP_124072824.1 | MFS transporter [Bacillus subtilis] |
| BSLIN78GL003966 | 100 | 2.10E-103 | WP_003227761.1 | MULTISPECIES: hydrolase [Bacillales |
| BSLIN78GL003967 | 98.7 | 3.50E-80 | WP_072173785.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL003968 | 100 | 2.70E-233 | WP_003227757.1 | MULTISPECIES: ammonium transporter AmtB [Bacillales] |
| BSLIN78GL003969 | 100 | 4.80E-58 | AFQ59504.1 | Nitrogen-regulated PII-like regulator protein [Bacillus subtilis QB928] |
| BSLIN78GL003970 | 100 | 3.40E-92 | WP_015483805.1 | undecaprenyl-diphosphate phosphatase BcrC [Bacillus subtilis] |
| BSLIN78GL003971 | 96.6 | 2.80E-94 | AFQ59506.1 | Putative integral inner membrane protein [Bacillus subtilis QB928] |
| BSLIN78GL003972 | 100 | 3.50E-158 | WP_014481160.1 | MULTISPECIES: stage II sporulation protein spoIIQ [Bacillus |
| BSLIN78GL003973 | 99.4 | 5.70E-89 | ADV94463.1 | putative phosphinothricin acetyltransferase [Bacillus subtilis BSn5] |
| BSLIN78GL003974 | 100 | 1.90E-87 | WP_015714857.1 | MULTISPECIES: DUF5362 family protein [Bacillus |
| BSLIN78GL003975 | 100 | 1.20E-17 | WP_003227748.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL003976 | 99.4 | 1.30E-79 | BAI87308.2 | hypothetical protein BSNT_10308 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL003977 | 100 | 1.10E-284 | AFQ59511.1 | Cardiolipin synthase [Bacillus subtilis QB928] |
| BSLIN78GL003978 | 98.9 | 1.90E-150 | AFQ59512.1 | Transcriptional regulator (MerR family) [Bacillus subtilis QB928] |
| BSLIN78GL003979 | 100 | 2.10E-62 | WP_014478231.1 | MULTISPECIES: DUF5362 family protein [Bacillus |
| BSLIN78GL003980 | 100 | 1.60E-115 | WP_029726052.1 | MULTISPECIES: NAD(P)-dependent oxidoreductase [Bacillus |
| BSLIN78GL003981 | 100 | 9.40E-66 | WP_003227734.1 | MULTISPECIES: Rrf2 family transcriptional regulator [Bacillales] |
| BSLIN78GL003982 | 99.5 | 0.00E+00 | WP_046663993.1 | MULTISPECIES: urease subunit alpha [Bacillus] |
| BSLIN78GL003983 | 100 | 1.20E-62 | WP_029726054.1 | MULTISPECIES: urease subunit beta [Bacillus] |
| BSLIN78GL003984 | 100 | 9.80E-56 | AFQ59518.1 | Urease (gamma subunit) [Bacillus subtilis QB928] |
| BSLIN78GL003985 | 100 | 2.30E-21 | AOA56449.1 | hypothetical protein BSHJ0_03906 [Bacillus subtilis] |
| BSLIN78GL003986 | 100 | 1.20E-25 | WP_003227720.1 | MULTISPECIES: transporter substrate-binding protein [Bacillus] |
| BSLIN78GL003987 | 100 | 1.10E-27 | WP_003227718.1 | MULTISPECIES: stress response protein CsbD [Bacillales] |
| BSLIN78GL003988 | 100 | 2.30E-119 | AHA79619.1 | putative membrane protein ywmF [Bacillus subtilis PY79] |
| BSLIN78GL003989 | 100 | 1.10E-215 | WP_003227715.1 | MULTISPECIES: response regulator aspartate phosphatase RapB [Bacillales] |
| BSLIN78GL003990 | 100 | 1.10E-187 | WP_003243488.1 | MULTISPECIES: GTP 3',8-cyclase MoaA [Bacillales |
| BSLIN78GL003991 | 100 | 3.10E-145 | WP_003227709.1 | MULTISPECIES: formate dehydrogenase accessory sulfurtransferase FdhD |
| BSLIN78GL003992 | 100 | 1.50E-19 | WP_003227706.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL003993 | 99.6 | 2.30E-128 | AGE65278.1 | hypothetical protein C663_3569 [Bacillus subtilis XF-1] |
| BSLIN78GL003994 | 100 | 5.10E-19 | WP_003227702.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL003995 | 100 | 2.90E-123 | WP_024571497.1 | MULTISPECIES: VWA domain-containing protein [Bacillus] |
| BSLIN78GL003996 | 100 | 1.20E-178 | WP_029726056.1 | MULTISPECIES: stage II sporulation protein D [Bacillus] |
| BSLIN78GL003997 | 100 | 2.40E-243 | WP_029726057.1 | MULTISPECIES: UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus |
| BSLIN78GL003998 | 100 | 2.60E-138 | RAP07936.1 | hypothetical protein HS3_01869 [Bacillus subtilis] |
| BSLIN78GL003999 | 100 | 3.20E-34 | WP_003227691.1 | MULTISPECIES: DUF1146 family protein [Bacillales |
| BSLIN78GL004000 | 100 | 5.40E-95 | WP_029726058.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004001 | 100 | 2.70E-65 | WP_014478254.1 | MULTISPECIES: F0F1 ATP synthase subunit epsilon [Bacillus |
| BSLIN78GL004002 | 95.9 | 1.80E-249 | WP_065982546.1 | MULTISPECIES: F0F1 ATP synthase subunit beta [Bacillus |
| BSLIN78GL004003 | 99.7 | 2.40E-154 | QHF59832.1 | synthase gamma chain [Bacillus subtilis] |
| BSLIN78GL004004 | 92.2 | 7.40E-265 | WP_326070032.1 | F0F1 ATP synthase subunit alpha [Bacillus licheniformis] |
| BSLIN78GL004005 | 100 | 6.10E-92 | WP_029726059.1 | MULTISPECIES: F0F1 ATP synthase subunit delta [Bacillus |
| BSLIN78GL004006 | 100 | 2.40E-70 | WP_029726060.1 | MULTISPECIES: F0F1 ATP synthase subunit B [Bacillus |
| BSLIN78GL004007 | 100 | 6.30E-29 | WP_003151167.1 | MULTISPECIES: F0F1 ATP synthase subunit C [Bacteria |

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|---|---|---|---|---|
| BSLIN78GL004008 | 100 | 1.30E-120 | AEP92744.1 | ATP synthase F0, A subunit [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL004009 | 100 | 6.30E-55 | WP_031601086.1 | ATP synthase subunit I [Bacillus subtilis] |
| BSLIN78GL004010 | 100 | 1.10E-113 | AFQ59540.1 | Uracil phosphoribosyltransferase [Bacillus subtilis QB928] |
| BSLIN78GL004011 | 100 | 1.10E-237 | WP_003227669.1 | MULTISPECIES: serine hydroxymethyltransferase [Bacillales |
| BSLIN78GL004012 | 100 | 4.50E-95 | WP_029318713.1 | MULTISPECIES: TIGR01440 family protein [Bacillus |
| BSLIN78GL004013 | 100 | 2.60E-80 | WP_003221910.1 | MULTISPECIES: ribose 5-phosphate isomerase B [Bacillales] |
| BSLIN78GL004014 | 100 | 2.90E-79 | WP_015384897.1 | MULTISPECIES: protein arginine phosphatase PrpB [Bacillus] |
| BSLIN78GL004015 | 100 | 5.40E-96 | WP_003227661.1 | MULTISPECIES: manganese efflux pump MntP family protein [Bacillales] |
| BSLIN78GL004016 | 100 | 6.60E-196 | WP_088327167.1 | L-threonylcarbamoyladenylate synthase [Bacillus subtilis |
| BSLIN78GL004017 | 99.4 | 7.70E-83 | AGE65303.1 | hypothetical protein C663_3595 [Bacillus subtilis XF-1] |
| BSLIN78GL004018 | 99.1 | 5.90E-121 | WP_174222771.1 | stage II sporulation protein R [Bacillus subtilis] |
| BSLIN78GL004019 | 100 | 1.40E-60 | WP_015251010.1 | UPF0715 family protein [Bacillus subtilis] |
| BSLIN78GL004020 | 100 | 7.00E-54 | AFQ59550.1 | YwkF [Bacillus subtilis QB928] |
| BSLIN78GL004021 | 100 | 4.10E-159 | WP_003227647.1 | MULTISPECIES: peptide chain release factor N(5)-glutamine methyltransferase |
| BSLIN78GL004022 | 100 | 1.60E-197 | WP_003227645.1 | MULTISPECIES: peptide chain release factor 1 [Bacillales] |
| BSLIN78GL004023 | 100 | 9.60E-68 | AFQ59553.1 | Putative lyase [Bacillus subtilis QB928] |
| BSLIN78GL004024 | 100 | 4.60E-95 | WP_015251007.1 | MULTISPECIES: chromosome-anchoring protein RacA [Bacillus] |
| BSLIN78GL004025 | 100 | 8.10E-172 | AFQ59555.1 | Putative transporter [Bacillus subtilis QB928] |
| BSLIN78GL004026 | 100 | 0.00E+00 | WP_003244309.1 | MULTISPECIES: oxaloacetate-decarboxylating malate dehydrogenase [Bacillales |
| BSLIN78GL004027 | 97.9 | 4.00E-19 | KIN27388.1 | hypothetical protein B4070_3760 [Bacillus subtilis] |
| BSLIN78GL004028 | 100 | 1.80E-105 | WP_017696004.1 | MULTISPECIES: thymidine kinase [Bacillus |
| BSLIN78GL004029 | 100 | 4.90E-34 | AFQ59558.1 | Ribosomal protein L31 [Bacillus subtilis QB928] |
| BSLIN78GL004030 | 100 | 4.10E-240 | WP_003221939.1 | MULTISPECIES: transcription termination factor Rho [Bacillales] |
| BSLIN78GL004031 | 100 | 1.10E-20 | WP_003227632.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL004032 | 100 | 6.60E-171 | AGE65317.1 | fructose 1,6-bisphosphatase II [Bacillus subtilis XF-1] |
| BSLIN78GL004033 | 100 | 1.60E-239 | WP_003227628.1 | MULTISPECIES: UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillales |
| BSLIN78GL004034 | 100 | 1.20E-112 | WP_003227626.1 | MULTISPECIES: fructose-6-phosphate aldolase [Bacillales |
| BSLIN78GL004035 | 100 | 2.10E-155 | AFQ59563.1 | Fructose-1,6-bisphosphate aldolase [Bacillus subtilis QB928] |
| BSLIN78GL004036 | 100 | 2.60E-62 | WP_003227621.1 | MULTISPECIES: sporulation initiation phosphotransferase Spo0F [Bacillales] |
| BSLIN78GL004037 | 100 | 2.60E-92 | WP_029726065.1 | MULTISPECIES: DUF2529 domain-containing protein [Bacillus] |
| BSLIN78GL004038 | 99.8 | 3.6e-311 | WP_172850329.1 | CTP synthase (glutamine hydrolyzing) [Bacillus subtilis |
| BSLIN78GL004039 | 100 | 6.20E-94 | WP_014665742.1 | MULTISPECIES: DNA-directed RNA polymerase subunit delta [Bacillus |
| BSLIN78GL004040 | 100 | 9.40E-18 | AFI30332.1 | hypothetical protein MY9_3800 [Bacillus sp. JS] |
| BSLIN78GL004041 | 95.5 | 1.00E-202 | WP_215797748.1 | acyl-CoA dehydrogenase AcdA [Bacillus cabrialesii |
| BSLIN78GL004042 | 100 | 0.00E+00 | WP_326253730.1 | heterodisulfide reductase-related iron-sulfur binding cluster [Bacillus subtilis] |
| BSLIN78GL004043 | 100 | 1.80E-229 | WP_147797745.1 | cardiolipin synthase [Bacillus subtilis] |
| BSLIN78GL004044 | 100 | 3.10E-184 | WP_147797744.1 | UV DNA damage repair endonuclease UvsE [Bacillus subtilis] |
| BSLIN78GL004045 | 100 | 5.80E-43 | WP_003227597.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL004046 | 98.5 | 6.90E-72 | WP_128480837.1 | dihydrofolate reductase family protein [Bacillus subtilis] |
| BSLIN78GL004047 | 98.6 | 0.00E+00 | WP_166443861.1 | ABC transporter ATP-binding protein [Bacillus subtilis] |
| BSLIN78GL004048 | 100 | 1.10E-289 | WP_147797742.1 | cardiolipin synthase [Bacillus subtilis] |
| BSLIN78GL004049 | 100 | 2.30E-125 | WP_147797741.1 | respiratory nitrate reductase subunit gamma [Bacillus subtilis] |
| BSLIN78GL004050 | 100 | 2.60E-98 | WP_015384918.1 | nitrate reductase molybdenum cofactor assembly chaperone [Bacillus subtilis] |
| BSLIN78GL004051 | 100 | 3.10E-292 | QHF59878.1 | reductase beta chain [Bacillus subtilis] |
| BSLIN78GL004052 | 99.9 | 0.00E+00 | WP_046381395.1 | MULTISPECIES: nitrate reductase subunit alpha [Bacillus] |
| BSLIN78GL004053 | 100 | 1.30E-16 | KIN54826.1 | hypothetical protein B4146_4146 [Bacillus subtilis] |
| BSLIN78GL004054 | 100 | 9.80E-77 | WP_147797739.1 | Crp/Fnr family transcriptional regulator ArfM [Bacillus subtilis] |
| BSLIN78GL004055 | 98 | 1.90E-147 | AFQ59581.1 | Putative integral inner membrane protein [Bacillus subtilis QB928] |
| BSLIN78GL004056 | 100 | 5.70E-130 | WP_003227573.1 | MULTISPECIES: fumarate/nitrate reduction transcriptional regulator Fnr [Bacillus] |
| BSLIN78GL004057 | 100 | 2.70E-228 | AIX09362.1 | putative nitrate transporter NarT [Bacillus subtilis] |
| BSLIN78GL004058 | 100 | 0.00E+00 | WP_147797738.1 | arginine--tRNA ligase [Bacillus subtilis] |
| BSLIN78GL004059 | 100 | 6.30E-67 | AGE65343.1 | hypothetical protein C663_3635 [Bacillus subtilis XF-1] |
| BSLIN78GL004060 | 100 | 1.50E-17 | WP_003222002.1 | MULTISPECIES: subtilosin A [Bacillales] |
| BSLIN78GL004061 | 100 | 2.30E-265 | WP_322393848.1 | subtilosin maturase AlbA [Bacillus stercoris] |
| BSLIN78GL004062 | 100 | 4.00E-20 | WP_003222006.1 | MULTISPECIES: antilisterial bacteriocin subtilosin biosynthesis protein AlbB |
| BSLIN78GL004063 | 100 | 4.60E-132 | WP_130572964.1 | ABC transporter ATP-binding protein [Bacillus subtilis] |
| BSLIN78GL004064 | 100 | 2.60E-242 | WP_326253722.1 | antilisterial bacteriocin subtilosin biosynthesis protein AlbD [Bacillus subtilis] |
| BSLIN78GL004065 | 99.7 | 3.30E-223 | QHM13683.1 | Antilisterial bacteriocin subtilosin biosynthesis protein AlbE [Bacillus subtilis |
| BSLIN78GL004066 | 100 | 1.10E-248 | WP_032722698.1 | pitrilysin family protein [Bacillus subtilis] |
| BSLIN78GL004067 | 100 | 3.40E-127 | WP_029726080.1 | MULTISPECIES: antilisterial bacteriocin subtilosin biosynthesis protein AlbG |
| BSLIN78GL004068 | 100 | 3.40E-264 | WP_046381401.1 | MULTISPECIES: YncE family protein [Bacillus] |
| BSLIN78GL004069 | 100 | 1.70E-260 | WP_046381402.1 | MULTISPECIES: YncE family protein [Bacillus] |
| BSLIN78GL004070 | 100 | 2.00E-13 | WP_038429796.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004071 | 100 | 8.80E-218 | WP_086344441.1 | MULTISPECIES: response regulator aspartate phosphatase RapF [Bacillus] |
| BSLIN78GL004072 | 100 | 4.60E-166 | WP_003227545.1 | MULTISPECIES: agmatinase [Bacillales] |
| BSLIN78GL004073 | 100 | 3.30E-158 | WP_003227543.1 | MULTISPECIES: spermidine synthase [Bacillales |
| BSLIN78GL004074 | 100 | 0.00E+00 | WP_038427996.1 | transglycosylase domain-containing protein [Bacillus subtilis] |
| BSLIN78GL004075 | 100 | 7.30E-95 | WP_015250981.1 | MULTISPECIES: YwhD family protein [Bacillus |
| BSLIN78GL004076 | 100 | 6.50E-114 | WP_041338298.1 | site-2 protease family protein [Bacillus subtilis] |
| BSLIN78GL004077 | 100 | 3.40E-26 | AFQ59605.1 | 4-oxalocrotonate tautomerase [Bacillus subtilis QB928] |
| BSLIN78GL004078 | 100 | 1.20E-71 | AFQ59606.1 | Putative transcriptional regulator (MarR family) [Bacillus subtilis QB928] |
| BSLIN78GL004079 | 99.8 | 0.00E+00 | AAA22863.1 | threonyl-tRNA synthetase (thrS2) (EC 6.1.1.3) [Bacillus subtilis] |
| BSLIN78GL004080 | 100 | 1.00E-20 | WP_003244574.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004081 | 100 | 8.50E-255 | WP_029726233.1 | MFS transporter [Bacillus subtilis] |
| BSLIN78GL004082 | 100 | 3.50E-80 | WP_029726232.1 | Rrf2 family transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL004083 | 100 | 4.00E-90 | AFQ59610.1 | YwgA [Bacillus subtilis QB928] |
| BSLIN78GL004084 | 100 | 1.20E-255 | QHF59912.1 | triphosphate triphosphohydrolase SAMHD1 [Bacillus subtilis] |
| BSLIN78GL004085 | 100 | 1.30E-24 | AGE65374.1 | hypothetical protein C663_3666 [Bacillus subtilis XF-1] |
| BSLIN78GL004086 | 100 | 3.10E-142 | WP_029726231.1 | MULTISPECIES: prespore-specific transcription regulator RsfA [Bacillus |
| BSLIN78GL004087 | 100 | 1.30E-163 | WP_029726230.1 | MULTISPECIES: carboxylate/amino acid/amine transporter [Bacillus] |

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| BSLIN78GL004088 | 100 | 1.30E-20 | QJD02102.1 | Permease of the drug/metabolite transporter (DMT) superfamily [Bacillus subtilis |
| BSLIN78GL004089 | 100 | 6.00E-155 | WP_003227511.1 | MULTISPECIES: octanoyl-[GcvH]:protein N-octanoyltransferase [Bacillales |
| BSLIN78GL004090 | 99 | 3.30E-167 | AGE65378.1 | regulator of sulfur assimilation CysL, activates cysJI expression [Bacillus subtilis XF- |
| BSLIN78GL004091 | 100 | 1.90E-176 | WP_003235941.1 | MULTISPECIES: phosphate acetyltransferase [Bacillus |
| BSLIN78GL004092 | 100 | 1.30E-145 | WP_003242896.1 | MULTISPECIES: hydrogen peroxide-dependent heme synthase [Bacillales |
| BSLIN78GL004093 | 100 | 1.90E-136 | WP_029726228.1 | MULTISPECIES: NADPH-dependent reductase BacG [Bacillus |
| BSLIN78GL004094 | 100 | 7.80E-233 | WP_029726227.1 | MULTISPECIES: transaminase BacF [Bacillus] |
| BSLIN78GL004095 | 100 | 1.80E-218 | WP_029726226.1 | MULTISPECIES: bacilysin exporter BacE [Bacillus |
| BSLIN78GL004096 | 100 | 1.00E-271 | WP_003242921.1 | MULTISPECIES: alanine--anticapsin ligase [Bacillales] |
| BSLIN78GL004097 | 99.6 | 1.70E-140 | KAF1339842.1 | Dihydroanticapsin 7-dehydrogenase [Bacillus subtilis] |
| BSLIN78GL004098 | 100 | 8.90E-136 | WP_003244300.1 | MULTISPECIES: 3-((4R)-4-hydroxycyclohexa-1,5-dien-1-yl)-2-oxopropanoate |
| BSLIN78GL004099 | 100 | 3.50E-112 | WP_009968341.1 | MULTISPECIES: prephenate decarboxylase [Bacillales |
| BSLIN78GL004100 | 100 | 2.00E-13 | AHA79735.1 | Hypothetical Protein U712_19025 [Bacillus subtilis PY79] |
| BSLIN78GL004101 | 100 | 4.90E-230 | WP_003242790.1 | MULTISPECIES: MFS transporter [Bacillales] |
| BSLIN78GL004102 | 99.8 | 1.90E-270 | KIL31848.1 | hypothetical protein B4067_4237 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL004103 | 100 | 0.00E+00 | WP_147797734.1 | M20/M25/M40 family metallo-hydrolase [Bacillus subtilis] |
| BSLIN78GL004104 | 100 | 6.80E-298 | WP_014478322.1 | MULTISPECIES: L-glutamate gamma-semialdehyde dehydrogenase [Bacillus |
| BSLIN78GL004105 | 97.5 | 4.30E-14 | RPK13733.1 | hypothetical protein EH5_00357 [Bacillus subtilis] |
| BSLIN78GL004106 | 100 | 1.60E-244 | QHF59932.1 | NAD-specific glutamate dehydrogenase [Bacillus subtilis] |
| BSLIN78GL004107 | 100 | 6.10E-16 | KIL31843.1 | hypothetical protein B4067_4232 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL004108 | 100 | 8.60E-79 | WP_101172258.1 | biofilm surface layer hydrophobin BslB [Bacillus subtilis] |
| BSLIN78GL004109 | 100 | 2.40E-86 | WP_003242881.1 | MULTISPECIES: dTDP-4-dehydrorhamnose 3,5-epimerase family protein |
| BSLIN78GL004110 | 99.6 | 1.30E-157 | WP_015250965.1 | MULTISPECIES: dTDP-4-dehydrorhamnose reductase [Bacillus |
| BSLIN78GL004111 | 100 | 2.10E-180 | WP_072173258.1 | MULTISPECIES: dTDP-glucose 4,6-dehydratase [Bacillus |
| BSLIN78GL004112 | 100 | 1.70E-137 | WP_147797733.1 | sugar phosphate nucleotidyltransferase [Bacillus subtilis] |
| BSLIN78GL004113 | 100 | 4.80E-191 | WP_326253710.1 | PseG/SpsG family protein [Bacillus subtilis] |
| BSLIN78GL004114 | 100 | 1.40E-131 | WP_326253709.1 | spore coat protein [Bacillus subtilis] |
| BSLIN78GL004115 | 100 | 1.90E-212 | WP_029726215.1 | MULTISPECIES: N-acetylneuraminate synthase family protein [Bacillus |
| BSLIN78GL004116 | 100 | 2.50E-164 | WP_029726214.1 | MULTISPECIES: GNAT family N-acetyltransferase [Bacillus |
| BSLIN78GL004117 | 100 | 3.40E-225 | WP_326253708.1 | DegT/DnrJ/EryC1/StrS family aminotransferase [Bacillus subtilis] |
| BSLIN78GL004118 | 99.8 | 1.90E-267 | KIL31833.1 | hypothetical protein B4067_4222 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL004119 | 100 | 1.00E-142 | WP_147797730.1 | spore coat dTDP-glycosyltransferase SpsA [Bacillus subtilis |
| BSLIN78GL004120 | 100 | 7.60E-103 | WP_014481253.1 | MULTISPECIES: spore coat protein GerQ [Bacillus] |
| BSLIN78GL004121 | 100 | 4.50E-62 | WP_003227446.1 | MULTISPECIES: DUF423 domain-containing protein [Bacillales] |
| BSLIN78GL004122 | 100 | 7.50E-245 | WP_029726212.1 | purine/pyrimidine permease [Bacillus subtilis] |
| BSLIN78GL004123 | 97.4 | 2.90E-79 | AII37505.1 | hypothetical protein M036_19425 [Bacillus subtilis TO-A] |
| BSLIN78GL004124 | 99.8 | 1.20E-261 | WP_019712832.1 | aldehyde dehydrogenase [Bacillus subtilis] |
| BSLIN78GL004125 | 100 | 2.00E-129 | WP_003242965.1 | MULTISPECIES: uracil-DNA glycosylase [Bacillales |
| BSLIN78GL004126 | 100 | 2.00E-152 | WP_015714916.1 | MULTISPECIES: glycosyltransferase family 2 protein [Bacillus |
| BSLIN78GL004127 | 100 | 6.70E-151 | EHA32137.1 | pyridoxal kinase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004128 | 100 | 1.10E-30 | AGE65413.1 | hypothetical protein C663_3708 [Bacillus subtilis XF-1] |
| BSLIN78GL004129 | 100 | 3.60E-293 | WP_003227428.1 | MULTISPECIES: sucrose-6-phosphate hydrolase [Bacillales |
| BSLIN78GL004130 | 100 | 1.10E-259 | WP_003227426.1 | MULTISPECIES: PTS system sucrose transporter subunit IIBC [Bacillales |
| BSLIN78GL004131 | 100 | 3.20E-150 | AKE25634.1 | hypothetical protein BsLM_3837 [Bacillus sp. LM 4-2] |
| BSLIN78GL004132 | 100 | 1.20E-152 | WP_003227423.1 | MULTISPECIES: sac operon transcriptional antiterminator SacT [Bacillus] |
| BSLIN78GL004133 | 100 | 1.40E-69 | AEP92867.1 | hypothetical protein I33_3959 [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL004134 | 100 | 0.00E+00 | WP_029726207.1 | MULTISPECIES: serine protease Vpr [Bacillus] |
| BSLIN78GL004135 | 100 | 3.20E-187 | WP_029726206.1 | MULTISPECIES: LLM class flavin-dependent oxidoreductase [Bacillus |
| BSLIN78GL004136 | 100 | 4.00E-145 | BAI87476.2 | FMN-containing NADPH-linked nitro/flavin reductase [Bacillus subtilis subsp. natto |
| BSLIN78GL004137 | 100 | 1.40E-218 | WP_015250943.1 | MULTISPECIES: cell shape-determining peptidoglycan glycosyltransferase RodA |
| BSLIN78GL004138 | 100 | 1.40E-41 | WP_081638379.1 | MULTISPECIES: spore morphogenesis/germination protein YwcE [Bacillus] |
| BSLIN78GL004139 | 100 | 2.70E-67 | WP_003227410.1 | MULTISPECIES: cytochrome aa3 quinol oxidase subunit IV [Bacillales |
| BSLIN78GL004140 | 100 | 1.10E-113 | WP_003227409.1 | MULTISPECIES: cytochrome aa3 quinol oxidase subunit III [Bacillales |
| BSLIN78GL004141 | 100 | 0.00E+00 | WP_003227407.1 | MULTISPECIES: cytochrome aa3 quinol oxidase subunit I [Bacillales |
| BSLIN78GL004142 | 100 | 1.00E-182 | AIC42300.1 | cytochrome aa3-600 quinol oxidase subunit II [Bacillus subtilis subsp. subtilis str. |
| BSLIN78GL004143 | 100 | 9.70E-13 | EME09230.1 | hypothetical protein BS732_0783 [Bacillus subtilis MB73/2] |
| BSLIN78GL004144 | 100 | 1.30E-38 | AEP92877.1 | integral membrane protein [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL004145 | 100 | 2.20E-304 | WP_003227402.1 | MULTISPECIES: UDP-glucose--hexose-1-phosphate uridylyltransferase [Bacillales |
| BSLIN78GL004146 | 100 | 7.40E-228 | WP_003227400.1 | MULTISPECIES: galactokinase [Bacillales] |
| BSLIN78GL004147 | 100 | 1.20E-62 | AIC42304.1 | hypothetical protein BSUA_04057 [Bacillus subtilis subsp. subtilis str. JH642 substr. |
| BSLIN78GL004148 | 100 | 4.80E-123 | WP_003227396.1 | MULTISPECIES: transcriptional regulator SlrC [Bacillales] |
| BSLIN78GL004149 | 100 | 1.30E-12 | AGE65434.1 | hypothetical protein C663_3730 [Bacillus subtilis XF-1] |
| BSLIN78GL004150 | 100 | 2.90E-51 | WP_003227392.1 | MULTISPECIES: DUF485 domain-containing protein [Bacillales] |
| BSLIN78GL004151 | 100 | 1.10E-282 | WP_110109522.1 | MULTISPECIES: cation acetate symporter [Bacillus |
| BSLIN78GL004152 | 100 | 5.30E-116 | WP_021480940.1 | MULTISPECIES: DsbA family protein [Bacillus |
| BSLIN78GL004153 | 100 | 1.90E-242 | WP_029318658.1 | MULTISPECIES: iron uptake transporter deferrochelatase/peroxidase subunit |
| BSLIN78GL004154 | 100 | 6.60E-213 | WP_029726199.1 | MULTISPECIES: iron uptake system lipoprotein EfeM [Bacillus |
| BSLIN78GL004155 | 100 | 6.00E-264 | WP_029726198.1 | MULTISPECIES: ferrous ion permease EfeU [Bacillus] |
| BSLIN78GL004156 | 97 | 2.30E-120 | WP_214287112.1 | thiamine phosphate synthase [Bacillus subtilis] |
| BSLIN78GL004157 | 99.6 | 1.80E-134 | WP_046160984.1 | MULTISPECIES: hydroxyethylthiazole kinase [Bacillus |
| BSLIN78GL004158 | 100 | 2.00E-172 | WP_003227377.1 | MULTISPECIES: LysR family transcriptional regulator [Bacillales |
| BSLIN78GL004159 | 100 | 5.50E-63 | TWH32667.1 | holin-like protein [Bacillus subtilis J22] |
| BSLIN78GL004160 | 100 | 4.70E-118 | WP_003227371.1 | MULTISPECIES: CidB/LrgB family autolysis modulator [Bacillales |
| BSLIN78GL004161 | 100 | 7.60E-228 | EHA32104.1 | putative sugar permease [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004162 | 100 | 2.90E-28 | WP_003227367.1 | MULTISPECIES: YwbE family protein [Bacillus |
| BSLIN78GL004163 | 100 | 5.50E-223 | WP_015714924.1 | MULTISPECIES: class I SAM-dependent rRNA methyltransferase [Bacillus |
| BSLIN78GL004164 | 100 | 8.00E-67 | WP_014665869.1 | MULTISPECIES: glyoxalase GlxA [Bacillus |
| BSLIN78GL004165 | 100 | 1.00E-246 | WP_326253700.1 | PTS cellobiose transporter subunit IIC [Bacillus subtilis] |
| BSLIN78GL004166 | 100 | 0.00E+00 | WP_046381425.1 | MULTISPECIES: minor protease Epr [Bacillus] |
| BSLIN78GL004167 | 97.6 | 3.70E-16 | AHA79804.1 | Hypothetical Protein U712_19380 [Bacillus subtilis PY79] |

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| BSLIN78GL004168 | 100 | 4.00E-257 | WP_046381426.1 | MULTISPECIES: SacY negative regulator SacX [Bacillus] |
| BSLIN78GL004169 | 100 | 1.30E-154 | WP_046381427.1 | MULTISPECIES: transcription antiterminator SacY [Bacillus] |
| BSLIN78GL004170 | 100 | 3.40E-149 | EHA32093.1 | putative glycosyl transferase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004171 | 100 | 3.00E-131 | WP_033882895.1 | MULTISPECIES: TIGR02206 family membrane protein [Bacillus] |
| BSLIN78GL004172 | 100 | 2.00E-89 | WP_046381428.1 | MULTISPECIES: tyrZ transcriptional regulator YwaE [Bacillus] |
| BSLIN78GL004173 | 100 | 9.50E-234 | WP_080480990.1 | MULTISPECIES: tyrosine--tRNA ligase [Bacillus] |
| BSLIN78GL004174 | 100 | 5.70E-256 | AKE25678.1 | hypothetical protein BsLM_3881 [Bacillus sp. LM 4-2] |
| BSLIN78GL004175 | 100 | 2.00E-166 | WP_202926374.1 | helix-turn-helix transcriptional regulator [Bacillus subtilis] |
| BSLIN78GL004176 | 100 | 5.80E-65 | WP_033882888.1 | MULTISPECIES: carboxymuconolactone decarboxylase family protein [Bacillus] |
| BSLIN78GL004177 | 100 | 2.80E-222 | WP_046381432.1 | MULTISPECIES: MFS transporter [Bacillus] |
| BSLIN78GL004178 | 100 | 1.60E-129 | EHA32088.1 | hypothetical protein BSSC8_03450 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004179 | 100 | 1.10E-162 | WP_015714937.1 | MULTISPECIES: 1,4-dihydroxy-2-naphthoate polyprenyltransferase [Bacillus |
| BSLIN78GL004180 | 100 | 1.50E-26 | AFI30489.1 | hypothetical protein MY9_3957 [Bacillus sp. JS] |
| BSLIN78GL004181 | 100 | 7.00E-18 | WP_003227332.1 | MULTISPECIES: hypothetical protein [Bacillales] |
| BSLIN78GL004182 | 100 | 6.80E-22 | ADM39851.1 | conserved hypothetical protein [Bacillus spizizenii str. W23] |
| BSLIN78GL004183 | 100 | 1.20E-291 | WP_041054155.1 | MULTISPECIES: D-alanine--poly(phosphoribitol) ligase subunit DltA [Bacillus] |
| BSLIN78GL004184 | 100 | 1.60E-238 | WP_046381433.1 | MULTISPECIES: D-alanyl-lipoteichoic acid biosynthesis protein DltB [Bacillus |
| BSLIN78GL004185 | 100 | 1.20E-36 | WP_003227325.1 | MULTISPECIES: D-alanine--poly(phosphoribitol) ligase subunit DltC [Bacillales] |
| BSLIN78GL004186 | 100 | 1.20E-230 | WP_003227323.1 | MULTISPECIES: D-alanyl-lipoteichoic acid biosynthesis protein DltD [Bacillales |
| BSLIN78GL004187 | 100 | 2.70E-138 | WP_046381434.1 | MULTISPECIES: SDR family oxidoreductase [Bacillus] |
| BSLIN78GL004188 | 100 | 1.90E-206 | AFQ59708.1 | Branched-chain amino acid aminotransferase [Bacillus subtilis QB928] |
| BSLIN78GL004189 | 100 | 2.20E-252 | WP_003244285.1 | MULTISPECIES: 6-phospho-beta-glucosidase LicH [Bacillales] |
| BSLIN78GL004190 | 100 | 2.60E-53 | WP_041850365.1 | PTS lichenan transporter subunit IIA [Bacillus subtilis] |
| BSLIN78GL004191 | 100 | 8.20E-255 | WP_046381435.1 | MULTISPECIES: PTS lichenan transporter subunit IIC [Bacillus] |
| BSLIN78GL004192 | 100 | 3.20E-40 | WP_003218755.1 | MULTISPECIES: PTS lichenan transporter subunit IIB [Bacillales] |
| BSLIN78GL004193 | 100 | 0.00E+00 | WP_147797726.1 | transcriptional regulator LicR [Bacillus subtilis] |
| BSLIN78GL004194 | 100 | 1.30E-25 | AEP92923.1 | conserved hypothetical protein [Bacillus subtilis subsp. subtilis str. RO-NN-1] |
| BSLIN78GL004195 | 100 | 1.80E-110 | WP_003227303.1 | MULTISPECIES: DNA-3-methyladenine glycosylase [Bacillales |
| BSLIN78GL004196 | 100 | 0.00E+00 | WP_015250908.1 | MULTISPECIES: catalase KatX [Bacillus] |
| BSLIN78GL004197 | 100 | 7.10E-53 | AOA56654.1 | putative MFS-type transporter YxlH [Bacillus subtilis] |
| BSLIN78GL004198 | 100 | 8.00E-166 | WP_015250907.1 | MULTISPECIES: MFS transporter [Bacillus] |
| BSLIN78GL004199 | 100 | 2.80E-143 | WP_003243335.1 | MULTISPECIES: ABC transporter permease subunit [Bacillales] |
| BSLIN78GL004200 | 100 | 7.20E-167 | WP_015250906.1 | MULTISPECIES: ABC transporter ATP-binding protein [Bacillus] |
| BSLIN78GL004201 | 100 | 8.00E-28 | WP_003227293.1 | MULTISPECIES: sigma Y negative regulator YxlE [Bacillales] |
| BSLIN78GL004202 | 100 | 1.70E-31 | WP_003227291.1 | MULTISPECIES: sigma Y negative regulator YxlD [Bacillus] |
| BSLIN78GL004203 | 100 | 1.00E-51 | WP_003227289.1 | MULTISPECIES: YxlC family protein [Bacillales] |
| BSLIN78GL004204 | 100 | 6.60E-99 | WP_015250905.1 | MULTISPECIES: RNA polymerase sigma factor SigY [Bacillus] |
| BSLIN78GL004205 | 99.8 | 3.40E-264 | AGA22674.1 | hypothetical protein YxlA [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL004206 | 100 | 1.00E-159 | WP_029726189.1 | MULTISPECIES: NAD(P)H-hydrate dehydratase [Bacillus] |
| BSLIN78GL004207 | 100 | 0.00E+00 | WP_326253691.1 | thiol reductant ABC exporter subunit CydC [Bacillus subtilis] |
| BSLIN78GL004208 | 100 | 0.00E+00 | WP_029726187.1 | MULTISPECIES: thiol reductant ABC exporter subunit CydD [Bacillus] |
| BSLIN78GL004209 | 100 | 5.10E-193 | WP_029318635.1 | cytochrome d ubiquinol oxidase subunit II [Bacillus subtilis] |
| BSLIN78GL004210 | 100 | 1.00E-279 | AFQ59729.1 | Cytochrome bd ubiquinol oxidase (subunit I) [Bacillus subtilis QB928] |
| BSLIN78GL004211 | 100 | 1.20E-250 | WP_003227271.1 | MULTISPECIES: citrate/malate transporter CimH [Bacillales] |
| BSLIN78GL004212 | 100 | 0.00E+00 | AID00178.1 | peptidase [Bacillus subtilis subsp. subtilis str. OH 131.1] |
| BSLIN78GL004213 | 100 | 1.10E-29 | EHA32054.1 | hypothetical protein BSSC8_03110 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004214 | 100 | 1.80E-159 | WP_326253688.1 | polysaccharide deacetylase family protein [Bacillus subtilis] |
| BSLIN78GL004215 | 100 | 8.20E-205 | WP_003227263.1 | MULTISPECIES: maltodextrin ABC transporter ATP-binding protein MsmX |
| BSLIN78GL004216 | 100 | 1.20E-166 | WP_003227261.1 | MULTISPECIES: PucR family transcriptional regulator [Bacillus] |
| BSLIN78GL004217 | 100 | 5.90E-275 | WP_003227259.1 | MULTISPECIES: aldehyde dehydrogenase family protein [Bacillus] |
| BSLIN78GL004218 | 100 | 4.70E-152 | AGA22661.1 | Hypothetical protein YxkD [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL004219 | 100 | 8.40E-94 | WP_003227255.1 | MULTISPECIES: DUF4352 domain-containing protein [Bacillus] |
| BSLIN78GL004220 | 94.6 | 1.70E-183 | WP_106033671.1 | UDP-glucose 4-epimerase GalE [Bacillus atrophaeus] |
| BSLIN78GL004221 | 100 | 3.20E-95 | WP_003227251.1 | MULTISPECIES: YbhB/YbcL family Raf kinase inhibitor-like protein [Bacillus] |
| BSLIN78GL004222 | 100 | 4.10E-167 | WP_029726185.1 | MULTISPECIES: LysR family transcriptional regulator [Bacillus] |
| BSLIN78GL004223 | 100 | 5.00E-85 | EHA32044.1 | hypothetical protein BSSC8_03010 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004224 | 100 | 7.20E-226 | WP_003227246.1 | MULTISPECIES: two-component system sensor histidine kinase YxjM [Bacillus] |
| BSLIN78GL004225 | 100 | 8.60E-117 | WP_147797723.1 | two-component system response regulator YxJL [Bacillus subtilis] |
| BSLIN78GL004226 | 100 | 1.30E-235 | WP_046161014.1 | MULTISPECIES: peptidase T [Bacillus] |
| BSLIN78GL004227 | 100 | 1.80E-15 | WP_003227241.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL004228 | 100 | 2.90E-24 | WP_072692799.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004229 | 100 | 1.40E-87 | WP_042976786.1 | MULTISPECIES: LURP-one-related/scramblase family protein [Bacillus] |
| BSLIN78GL004230 | 100 | 6.00E-219 | WP_088467444.1 | 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase [Bacillus |
| BSLIN78GL004231 | 99.7 | 8.50E-221 | AFW16639.1 | putative methyltetrahydrofolate methyltransferase [Bacillus sp. UEB-S] |
| BSLIN78GL004232 | 100 | 6.00E-141 | AGA22650.1 | putative oxidoreductase YxjF [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL004233 | 100 | 6.50E-117 | WP_003227231.1 | MULTISPECIES: CoA transferase subunit B [Bacillus] |
| BSLIN78GL004234 | 100 | 3.30E-130 | WP_003227229.1 | MULTISPECIES: succinyl-CoA--3-ketoacid CoA transferase subunit A [Bacillus |
| BSLIN78GL004235 | 100 | 3.80E-263 | WP_003243205.1 | MULTISPECIES: GntP family permease [Bacillales] |
| BSLIN78GL004236 | 100 | 1.10E-164 | AFQ59754.1 | Putative ribosomal RNA methyltransferase [Bacillus subtilis QB928] |
| BSLIN78GL004237 | 100 | 2.80E-222 | WP_038428024.1 | NupC/NupG family nucleoside CNT transporter [Bacillus subtilis] |
| BSLIN78GL004238 | 95.4 | 7.00E-128 | AGE65519.1 | hypothetical protein C663_3820 [Bacillus subtilis XF-1] |
| BSLIN78GL004239 | 100 | 3.70E-48 | WP_038428028.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004240 | 100 | 0.00E+00 | WP_038428030.1 | catalase [Bacillus subtilis] |
| BSLIN78GL004241 | 100 | 4.60E-253 | AFQ59758.1 | Secondary transporter of divalent metalions/citrate [Bacillus subtilis QB928] |
| BSLIN78GL004242 | 100 | 3.20E-141 | QHF60071.1 | hypothetical protein Bateq7PJ16_4265 [Bacillus subtilis] |
| BSLIN78GL004243 | 95.2 | 1.20E-14 | AKN11861.1 | hypothetical protein ABU16_0785 [Bacillus subtilis] |
| BSLIN78GL004244 | 100 | 1.90E-153 | AFQ59760.1 | Transcriptional antiterminator (BglG family) [Bacillus subtilis QB928] |
| BSLIN78GL004245 | 100 | 7.00E-17 | AHA79880.1 | Hypothetical Protein U712_19765 [Bacillus subtilis PY79] |
| BSLIN78GL004246 | 100 | 1.30E-103 | AFQ59761.1 | Putative lipoprotein [Bacillus subtilis QB928] |
| BSLIN78GL004247 | 100 | 2.60E-13 | AFI30561.1 | hypothetical protein MY9_4029 [Bacillus sp. JS] |

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| BSLIN78GL004248 | 100 | 2.10E-239 | WP_009968391.1 | MULTISPECIES: MFS transporter [Bacillales] |
| BSLIN78GL004249 | 100 | 7.10E-273 | WP_032725080.1 | ATP-dependent RNA helicase DbpA [Bacillus subtilis] |
| BSLIN78GL004250 | 100 | 6.10E-219 | WP_163182270.1 | GDSL-type esterase/lipase family protein [Bacillus subtilis] |
| BSLIN78GL004251 | 100 | 2.60E-17 | WP_015714975.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL004252 | 100 | 3.70E-73 | CAF1884933.1 | hypothetical protein NRS6185_02715 [Bacillus subtilis] |
| BSLIN78GL004253 | 100 | 1.50E-49 | WP_144500449.1 | YxiJ family protein [Bacillus subtilis] |
| BSLIN78GL004254 | 100 | 2.40E-95 | WP_021480992.1 | DUF2716 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL004255 | 100 | 1.10E-150 | TWH32583.1 | hypothetical protein L609_000100001870 [Bacillus subtilis J22] |
| BSLIN78GL004256 | 100 | 3.30E-74 | WP_172851086.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004257 | 98.8 | 4.60E-42 | WP_250634986.1 | DNA-binding protein [Bacillus subtilis] |
| BSLIN78GL004258 | 100 | 1.70E-171 | CAF1798615.1 | hypothetical protein NRS6085_02631 [Bacillus subtilis] |
| BSLIN78GL004259 | 100 | 2.70E-74 | WP_003227162.1 | MULTISPECIES: universal stress protein [Bacillales] |
| BSLIN78GL004260 | 99.8 | 3.50E-280 | CAF1742425.1 | Aryl-phospho-beta-D-glucosidase BglH [Bacillus subtilis] |
| BSLIN78GL004261 | 100 | 0.00E+00 | WP_015714987.1 | MULTISPECIES: PTS beta-glucoside transporter subunit IIABC [Bacillus] |
| BSLIN78GL004262 | 93.4 | 6.90E-24 | WP_232567303.1 | contact-dependent growth inhibition system immunity protein [Bacillus subtilis] |
| BSLIN78GL004263 | 100 | 2.80E-79 | WP_029726169.1 | type II toxin-antitoxin system antitoxin YxxD [Bacillus subtilis] |
| BSLIN78GL004264 | 100 | 0.00E+00 | WP_029726168.1 | LXG family T7SS effector ribonuclease toxin YxiD [Bacillus subtilis] |
| BSLIN78GL004265 | 100 | 1.60E-40 | WP_029726167.1 | YwqI/YxiC family protein [Bacillus subtilis] |
| BSLIN78GL004266 | 100 | 1.80E-60 | WP_041338026.1 | DUF5082 family protein [Bacillus subtilis] |
| BSLIN78GL004268 | 100 | 2.70E-274 | WP_151262478.1 | arabinan endo-1,5-alpha-L-arabinosidase AbnB [Bacillus subtilis] |
| BSLIN78GL004269 | 97.6 | 4.40E-14 | RAP07662.1 | hypothetical protein HS3_01588 [Bacillus subtilis] |
| BSLIN78GL004271 | 95.1 | 1.70E-13 | KIN51491.1 | hypothetical protein B4146_4258 [Bacillus subtilis] |
| BSLIN78GL004272 | 100 | 1.70E-79 | AAA22537.1 | hut operon positive regulatory protein [Bacillus subtilis] |
| BSLIN78GL004273 | 100 | 1.10E-284 | WP_326253668.1 | histidine ammonia-lyase [Bacillus subtilis] |
| BSLIN78GL004274 | 92 | 1.70E-302 | WP_214800189.1 | MULTISPECIES: urocanate hydratase [Bacteria] |
| BSLIN78GL004275 | 100 | 1.40E-237 | WP_326253666.1 | imidazolonepropionase [Bacillus subtilis] |
| BSLIN78GL004276 | 100 | 3.20E-181 | WP_048655066.1 | MULTISPECIES: formimidoylglutamase [Bacillus] |
| BSLIN78GL004277 | 100 | 1.10E-270 | WP_048655067.1 | amino acid permease [Bacillus subtilis] |
| BSLIN78GL004278 | 99.8 | 1.60E-236 | WP_033882814.1 | pyrimidine-nucleoside phosphorylase [Bacillus subtilis] |
| BSLIN78GL004279 | 100 | 4.70E-214 | WP_003244143.1 | MULTISPECIES: nucleoside permease NupC [Bacillales] |
| BSLIN78GL004280 | 100 | 1.20E-118 | WP_015385091.1 | MULTISPECIES: deoxyribose-phosphate aldolase [Bacillus] |
| BSLIN78GL004281 | 100 | 1.90E-173 | WP_014478458.1 | MULTISPECIES: DNA-binding transcriptional repressor DeoR [Bacillus] |
| BSLIN78GL004282 | 100 | 5.00E-154 | WP_101172298.1 | DUF1206 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL004283 | 100 | 3.40E-217 | EHA31982.1 | hypothetical protein BSSC8_02390 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004284 | 100 | 4.00E-254 | WP_003227118.1 | MULTISPECIES: MmgE/PrpD family protein [Bacillus] |
| BSLIN78GL004285 | 100 | 1.80E-215 | WP_003227116.1 | MULTISPECIES: N-acetyl-sulfur-metabolite deacetylase SndB [Bacillus |
| BSLIN78GL004286 | 100 | 4.00E-134 | WP_014478463.1 | MULTISPECIES: amino acid ABC transporter ATP-binding protein [Bacillus] |
| BSLIN78GL004287 | 100 | 1.90E-119 | WP_003227111.1 | MULTISPECIES: amino acid ABC transporter permease [Bacillus] |
| BSLIN78GL004288 | 100 | 6.20E-146 | WP_003227109.1 | MULTISPECIES: amino acid ABC transporter substrate-binding protein [Bacillales] |
| BSLIN78GL004289 | 100 | 3.20E-92 | WP_003227107.1 | MULTISPECIES: sulfur-containing aminoacid acetyltransferase SnaB [Bacillus] |
| BSLIN78GL004290 | 100 | 5.20E-254 | WP_003227105.1 | MULTISPECIES: LLM class flavin-dependent oxidoreductase [Bacillus] |
| BSLIN78GL004291 | 100 | 2.20E-24 | AOA56753.1 | uncharacterized protein BSHJ0_04210 [Bacillus subtilis] |
| BSLIN78GL004292 | 100 | 2.30E-190 | WP_317680486.1 | penicillin V amidase [Bacillus subtilis] |
| BSLIN78GL004293 | 99.6 | 6.60E-151 | WP_134983162.1 | sugar-phosphatase [Bacillus subtilis] |
| BSLIN78GL004294 | 100 | 2.20E-97 | WP_003242636.1 | MULTISPECIES: hypothetical protein [Bacillales] |
| BSLIN78GL004295 | 97.2 | 2.20E-73 | WP_015715009.1 | MULTISPECIES: DUF3255 family protein [Bacillus] |
| BSLIN78GL004296 | 100 | 2.70E-64 | WP_003227093.1 | MULTISPECIES: inner spore coat protein CotNE [Bacillales] |
| BSLIN78GL004297 | 99.1 | 4.30E-56 | WP_014666007.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL004298 | 100 | 3.00E-72 | WP_003243293.1 | MULTISPECIES: hypothetical protein [Bacillales] |
| BSLIN78GL004299 | 100 | 2.10E-183 | BAI87657.2 | hypothetical protein BSNT_10646 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL004300 | 100 | 1.10E-59 | WP_003227084.1 | MULTISPECIES: YxeA family protein [Bacillales] |
| BSLIN78GL004301 | 100 | 0.00E+00 | WP_017696088.1 | MULTISPECIES: ABC transporter permease YxdM [Bacillus] |
| BSLIN78GL004302 | 99.6 | 1.80E-148 | AGE65578.1 | ABC transporter ATP-binding protein [Bacillus subtilis XF-1] |
| BSLIN78GL004303 | 100 | 1.30E-185 | WP_326253658.1 | two-component system sensor histidine kinase YxdK [Bacillus subtilis] |
| BSLIN78GL004304 | 100 | 2.00E-124 | WP_003243527.1 | MULTISPECIES: two-component system response regulator YxdJ [Bacillales] |
| BSLIN78GL004305 | 99.3 | 3.40E-164 | BAI87665.2 | fructose-1,6-bisphosphate aldolase [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL004306 | 100 | 3.70E-160 | AGE65582.1 | putative sugar-phosphate epimerase/isomerase [Bacillus subtilis XF-1] |
| BSLIN78GL004307 | 100 | 2.50E-161 | EHA31957.1 | putative sugar-phosphate epimerase/isomerase [Bacillus subtilis subsp. subtilis str. SC- |
| BSLIN78GL004308 | 99.7 | 2.30E-196 | WP_003227066.1 | MULTISPECIES: bifunctional inositol 2-dehydrogenase/D-chiro-inositol 1- |
| BSLIN78GL004309 | 100 | 5.60E-248 | EHA31955.1 | inositol transport protein [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004310 | 100 | 4.00E-173 | WP_003227062.1 | MULTISPECIES: myo-inosose-2 dehydratase [Bacillus] |
| BSLIN78GL004311 | 100 | 0.00E+00 | WP_003227059.1 | MULTISPECIES: 3D-(3,5/4)-trihydroxycyclohexane-1,2-dione acylhydrolase |
| BSLIN78GL004312 | 99.4 | 2.90E-188 | AGE65588.1 | 5-dehydro-2-deoxygluconokinase [Bacillus subtilis XF-1] |
| BSLIN78GL004313 | 99.6 | 1.10E-144 | WP_003243247.1 | MULTISPECIES: 5-deoxy-glucuronate isomerase [Bacillales] |
| BSLIN78GL004314 | 99.8 | 2.40E-284 | EHA31950.1 | methylmalonate-semialdehyde dehydrogenase [Bacillus subtilis subsp. subtilis str. SC- |
| BSLIN78GL004315 | 100 | 9.20E-139 | WP_038828963.1 | MULTISPECIES: myo-inositol utilization transcriptional regulator IolR [Bacillus] |
| BSLIN78GL004316 | 100 | 2.60E-175 | WP_003227049.1 | MULTISPECIES: aldo/keto reductase [Bacillus] |
| BSLIN78GL004317 | 100 | 8.00E-31 | KIL32279.1 | hypothetical protein B4067_4493 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL004318 | 98.1 | 1.80E-114 | WP_264240191.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004319 | 100 | 2.20E-51 | WP_003227046.1 | MULTISPECIES: YxcD family protein [Bacillales] |
| BSLIN78GL004320 | 100 | 1.80E-257 | WP_003227045.1 | MULTISPECIES: sugar porter family MFS transporter [Bacillus] |
| BSLIN78GL004321 | 100 | 0.00E+00 | WP_003227044.1 | molecular chaperone HtpG [Bacillus subtilis] |
| BSLIN78GL004322 | 100 | 2.00E-42 | WP_003227043.1 | MULTISPECIES: hypothetical protein [Bacillus] |
| BSLIN78GL004323 | 100 | 6.00E-152 | WP_003227042.1 | MULTISPECIES: SDR family oxidoreductase [Bacillus] |
| BSLIN78GL004324 | 100 | 1.20E-217 | EHA31940.1 | putative transcriptional regulator [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004325 | 100 | 3.40E-253 | WP_003227040.1 | MULTISPECIES: aldehyde dehydrogenase family protein [Bacillus |
| BSLIN78GL004326 | 100 | 3.60E-42 | EHA31938.1 | hypothetical protein BSSC8_01950 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004327 | 100 | 1.90E-29 | WP_042976894.1 | RDD family protein [Bacillus subtilis] |
| BSLIN78GL004328 | 100 | 7.60E-236 | WP_017696075.1 | MULTISPECIES: PQQ-binding-like beta-propeller repeat protein [Bacillus] |
| BSLIN78GL004329 | 100 | 1.70E-67 | AID00283.1 | hypothetical protein Q433_22015 [Bacillus subtilis subsp. subtilis str. OH 131.1] |

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| BSLIN78GL004330 | 100 | 1.40E-78 | EHA31934.1 | putative integral inner membrane protein [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004331 | 100 | 3.00E-232 | WP_003227027.1 | MULTISPECIES: DUF418 domain-containing protein [Bacillus] |
| BSLIN78GL004332 | 99.7 | 1.60E-191 | WP_038428088.1 | quercetin 2,3-dioxygenase [Bacillus subtilis] |
| BSLIN78GL004333 | 100 | 7.60E-101 | WP_087614830.1 | transcriptional regulator YxaF [Bacillus subtilis] |
| BSLIN78GL004334 | 100 | 1.20E-203 | WP_128473445.1 | SDR family oxidoreductase [Bacillus subtilis] |
| BSLIN78GL004335 | 100 | 7.70E-86 | AKE25842.1 | MarR family transcriptional regulator [Bacillus sp. LM 4-2] |
| BSLIN78GL004336 | 100 | 7.70E-56 | WP_038428093.1 | CidA/LrgA family holin-like protein [Bacillus subtilis] |
| BSLIN78GL004337 | 100 | 1.50E-124 | WP_038428094.1 | MULTISPECIES: LrgB family protein [Bacillus |
| BSLIN78GL004338 | 100 | 5.50E-195 | WP_014481442.1 | MULTISPECIES: polysaccharide pyruvyl transferase family protein [Bacillus |
| BSLIN78GL004339 | 97.4 | 3.60E-206 | WP_272515853.1 | glycerate kinase [Bacillus subtilis] |
| BSLIN78GL004340 | 99.6 | 1.90E-125 | EHA31924.1 | GntR family transcriptional regulator [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004341 | 100 | 1.20E-297 | WP_144453093.1 | gluconokinase [Bacillus subtilis] |
| BSLIN78GL004342 | 100 | 1.90E-243 | WP_003243139.1 | MULTISPECIES: gluconate permease GntP [Bacillales] |
| BSLIN78GL004343 | 100 | 2.00E-272 | WP_003227004.1 | MULTISPECIES: decarboxylating NADP(+)-dependent phosphogluconate |
| BSLIN78GL004344 | 100 | 2.50E-21 | WP_003227001.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004345 | 100 | 5.40E-113 | EHA31919.1 | alkyl hydroperoxide reductase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004346 | 100 | 2.80E-288 | WP_038428098.1 | MULTISPECIES: alkyl hydroperoxide reductase subunit F [Bacillus |
| BSLIN78GL004347 | 100 | 2.70E-258 | WP_038428099.1 | MULTISPECIES: polysaccharide pyruvyl transferase family protein [Bacillus |
| BSLIN78GL004348 | 100 | 2.40E-289 | WP_041334190.1 | 6-phospho-beta-glucosidase BglA [Bacillus subtilis] |
| BSLIN78GL004349 | 98.7 | 1.60E-33 | AMR45198.1 | PTS sugar transporter subunit IIA [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL004350 | 100 | 1.20E-129 | WP_003226988.1 | MULTISPECIES: GntR family transcriptional regulator [Bacillales |
| BSLIN78GL004351 | 100 | 0.00E+00 | POX32835.1 | class 3 fructose-bisphosphatase [Bacillus sp. Ru63] |
| BSLIN78GL004352 | 100 | 0.00E+00 | WP_326253650.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004353 | 100 | 8.00E-294 | WP_326253649.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004354 | 100 | 2.90E-82 | WP_003243164.1 | MULTISPECIES: 23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH |
| BSLIN78GL004355 | 100 | 4.80E-31 | AGE65632.1 | hypothetical protein C663_3939 [Bacillus subtilis XF-1] |
| BSLIN78GL004356 | 100 | 1.50E-65 | WP_014481457.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL004357 | 100 | 2.60E-236 | WP_014481458.1 | MULTISPECIES: formaldehyde dehydrogenase, glutathione-independent [Bacillus |
| BSLIN78GL004358 | 100 | 4.60E-22 | WP_014481459.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL004359 | 100 | 2.50E-37 | WP_014481460.1 | MULTISPECIES: DUF2651 family protein [Bacillus |
| BSLIN78GL004360 | 100 | 3.20E-223 | WP_046381471.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL004361 | 100 | 5.70E-127 | WP_326043275.1 | YiiX/YebB-like N1pC/P60 family cysteine hydrolase [Bacillus subtilis |
| BSLIN78GL004362 | 100 | 1.50E-86 | WP_119899989.1 | GNAT family N-acetyltransferase [Bacillus subtilis |
| BSLIN78GL004363 | 100 | 3.90E-207 | WP_014478534.1 | response regulator aspartate phosphatase RapG [Bacillus subtilis] |
| BSLIN78GL004364 | 100 | 4.50E-13 | WP_003226961.1 | MULTISPECIES: Phr family secreted Rap phosphatase inhibitor [Bacteria] |
| BSLIN78GL004365 | 100 | 8.00E-166 | WP_003226959.1 | MULTISPECIES: arginase [Bacillales] |
| BSLIN78GL004366 | 99.8 | 1.30E-266 | WP_014481465.1 | MULTISPECIES: amino acid permease [Bacillus] |
| BSLIN78GL004367 | 100 | 5.40E-237 | AOA56830.1 | Ornithine aminotransferase [Bacillus subtilis] |
| BSLIN78GL004368 | 100 | 2.10E-261 | WP_003226952.1 | MULTISPECIES: arginine utilization regulatory protein RocR [Bacillus |
| BSLIN78GL004369 | 100 | 9.40E-273 | WP_029726117.1 | MULTISPECIES: HAMP domain-containing sensor histidine kinase [Bacillus] |
| BSLIN78GL004370 | 100 | 7.00E-122 | WP_038428106.1 | MULTISPECIES: response regulator transcription factor [Bacillus] |
| BSLIN78GL004371 | 100 | 6.20E-166 | WP_046381473.1 | MULTISPECIES: PepSY domain-containing protein [Bacillus] |
| BSLIN78GL004372 | 100 | 2.30E-85 | WP_046381474.1 | MULTISPECIES: PepSY domain-containing protein [Bacillus] |
| BSLIN78GL004373 | 100 | 1.20E-222 | WP_046381475.1 | MULTISPECIES: serine protease HtrC [Bacillus] |
| BSLIN78GL004374 | 100 | 2.30E-148 | WP_046381476.1 | MULTISPECIES: MBL fold metallo-hydrolase [Bacillus |
| BSLIN78GL004375 | 100 | 5.80E-158 | WP_003244037.1 | MULTISPECIES: WalRK two-component regulatory system regulator WalI |
| BSLIN78GL004376 | 100 | 1.40E-262 | WP_042976993.1 | MULTISPECIES: WalRK two-component regulatory system regulator WalH |
| BSLIN78GL004377 | 100 | 0.00E+00 | EHA31886.1 | hypothetical protein BSSC8_01430 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004378 | 100 | 4.50E-138 | EHA31885.1 | two-component response regulator (YycG) [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004379 | 93.5 | 1.10E-232 | WP_197202619.1 | adenylosuccinate synthase [Bacillus safensis] |
| BSLIN78GL004380 | 97.3 | 1.50E-80 | EHA31883.1 | hypothetical protein BSSC8_01400 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004381 | 100 | 6.50E-252 | AGA21859.1 | Replicative DNA helicase [Bacillus subtilis subsp. subtilis str. BSP1] |
| BSLIN78GL004382 | 100 | 1.20E-29 | WP_003226922.1 | MULTISPECIES: DUF2188 domain-containing protein [Bacillales] |
| BSLIN78GL004383 | 100 | 1.40E-30 | WP_015250806.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL004384 | 100 | 7.10E-15 | EHA31878.1 | hypothetical protein BSSC8_01350 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004385 | 100 | 2.70E-225 | WP_003226917.1 | MULTISPECIES: CynX/NimT family MFS transporter [Bacillales |
| BSLIN78GL004386 | 100 | 0.00E+00 | WP_029726111.1 | glycosyltransferase family 39 protein [Bacillus subtilis |
| BSLIN78GL004387 | 100 | 1.50E-75 | WP_003226915.1 | MULTISPECIES: 50S ribosomal protein L9 [Bacillales] |
| BSLIN78GL004388 | 100 | 0.00E+00 | WP_017695791.1 | MULTISPECIES: cyclic-di-AMP phosphodiesterase GdpP [Bacillus |
| BSLIN78GL004389 | 100 | 1.40E-168 | WP_003226911.1 | MULTISPECIES: YbbS family protein [Bacillus |
| BSLIN78GL004390 | 100 | 1.10E-19 | WP_003226909.1 | MULTISPECIES: hypothetical protein [Terrabacteria group] |
| BSLIN78GL004391 | 100 | 2.90E-85 | WP_003226906.1 | MULTISPECIES: spore coat protein CotF [Bacillus] |
| BSLIN78GL004392 | 100 | 6.10E-67 | WP_085185303.1 | transcriptional regulator HypR [Bacillus subtilis] |
| BSLIN78GL004393 | 100 | 1.30E-166 | WP_003226902.1 | MULTISPECIES: manganese-dependent inorganic pyrophosphatase [Bacillales |
| BSLIN78GL004394 | 100 | 2.10E-77 | QHF60248.1 | lipoprotein [Bacillus subtilis] |
| BSLIN78GL004395 | 100 | 4.00E-51 | WP_003226899.1 | MULTISPECIES: hypothetical protein [Bacillales |
| BSLIN78GL004396 | 100 | 2.30E-254 | EHA31866.1 | putative permease [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004397 | 100 | 5.20E-142 | EHA31864.1 | hypothetical protein BSSC8_01210 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004398 | 99.2 | 8.50E-151 | BAI87778.2 | hypothetical protein BSNT_10781 [Bacillus subtilis subsp. natto BEST195] |
| BSLIN78GL004399 | 100 | 4.40E-71 | EHA31862.1 | hypothetical protein BSSC8_01190 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004400 | 99.6 | 2.20E-140 | WP_003244562.1 | MULTISPECIES: pentapeptide repeat-containing protein [Bacillales |
| BSLIN78GL004401 | 99 | 2.50E-226 | WP_326153459.1 | MFS transporter [Bacillus subtilis] |
| BSLIN78GL004402 | 100 | 7.30E-164 | WP_015715067.1 | MULTISPECIES: LysR family transcriptional regulator [Bacillus |
| BSLIN78GL004403 | 100 | 8.20E-79 | WP_015715068.1 | MULTISPECIES: GNAT family N-acetyltransferase [Bacillus |
| BSLIN78GL004404 | 100 | 6.50E-82 | WP_015715069.1 | hypothetical protein [Bacillus] |
| BSLIN78GL004405 | 100 | 2.10E-126 | WP_015715070.1 | MULTISPECIES: MBL fold metallo-hydrolase [Bacillus |
| BSLIN78GL004406 | 100 | 4.10E-78 | WP_003226875.1 | MULTISPECIES: MarR family transcriptional regulator [Bacillales] |
| BSLIN78GL004407 | 100 | 1.70E-79 | WP_003226873.1 | MULTISPECIES: GNAT family N-acetyltransferase [Bacillus |
| BSLIN78GL004408 | 100 | 1.50E-104 | WP_003226872.1 | MULTISPECIES: YitT family protein [Bacillus |
| BSLIN78GL004409 | 100 | 2.40E-98 | WP_106073188.1 | streptothricin N-acetyltransferase SatA [Bacillus subtilis] |

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| BSLIN78GL004410 | 100 | 1.40E-65 | WP_021481096.1 | MULTISPECIES: MmcQ/YjbR family DNA-binding protein [Bacillus |
| BSLIN78GL004411 | 100 | 1.70E-105 | WP_003226866.1 | MULTISPECIES: dihydrofolate reductase family protein [Bacillus |
| BSLIN78GL004412 | 99.8 | 7.30E-248 | WP_029726095.1 | tetracycline efflux MFS transporter Tet(L) [Bacillus subtilis |
| BSLIN78GL004413 | 100 | 4.50E-31 | AMR45139.1 | hypothetical protein KHRBS_00160 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL004414 | 100 | 2.00E-86 | WP_050496387.1 | MULTISPECIES: DUF4944 domain-containing protein [Bacillus subtilis group] |
| BSLIN78GL004416 | 100 | 1.80E-187 | WP_029726093.1 | amidase domain-containing protein [Bacillus subtilis] |
| BSLIN78GL004417 | 100 | 4.10E-41 | AFQ59938.1 | Putative transcriptional regulator (MerR family) [Bacillus subtilis QB928] |
| BSLIN78GL004418 | 100 | 7.70E-161 | WP_029726092.1 | EamA family transporter [Bacillus subtilis] |
| BSLIN78GL004419 | 100 | 3.10E-18 | QJD06408.1 | YyaL [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL004420 | 100 | 7.90E-121 | QAV98406.1 | LysE family translocator [Bacillus subtilis] |
| BSLIN78GL004421 | 94.9 | 3.80E-27 | SPU05088.1 | peptidase M14, carboxypeptidase A [Bacillus tequilensis] |
| BSLIN78GL004422 | 100 | 0.00E+00 | WP_326253638.1 | thioredoxin domain-containing protein [Bacillus subtilis] |
| BSLIN78GL004423 | 99.7 | 2.60E-175 | EHA31844.1 | putative integral inner membrane protein [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004424 | 100 | 4.20E-259 | WP_029318525.1 | MULTISPECIES: MFS transporter [Bacillus] |
| BSLIN78GL004425 | 100 | 3.90E-102 | WP_033884396.1 | MULTISPECIES: sugar O-acetyltransferase [Bacillus |
| BSLIN78GL004426 | 97.8 | 4.80E-70 | EHA31841.1 | hypothetical protein BSSC8_00980 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004427 | 100 | 5.60E-178 | WP_048654830.1 | MULTISPECIES: transcriptional regulator CcpB [Bacillus] |
| BSLIN78GL004428 | 100 | 1.50E-144 | WP_029726087.1 | MULTISPECIES: exodeoxyribonuclease III [Bacillus |
| BSLIN78GL004429 | 100 | 3.00E-96 | AFQ59948.1 | Single-strand DNA-binding protein [Bacillus subtilis QB928] |
| BSLIN78GL004430 | 100 | 9.70E-43 | EHA31837.1 | 30S ribosomal protein S6 [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004431 | 100 | 2.50E-209 | EHA31836.1 | translation-associated GTPase [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004432 | 99.9 | 0.00E+00 | QHF60285.1 | oxidoreductase [Bacillus subtilis] |
| BSLIN78GL004433 | 100 | 4.10E-33 | WP_003226838.1 | MULTISPECIES: DUF951 family protein [Bacillales |
| BSLIN78GL004434 | 100 | 8.10E-205 | AFQ59953.1 | Putative integral membrane protein [Bacillus subtilis QB928] |
| BSLIN78GL004435 | 100 | 1.70E-111 | WP_015715079.1 | MULTISPECIES: spore protease YyaC [Bacillus |
| BSLIN78GL004436 | 100 | 1.40E-151 | WP_015715080.1 | MULTISPECIES: stage 0 sporulation protein Spo0J [Bacillus] |
| BSLIN78GL004437 | 99.6 | 1.20E-138 | AFQ59956.1 | Chromosome partitioning protein [Bacillus subtilis QB928] |
| BSLIN78GL004438 | 100 | 5.80E-77 | WP_326253632.1 | PH domain-containing protein [Bacillus subtilis] |
| BSLIN78GL004439 | 100 | 6.70E-154 | WP_015250778.1 | MULTISPECIES: nucleoid occlusion protein [Bacillus |
| BSLIN78GL004440 | 100 | 7.90E-132 | WP_015250777.1 | MULTISPECIES: 16S rRNA (guanine(527)-N(7))-methyltransferase RsmG |
| BSLIN78GL004441 | 92 | 0.00E+00 | WP_251225369.1 | tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG [Bacillus |
| BSLIN78GL004442 | 99.8 | 1.60E-253 | AGI31270.1 | tRNA modification GTPase TrmE [Bacillus subtilis subsp. subtilis str. BAB-1] |
| BSLIN78GL004443 | 100 | 4.00E-108 | EHA31824.1 | spoIIIJ-associated protein [Bacillus subtilis subsp. subtilis str. SC-8] |
| BSLIN78GL004444 | 100 | 2.00E-138 | WP_010886648.1 | MULTISPECIES: YidC family membrane integrase SpoIIIJ [Bacillales |
| BSLIN78GL004445 | 100 | 5.80E-59 | AGE65721.1 | ribonuclease P protein component [Bacillus subtilis XF-1] |
| BSLIN78GL004446 | 99.1 | 1.20E-58 | WP_172688870.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004447 | 100 | 1.60E-163 | WP_198879101.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004448 | 100 | 1.30E-134 | WP_124048606.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004449 | 100 | 3.30E-118 | WP_214283062.1 | XF1762 family protein [Bacillus subtilis] |
| BSLIN78GL004450 | 100 | 1.20E-95 | WP_166852650.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL004451 | 100 | 5.00E-99 | WP_052475764.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004453 | 93.3 | 6.30E-42 | WP_326380242.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004454 | 97.4 | 4.70E-177 | WP_236830503.1 | trypsin-like peptidase domain-containing protein [Bacillus subtilis] |
| BSLIN78GL004455 | 100 | 4.40E-39 | APB62344.1 | hypothetical protein pBS72_0750 [Bacillus subtilis] |
| BSLIN78GL004457 | 100 | 1.60E-126 | WP_326380236.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004458 | 100 | 6.10E-297 | WP_172688840.1 | DNA cytosine methyltransferase [Bacillus subtilis |
| BSLIN78GL004459 | 100 | 8.10E-17 | KIN38149.1 | hypothetical protein B4071_4405 [Bacillus subtilis] |
| BSLIN78GL004460 | 98.7 | 1.30E-38 | AYK68256.1 | hypothetical protein D9C11_23340 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL004462 | 100 | 1.20E-48 | WP_124048636.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL004464 | 100 | 4.40E-39 | APB62344.1 | hypothetical protein pBS72_0750 [Bacillus subtilis] |
| BSLIN78GL004466 | 100 | 1.30E-28 | WP_302897270.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004467 | 100 | 1.20E-152 | WP_124048638.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004468 | 99.6 | 0.00E+00 | WP_268425040.1 | DEAD/DEAH box helicase [Bacillus inaquosorum] |
| BSLIN78GL004470 | 100 | 4.40E-39 | AYK68256.1 | hypothetical protein D9C11_23340 [Bacillus subtilis subsp. subtilis] |
| BSLIN78GL004472 | 100 | 2.20E-131 | WP_121592025.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004473 | 100 | 2.90E-48 | WP_069479522.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004474 | 98.7 | 7.10E-37 | WP_129134492.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004475 | 100 | 1.90E-150 | WP_326380228.1 | ATP-dependent DNA ligase [Bacillus subtilis] |
| BSLIN78GL004476 | 100 | 3.50E-118 | WP_127059443.1 | MULTISPECIES: restriction endonuclease [Bacillus |
| BSLIN78GL004477 | 100 | 2.70E-15 | WP_326380232.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004478 | 99.3 | 1.60E-79 | WP_127059442.1 | YopX family protein [Bacillus subtilis] |
| BSLIN78GL004479 | 100 | 2.80E-129 | WP_172688878.1 | MULTISPECIES: dUTP diphosphatase [Bacillus] |
| BSLIN78GL004480 | 100 | 1.70E-256 | WP_069479528.1 | MULTISPECIES: DNA cytosine methyltransferase [Bacillus |
| BSLIN78GL004481 | 100 | 2.70E-36 | WP_069479530.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL004482 | 100 | 1.80E-84 | WP_326380225.1 | single-stranded DNA-binding protein [Bacillus subtilis] |
| BSLIN78GL004483 | 99.8 | 0.00E+00 | APB62321.1 | hypothetical protein pBS72_0520 [Bacillus subtilis] |
| BSLIN78GL004485 | 100 | 2.10E-52 | WP_069479536.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL004486 | 99.9 | 0.00E+00 | WP_172688812.1 | MULTISPECIES: DNA topoisomerase [Bacillus] |
| BSLIN78GL004487 | 100 | 1.50E-101 | WP_175271379.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL004488 | 100 | 6.80E-30 | KIN40253.1 | hypothetical protein B4071_4373 [Bacillus subtilis] |
| BSLIN78GL004489 | 100 | 4.40E-62 | WP_069479539.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL004490 | 100 | 9.30E-173 | WP_172688809.1 | type IV secretory system conjugative DNA transfer family protein [Bacillus subtilis |
| BSLIN78GL004491 | 100 | 8.00E-233 | WP_326380223.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004492 | 100 | 3.60E-277 | WP_326380222.1 | pentapeptide repeat-containing protein [Bacillus subtilis] |
| BSLIN78GL004493 | 100 | 1.10E-92 | WP_069479543.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004494 | 100 | 1.10E-240 | WP_326380221.1 | MobP2 family relaxase [Bacillus subtilis] |
| BSLIN78GL004495 | 100 | 4.80E-35 | WP_175271376.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL004496 | 100 | 4.80E-163 | WP_069479547.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004497 | 100 | 2.70E-222 | WP_080320314.1 | bifunctional lytic transglycosylase/C40 family peptidase [Bacillus subtilis |
| BSLIN78GL004498 | 100 | 3.60E-109 | WP_069479548.1 | hypothetical protein [Bacillus subtilis] |

| | | | | |
|---|---|---|---|---|
| BSLIN78GL004499 | 100 | 0.00E+00 | WP_041335097.1 | MULTISPECIES: type IV secretion system VirB4 protein [Bacillus |
| BSLIN78GL004500 | 99.6 | 2.10E-141 | WP_041335101.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL004501 | 91.7 | 5.10E-294 | WP_127059428.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004502 | 100 | 2.10E-149 | ODV48163.1 | hypothetical protein BCM26_04240 [Bacillus subtilis] |
| BSLIN78GL004503 | 100 | 7.70E-214 | WP_326380217.1 | CpaF/VirB11 family protein [Bacillus subtilis] |
| BSLIN78GL004504 | 100 | 3.10E-122 | WP_069479552.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL004505 | 100 | 0.00E+00 | WP_069479553.1 | MULTISPECIES: type IV secretory system conjugative DNA transfer family protein |
| BSLIN78GL004506 | 98.9 | 1.20E-43 | WP_326380216.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004507 | 99.8 | 1.00E-268 | WP_172688799.1 | toprim domain-containing protein [Bacillus subtilis] |
| BSLIN78GL004508 | 100 | 1.60E-109 | WP_317906582.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004509 | 100 | 2.20E-285 | WP_326380214.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004510 | 100 | 7.20E-43 | WP_124048591.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004511 | 99.4 | 0.00E+00 | WP_172688794.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004512 | 100 | 2.00E-22 | WP_161792545.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL004513 | 98.9 | 1.90E-153 | WP_172688791.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004514 | 100 | 2.20E-123 | WP_041334430.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004515 | 100 | 1.20E-118 | WP_052475771.1 | class A sortase [Bacillus subtilis] |
| BSLIN78GL004516 | 97.2 | 2.40E-201 | WP_172688789.1 | LPXTG cell wall anchor domain-containing protein [Bacillus subtilis] |
| BSLIN78GL004517 | 100 | 8.70E-71 | WP_041334372.1 | MULTISPECIES: ArpU family phage packaging/lysis transcriptional regulator |
| BSLIN78GL004518 | 100 | 2.60E-14 | WP_041334369.1 | MULTISPECIES: helix-turn-helix domain-containing protein [Bacillus |
| BSLIN78GL004519 | 100 | 1.80E-54 | KIN41330.1 | hypothetical protein B4071_4337 [Bacillus subtilis] |
| BSLIN78GL004520 | 100 | 2.10E-91 | WP_032490595.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004521 | 100 | 8.30E-199 | WP_052475768.1 | helix-turn-helix domain-containing protein [Bacillus subtilis] |
| BSLIN78GL004522 | 100 | 1.30E-42 | WP_032490597.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL004523 | 100 | 3.20E-142 | WP_041334364.1 | MULTISPECIES: ParA family protein [Bacillus] |
| BSLIN78GL004524 | 100 | 1.20E-208 | WP_326380253.1 | DUF262 domain-containing protein [Bacillus subtilis] |
| BSLIN78GL004525 | 100 | 2.60E-250 | WP_069479490.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004526 | 98.9 | 3.80E-91 | APB62404.1 | hypothetical protein pBS72_1350 [Bacillus subtilis] |
| BSLIN78GL004527 | 100 | 2.90E-48 | WP_317906612.1 | YolD-like family protein [Bacillus subtilis] |
| BSLIN78GL004528 | 100 | 7.60E-239 | WP_124048599.1 | UV damage repair protein UvrX [Bacillus subtilis] |
| BSLIN78GL004529 | 100 | 3.40E-239 | WP_236830513.1 | tetratricopeptide repeat protein [Bacillus subtilis] |
| BSLIN78GL004530 | 100 | 7.10E-96 | WP_236830511.1 | MULTISPECIES: response regulator transcription factor [Bacillus] |
| BSLIN78GL004531 | 100 | 2.60E-261 | WP_124048600.1 | MULTISPECIES: sensor histidine kinase [Bacillus] |
| BSLIN78GL004532 | 99.7 | 1.80E-187 | WP_326380246.1 | alpha/beta hydrolase [Bacillus subtilis] |
| BSLIN78GL004533 | 100 | 3.20E-107 | WP_124048601.1 | MULTISPECIES: hypothetical protein [Bacillus |
| BSLIN78GL004534 | 100 | 4.80E-79 | WP_069479497.1 | hypothetical protein [Bacillus subtilis] |
| BSLIN78GL004535 | 99.5 | 9.00E-119 | WP_236830509.1 | recombinase family protein [Bacillus subtilis] |
| BSLIN78GL004536 | 100 | 2.40E-93 | OJH64045.1 | hypothetical protein BOH71_06835 [Bacillus subtilis] |
| BSLIN78GL004537 | 100 | 2.60E-71 | WP_041334305.1 | MULTISPECIES: TIR domain-containing protein [Bacillus |
| BSLIN78GL004538 | 100 | 2.00E-183 | WP_069479501.1 | caspase family protein [Bacillus subtilis] |
| BSLIN78GL004539 | 100 | 1.20E-86 | WP_069479502.1 | hypothetical protein [Bacillus subtilis] |

Table S3. The predicted genomic islands (GIs)

| No. | Start | End | Size |
|---|---|---|---|
| 1 | 31,810 | 36,058 | 4,248 |
| 2 | 91,995 | 102,266 | 10,271 |
| 3 | 162,356 | 171,495 | 9,139 |
| 4 | 208,874 | 216,684 | 7,810 |
| 5 | 523,529 | 528,448 | 4,919 |
| 6 | 545,077 | 549,530 | 4,453 |
| 7 | 706,492 | 730,283 | 23,791 |
| 8 | 719,070 | 727,307 | 8,237 |
| 9 | 1,100,882 | 1,105,522 | 4,640 |
| 10 | 1,319,876 | 1,325,129 | 5,253 |
| 11 | 1,851,134 | 1,978,722 | 127,588 |
| 12 | 1,905,261 | 1,910,809 | 5,548 |
| 13 | 1,915,718 | 1,934,428 | 18,710 |
| 14 | 1,936,171 | 1,940,353 | 4,182 |
| 14 | 1,990,434 | 2,000,613 | 10,179 |
| 16 | 2,012,601 | 2,021,970 | 9,369 |
| 17 | 2,017,881 | 2,063,634 | 45,753 |
| 18 | 2,026,240 | 2,032,260 | 6,020 |
| 19 | 2,031,833 | 2,036,766 | 4,933 |
| 20 | 2,209,753 | 2,231,615 | 21,862 |
| 21 | 2,215,174 | 2,227,730 | 12,556 |
| 22 | 2,219,976 | 2,224,144 | 4,168 |
| 23 | 2,674,154 | 2,725,817 | 51,663 |
| 24 | 2,675,217 | 2,680,482 | 5,265 |
| 25 | 2,809,287 | 2,825,359 | 16,072 |
| 26 | 2,809,649 | 2,824,989 | 15,340 |
| 27 | 3,727,220 | 3,734,116 | 6,896 |
| 28 | 4,174,636 | 4,182,856 | 8,220 |

Table S4. The predicted prophage regions in LIN78 chromosome.

| NO. | REGION POSITION | RNA NUM | TOTAL PROTEIN NUM | PHAGE HIT PROTEIN NUM | HYPOTHETICAL PROTEIN NUM | PHAGE+HYPO PROTEIN PERCENTAGE |
|---|---|---|---|---|---|---|
| 1 | 1292318-1327516 | 0 | 44 | 33 | 1 | 77.20% |
| 2 | 1839471-1981937 | 0 | 185 | 129 | 45 | 94% |
| 3 | 1983340-2025413 | 0 | 56 | 35 | 10 | 80.30% |
| 4 | 2686343-2715670 | 0 | 36 | 27 | 6 | 91.60% |

Table S5. Repetitive DNA elements in LIN78

| Sample Name (#) | Type (#) | Number (#) | Repeat Size (bp) | Total Length (bp) | In Genome (%) |
|---|---|---|---|---|---|
| BSLIN78 | TRF | 69 | 6-253 | 11,507 | 0.264 |
| | Minisatellite DNA | 44 | 15-60 | 4,592 | 0.1053 |
| | Microsatellite DNA | 4 | 6-9 | 4,054 | 0.093 |

Table S6. CRISPRS Report

| Strain | Sequence | Sequence basename | Duplicated Spacers | CRISPR Id | CRISPR Start | CRISPR End | CRISPR Length | Potential Orientation (AT%) |
|---|---|---|---|---|---|---|---|---|
| circular | Chromosome1 | Chromosome1 | 0 | Chromosome1_1 | 913929 | 914034 | 106 | Forward |
| circular | Chromosome1 | Chromosome1 | 0 | Chromosome1 2 | 3223972 | 3224079 | 108 | Unknown |

| CRISPRDirection | Consensus Repeat | Repeat ID (CRISPRdb) | Nb CRISPRs with same Repeat (CRISPRdb) | Repeat Length | Spacers Nb | Mean size Spacers | Standard Deviation Spacers | Nb Repeats matching Consensus |
|---|---|---|---|---|---|---|---|---|
| Unknown | GAAAACAAAACCAACAATCAGCT | Unknown | 0 | 25 | 1 | 56 | 0 | 1 |
| Unknown | TGATGGGAATCGAACCCACGACAT | Unknown | 0 | 24 | 1 | 60 | 0 | 1 |

| Ratio Repeats match/TotalRepeat | Conservation Repeats (% identity) | EBcons Repeats | Conservation Spacers (% identity) | EBcons Spacers | Repeat Length plus mean size Spacers | Ratio Repeat/mean Spacers Length | CRISPR found in DB | Evidence Level |
|---|---|---|---|---|---|---|---|---|
| 0.5 | 96 | 96 | 100 | 100 | 81 | 0.446428571 | 0 | 1 |
| 0.5 | 87.5 | 87.5 | 100 | 100 | 84 | 0.4 | 0 | 1 |

Table S7. Gene function annotation statistics

| Sample Name (# | Total (#) | VFDB (#) | ARDB (#) | CAZY (#) | IPR (#) | SWISSPROT (# | COG (#) | CARD (#) | GO (#) | KEGG (#) | NR (#) | T3SS (#) | OverAll (#) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| BSLIN78 | 4,539 | 209 (4.6%) | 30 (0.66%) | 253 (5.57%) | 3,766 (82.96%) | 3,936 (86.71%) | 3,302 (72.74%) | 13 (0.28%) | 2,578 (56.79%) | 2,734 (60.23%) | 4,510 (99.36%) | 475 (10.46%) | 4,513 (99.42%) |

Table S8. Virulence factor expression or prediction in LIN78

| Gene id | Identity | E value | VF id | GI id | Type | Description |
|---|---|---|---|---|---|---|
| BSLIN78 | 40 | 2.70E-39 | VFG041139 | gb\|WP_006485337 | Predicted | (QU43_RS38205) transporter substrate-binding domain-containing protein [T6SS (VF0698) - Effector delivery sy [Burkholderia cenocepacia J2315] |
| BSLIN78 | 40 | 7.00E-37 | VFG013192 | gb\|WP_012340414 | Predicted | (hitC) iron(III) ABC transporter, ATP-binding protein [HitABC (VF0268) - Nutritional/Metabolic factor (VFC027 somnus 2336] |
| BSLIN78 | 40 | 1.50E-81 | VFG009135 | gb\|YP_005360856 | Predicted | (kasB) 3-oxoacyl-(acyl carrier protein) synthase II [FAS-II (VF0809) - Nutritional/Metabolic factor (VFC0272)] [ tuberculosis RGTB327] |
| BSLIN78 | 40 | 7.10E-58 | VFG044190 | gb\|WP_011179201 | Predicted | (BQ_RS02100) iron ABC transporter permease [Direct heme uptake system (VF0681) - Nutritional/Metabolic fac [Bartonella quintana str. Toulouse] |
| BSLIN78 | 40 | 1.20E-08 | VFG045302 | gb\|WP_010946491 | Verified | (LPG_RS03740) acetyltransferase [LPS (VF0171) - Immune modulation (VFC0258)] [Legionella pneumophila su str. Philadelphia 1] |
| BSLIN78 | 40.1 | 7.10E-39 | VFG006259 | gb\|WP_003687540 | Predicted | (fbpC) iron(III) ABC transporter, ATP-binding protein [FbpABC (VF0272) - Nutritional/Metabolic factor (VFC02 gonorrhoeae FA 1090] |
| BSLIN78 | 40.2 | 2.50E-42 | VFG031685 | gb\|YP_001704776 | Predicted | (senX3) Sensor-like histidine kinase senX3 [SenX3 (VF0857) - Regulation (VFC0301)] [Mycobacterium abscessu |
| BSLIN78 | 40.2 | 3.70E-62 | VFG016170 | gb\|WP_011267802 | Predicted | (cbrC) iron ABC transporter permease [Achromobactin biosynthesis and transport (VF0922) - Nutritional/Metabol (VFC0272)] [Pseudomonas syringae pv. syringae B728a] |
| BSLIN78 | 40.2 | 2.20E-47 | VFG006089 | gb\|WP_011681446 | Predicted | (rfbD) dTDP-4-dehydrorhamnose reductase [Capsule (VF0144) - Immune modulation (VFC0258)] [Streptococcus LMD-9] |
| BSLIN78 | 40.3 | 7.30E-09 | VFG001379 | gb\|NP_214867 | Verified | (hspR) heat shock protein transcriptional repressor HspR [HspR (VF0297) - Regulation (VFC0301)] [Mycobacteri H37Rv] |
| BSLIN78 | 40.3 | 5.60E-33 | VFG013192 | gb\|WP_012340414 | Predicted | (hitC) iron(III) ABC transporter, ATP-binding protein [HitABC (VF0268) - Nutritional/Metabolic factor (VFC027 somnus 2336] |
| BSLIN78 | 40.4 | 3.00E-31 | VFG045340 | gb\|WP_002964382 | Verified | (ricA) type IV secretion system effector RicA, Rab2 interacting conserved protein A [T4SS secreted effectors (VF delivery system (VFC0086)] [Brucella melitensis bv. 1 str. 16M] |
| BSLIN78 | 40.5 | 8.60E-59 | VFG044253 | gb\|WP_001045111 | Predicted | (sirA) staphyloferrin B ABC transporter substrate-binding protein SirA [Staphyloferrin B (VF1014) - Nutritional/ (VFC0272)] [Staphylococcus aureus subsp. aureus str. Newman] |
| BSLIN78 | 40.5 | 4.10E-15 | VFG005951 | gb\|WP_148148905 | Predicted | (STU_RS19955) acyltransferase [Capsule (VF0144) - Immune modulation (VFC0258)] [Streptococcus thermophi |
| BSLIN78 | 40.5 | 6.40E-42 | VFG022905 | gb\|YP_001701425 | Predicted | (phoP) Possible two component system response transcriptional positive regulator PhoP [PhoP (VF0286) - Regula [Mycobacterium abscessus ATCC 19977] |
| BSLIN78 | 40.6 | 2.50E-66 | VFG046913 | gb\|WP_013922683 | Predicted | (flmF2) glycosyl transferase family protein [LPS (VF0542) - Immune modulation (VFC0258)] [Francisella sp. TX |
| BSLIN78 | 40.6 | 3.50E-66 | VFG013612 | gb\|WP_011609686 | Predicted | (hemE) uroporphyrinogen decarboxylase [Heme biosynthesis (VF0758) - Nutritional/Metabolic factor (VFC0272) somnus 129PT] |
| BSLIN78 | 40.6 | 4.30E-35 | VFG016510 | gb\|WP_011290050 | Predicted | (hlyA) TlyA family RNA methyltransferase [Hemolysin (VF0879) - Exotoxin (VFC0235)] [Mycoplasma hyopneu |
| BSLIN78 | 40.6 | 5.90E-53 | VFG043303 | gb\|WP_003425220 | Predicted | (CD630_RS01810) MotA/TolQ/ExbB proton channel family protein [Peritrichous flagella (VF0732) - Motility (V [Clostridium difficile 630] |
| BSLIN78 | 40.7 | 1.30E-64 | VFG043148 | gb\|WP_005478291 | Predicted | (VP_RS22515) sigma-54 dependent transcriptional regulator [Lateral flagella (VF0625) - Biofilm (VFC0271)] [Vi parahaemolyticus RIMD 2210633] |
| BSLIN78 | 40.8 | 7.50E-63 | VFG016507 | gb\|WP_011949275 | Predicted | (pdhB) alpha-ketoacid dehydrogenase subunit beta [PDH-B (VF0878) - Adherence (VFC0001)] [Mycoplasma aga |
| BSLIN78 | 40.9 | 1.80E-06 | VFG045470 | gb\|AAM75247 | Verified | (cylR2) cytolysin regulator R2 [Cytolysin (VF0356) - Exotoxin (VFC0235)] [Enterococcus faecalis str. MMH594] |
| BSLIN78 | 41 | 1.90E-39 | VFG023850 | gb\|WP_043955033 | Predicted | (ddrA) daunorubicin resistance protein DrrA family ABC transporter ATP-binding protein [PDIM (VF0309) - Imn (VFC0258)] [Mycobacterium indicus pranii MTCC 9506] |
| BSLIN78 | 41 | 2.60E-71 | VFG043295 | gb\|WP_011860698 | Predicted | (fliG) flagellar motor switch protein FliG [Peritrichous flagella (VF0732) - Motility (VFC0204)] [Clostridium diff |
| BSLIN78 | 41.1 | 3.30E-33 | VFG001404 | gb\|NP_216944 | Verified | (ahpC) alkyl hydroperoxide reductase subunit AhpC [AhpC (VF0306) - Stress survival (VFC0282)] [Mycobacteri H37Rv] |
| BSLIN78 | 41.2 | 1.90E-30 | VFG043453 | gb\|WP_001829380 | Predicted | (aae) autolysin/adhesin Aae [SE2319 (VF1000) - Adherence (VFC0001)] [Staphylococcus epidermidis ATCC 122 |
| BSLIN78 | 41.2 | 2.40E-47 | VFG038840 | gb\|WP_005300916 | Verified | (flmH) short chain dehydrogenase/reductase family oxidoreductase [Polar flagella (VF0473) - Motility (VFC0204 hydrophila ML09-119] |
| BSLIN78 | 41.3 | 1.40E-68 | VFG001314 | gb\|WP_001225025 | Verified | (aur) zinc metalloproteinase aureolysin [Aureolysin (VF0024) - Exoenzyme (VFC0251)] [Staphylococcus aureus MW2] |
| BSLIN78 | 41.3 | 3.40E-07 | VFG043277 | gb\|WP_011860681 | Predicted | (flgM) flagellar biosynthesis anti-sigma factor FlgM [Peritrichous flagella (VF0732) - Motility (VFC0204)] [Clost 630] |
| BSLIN78 | 41.3 | 5.50E-49 | VFG006818 | gb\|NP_465270 | Predicted | (virR) two-component response regulator [VirR/VirS (VF0791) - Regulation (VFC0301)] [Listeria monocytogene |
| BSLIN78 | 41.4 | 2.70E-63 | VFG038766 | gb\|WP_005350678 | Predicted | (flrA) FleQ protein [Polar flagella (VF0473) - Motility (VFC0204)] [Aeromonas veronii B565] |
| BSLIN78 | 41.4 | 7.40E-66 | VFG044357 | gb\|WP_013317300 | Predicted | (DDA3937_RS07760) iron ABC transporter permease [Achromobactin (VF1243) - Nutritional/Metabolic factor ( [Dickeya dadantii 3937] |
| BSLIN78 | 41.4 | 1.10E-72 | VFG049124 | gb\|WP_012737540 | Verified | (allD) ureidoglycolate dehydrogenase [Allantion utilization (VF0572) - Nutritional/Metabolic factor (VFC0272)] [ pneumoniae subsp. pneumoniae NTUH-K2044] |
| BSLIN78 | 41.4 | 1.30E-33 | VFG041486 | gb\|WP_004155373 | Predicted | (EAMY_RS20020) pectate lyase [T3SS (VF1270) - Effector delivery system (VFC0086)] [Erwinia amylovora CF |
| BSLIN78 | 41.6 | 5.00E-39 | VFG043410 | gb\|WP_001114998 | Predicted | (fliY) flagellar motor switch protein [Peritrichous flagella (VF0670) - Motility (VFC0204)] [Bacillus cereus ATC |
| BSLIN78 | 41.6 | 5.00E-46 | VFG044236 | gb\|WP_011815405 | Predicted | (YE_RS01715) heme ABC transporter ATP-binding protein [Direct heme uptake system (VF1031) - Nutritional/ (VFC0272)] [Yersinia enterocolitica subsp. enterocolitica 8081] |
| BSLIN78 | 41.6 | 8.30E-68 | VFG005841 | gb\|WP_002262748 | Predicted | (SMU_RS01255) rhamnose-glucose polysaccharide biosynthesis protein RgpB [Capsule (VF0144) - Immune mod (VFC0258)] [Streptococcus mutans UA159] |
| BSLIN78 | 41.7 | 3.90E-94 | VFG047258 | gb\|WP_014547756 | Predicted | (lpxA/glmU) UDP-N-acetylglucosamine pyrophosphorylase/glucosamine-1-phosphate N-acetyltransferase [LPS ( modulation (VFC0258)] [Francisella cf. tularensis subsp. novicida 3523] |
| BSLIN78 | 41.7 | 6.80E-62 | VFG002180 | gb\|WP_002362627 | Verified | (cpsK) ABC transporter, permease protein [Capsule (VF0361) - Immune modulation (VFC0258)] [Enterococcus f |
| BSLIN78 | 41.8 | 3.60E-122 | VFG009226 | gb\|WP_010908708 | Predicted | (secA2) accessory Sec system translocase SecA2 [Accessory secretion factor (VF0808) - Others (VFC0346)] [My leprae TN] |
| BSLIN78 | 41.8 | 7.10E-103 | VFG037029 | gb\|WP_010951343 | Predicted | (katA) catalase [KatA (VF0454) - Stress survival (VFC0282)] [Neisseria gonorrhoeae FA 1090] |
| BSLIN78 | 41.9 | 1.90E-56 | VFG002189 | gb\|WP_002359680 | Verified | (cpsB/cdsA) phosphatidate cytidylyltransferase [Capsule (VF0361) - Immune modulation (VFC0258)] [Enterococ |
| BSLIN78 | 41.9 | 5.60E-19 | VFG005382 | gb\|WP_011681303 | Predicted | (srtA) sortase [Sortase A (VF1048) - Exoenzyme (VFC0251)] [Streptococcus thermophilus LMD-9] |

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| BSLIN78 | 42 | 1.00E-62 | VFG014129 | gb\|WP_003150889 | Predicted | (PSPA7_RS09470) polysaccharide biosynthesis protein [LPS (VF0085) - Immune modulation (VFC0258)] [Pseud aeruginosa PA7] |
| BSLIN78 | 42 | 7.20E-37 | VFG023954 | gb\|WP_013472160 | Predicted | (leuD) 3-isopropylmalate dehydratase small subunit [Leucine synthesis (VF0814) - Nutritional/Metabolic factor ( [Mycobacterium gilvum Spyr1] |
| BSLIN78 | 42 | 2.00E-102 | VFG037032 | gb\|WP_003689973 | Predicted | (katA) catalase [KatA (VF0454) - Stress survival (VFC0282)] [Neisseria gonorrhoeae NCCP11945] |
| BSLIN78 | 42.2 | 4.50E-66 | VFG015352 | gb\|WP_011168041 | Predicted | (hopAK1) type III helper protein HopAK1 [P. syringae TTSS effectors (VF0911) - Effector delivery system (VFC [Pseudomonas syringae pv. phaseolicola 1448A] |
| BSLIN78 | 42.2 | 3.60E-53 | VFG009638 | gb\|WP_011558671 | Predicted | (narI) respiratory nitrate reductase subunit gamma [Nitrate reductase (VF0302) - Nutritional/Metabolic factor (VF [Mycobacterium sp. KMS] |
| BSLIN78 | 42.5 | 3.90E-57 | VFG000182 | gb\|NP_251793 | Verified | (xcpR) general secretion pathway protein E [Xcp secretion system (VF0084) - Effector delivery system (VFC0086 aeruginosa PAO1] |
| BSLIN78 | 42.7 | 1.50E-32 | VFG000320 | gb\|WP_001169234 | Verified | (kdtB) lipopolysaccharide core biosynthesis protein [LPS (VF0056) - Immune modulation (VFC0258)] [Helicobac |
| BSLIN78 | 42.9 | 3.20E-75 | VFG047736 | gb\|WP_013921813 | Predicted | (carA) carbamoyl phosphate synthase small subunit [Pyrimidine biosynthesis (VF0558) - Nutritional/Metabolic fa [Francisella sp. TX077308] |
| BSLIN78 | 42.9 | 1.10E-72 | VFG005533 | gb\|WP_002262650 | Predicted | (htrA/degP) trypsin-like peptidase domain-containing protein [Serine protease (VF1055) - Exoenzyme (VFC0251) mutans UA159] |
| BSLIN78 | 42.9 | 1.70E-63 | VFG044356 | gb\|WP_013317299 | Predicted | (DDA3937_RS07755) iron ABC transporter permease [Achromobactin (VF1243) - Nutritional/Metabolic factor ( [Dickeya dadantii 3937] |
| BSLIN78 | 42.9 | 1.50E-61 | VFG043148 | gb\|WP_005478291 | Predicted | (VP_RS22515) sigma-54 dependent transcriptional regulator [Lateral flagella (VF0625) - Biofilm (VFC0271)] [Vi parahaemolyticus RIMD 2210633] |
| BSLIN78 | 43.1 | 4.00E-75 | VFG019090 | gb\|WP_000681598 | Predicted | (htrA/degP) S1C family serine protease [Serine protease (VF1055) - Exoenzyme (VFC0251)] [Streptococcus pneu |
| BSLIN78 | 43.2 | 3.30E-80 | VFG043309 | gb\|WP_011860706 | Predicted | (CD630_RS01840) fused FliR family export protein/FlhB family type III secretion system protein [Peritrichous fla Motility (VFC0204)] [Clostridium difficile 630] |
| BSLIN78 | 43.2 | 4.10E-38 | VFG014106 | gb\|NP_251842 | Verified | (hisH2) imidazole glycerol phosphate synthase subunit HisH [LPS (VF0085) - Immune modulation (VFC0258)] [ aeruginosa PAO1] |
| BSLIN78 | 43.3 | 1.30E-52 | VFG009301 | gb\|WP_011731036 | Predicted | (panC) pantoate--beta-alanine ligase [PanC/PanD (VF0319) - Nutritional/Metabolic factor (VFC0272)] [Mycobact str. MC2 155] |
| BSLIN78 | 43.3 | 7.10E-15 | VFG001306 | gb\|WP_000636149 | Verified | (cap8J) type 8 capsular polysaccharide synthesis protein Cap8J [Capsule (VF0003) - Immune modulation (VFC02 [Staphylococcus aureus subsp. aureus MW2] |
| BSLIN78 | 43.5 | 1.50E-44 | VFG039536 | gb\|NP_820549 | Verified | (CBU_1566) Coxiella Dot/Icm type IVB secretion system translocated effector [T4SS secreted effectors (VF0696 delivery system (VFC0086)] [Coxiella burnetii RSA 493] |
| BSLIN78 | 43.5 | 3.10E-79 | VFG005533 | gb\|WP_002262650 | Predicted | (htrA/degP) trypsin-like peptidase domain-containing protein [Serine protease (VF1055) - Exoenzyme (VFC0251) mutans UA159] |
| BSLIN78 | 43.6 | 1.70E-49 | VFG031730 | gb\|WP_014876914 | Predicted | (regX3) two-component sensory transduction protein RegX [RegX3 (VF0858) - Regulation (VFC0301)] [Mycoba str. MC2 155] |
| BSLIN78 | 43.6 | 3.80E-72 | VFG046913 | gb\|WP_013922683 | Predicted | (flmF2) glycosyl transferase family protein [LPS (VF0542) - Immune modulation (VFC0258)] [Francisella sp. TX |
| BSLIN78 | 43.6 | 2.20E-51 | VFG012578 | gb\|WP_000983714 | Predicted | (sitB) iron/manganese ABC transporter ATP-binding protein SitB [Iron/manganese transport (VF1116) - Nutrition factor (VFC0272)] [Escherichia coli UTI89] |
| BSLIN78 | 43.7 | 2.00E-50 | VFG006700 | gb\|WP_000946433 | Predicted | (flgG_2) flagellar basal-body rod protein (flgG) [Flagella (VF0051) - Motility (VFC0204)] [Helicobacter pylori J9 |
| BSLIN78 | 43.8 | 1.90E-77 | VFG047566 | gb\|WP_014547701 | Predicted | (purM) phosphoribosylaminoimidazole synthetase [Purine biosynthesis (VF0559) - Nutritional/Metabolic factor ( [Francisella cf. tularensis subsp. novicida 3523] |
| BSLIN78 | 43.8 | 1.10E-16 | VFG043551 | gb\|WP_010908478 | Predicted | (ML_RS08565) HU family DNA-binding protein [ML1683 (VF0867) - Adherence (VFC0001)] [Mycobacterium |
| BSLIN78 | 43.9 | 3.10E-60 | VFG013198 | gb\|WP_011608203 | Predicted | (hemC) hydroxymethylbilane synthase [Heme biosynthesis (VF0758) - Nutritional/Metabolic factor (VFC0272)] [ somnus 2336] |
| BSLIN78 | 43.9 | 1.60E-51 | VFG031746 | gb\|WP_013470606 | Predicted | (regX3) two-component sensory transduction protein RegX [RegX3 (VF0858) - Regulation (VFC0301)] [Mycoba Spyr1] |
| BSLIN78 | 44 | 2.10E-28 | VFG043292 | gb\|WP_003425244 | Predicted | (flgC) flagellar basal body rod protein FlgC [Peritrichous flagella (VF0732) - Motility (VFC0204)] [Clostridium d |
| BSLIN78 | 44 | 2.40E-161 | VFG043409 | gb\|WP_001192590 | Predicted | (BCE_RS08705) chemotaxis protein CheA [Peritrichous flagella (VF0670) - Motility (VFC0204)] [Bacillus cereu |
| BSLIN78 | 44 | 8.70E-56 | VFG045297 | gb\|WP_011213307 | Verified | (wbuZ) glycosyl amidation-associated protein WbuZ [LPS (VF0171) - Immune modulation (VFC0258)] [Legione subsp. pneumophila str. Philadelphia 1] |
| BSLIN78 | 44.1 | 9.00E-52 | VFG030675 | gb\|WP_003875535 | Predicted | (sugC) sn-glycerol-3-phosphate ABC transporter ATP-binding protein UgpC [Trehalose-recycling ABC transporte Nutritional/Metabolic factor (VFC0272)] [Mycobacterium avium subsp. paratuberculosis K-10] |
| BSLIN78 | 44.2 | 1.10E-98 | VFG026433 | gb\|YP_005360830 | Predicted | (glnA1) glutamine synthetase [Glutamine synthesis (VF0816) - Nutritional/Metabolic factor (VFC0272)] [Mycoba tuberculosis RGTB327] |
| BSLIN78 | 44.2 | 1.50E-39 | VFG026357 | gb\|YP_007962086 | Predicted | (trpD) anthranilate phosphoribosyltransferase [Tryptophan synthesis (VF0813) - Nutritional/Metabolic factor (VF [Mycobacterium tuberculosis CAS/NITR204] |
| BSLIN78 | 44.2 | 2.90E-94 | VFG009393 | gb\|WP_011781504 | Predicted | (lysA) diaminopimelate decarboxylase [Lysine synthesis (VF0815) - Nutritional/Metabolic factor (VFC0272)] [M vanbaalenii PYR-1] |
| BSLIN78 | 44.3 | 1.10E-38 | VFG004738 | gb\|WP_000141557 | Predicted | (nuc) thermonuclease family protein [Thermonuclease nuc (VF0993) - Exoenzyme (VFC0251)] [Staphylococcus a aureus Mu50] |
| BSLIN78 | 44.4 | 5.70E-94 | VFG002188 | gb\|WP_002362618 | Verified | (cpsC) teichoic acid biosynthesis protein, putative [Capsule (VF0361) - Immune modulation (VFC0258)] [Enteroc V583] |
| BSLIN78 | 44.5 | 1.10E-63 | VFG044273 | gb\|WP_001214661 | Predicted | (NWMN_RS12035) ABC transporter substrate-binding protein [Staphyloferrin A (VF1013) - Nutritional/Metaboli (VFC0272)] [Staphylococcus aureus subsp. aureus str. Newman] |
| BSLIN78 | 44.5 | 2.10E-182 | VFG022971 | gb\|WP_041319925 | Predicted | (relA) Probable GTP pyrophosphokinase RelA (ATP:GTP 3'-pyrophosphotransferase) (PPGPP synthetase I) ((P)P (GTP diphosphokinase) [RelA (VF0287) - Regulation (VFC0301)] [Mycobacterium sp. JDM601] |
| BSLIN78 | 44.7 | 4.60E-53 | VFG009859 | gb\|WP_003872811 | Predicted | (mprA) two-component system response regulator MprA [MprAB (VF0298) - Regulation (VFC0301)] [Mycobact subsp. paratuberculosis K-10] |
| BSLIN78 | 44.7 | 7.60E-37 | VFG004737 | gb\|WP_001643461 | Predicted | (nuc) thermonuclease family protein [Thermonuclease nuc (VF0993) - Exoenzyme (VFC0251)] [Staphylococcus a aureus MRSA252] |
| BSLIN78 | 44.7 | 8.70E-28 | VFG032845 | gb\|NP_466072 | Verified | (gtcA) wall teichoic acid glycosylation protein GtcA [GtcA (VF0607) - Post-translational modification (VFC0315 monocytogenes EGD-e] |
| BSLIN78 | 44.8 | 2.80E-101 | VFG001314 | gb\|WP_001225025 | Verified | (aur) zinc metalloproteinase aureolysin [Aureolysin (VF0024) - Exoenzyme (VFC0251)] [Staphylococcus aureus MW2] |
| BSLIN78 | 45.1 | 9.30E-38 | VFG016416 | gb\|WP_000060578 | Predicted | (BT9727_RS25850) sugar transferase [Polysaccharide capsule (VF0659) - Immune modulation (VFC0258)] [Baci serovar konkukian str. 97-27] |
| BSLIN78 | 45.3 | 2.20E-07 | VFG027273 | gb\|YP_005361686 | Predicted | (devR/dosR) two component transcriptional regulator [DevRS (VF0317) - Regulation (VFC0301)] [Mycobacteriu RGTB327] |
| BSLIN78 | 45.3 | 8.50E-57 | VFG016402 | gb\|WP_000757828 | Predicted | (galU) UTP--glucose-1-phosphate uridylyltransferase GalU [Polysaccharide capsule (VF0659) - Immune modulati [Bacillus cereus ATCC 10987] |

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| BSLIN78 | 45.4 | 5.40E-37 | VFG013265 | gb\|WP_005694045 | Verified | (orfM) deoxyribonucleotide triphosphate pyrophosphatase [LOS (VF0044) - Immune modulation (VFC0258)] [Ha influenzae Rd KW20] |
| BSLIN78 | 45.5 | 1.00E-64 | VFG003392 | gb\|WP_032466628 | Predicted | (rfbF) glucose-1-phosphate cytidylyltransferase [O-antigen (VF0392) - Immune modulation (VFC0258)] [Yersinia pseudotuberculosis IP 32953] |
| BSLIN78 | 45.5 | 3.70E-25 | VFG041304 | gb\|WP_010947678 | Verified | (lirB) Dot/Icm type IV secretion system effector LirB [Dot/Icm T4SS secreted effectors (VF0798) - Effector deliv (VFC0086)] [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] |
| BSLIN78 | 45.6 | 2.40E-55 | VFG006818 | gb\|NP_465270 | Predicted | (virR) two-component response regulator [VirR/VirS (VF0791) - Regulation (VFC0301)] [Listeria monocytogene |
| BSLIN78 | 45.7 | 1.40E-80 | VFG044271 | gb\|WP_000989091 | Predicted | (NWMN_RS12025) iron chelate uptake ABC transporter family permease subunit [Staphyloferrin A (VF1013) - Nutritional/Metabolic factor (VFC0272)] [Staphylococcus aureus subsp. aureus str. Newman] |
| BSLIN78 | 45.8 | 1.30E-102 | VFG013515 | gb\|WP_011961967 | Predicted | (mrsA/glmM) phosphoglucosamine mutase [Exopolysaccharide (VF0755) - Immune modulation (VFC0258)] [Ha influenzae PittEE] |
| BSLIN78 | 45.8 | 1.40E-49 | VFG046612 | gb\|WP_014548584 | Predicted | (rpe) ribulose-phosphate 3-epimerase [Capsule (VF0543) - Immune modulation (VFC0258)] [Francisella cf. tular novicida 3523] |
| BSLIN78 | 46.2 | 1.10E-46 | VFG009705 | gb\|WP_011731275 | Predicted | (sodA) superoxide dismutase [SodA (VF0304) - Stress survival (VFC0282)] [Mycobacterium smegmatis str. MC2 |
| BSLIN78 | 46.2 | 3.10E-18 | VFG043551 | gb\|WP_010908478 | Predicted | (ML_RS08565) HU family DNA-binding protein [ML1683 (VF0867) - Adherence (VFC0001)] [Mycobacterium |
| BSLIN78 | 46.2 | 3.80E-80 | VFG016502 | gb\|WP_011265103 | Predicted | (pdhB) alpha-ketoacid dehydrogenase subunit beta [PDH-B (VF0878) - Adherence (VFC0001)] [Mycoplasma mo |
| BSLIN78 | 46.2 | 3.10E-52 | VFG030700 | gb\|WP_005098896 | Predicted | (sugC) sn-glycerol-3-phosphate ABC transporter ATP-binding protein UgpC [Trehalose-recycling ABC transport Nutritional/Metabolic factor (VFC0272)] [Mycobacterium abscessus subsp. bolletii 50594] |
| BSLIN78 | 46.3 | 3.10E-240 | VFG047710 | gb\|WP_014547360 | Predicted | (carB) carbamoyl phosphate synthase large subunit [Pyrimidine biosynthesis (VF0558) - Nutritional/Metabolic fac [Francisella cf. tularensis subsp. novicida 3523] |
| BSLIN78 | 46.4 | 7.30E-62 | VFG032880 | gb\|WP_011702987 | Predicted | (prsA2) post translocation chaperone PrsA2 [PrsA2 (VF0449) - Post-translational modification (VFC0315)] [Liste serovar 6b str. SLCC5334] |
| BSLIN78 | 46.4 | 5.20E-172 | VFG043310 | gb\|WP_011860707 | Predicted | (flhA) flagellar biosynthesis protein FlhA [Peritrichous flagella (VF0732) - Motility (VFC0204)] [Clostridium diff |
| BSLIN78 | 46.7 | 1.00E-85 | VFG016506 | gb\|WP_020002786 | Predicted | (pdhB) alpha-ketoacid dehydrogenase subunit beta [PDH-B (VF0878) - Adherence (VFC0001)] [Mycoplasma syn |
| BSLIN78 | 46.7 | 2.30E-275 | VFG047710 | gb\|WP_014547360 | Predicted | (carB) carbamoyl phosphate synthase large subunit [Pyrimidine biosynthesis (VF0558) - Nutritional/Metabolic fac [Francisella cf. tularensis subsp. novicida 3523] |
| BSLIN78 | 46.8 | 6.20E-81 | VFG043556 | gb\|WP_009885879 | Predicted | (gap) type I glyceraldehyde-3-phosphate dehydrogenase [MG_301/GAPDH (VF0887) - Adherence (VFC0001)] [ genitalium G37] |
| BSLIN78 | 46.9 | 4.10E-87 | VFG007249 | gb\|WP_011151968 | Predicted | (vctD) iron chelate uptake ABC transporter permease subunit VctD [VctPDGC system (VF0638) - Nutritional/Me (VFC0272)] [Vibrio vulnificus YJ016] |
| BSLIN78 | 47 | 2.50E-84 | VFG044272 | gb\|WP_000974906 | Predicted | (NWMN_RS12030) iron ABC transporter permease [Staphyloferrin A (VF1013) - Nutritional/Metabolic factor ( [Staphylococcus aureus subsp. aureus str. Newman] |
| BSLIN78 | 47 | 1.70E-104 | VFG049122 | gb\|WP_012737539 | Verified | (allC) allantoate amidohydrolase [Allantion utilization (VF0572) - Nutritional/Metabolic factor (VFC0272)] [Kleb subsp. pneumoniae NTUH-K2044] |
| BSLIN78 | 47.1 | 2.20E-24 | VFG041578 | gb\|WP_012847749 | Predicted | (ETAE_RS04220) transglycosylase SLT domain-containing protein [T3SS (VF1266) - Effector delivery system ( [Edwardsiella tarda EIB202] |
| BSLIN78 | 47.1 | 2.80E-56 | VFG006818 | gb\|NP_465270 | Predicted | (virR) two-component response regulator [VirR/VirS (VF0791) - Regulation (VFC0301)] [Listeria monocytogene |
| BSLIN78 | 47.1 | 1.10E-55 | VFG006041 | gb\|WP_011681286 | Predicted | (rfbA) glucose-1-phosphate thymidylyltransferase RfbA [Capsule (VF0144) - Immune modulation (VFC0258)] [S thermophilus LMD-9] |
| BSLIN78 | 47.7 | 3.10E-82 | VFG013197 | gb\|WP_011608705 | Predicted | (hemB) porphobilinogen synthase [Heme biosynthesis (VF0758) - Nutritional/Metabolic factor (VFC0272)] [Hae 2336] |
| BSLIN78 | 47.8 | 4.10E-77 | VFG044356 | gb\|WP_013317299 | Predicted | (DDA3937_RS07755) iron ABC transporter permease [Achromobactin (VF1243) - Nutritional/Metabolic factor ( [Dickeya dadantii 3937] |
| BSLIN78 | 47.8 | 4.70E-43 | VFG016532 | gb\|NP_975942 | Predicted | (oppF) oligopeptide ABC transporter permease [Capsule (VF0881) - Immune modulation (VFC0258)] [Mycoplas subsp. mycoides SC str. PG1] |
| BSLIN78 | 47.9 | 8.60E-66 | VFG043411 | gb\|WP_000582894 | Predicted | (BCE_RS08725) protein-glutamate O-methyltransferase CheR [Peritrichous flagella (VF0670) - Motility (VFC02 cereus ATCC 10987] |
| BSLIN78 | 48 | 4.10E-73 | VFG043257 | gb\|NP_464216 | Predicted | (lmo0689) chemotaxis protein CheV [Peritrichous flagella (VF0796) - Motility (VFC0204)] [Listeria monocytoge |
| BSLIN78 | 48.1 | 1.40E-75 | VFG044358 | gb\|WP_013317301 | Predicted | (DDA3937_RS07765) ABC transporter ATP-binding protein [Achromobactin (VF1243) - Nutritional/Metabolic f [Dickeya dadantii 3937] |
| BSLIN78 | 48.2 | 1.00E-82 | VFG007659 | gb\|WP_011261022 | Predicted | (rmlB) dTDP-glucose 4,6-dehydratase [Capsular polysaccharide (VF0624) - Immune modulation (VFC0258)] [Vi ES114] |
| BSLIN78 | 48.3 | 2.00E-93 | VFG030679 | gb\|WP_011730288 | Predicted | (sugC) sn-glycerol-3-phosphate ABC transporter ATP-binding protein UgpC [Trehalose-recycling ABC transport Nutritional/Metabolic factor (VFC0272)] [Mycobacterium smegmatis str. MC2 155] |
| BSLIN78 | 48.3 | 1.30E-25 | VFG006470 | gb\|WP_011578335 | Predicted | (ureA) urease alpha subunit UreA [Urease (VF0050) - Stress survival (VFC0282)] [Helicobacter acinonychis str. |
| BSLIN78 | 48.3 | 8.10E-101 | VFG011157 | gb\|WP_003807107 | Predicted | (bplF) lipopolysaccharide biosynthesis protein [LPS (VF0033) - Immune modulation (VFC0258)] [Bordetella bro |
| BSLIN78 | 48.5 | 4.80E-80 | VFG007252 | gb\|WP_005482136 | Predicted | (vctG) iron chelate uptake ABC transporter permease subunit VctG [VctPDGC system (VF0638) - Nutritional/Me (VFC0272)] [Vibrio parahaemolyticus RIMD 2210633] |
| BSLIN78 | 48.5 | 6.00E-31 | VFG011402 | gb\|WP_004688426 | Predicted | (fabZ) (3R)-hydroxymyristoyl ACP dehydratase [LPS (VF0367) - Immune modulation (VFC0258)] [Brucella suis |
| BSLIN78 | 48.9 | 2.90E-56 | VFG031738 | gb\|YP_001704775 | Predicted | (regX3) Sensory transduction protein RegX3 [RegX3 (VF0858) - Regulation (VFC0301)] [Mycobacterium absces |
| BSLIN78 | 49 | 1.90E-50 | VFG015885 | gb\|WP_003381688 | Predicted | (cysC1) adenylyl-sulfate kinase [Phytotoxin phaseolotoxin (VF0917) - Exotoxin (VFC0235)] [Pseudomonas syrin phaseolicola 1448A] |
| BSLIN78 | 49 | 2.20E-46 | VFG015885 | gb\|WP_003381688 | Predicted | (cysC1) adenylyl-sulfate kinase [Phytotoxin phaseolotoxin (VF0917) - Exotoxin (VFC0235)] [Pseudomonas syrin phaseolicola 1448A] |
| BSLIN78 | 49 | 1.70E-24 | VFG032760 | gb\|WP_003746076 | Predicted | (cheY) response regulator [CheA/CheY (VF0794) - Regulation (VFC0301)] [Listeria ivanovii subsp. ivanovii PA |
| BSLIN78 | 49.3 | 2.10E-118 | VFG013203 | gb\|WP_012341659 | Predicted | (hemL) glutamate-1-semialdehyde 2,1-aminomutase [Heme biosynthesis (VF0758) - Nutritional/Metabolic factor [Haemophilus somnus 2336] |
| BSLIN78 | 49.4 | 2.10E-57 | VFG039536 | gb\|NP_820549 | Verified | (CBU_1566) Coxiella Dot/Icm type IVB secretion system translocated effector [T4SS secreted effectors (VF0696 delivery system (VFC0086)] [Coxiella burnetii RSA 493] |
| BSLIN78 | 49.6 | 8.50E-64 | VFG038840 | gb\|WP_005300916 | Verified | (flmH) short chain dehydrogenase/reductase family oxidoreductase [Polar flagella (VF0473) - Motility (VFC0204 hydrophila ML09-119] |
| BSLIN78 | 49.8 | 2.60E-122 | VFG016428 | gb\|WP_001017616 | Predicted | (BALH_RS26215) UDP-glucose/GDP-mannose dehydrogenase family protein [Polysaccharide capsule (VF0659) modulation (VFC0258)] [Bacillus thuringiensis str. Al Hakam] |
| BSLIN78 | 50 | 1.80E-67 | VFG043437 | gb\|WP_001256752 | Predicted | (motB) flagellar motor protein MotB [Peritrichous flagella (VF0670) - Motility (VFC0204)] [Bacillus cereus ATC |

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| BSLIN78 | 50.1 | 0.00E+00 | VFG026753 | gb\|WP_015302870 | Predicted | (narG) nitrate reductase subunit alpha [Nitrate reductase (VF0302) - Nutritional/Metabolic factor (VFC0272)] [My canettii CIPT 140070008] |
| BSLIN78 | 50.2 | 2.70E-183 | VFG031404 | gb\|WP_085981087 | Predicted | (ctpV) copper-translocating P-type ATPase [Copper exporter (VF0849) - Nutritional/Metabolic factor (VFC0272)] intracellulare ATCC 13950] |
| BSLIN78 | 50.4 | 2.20E-35 | VFG016532 | gb\|NP_975942 | Predicted | (oppF) oligopeptide ABC transporter permease [Capsule (VF0881) - Immune modulation (VFC0258)] [Mycoplas subsp. mycoides SC str. PG1] |
| BSLIN78 | 50.4 | 2.50E-66 | VFG006797 | gb\|WP_011702610 | Predicted | (stp) Stp1/IreP family PP2C-type Ser/Thr phosphatase [Serine-threonine phosphatase stp (VF0787) - Post-translati (VFC0315)] [Listeria welshimeri serovar 6b str. SLCC5334] |
| BSLIN78 | 50.5 | 3.70E-180 | VFG032996 | gb\|WP_012581401 | Predicted | (oatA) peptidoglycan O-acetyltransferase [OatA (VF0441) - Immune modulation (VFC0258)] [Listeria monocytog |
| BSLIN78 | 50.6 | 7.50E-87 | VFG049038 | gb\|WP_032448055 | Predicted | (KPN2242_RS16175) glycosyltransferase family 2 protein [LPS (VF0561) - Immune modulation (VFC0258)] [Kl pneumoniae KCTC 2242] |
| BSLIN78 | 50.6 | 9.00E-41 | VFG001867 | gb\|WP_016357051 | Verified | (sodB) superoxide dismutase [SodB (VF0169) - Stress survival (VFC0282)] [Legionella pneumophila subsp. pneu Philadelphia 1] |
| BSLIN78 | 50.6 | 3.20E-66 | VFG016398 | gb\|WP_000606280 | Predicted | (BCE_RS25850) glycosyltransferase family 2 protein [Polysaccharide capsule (VF0659) - Immune modulation (V [Bacillus cereus ATCC 10987] |
| BSLIN78 | 51 | 2.70E-141 | VFG032790 | gb\|WP_003727064 | Predicted | (dltA) D-alanine--poly(phosphoribitol) ligase subunit DltA [D-alanine-polyphosphoribitol ligase DltA (VF0795) - modification (VFC0315)] [Listeria monocytogenes serotype 4b str. F2365] |
| BSLIN78 | 51 | 3.40E-101 | VFG030724 | gb\|WP_015308640 | Predicted | (sugC) sn-glycerol-3-phosphate ABC transporter ATP-binding protein UgpC [Trehalose-recycling ABC transporte Nutritional/Metabolic factor (VFC0272)] [Mycobacterium smegmatis JS623] |
| BSLIN78 | 51.1 | 3.90E-23 | VFG006801 | gb\|WP_011701738 | Predicted | (srtA) class A sortase [Sortase A (VF0788) - Post-translational modification (VFC0315)] [Listeria welshimeri sero SLCC5334] |
| BSLIN78 | 51.2 | 1.20E-113 | VFG005552 | gb\|WP_011837486 | Predicted | (tig/ropA) trigger factor [Trigger factor (VF1056) - Stress survival (VFC0282)] [Streptococcus sanguinis SK36] |
| BSLIN78 | 51.5 | 1.30E-68 | VFG043285 | gb\|WP_011860690 | Predicted | (fliC) flagellin FliC [Peritrichous flagella (VF0732) - Motility (VFC0204)] [Clostridium difficile 630] |
| BSLIN78 | 51.5 | 4.80E-68 | VFG043285 | gb\|WP_011860690 | Predicted | (fliC) flagellin FliC [Peritrichous flagella (VF0732) - Motility (VFC0204)] [Clostridium difficile 630] |
| BSLIN78 | 51.7 | 6.50E-73 | VFG043438 | gb\|WP_000344868 | Predicted | (motA) flagellar motor stator protein MotA [Peritrichous flagella (VF0670) - Motility (VFC0204)] [Bacillus cereu |
| BSLIN78 | 51.7 | 1.10E-89 | VFG016389 | gb\|WP_000727070 | Predicted | (BCE_RS25805) LytR family transcriptional regulator [Polysaccharide capsule (VF0659) - Immune modulation ( [Bacillus cereus ATCC 10987] |
| BSLIN78 | 52 | 5.60E-167 | VFG031933 | gb\|WP_014093172 | Predicted | (fbpA) fibronectin-binding protein [FbpA (VF0349) - Adherence (VFC0001)] [Listeria ivanovii subsp. ivanovii P |
| BSLIN78 | 52.9 | 3.90E-13 | VFG001250 | gb\|NP_249791 | Verified | (fliE) flagellar hook-basal body complex protein FliE [Flagella (VF0273) - Motility (VFC0204)] [Pseudomonas ae |
| BSLIN78 | 52.9 | 3.10E-30 | VFG009317 | gb\|WP_011892322 | Predicted | (panD) aspartate 1-decarboxylase [PanC/PanD (VF0319) - Nutritional/Metabolic factor (VFC0272)] [Mycobacteri GCK] |
| BSLIN78 | 53 | 2.40E-66 | VFG016405 | gb\|WP_000393162 | Predicted | (BCE_RS25885) capsular polysaccharide biosynthesis protein [Polysaccharide capsule (VF0659) - Immune modul [Bacillus cereus ATCC 10987] |
| BSLIN78 | 53.2 | 4.70E-99 | VFG016424 | gb\|WP_000276321 | Predicted | (manA) mannose-6-phosphate isomerase, class I [Polysaccharide capsule (VF0659) - Immune modulation (VFC02 thuringiensis str. Al Hakam] |
| BSLIN78 | 53.4 | 7.10E-144 | VFG047162 | gb\|WP_003022298 | Verified | (wbtE) nucleotide sugar dehydrogenase [LPS (VF0542) - Immune modulation (VFC0258)] [Francisella tularensis SCHU S4] |
| BSLIN78 | 53.5 | 4.30E-67 | VFG006610 | gb\|WP_138091884 | Predicted | (fliP) flagellar biosynthetic protein FliP [Flagella (VF0051) - Motility (VFC0204)] [Helicobacter hepaticus ATCC |
| BSLIN78 | 53.7 | 3.90E-12 | VFG010906 | gb\|WP_011213314 | Verified | (csrA) carbon storage regulator CsrA [CsrA (VF0261) - Regulation (VFC0301)] [Legionella pneumophila subsp. Philadelphia 1] |
| BSLIN78 | 54.3 | 2.00E-79 | VFG016166 | gb\|WP_003372869 | Predicted | (cbrD) ABC transporter ATP-binding protein [Achromobactin biosynthesis and transport (VF0922) - Nutritional/ (VFC0272)] [Pseudomonas syringae pv. syringae B728a] |
| BSLIN78 | 54.3 | 1.40E-18 | VFG043067 | gb\|NP_460933 | Predicted | (fliQ) flagellar export apparatus protein FliQ [Peritrichous flagella (VF0967) - Motility (VFC0204)] [Salmonella e enterica serovar Typhimurium str. LT2] |
| BSLIN78 | 54.3 | 4.90E-104 | VFG016424 | gb\|WP_000276321 | Predicted | (manA) mannose-6-phosphate isomerase, class I [Polysaccharide capsule (VF0659) - Immune modulation (VFC02 thuringiensis str. Al Hakam] |
| BSLIN78 | 54.7 | 2.90E-190 | VFG016381 | gb\|WP_033685340 | Predicted | (BC_RS26295) polysaccharide biosynthesis protein [Polysaccharide capsule (VF0659) - Immune modulation (VF cereus ATCC 14579] |
| BSLIN78 | 54.9 | 1.80E-80 | VFG016434 | gb\|WP_000566198 | Predicted | (BALH_RS26245) hypothetical protein [Polysaccharide capsule (VF0659) - Immune modulation (VFC0258)] [Ba thuringiensis str. Al Hakam] |
| BSLIN78 | 55.1 | 4.60E-154 | VFG037029 | gb\|WP_010951343 | Predicted | (katA) catalase [KatA (VF0454) - Stress survival (VFC0282)] [Neisseria gonorrhoeae FA 1090] |
| BSLIN78 | 55.3 | 1.80E-147 | VFG048959 | gb\|WP_020956638 | Predicted | (gndA) NADP-dependent phosphogluconate dehydrogenase [Capsule (VF0560) - Immune modulation (VFC0258) pneumoniae JM45] |
| BSLIN78 | 55.5 | 6.10E-97 | VFG005360 | gb\|WP_002262489 | Predicted | (plr/gapA) type I glyceraldehyde-3-phosphate dehydrogenase [Streptococcal plasmin receptor/GAPDH (VF1042) (VFC0001)] [Streptococcus mutans UA159] |
| BSLIN78 | 55.6 | 1.50E-79 | VFG007257 | gb\|WP_005482130 | Predicted | (vctC) iron chelate ABC transporter ATP-binding protein VctC [VctPDGC system (VF0638) - Nutritional/Metabo (VFC0272)] [Vibrio parahaemolyticus RIMD 2210633] |
| BSLIN78 | 55.8 | 1.10E-62 | VFG050210 | gb\|WP_000467926 | Predicted | (BCAH187_RS26575) CpsD/CapB family tyrosine-protein kinase [Polysaccharide capsule (VF0659) - Immune m (VFC0258)] [Bacillus cereus AH187] |
| BSLIN78 | 56.2 | 3.50E-129 | VFG043297 | gb\|WP_011860700 | Predicted | (fliI) flagellar protein export ATPase FliI [Peritrichous flagella (VF0732) - Motility (VFC0204)] [Clostridium diffi |
| BSLIN78 | 56.2 | 2.10E-25 | VFG006470 | gb\|WP_011578335 | Predicted | (ureA) urease alpha subunit UreA [Urease (VF0050) - Stress survival (VFC0282)] [Helicobacter acinonychis str. |
| BSLIN78 | 56.5 | 1.80E-102 | VFG026966 | gb\|WP_041300173 | Predicted | (sigA/rpoV) RNA polymerase sigma factor [SigA (VF0257) - Regulation (VFC0301)] [Mycobacterium liflandii 1 |
| BSLIN78 | 57.1 | 3.20E-45 | VFG002161 | gb\|NP_465369 | Verified | (lspA) signal peptidase II [Lsp (VF0351) - Post-translational modification (VFC0315)] [Listeria monocytogenes E |
| BSLIN78 | 57.9 | 7.20E-108 | VFG016424 | gb\|WP_000276321 | Predicted | (manA) mannose-6-phosphate isomerase, class I [Polysaccharide capsule (VF0659) - Immune modulation (VFC02 thuringiensis str. Al Hakam] |
| BSLIN78 | 57.9 | 5.40E-138 | VFG013203 | gb\|WP_012341659 | Predicted | (hemL) glutamate-1-semialdehyde 2,1-aminomutase [Heme biosynthesis (VF0758) - Nutritional/Metabolic factor [Haemophilus somnus 2336] |
| BSLIN78 | 58.1 | 5.20E-19 | VFG029673 | gb\|WP_011725355 | Predicted | (mbtH) MbtH family protein [GPL locus (VF0841) - Immune modulation (VFC0258)] [Mycobacterium avium 10 |
| BSLIN78 | 58.5 | 2.00E-91 | VFG016433 | gb\|WP_000757777 | Predicted | (galU) UTP--glucose-1-phosphate uridylyltransferase GalU [Polysaccharide capsule (VF0659) - Immune modulati [Bacillus thuringiensis str. Al Hakam] |
| BSLIN78 | 58.7 | 2.40E-65 | VFG050208 | gb\|WP_001207190 | Predicted | (BCAH187_RS26565) CpsD/CapB family tyrosine-protein kinase [Polysaccharide capsule (VF0659) - Immune m (VFC0258)] [Bacillus cereus AH187] |
| BSLIN78 | 58.8 | 5.80E-86 | VFG002181 | gb\|WP_002387127 | Verified | (cpsJ) ABC transporter, ATP-binding protein [Capsule (VF0361) - Immune modulation (VFC0258)] [Enterococcu |

| | | | | | | |
|---|---|---|---|---|---|---|
| BSLIN78 | 59 | 8.90E-99 | VFG032466 | gb\|WP_014093697 | Predicted | (lgt) prolipoprotein diacylglyceryl transferase [Lipoprotein diacylglyceryl transferase lgt (VF0790) - Post-translati (VFC0315)] [Listeria ivanovii subsp. ivanovii PAM 55] |
| BSLIN78 | 59.3 | 6.80E-109 | VFG047143 | gb\|WP_011733708 | Predicted | (wbtF) NAD dependent epimerase [LPS (VF0542) - Immune modulation (VFC0258)] [Francisella novicida U112] |
| BSLIN78 | 59.5 | 6.60E-124 | VFG045303 | gb\|WP_010946492 | Verified | (LPG_RS03745) aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme [LPS (VF0171) - Immun (VFC0258)] [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] |
| BSLIN78 | 59.7 | 2.40E-179 | VFG022803 | gb\|WP_041317387 | Predicted | (narH) nitrate reductase subunit beta [Nitrate reductase (VF0302) - Nutritional/Metabolic factor (VFC0272)] [Myc JDM601] |
| BSLIN78 | 60.2 | 1.10E-82 | VFG045688 | gb\|WP_002294134 | Predicted | (cpsA/uppS) undecaprenyl diphosphate synthase [Capsule (VF0361) - Immune modulation (VFC0258)] [Enteroco Aus0004] |
| BSLIN78 | 60.2 | 4.20E-26 | VFG031470 | gb\|WP_011741443 | Predicted | (ndk) nucleoside-diphosphate kinase [Nucleoside diphosphate kinase (VF0851) - Immune modulation (VFC0258) ulcerans Agy99] |
| BSLIN78 | 60.2 | 8.80E-203 | VFG043573 | gb\|NP_219906 | Predicted | (dnaK) chaperone protein DnaK [Adherence; porin (VF0713) - Adherence (VFC0001)] [Chlamydia trachomatis D |
| BSLIN78 | 61.5 | 1.30E-211 | VFG019522 | gb\|WP_000724279 | Predicted | (ureB) urease beta subunit UreB, urea amidohydrolase [Urease (VF0050) - Stress survival (VFC0282)] [Helicobac |
| BSLIN78 | 62.1 | 6.70E-155 | VFG016428 | gb\|WP_001017616 | Predicted | (BALH_RS26215) UDP-glucose/GDP-mannose dehydrogenase family protein [Polysaccharide capsule (VF0659) modulation (VFC0258)] [Bacillus thuringiensis str. Al Hakam] |
| BSLIN78 | 63 | 6.40E-18 | VFG011430 | gb\|WP_002963616 | Verified | (acpXL) acyl carrier protein [LPS (VF0367) - Immune modulation (VFC0258)] [Brucella melitensis bv. 1 str. 16 |
| BSLIN78 | 63.2 | 3.90E-132 | VFG001373 | gb\|WP_000758382 | Verified | (cps4I) capsular polysaccharide biosynthesis protein Cps4I [Capsule (VF0144) - Immune modulation (VFC0258)] pneumoniae TIGR4] |
| BSLIN78 | 64.1 | 2.00E-96 | VFG016166 | gb\|WP_003372869 | Predicted | (cbrD) ABC transporter ATP-binding protein [Achromobactin biosynthesis and transport (VF0922) - Nutritional/ (VFC0272)] [Pseudomonas syringae pv. syringae B728a] |
| BSLIN78 | 65.3 | 4.90E-131 | VFG002158 | gb\|NP_464456 | Verified | (lplA1) lipoate protein ligase [LplA1 (VF0347) - Nutritional/Metabolic factor (VFC0272)] [Listeria monocytogen |
| BSLIN78 | 66.4 | 1.40E-241 | VFG000080 | gb\|NP_464522 | Verified | (clpE) ATP-dependent protease [ClpE (VF0073) - Stress survival (VFC0282)] [Listeria monocytogenes EGD-e] |
| BSLIN78 | 67.7 | 3.10E-63 | VFG007642 | gb\|WP_011149334 | Predicted | (wcaJ) sugar transferase [Capsular polysaccharide (VF0624) - Immune modulation (VFC0258)] [Vibrio vulnificus |
| BSLIN78 | 68.6 | 5.30E-43 | VFG043408 | gb\|WP_000940577 | Predicted | (BCE_RS08700) response regulator [Peritrichous flagella (VF0670) - Motility (VFC0204)] [Bacillus cereus ATC |
| BSLIN78 | 70.4 | 1.20E-191 | VFG048830 | gb\|WP_014907233 | Verified | (gndA) NADP-dependent phosphogluconate dehydrogenase [Capsule (VF0560) - Immune modulation (VFC0258) pneumoniae subsp. pneumoniae NTUH-K2044] |
| BSLIN78 | 71.9 | 3.10E-178 | VFG018662 | gb\|WP_012130507 | Predicted | (eno) phosphopyruvate hydratase [Streptococcal enolase (VF1060) - Exoenzyme (VFC0251)] [Streptococcus gord substr. CH1] |
| BSLIN78 | 74.5 | 3.60E-224 | VFG012103 | gb\|WP_003514589 | Predicted | (groEL) chaperonin GroEL [GroEL (VF0594) - Adherence (VFC0001)] [Clostridium thermocellum ATCC 27405 |
| BSLIN78 | 75 | 8.30E-178 | VFG046474 | gb\|WP_014714676 | Predicted | (tufA) elongation factor Tu [EF-Tu (VF0460) - Adherence (VFC0001)] [Francisella noatunensis subsp. orientalis |
| BSLIN78 | 76.1 | 7.30E-82 | VFG000077 | gb\|NP_465991 | Verified | (clpP) ATP-dependent Clp protease proteolytic subunit [ClpP (VF0074) - Stress survival (VFC0282)] [Listeria mo e] |
| BSLIN78 | 79 | 0.00E+00 | VFG000079 | gb\|NP_463763 | Verified | (clpC) endopeptidase Clp ATP-binding chain C [ClpC (VF0072) - Stress survival (VFC0282)] [Listeria monocyto |
| BSLIN78 | 79.7 | 4.30E-131 | VFG016417 | gb\|WP_000757774 | Predicted | (galU) UTP--glucose-1-phosphate uridylyltransferase GalU [Polysaccharide capsule (VF0659) - Immune modulati [Bacillus thuringiensis serovar konkukian str. 97-27] |
| BSLIN78 | 80.4 | 4.90E-163 | VFG050194 | gb\|WP_000996524 | Predicted | (galE) UDP-glucose 4-epimerase GalE [Polysaccharide capsule (VF0659) - Immune modulation (VFC0258)] [Bac AH187] |
| BSLIN78 | 99.2 | 0.00E+00 | VFG050043 | gb\|NP_391076 | Predicted | (dhbF) non-ribosomal peptide synthetase, DhbF [Bacillibactin (VF0586) - Nutritional/Metabolic factor (VFC0272 subtilis subsp. subtilis str. 168] |
| BSLIN78 | 99.2 | 4.00E-228 | VFG050010 | gb\|NP_391079 | Predicted | (dhbC) isochorismate synthase DhbC [Bacillibactin (VF0586) - Nutritional/Metabolic factor (VFC0272)] [Bacillu subtilis str. 168] |
| BSLIN78 | 99.4 | 0.00E+00 | VFG050021 | gb\|NP_391078 | Predicted | (dhbE) 2,3-dihydroxybenzoate adenylase DhbE [Bacillibactin (VF0586) - Nutritional/Metabolic factor (VFC0272) subtilis subsp. subtilis str. 168] |
| BSLIN78 | 99.5 | 0.00E+00 | VFG016303 | gb\|NP_389723 | Predicted | (dep/capD) gamma-glutamyltranspeptidase, required for polyglutamate anchoring to peptidoglycan [Capsule (VF0 modulation (VFC0258)] [Bacillus subtilis subsp. subtilis str. 168] |
| BSLIN78 | 99.5 | 1.10E-118 | VFG016234 | gb\|NP_390062 | Predicted | (hlyIII) putative membrane hydrolase [Hemolysin III (VF0655) - Exotoxin (VFC0235)] [Bacillus subtilis subsp. s |
| BSLIN78 | 99.6 | 6.80E-144 | VFG049999 | gb\|NP_391080 | Predicted | (dhbA) 2,3-dihydroxybenzoate-2,3-dehydrogenase, DhbA [Bacillibactin (VF0586) - Nutritional/Metabolic factor ( [Bacillus subtilis subsp. subtilis str. 168] |
| BSLIN78 | 99.7 | 9.10E-180 | VFG050032 | gb\|NP_391077 | Predicted | (dhbB) isochorismatase, DhbB [Bacillibactin (VF0586) - Nutritional/Metabolic factor (VFC0272)] [Bacillus subtil str. 168] |
| BSLIN78 | 100 | 1.20E-221 | VFG016291 | gb\|NP_391469 | Predicted | (capA) CapA, required for Poly-gamma-glutamate transport [Capsule (VF0141) - Immune modulation (VFC0258) subsp. subtilis str. 168] |
| BSLIN78 | 100 | 2.40E-77 | VFG016295 | gb\|NP_391470 | Predicted | (capC) CapC, involved in Poly-gamma-glutamate synthesis [Capsule (VF0141) - Immune modulation (VFC0258) subsp. subtilis str. 168] |
| BSLIN78 | 100 | 5.60E-227 | VFG016299 | gb\|NP_391471 | Predicted | (capB) CapB, involved in Poly-gamma-glutamate synthesis [Capsule (VF0141) - Immune modulation (VFC0258) subsp. subtilis str. 168] |

Table S9. antibiotic resistent genes card

| ORF_ID | Start | Stop | Orientation | Cut_Off | Pass_Bitscore | Best_Hit_Bitscore | Best_Hit_ARO | Best_Identities | ARO | SNPs_in_Best_Hit_ARO | Drug Class |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Chromosome1_252 | 269214 | 270134 | + | Strict | 500 | 626.706 | mphK | 99.02 | 3004541 | n/a | macrolide antibiotic |
| Chromosome1_267 | 282031 | 283464 | - | Strict | 900 | 933.71 | lmrB | 99.37 | 3002813 | n/a | lincosamide antibiotic |
| Chromosome1_314 | 332556 | 333149 | - | Strict | 375 | 407.527 | tmrB | 98.48 | 3003059 | n/a | nucleoside antibiotic |
| Chromosome1_470 | 510629 | 511798 | + | Strict | 175 | 184.111 | vanT gene in vanG cluster | 31.78 | 3002972 | n/a | glycopeptide antibiotic |
| Chromosome1_555 | 582936 | 584579 | - | Strict | 1000 | 1103.58 | vmlR | 98.54 | 3004476 | n/a | lincosamide antibiotic; streptogramin antibiotic; streptogramin |
| Chromosome1_837 | 892763 | 895333 | + | Strict | 1650 | 1725.68 | Bacillus subtilis mprF | 99.88 | 3003324 | n/a | peptide antibiotic |
| Chromosome1_1318 | 1355822 | 1356160 | + | Perfect | 180 | 214.542 | ykkC | 100 | 3003063 | n/a | aminoglycoside antibiotic; tetracycline antibiotic; phenicol |
| Chromosome1_1319 | 1356160 | 1356477 | + | Strict | 180 | 206.453 | ykkD | 99.05 | 3003064 | n/a | aminoglycoside antibiotic; tetracycline antibiotic; phenicol |
| Chromosome1_1748 | 1840941 | 1841294 | - | Strict | 75 | 78.1814 | qacJ | 43.75 | 3007014 | n/a | disinfecting agents and antiseptics |
| Chromosome1_1749 | 1841308 | 1841628 | - | Strict | 75 | 82.0333 | qacG | 47.47 | 3007015 | n/a | disinfecting agents and antiseptics |
| Chromosome1_2023 | 2054547 | 2055731 | - | Strict | 175 | 217.624 | vanT gene in vanG cluster | 34.59 | 3002972 | n/a | glycopeptide antibiotic |
| Chromosome1_2047 | 2072346 | 2072780 | + | Strict | 150 | 182.956 | FosBx1 | 62.04 | 3007372 | n/a | phosphonic acid antibiotic |
| Chromosome1_2143 | 2201031 | 2201942 | - | Strict | 50 | 119.783 | vanW gene in vanI cluster | 40 | 3003724 | n/a | glycopeptide antibiotic |
| Chromosome1_2151 | 2207666 | 2208586 | + | Strict | 350 | 423.32 | BcI | 66.34 | 3002877 | n/a | cephalosporin; penem |
| Chromosome1_2249 | 2288610 | 2289431 | - | Strict | 50 | 119.013 | vanY gene in vanG cluster | 36.44 | 3002959 | n/a | glycopeptide antibiotic |
| Chromosome1_2511 | 2514102 | 2515271 | + | Strict | 750 | 762.296 | bmr | 99.23 | 3003007 | n/a | fluoroquinolone antibiotic; nucleoside antibiotic; phenicol antibiotic; disinfecting agents and antiseptics |
| Chromosome1_2782 | 2743544 | 2744746 | + | Strict | 750 | 787.719 | blt | 99.5 | 3003006 | n/a | fluoroquinolone antibiotic; disinfecting agents and antiseptics |
| Chromosome1_2801 | 2762721 | 2763575 | - | Strict | 500 | 582.793 | aadK | 98.24 | 3002627 | n/a | aminoglycoside antibiotic |
| Chromosome1_4241 | 4230664 | 4232040 | - | Strict | 450 | 706.057 | tet(45) | 75.6 | 3003196 | n/a | tetracycline antibiotic |

Table S10. Core pan genes of *Bacillus subtilis* strains

| SampleName | TotalGeneNum |
|---|---|
| AMR1 | 4,198 |
| BS11774 | 4,064 |
| BS16045 | 4,076 |
| BSA10 | 4,167 |
| BSDKU | 3,861 |
| BSLIN78 | 4,539 |

Table S11. BSLIN78 specific COG list class catalog.

| First class | Second class | Class description | Gene number | Gene id |
|---|---|---|---|---|
| CELLULAR | D | Cell cycle control, cell division, chromosome partitioning | 1 | [BSLIN78] BSLIN78GL004523 |
| METABOLISM | E | Amino acid transport and metabolism | 3 | [BSLIN78] BSLIN78GL002953;[BSLIN78] BSLIN78GL004420;[BSLIN78] BSLIN78GL004418 |
| METABOLISM | G | Carbohydrate transport and metabolism | 2 | [BSLIN78] BSLIN78GL004418;[BSLIN78] BSLIN78GL004349 |
| METABOLISM | I | Lipid transport and metabolism | 1 | [BSLIN78] BSLIN78GL000533 |
| INFORMATION | J | Translation, ribosomal structure and biogenesis | 1 | [BSLIN78] BSLIN78GL000144 |
| INFORMATION | K | Transcription | 4 | [BSLIN78]_BSLIN78GL000534;[BSLIN78]_BSLIN78GL004530;[BSLIN78]_BSLIN78GL004222;[BSLIN78] BSLIN78GL004417 |
| INFORMATION | L | Replication, recombination and repair | 5 | [BSLIN78]_BSLIN78GL000702;[BSLIN78]_BSLIN78GL004535;[BSLIN78]_BSLIN78GL004486;[BSLIN78] BSLIN78GL004480;[BSLIN78] BSLIN78GL002020 |
| CELLULAR | M | Cell wall/membrane/envelope biogenesis | 4 | [BSLIN78]_BSLIN78GL004497;[BSLIN78]_BSLIN78GL002960;[BSLIN78]_BSLIN78GL004515;[BSLIN78] BSLIN78GL002959 |
| CELLULAR | N | Cell motility | 1 | [BSLIN78] BSLIN78GL004523 |
| METABOLISM | P | Inorganic ion transport and metabolism | 1 | [BSLIN78] BSLIN78GL002868 |
| METABOLISM | Q | Secondary metabolites biosynthesis, transport and catabolism | 1 | [BSLIN78] BSLIN78GL002796 |
| POORLY | R | General function prediction only | 8 | [BSLIN78]_BSLIN78GL004221;[BSLIN78]_BSLIN78GL002868;[BSLIN78]_BSLIN78GL002957;[BSLIN78]_BSLIN78GL004538;[BSLIN78]_BSLIN78GL002958;[BSLIN78]_BSLIN78GL000717;[BSLIN78] BSLIN78GL002956;[BSLIN78] BSLIN78GL004418 |
| POORLY | S | Function unknown | 2 | [BSLIN78] BSLIN78GL002792;[BSLIN78] BSLIN78GL004448 |
| CELLULAR | T | Signal transduction mechanisms | 4 | [BSLIN78]_BSLIN78GL000534;[BSLIN78]_BSLIN78GL004531;[BSLIN78]_BSLIN78GL004530;[BSLIN78] BSLIN78GL000535 |
| CELLULAR | U | Intracellular trafficking, secretion, and vesicular transport | 2 | [BSLIN78] BSLIN78GL004505;[BSLIN78] BSLIN78GL004499 |
| CELLULAR | V | Defense mechanisms | 6 | [BSLIN78]_BSLIN78GL000511;[BSLIN78]_BSLIN78GL000206;[BSLIN78]_BSLIN78GL000633;[BSLIN78] BSLIN78GL004476;[BSLIN78] BSLIN78GL000632;[BSLIN78] BSLIN78GL000634 |
| METABOLISM | X | Mobilome: prophages, transposons | 5 | [BSLIN78]_BSLIN78GL002060;[BSLIN78]_BSLIN78GL002055A1:E20;[BSLIN78]_BSLIN78GL002048;[BSLIN78] BSLIN78GL002047;[BSLIN78] BSLIN78GL002020 |