Figure S1. Screening for amylase activity in isolates from wastewater sludge compost (Kazan, Tatarstan, Russia). The MGMM159 isolate is marked with an arrow.



Figure S2. Genetic map and annotated nucleotide sequence of the pET22-amyBL159 recombinant plasmid.

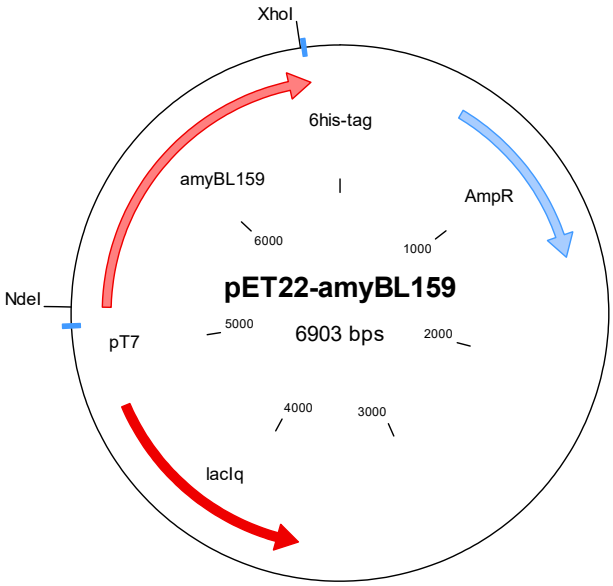


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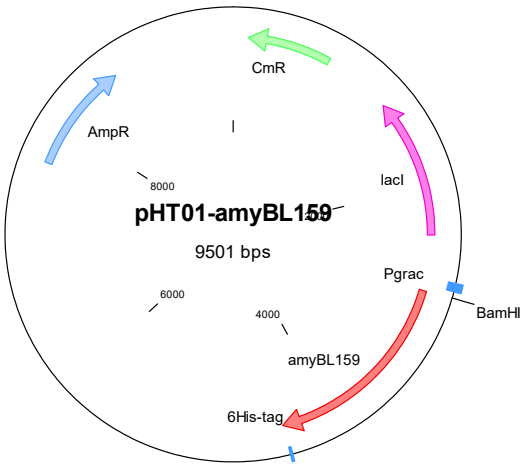
Figure S3. Genetic map and annotated nucleotide sequence of the pHT01-amyBL159 recombinant plasmid



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4141 cgacagctcg gttgcaaatt caggtttggc ggcattaata acagacggac ccggtggggc
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4261 ccgttcggag ccggttgtca tcaattcgga aggctgggga gagtttcacg taaacggcgg
4321 gtcggtttca atttatgttc aaagagagca ccaccaccac caccactgac ccggggcagc
4381 ccgcctaatg agcgggcttt tttcacgtca cgcgtccatg gagatctttg tctgcaactg
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4621 taaagcgatt tgatgttcaa ggaatcacgg aagaagatac tcatgataaa gaagctctaa
4681 aactattcaa taaccttaca atggaattga tcgaaagggt ggaaggttaa tggtacgaaa
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5581 caaataaaaa acttttcttt agacaaattt ggtacgcata taccttacat agaaggtcat
5641 tatacaatct taaataatta cttctttgat ttttggggct atttttagg tgctgaagga
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6481 cagttttttt tatttagaaa tagtgaaaaa aatataatca gggaggtatc aatatttaat

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     6541 gagtactgat ttaaatttat ttagactgga attaataatt aacacgtaga ctaattaaaa
     6601 tttaatgagg gataaagagg atacaaaaat attaatttca atccctatta aattttaaca
     6661 agggggggat taaaatttaa ttagaggttt atccacaaga aaagacccta ataaaatttt
     6721 tactagggtt ataacactga ttaatttctt aatgggggag ggattaaaat ttaatgacaa
     6781 agaaaacaat cttttaagaa aagcttttaa aagataataa taaaaagagc tttgcgatta
     6841 agcaaaactc tttacttttt cattgacatt atcaaattca tcgatttcaa attgttgttg
     6901 tatcataaag ttaattctgt tttgcacaac cttttcagga atataaaaca catctgaggc
     6961 ttgttttata aactcagggt cgctaaagtc aatgtaacgt agcatatgat atggtatagc
     7021 ttccacccaa gttagccttt ctgcttcttc tgaatgtttt tcatatactt ccatgggtat
     7081 ctctaaatga ttttcctcat gtagcaaggt atgagcaaaa agtttatgga attgatagtt
     7141 cctctctttt tcttcaactt ttttatctaa aacaaacact ttaacatctg agtcaatgta
     7201 agcataagat gtttttccag tcataatttc aatcccaaat cttttagaca gaaattctgg
     7261 acgtaaatct tttggtgaaa gaatttttt atgtagcaat atatccgata cagcaccttc
     7321 taaaagcgtt ggtgaatagg gcattttacc tatctcctct cattttgtgg aataaaaata
     7381 gtcatattcg tccatctacc tatcctatta tcgaacagtt gaacttttta atcaaggatc
     7441 agtccttttt ttcattattc ttaaactgtg ctcttaactt taacaactcg atttgttttt
     7501 ccagatctcg agggtaacta gcctcgccga tcccgcaaga ggcccggcag tcaggtggca
     7561 cttttcgggg aaatgtgcgc ggaaccccta tttgtttatt tttctaaata cattcaaata
     7621 tgtatccgct catgagacaa taaccctgat aaatgcttca ataatattga aaaaggaaga
     7681 gtatgagtat tcaacatttc cgtgtcgccc ttattccctt ttttgcggca ttttgccttc
     7741 ctgtttttgc tcacccagaa acgctggtga aagtaaaaga tgctgaagat cagttgggtg
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     7921 cccgtattga cgccgggcaa gagcaactcg gtcgccgcat acactattct cagaatgact
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     8041 tatgcagtgc tgccataacc atgagtgata acactgcggc caacttactt ctgacaacga
     8101 tcggaggacc gaaggagcta accgcttttt tgcacaacat gggggatcat gtaactcgcc
     8161 ttgatcgttg ggaaccggag ctgaatgaag ccataccaaa cgacgagcgt gacaccacga
     8221 tgcctgtagc aatggcaaca acgttgcgca aactattaac tggcgaacta cttactctag
     8281 cttcccggca acaattaata gactggatgg aggcggataa agttgcagga ccacttctgc
     8341 gctcggccct tccggctggc tggtttattg ctgataaatc tggagccggt gagcgtgggt
     8401 ctcgcggtat cattgcagca ctggggccag atggtaagcc ctcccgtatc gtagttatct
     8461 acacgacggg gagtcaggca actatggatg aacgaaatag acagatcgct gagataggtg
     8521 cctcactgat taagcattgg taactgtcag accaagttta ctcatatata ctttagattg
     8581 atttaaaact tcatttttaa tttaaaagga tctaggtgaa gatccttttt gataatctca
     8641 tgaccaaaat cccttaacgt gagttttcgt tccactgagc gtcagacccc gtagaaaaga
     8701 tcaaaggatc ttcttgagat cctttttttc tgcgcgtaat ctgctgcttg caaacaaaaa
     8761 aaccaccgct accagcggtg gtttgtttgc cggatcaaga gctaccaact ctttttccga
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     9121 cgcttcccga agggagaaag gcggacaggt atccggtaag cggcagggtc ggaacaggag
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     9241 gccacctctg acttgagcgt cgatttttgt gatgctcgtc agggggggcgg agcctatgga
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     9361 tgttctttcc tgcgttatcc cctgattctg tggataaccg tattaccgcc tttgagtgag
     9421 ctgataccgc tcgccgcagc cgaacgaccg agcgcagcga gtcagtgagc gaggaagcgg
     9481 aagagcgccc aatacgcatg c
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Figure S4. Multiple sequence alignment of amylase from closely related *B. licheniformis* strains. The AmyBL159 protein sequence utilized in this work is colored (orange). The signal peptide identified using SignalP 6.0 is indicated in bold type and gray shading

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WP_268400763.1      MKQQKRLYARLLPLLFALIFLLPHSAAAAANLKGTLMQYFEWYMPNDGQHWKRLQNDSAY
AMJ27400.1          ----------------------PHSAAAAANLNGTLMQYFEWYMPNDGQHWKRLQNDSAY
amyBL159            MKQQKRLYARLLTLLFALIFLLPHSAAAANLNGTLMQYFEWYMPNDGQHWKRLQNDSAY
ABW90124.1          --------------------------AAANLNGTLMQYFEWYMPNDGQHWKRLQNDSAY
ACN88151.1          MKQQKRLYARLLTLLFALIFLLPHSAAAAANLNGTLMQYFEWYMPNDGQHWKRLQNDSAY
1BLI_A              ----------------------------ANLNGTLMQYFEWYMPNDGQHWKRLQNDSAY
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1OB0_A              ----------------------------ANLNGTLMQYFEWYMPNDGQHWKRLQNDSAY
ABW94981.1          -----------------------------------MQYFEWYMPNDGQHWKRLQNDSAY
1VJS_A              ----------------------------ANLNGTLMQYFEWYMPNDGQHWKRLQNDSAY
6TOY_A              ----------------------------ASLNGTLMQYFEWYMPNDGQHWKRLQNDSAY
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WP_268400763.1      LAEHGITAVWIPPAYKGTSQADVGYGAYDLYDLGEFHQKGTVRTKYGTKGELQSAIKSLH
AMJ27400.1          LAEHGITAVWIPPAYKGTSQADVGYGAYDLYDLGEFHQKGTVRTKYGTKGELQSAIKSLH
amyBL159            LAEHGITAVWIPPAYKGTSQADVGYGAYDLYDLGEFHQKGTVRTKYGTKGELQSAIKSLH
ABW90124.1          LAEHGITAVWIPPAYKGTSQADVGYGAYDLYDLGEFHQKGTVRTKYSTKGELQSAIKSLH
ACN88151.1          LAEHGITAVWIPPAYKGTSQADVGYGAYDLYDLGEFHQKGTVRTKYSTKGELQSAIKSLH
1BLI_A              LAEHGITAVWIPPAYKGTSQADVGYGAYDLYDLGEFHQKGTVRTKYGTKGELQSAIKSLH
1OB0_A              LAEHGITAVWIPPAYKGTSQADVGYGAYDLYDLGEFHQKGTVRTKYGTKGELQSAIKSLH
ABW94981.1          LAEHGITAVWIPPAYKGTSQADVGYGAYDLYDLGEFHQKGTVRTKYGTKGELQSAIKSLH
1VJS_A              LAEHGITAVWIPPAYKGTSQADVGYGAYDLYDLGEFHQKGTVRTKYGTKGELQSAIKSLH
6TOY_A              LAEHGITAVWIPPAYKGTSQDDVGYGAYDLYDLGEFHQKGTVRTKYGTKGELQSAINSLH
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WP_268400763.1      SRDINVYGDVVINHKGGADATEDVTAVEVDPADRNRVISGEHRIKAWTHFHFPGRGSTYS
AMJ27400.1          SRDINVYGDVVINHKGGADATEDVTAVEVDPADRNRVISGEHRIKAWTHFHFPGRGSTYS
amyBL159            SRDINVYGDVVINHKGGADATEDVTAVEVDPADRNRVISGEHRIKAWTHFHFPGRGSTYS
ABW90124.1          SRDINVYGDVVINHKGGADATEDVTAVEVDPADRNRVISGEHRIKAWTHFHFPGRGSTYS
ACN88151.1          SRDINVYGDVVINHKGGADATEDVTAVEVDPADRNRVISGEHRIKAWTHFHFPGRGSTYS
1BLI_A              SRDINVYGDVVINHKGGADATEDVTAVEVDPADRNRVISGEHLIKAWTHFHFPGRGSTYS
1OB0_A              SRDINVYGDVVINHKGGADATEDVTAVEVDPADRNRVISGEVLIKAWTHFHFPGRGSTYS
ABW94981.1          SRDINVYGDVVITTKGGADATEDVTAVVVDPADRNRVISGEHLIKAWTHFHFPGRGSTYS
1VJS_A              SRDINVYGDVVINHKGGADATEDVTAVEVDPADRNRVISGEHLIKAWTHFHFPGRGSTYS
6TOY_A              SRDINVYGDVVINHKGGADATEYVTAVEVDPADRNRVTSGEQRIKAWTHFQFPGRGSTYS
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WP_268400763.1      DFKWHWYHFDGTDWDESRKLNRIYKFQGKAWDWEVSNENGNYDYLMYADIDYDHPDVAAE
AMJ27400.1          DFKWHWYHFDGTDWDESRKLNRIYKFQGKAWDWEVSNENGNYDYLMYADIDYDHPDVAAE
amyBL159            DFKWHWYHFDGTDWDESRKLNRIYKFQGKAWDWEVSNENGNYDYLMYADIDYDHPDVAAE
ABW90124.1          DFKWHWYHFDGTDWDESRKLNRIYKFQGKAWDWEVSNENGNYDYLMYADIDYDHPDVAAE
ACN88151.1          DFKWHWYHFDGTDWDESRKLNRIYKFQGKAWDWEVSNENGNYDYLMYADIDYDHPDVAAE
1BLI_A              DFKWHWYHFDGTDWDESRKLNRIYKFQGKAWDWEVSNEFGNYDYLMYADIDYDHPDVAAE
1OB0_A              DFKWHWYHFDGTDWDESRKLNRIYKFQGKAWDWEVSNEFGNYDYLMYADIDYDHPDVVAE
ABW94981.1          DFKWHWYHFDGTDWDESRKLNRIYKFQGKAWDWEVSNENGNYDYLMYADIDYDHPDVAAE
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1VJS_A              DFKWHWYHFDGTDWDESRKLNRIYKFQGKAWDWEVSNENGNYDYLMYADIDYDHPDVAAE
6TOY_A              DFKWYWYHFDGTDWDESRKLNRIYKFQGKAWDWEVSNENGNYDYLMYADIDYDHPDVTAE
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WP_268400763.1      IKRWGTWYANELQLDGFRLDAVKHIKFSFLRDWVNHVREKTGKEMFTVAEYWQNDLGALE
AMJ27400.1          IKRWGTWYANELQLDGFRLDAVKHIKFSFLRDWVNHVREKTGKEMFTVAEYWQNDLGALE
amyBL159            IKRWGTWYANELQLDGFRLDAVKHIKFSFLRDWVNHVREKTGKEMFTVAEYWQNDLGALE
ABW90124.1          IKRWGTWYANELQLDGFRLDAVKHIKFSFLRDWVNHVREKTGKEMFTVAEYWQNDLGALE
ACN88151.1          IKRWGTWYANELQLDGFRLDAVKHIKFSFLRDWVNHVREKTGKEMFTVAEYWQNDLGALE
1BLI_A              IKRWGTWYANELQLDGFRLDAVKHIKFSFLRDWVNHVREKTGKEMFTVAEYWSYDLGALE
1OB0_A              IKRWGTWYANELQLDGFRLDAVKHIKFSFLRDWVNHVREKTGKEMFTVAEYWSYDLGALE
ABW94981.1          IKRWGTWYANELLLDGFRLDAVKHIKFSFLRDWVNHVREKTGKEMFTVAEYWQNDLGALE
1VJS_A              IKRWGTWYANELQLDGFRLDAVKHIKFSFLRDWVNHVREKTGKEMFTVAEYWQNDLGALE
6TOY_A              IKRWGTWYANELQLDGFRLDAVKHIKFSFLRDWVNHVREKTGKEMFTVAEYWQNDLGALE
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WP_268400763.1      NYLNKTNFNHSVFDVPLHYQFHAASTQGGGYDMRKLLNGTVVSKHPLKAVIFVDNHDTQP
AMJ27400.1          NYLNKTNFNHSVFDVPLHYQFHAASTQGGGYDMRKLLNSTVVSKHPLKAVTFVDNHDTQP
amyBL159            NYLNKTNFNHSVFDVPLHYQFHAASTQGGGYDMRKLLNGTVVSKHPLKSVTFVDNHDTQP
ABW90124.1          NYLNKTNFNHSVFDVPLHYQFHAASTQGGGYDMRKLLNGTVVSKHPLKAVTFVDNHDTQP
ACN88151.1          NYLNKTNFNHSVFDVPLHYQFHAASTQGGGYDMRKLLNGTVVSKHPLKAVTFVDNHDTQP
1BLI_A              NYLNKTNFNHSVFDVPLHYQFHAASTQGGGYDMRKLLNGTVVSKHPLKSVTFVDNHDTQP
1OB0_A              NYLNKTNFNHSVFDVPLHYQFHAASTQGGGYDMRKLLNGTVVSKHPLKSVTFVDNHDTQP
ABW94981.1          NYLNKTNFNHSVFDVPLHYQFHAASTQEGGYDMRKLLIGTVVSKHPLKSVTFVDNHDTQP
1VJS_A              NYLNKTNFNHSVFDVPLHYQFHAASTQGGGYDMRKLLNSTVVSKHPLKAVTFVDNHDTQP
6TOY_A              NYLNKTNFNHSVFDVPLHYQFHAASTQGGGYDMRKLLNGTVVSKHPVKAVTFVDNHDTQP
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WP_268400763.1      GQSLESTVQTWFKPLAYAFILTRESGYPQVFYGDMYGTKGDSQREIPALKHKIEPILKAR
AMJ27400.1          GQSLESTVQTWFKPLAYAFILTRKSGYPHVFSGDMYGTKRNSPPEILALKHKIEPILKAR
amyBL159            GQSLESTVQTWFKPLAYAFILTRESGYPQVFYGDMYGTKGDSQREIPALKHKIEPILKAR
ABW90124.1          GQSLESTVQTWFKPLAYAFILTRESGYPQVFYGDMYGTKGDSQREIPALKHKIEPILKAR
ACN88151.1          GQSLESTVQTWFKPLAYAFILTRESGYPQVFYGDMYGTKGDSQREIPALKHKIEPILKAR
1BLI_A              GQSLESTVQTWFKPLAYAFILTRESGYPQVFYGDMYGTKGDSQREIPALKHKIEPILKAR
1OB0_A              GQSLESTVQTWFKPLAYAFILTRESGYPQVFYGDMYGTKGDSQREIPALKHKIEPILKAR
ABW94981.1          GQSLESTVQTWFKPLAYAFILTRESGYPQVFYGDMWGTKGDSQREIPALKHKIEPILKAR
1VJS_A              GQSLESTVQTWFKPLAYAFILTRESGYPQVFYGDMYGTKGDSQREIPALKHKIEPILKAR
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6TOY_A              GQSLESTVQTWFKPLAYAFILTREAGYPQIFYGDMYGTKGASQREIPALKHKIEPILKAR
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WP_268400763.1      KQYAYGAQHDYFDHHDIVGWTREGDSSVANSGLAALITDGPGGAKRMYVGRQNAGETWHD
AMJ27400.1          KQYAYGAQHDYFDHHDIVGWTREGDSSVANSGLAALITDGPGGAKRMYVGRQNAGETWHD
amyBL159            KPYAYGAQHDYFDHHDIVGWTREGDSSVANSGLAALITDGPGGAKRMYVGRQNAGETWHD
ABW90124.1          KQYAYGAQHDYFDHHDIVGWTREGDSSVANSGLAALITDGPGGAKRMYVGRQNAGETWHD
ACN88151.1          KQYAYGAQHDYFDHHDIVGWTREGDSSVANSGLAALITDGPGGAKRMYVGRQNAGETWHD
1BLI_A              KQYAYGAQHDYFDHHDIVGWTREGDSSVANSGLAALITDGPGGAKRMYVGRQNAGETWHD
1OB0_A              KQYAYGAQHDYFDHHDIVGWTREGDSSVANSGLAALITDGPGGAKRMYVGRQNAGETWHD
ABW94981.1          KQYAYGAQHDYFDHHDIVGWTREGDSSVANSGLAALITDGPGGAKRMYVGRQNAGETWHD
1VJS_A              KQYAYGAQHDYFDHHDIVGWTREGDSSVANSGLAALITDGPGGAKRMYVGRQNAGETWHD
6TOY_A              KQYAYGAQHDYFDHHNIVGWTREGDSSVANSGLAALITDGPGGTKRMYVGRQNAGETWHD
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WP_268400763.1      ITGNRSEPVVINSEGWGEFHVNGGSVSIYVQR
AMJ27400.1          ITGNRSEPVVI----------------------
amyBL159            ITGNRSEPVVINSEGWGEFHVNGGSVSIYVQR
ABW90124.1          ITGNRSEPVVINSEGWGEFHVNGGSVSIYVQR
ACN88151.1          ITGNRSEPVVINSEGWGEFHVNGGSVSIYVQR
1BLI_A              ITGNRSEPVVINSAGWGEFHVNGGSVSIYVQR
1OB0_A              ITGNRSEPVVINSEGWGEFHVNGGSVSIYVQR
ABW94981.1          ITGNRSEPVVIYSEGWGEFHVNGGSVSIYVQR
1VJS_A              ITGNRSEPVVINSEGWGEFHVNGGSVSIYVQR
6TOY_A              ITGNRSDSVVINAEGWGEFHVNGGSVSIYVQR
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