# Supporting Information:

**Supplementary List 1**: Nucleotide and amino acid sequences for the genes closA, closM, closPt, cellA, cellM, and cellPt in the supporting information:

**Nucleotide sequence closPt**

ATGAAGTTGTTTGGAATAGATATAACTGAAATATTTTCGCTATCTTTTAGGAAGGAAAAGTATGTTATGAAAAAGGTCGATATAGTAAAGCAAATATCTCAAACAGAATGTGGGGTATGTTGTTGTGTAATGATTCAAAATTATTATAATGTTAATACTTCATTAGGGCAGGTTAGAAAAGAATTAGATGTTGGCCGAGATGGAATGTCAATGATTCAGATTTATGAGTACTTAACAAGTAAAGGCTTTTCATGCAAACCCTTCAAGACAAATAATGTTCTTAAGCTATCTGAGATTACGTTGCCATGCATTGCTTTTTTTGGTGAAAATCATTTTGTTGTTGTTGAATCAATAAAAAATCAAAAGGTTATTGTCTGCAATCCAAGTATTGGAAGAAAAGTTATGTCAATTCAGGAGTTTGATAAAGATTTTAGTGGAATAATTCTACAAGTGTTACCTACAGATAAAGTTGAAAAAGTTTCAAAGAAAGAAAACCCATGGCATGTAGTTATTAAGTTGTTAAAAGAAAACAAGCGTTTACTCCTTGTAGCAGTATTATATATGATCCTAGCATATGCTATATACTTGGGTGTACCCATGTTTGAACAAAATTTGATAGATAAAGTAATAGTTTTATCTAACCTTGATACAGTCTATATTTTCTCATTAATTTTAGGTTGTTTACTTATTGGCTATGCAATTATTAGCCTTTTGAGAGGATTTAAGTTATTAACTTTAAATATTAATATAGCTAATAAGATGGAGATTGGAACGTATAATAAATTATTACGACTTCCATATAAGTATTTTGAAGTTAGAAATACTGGGGAATTATTGTATAGTTTAATCTGTGTTTCTTCTGTAAGAGAACTATTAGCTACATATATTGTTAATGGAGTAATAGATGTTGGTGCAGTGATAATAGTAAGTATATATATGTTTCAGAAGTCATGGTTATTAGGAATTTTTGCTTTAGTTTTATGGATACTAAACGTAGTTTTTTTATTTTTAATGCAGCCTAAGTTAAGTGGAGTTGTTGATGAAGAATTAGTGCAAAGAGCTACTGCACAATCGTTACAAACAGAAGCTTTAGGATCAATAATGTCTATAAAAATGATGGGGTTAGAAAAACAGGTATTAAATGATTGGAAAATAGTATATGAAAAAGTAATAAGAAAATTTTCAAGGAGAATTAATATTCAAAATATAATTGGTGCATTCAATAGTAGTATTAATTTGTTTGGACCAGCATTCATAGTATGCAGTAGCATGGTTTTATATTTTTATGGATTACTGTCTATTGGTGAAATAGTTGCTTTTCAAACAATATCATCAATTTTTTTTGGAATTGCAAATAATATATGTACTGCATATTCTCAGTTTATTCTTGCTTCTTCATATTTAGAAAGAGTAGATGAAATTTGGTCTACTGAAGAAGAAAATTATAATGAAAATGGTATAGCAAAAGATATTAAAGGAGATATTGAAGTCAATGATATAACTTTCAGATATTCTAAAACTTCTCCATATGTAATTGAGAAGATTAACTTAAAAATTAAAGCTGGTTCAAATGTAGCAGTTGTGGGACCTTCTGGTTCAGGAAAAAGCACACTAGGAAAAATTTTAAGTGGTCTATATGATATTGAAAGTGGAGATATTAATTATGATGGTATCAGCATCAGAGAATATAATAAAAATGAATTGTGTAAAATGATAGGCATTGTACCTCAGGAAGTAATGCTTTTTAATAAATCAATTTATCACAATATTGTAATGAATAATGGAAGTATACCGCTTAATGAAGTAAGAGAAATATGTAAATTGGTATGTATTGATGAAGAAATAATGAGTATGCCAATGCAATATAATACTATAATATCAGAAATGGGATTGAATTTATCTGGTGGACAAAGGCAAAGGATACTGTTGGCACGAATCCTCATCAGTAAACCTAAAATTCTAATTTTAGATGAAGCTACAAGCTCGATAGATACTATAAGTGAAGAAAAAATATCAAGGTATCTAGCTGATTTAGGATGCACTAGAATTACAATTGCACACCGCTTATCAACAATTATAAATGCAGATTGCATCTATGTAATGAATAAGGGAAGAATTATCGAGTCGGGAACGCATAATGAATTAATAGAGAATGGTAAGGTATATAATGAGTTGTACTATTCTGGAAACACAGATTAA

**Amino acid sequence ClosPt**

MKLFGIDITEIFSLSFRKEKYVMKKVDIVKQISQTECGVCCCVMIQNYYNVNTSLGQVRKELDVGRDGMSMIQIYEYLTSKGFSCKPFKTNNVLKLSEITLPCIAFFGENHFVVVESIKNQKVIVCNPSIGRKVMSIQEFDKDFSGIILQVLPTDKVEKVSKKENPWHVVIKLLKENKRLLLVAVLYMILAYAIYLGVPMFEQNLIDKVIVLSNLDTVYIFSLILGCLLIGYAIISLLRGFKLLTLNINIANKMEIGTYNKLLRLPYKYFEVRNTGELLYSLICVSSVRELLATYIVNGVIDVGAVIIVSIYMFQKSWLLGIFALVLWILNVVFLFLMQPKLSGVVDEELVQRATAQSLQTEALGSIMSIKMMGLEKQVLNDWKIVYEKVIRKFSRRINIQNIIGAFNSSINLFGPAFIVCSSMVLYFYGLLSIGEIVAFQTISSIFFGIANNICTAYSQFILASSYLERVDEIWSTEEENYNENGIAKDIKGDIEVNDITFRYSKTSPYVIEKINLKIKAGSNVAVVGPSGSGKSTLGKILSGLYDIESGDINYDGISIREYNKNELCKMIGIVPQEVMLFNKSIYHNIVMNNGSIPLNEVREICKLVCIDEEIMSMPMQYNTIISEMGLNLSGGQRQRILLARILISKPKILILDEATSSIDTISEEKISRYLADLGCTRITIAHRLSTIINADCIYVMNKGRIIESGTHNELIENGKVYNELYYSGNTD

**Nucleotide sequence closM**

ATGGAAAAGTTGTTTGGAAACTACATTAAAAAATCTTTTGAAATTAAGGAAATAAATAAAATTGTTCATAGGACTAAAGAATATTTTGGAGAGTTTTCTAGATATTATTTATATATTTTTTATTACGAATTTGACAATGCAATAATCAGAAAATATGGTGATTTATTTGATCAATTTAATAGCATAATTCAACAACAATTAGATATATTTTTCAAGGATATATTTTATATAAGCATAAGAGTGTTAATTGTTGAAATGAATATTATGAAAGATGAAAATAAGCTAGTTGGTGCAAATAGCCAAGAAAGATACTTGTATTATTCGGAACTTTTAACAAAAGAAGAATACATTGATTACCTAATAAGCAAGTATCCGGTTTTAAATAGAATTTTATTGGAAAAGTGTAAAAATCAAATTAGACTAATTAATGAATGTTTAAGTAATTATATACAAGATTTTGAACCGATGTGTGAAACTTTTGAAATTTCAGCTCAAAGTAAAATTAAGCAAATAATTGTTACATCGGGGGACTCACATAATGGAGGTAAGAAGGTTATCTTATTAGAACTTTCAGAAAACAAAATATTATATAAGCCTCATGATTTTTCATCAGAAAAAATATTTAATGAAATACTAGAATCCATAAATAAAGAACAGTGCATAAAGTATAAGTTAAAGACTATTAAGAATATTACTAGGGATAATTATGCATGGCAGGATTATATCAAAGCAATTGGATGTACGAAGATTCAAGAGGTGGAGGAATATTACTACAAGATTGGAGCATATTTGGCGGTATTGTATTCTTTGGGATGCGAGGATATTCACAAGGAAAATATTATAGCTTCTGGTAACAATCCATATCTAATTGATATGGAGACACTATCAAATTGTCAGGCACCTTTAATAAATGATAAAGCTACAATGCTAGAGCACTTTTTTTATGAGAATAGCCAATCAGTCTTCGGAACAATGCTTTTACCTACTAATTCAGCAGTGTCTATATTTGATTATGACATTGGAGGAATCTCTGGAGATGATAACATTGAAACATCAAAATGGGAAGCTTTTGATATAAAAAATCAAGGAACTGATAATTTACAATTTGTTAAGGAATCTAAGTTTATAACTGGTGGATGTGATAACATAGTAAAACTTAATGGTGAGGCTACTCGTGCTAGAGATTATTACAAGAATATTATAGAAGGATTTTCTGATTGTTATAAAATATTTATAAAAACTCCAAATAAAGTTGTAGATATATTAAAAGAGAGTGAAGTTATAATACGACAGGTTTTAAGACCAACAGCAGTTTATAGTAAATTTTTAGAAGCTTCTACTTATCCAACTTATCTAACAAATGAAGAATCTTTTAGAGGTCTCTTTGCAAAGTTAGATAATTTGGAAGAGGTAAAAGAAAAGAAAAAAGCACAAATTGAAATAGATAGTTTATATGAGTTTGATATACCATATTTTTATTCCGATTTAAATACAACTAACATTTATTCAGTCAAAGGAAAAGTTGATAATTACATAAATTATTCTGTTATGGATGCTATAAGCGGAAAGGCTAGGAAGTTTTCGGAAAAGGATTTAAAGGTGCAAATATATTATATTAACCTTGCACTATCAACCCAACCTAACACATCTGAGATGATTTATAAATATAATTTATTCAGTAAATCACAAAATTTAAAGAATATTACAATTAATCATATTGCTAAACAGATAGGAGATGTAATTGAAGAAAAACTAATTTGGGATTATAGAAAACAAAGTTGCTTTTTTATGATTGATACGGTAGTAAAAGAAAAGAGAAAATACTGTAGCATGGATTCTAGTTTGTATGGTTCGGGTGGAGTAATTCTGTACTATCTATCGCTATACAAAGCTACTTGTGATTTGAAGTATAAACATATAGTCGAAGGATTAATTAATGGACATATAGGGTTACATTCAAAAAAATCCTTAGAGGAGGGGATAGGATTATTTTCAGGGTTAACTTCATTAGCATATATATACTATCAATGTTATAGGGTTTTAGGAAAGAAACAGTATTTAGAAGATGTCTTAGAAGTTCTAAAGGAAATAGAAGAAAATTTACATATGTGGGATGAGCTAGATTTATCAACAGGGTTATCAGGTGTTATCATATTTCTATCAGAACTTTATAAAACAGAAAATAATGAACAGTATCTATTAATTGCAAATGGCTTAGCTGATAAATTATATAAATTAGTGTTGAAAGCTAATTTTAATATGTTAACAGGATTAGCACATGGATATGCAGGAGTTGCTTGGGCTTTATATAGTATAGGGCATATAGTTAATAATGAGGATTATATTAATTGCGCTATGAAATGCATTGAAGAGGAAAATATGTATTATGATTCAGAAAAAAACAACTGGAAAGATAAAAGAAATGGTAGTTCAGAAAGCTTCTATTGGTGTTATGGTGCTTTTGGGATAGGTATCGCAAGATTAAAGATGTATGAAATAGCTCATAATGATATTTTATTAAAGGATATTGAAAAATGCAGATATATATATATTAATTATAATTTAATTAATAGTAAGTATAATCATTCTTTATGCCATGGGCTTACAGGAAACTTATCAGCAATAAAGATGTTTAGTGATTTTTATAAGAATGACAATAAGTTAAAAAAGAAATATAAGGAAATGTTGGATATATTATTAAATGATGTTGTAAATGGCAAAGTTATATGGGGTGATAAGGAGCTCATAGAAGATTATTCATTTATGATTGGTTTATCGGGTATTGGGTATGAGTTATTAAGGCACGAAGCTACAAACTCTGTAAATATTTTAGCATTAGAAGTGTAA

**Amino acid sequence ClosM**

MEKLFGNYIKKSFEIKEINKIVHRTKEYFGEFSRYYLYIFYYEFDNAIIRKYGDLFDQFNSIIQQQLDIFFKDIFYISIRVLIVEMNIMKDENKLVGANSQERYLYYSELLTKEEYIDYLISKYPVLNRILLEKCKNQIRLINECLSNYIQDFEPMCETFEISAQSKIKQIIVTSGDSHNGGKKVILLELSENKILYKPHDFSSEKIFNEILESINKEQCIKYKLKTIKNITRDNYAWQDYIKAIGCTKIQEVEEYYYKIGAYLAVLYSLGCEDIHKENIIASGNNPYLIDMETLSNCQAPLINDKATMLEHFFYENSQSVFGTMLLPTNSAVSIFDYDIGGISGDDNIETSKWEAFDIKNQGTDNLQFVKESKFITGGCDNIVKLNGEATRARDYYKNIIEGFSDCYKIFIKTPNKVVDILKESEVIIRQVLRPTAVYSKFLEASTYPTYLTNEESFRGLFAKLDNLEEVKEKKKAQIEIDSLYEFDIPYFYSDLNTTNIYSVKGKVDNYINYSVMDAISGKARKFSEKDLKVQIYYINLALSTQPNTSEMIYKYNLFSKSQNLKNITINHIAKQIGDVIEEKLIWDYRKQSCFFMIDTVVKEKRKYCSMDSSLYGSGGVILYYLSLYKATCDLKYKHIVEGLINGHIGLHSKKSLEEGIGLFSGLTSLAYIYYQCYRVLGKKQYLEDVLEVLKEIEENLHMWDELDLSTGLSGVIIFLSELYKTENNEQYLLIANGLADKLYKLVLKANFNMLTGLAHGYAGVAWALYSIGHIVNNEDYINCAMKCIEEENMYYDSEKNNWKDKRNGSSESFYWCYGAFGIGIARLKMYEIAHNDILLKDIEKCRYIYINYNLINSKYNHSLCHGLTGNLSAIKMFSDFYKNDNKLKKKYKEMLDILLNDVVNGKVIWGDKELIEDYSFMIGLSGIGYELLRHEATNSVNILALEV

**Nucleotide sequence closA**

ATGCAAAATTATGAAAGCAAAGCAGGATTTATTTCTGAAATGGAACTAGATGAATTAGTTTCAAACAAAACTGTTGGTGGTGCTACTACTGTACCTTGTGCAATTGCTATTATTGGAATTACACTTTCAGCTGGTATCTGCCCAACTTCAGCATGCTCAAAAGATTGTCCATGGAATAACTAA

**Amino acid sequence pre-Clostrisin**

MQNYESKAGFISEMELDELVSNKTVGGATTVPCAIAIIGITLSAGICPTSACSKDCPWNN

**Nucleotide sequence cellPt**

ATGATCAAGAGAAGCGGTATACGAATAATTAAACAATTAACAGAAACAGAATGTGGCTTATGTTGTTGTGCCATGATATTGAGATATTACGGAAGTAAGGAATCAATAAGAGAGTTACAAGATTATATGGATGTCGGCAGAGATGGGATATCTATGTTTCAGATTAAGCATTTCTTAAATGAAAAAGGTGTTTCTGCCAAAGTATATGAAGTCAATGAGATTGATAAGTTAGTTCATATAGATAAACCATTTATATGTTATTGGAATCAAAAGCATTTCGTTATTGTAGAAAAAATAAAAAATAATATGTTTTATATAGCAGATCCAGCAGATGGGAAAGTAGTTCTTAATAGAGAAGAATTTTCTAAAAAATTTTCAAAAACCATTTTAGTAAGTGATGTTACGGAAGCATTTAAACCTACGAAAAATAGAAATTACAATCCGTGGATAACTATTTTACAGTATCTTAAAGAAAATAAAATATTAATTCTTGAGATTTTGATATTGCTTGGAATAACTTATGGAATAACGTTGGAAATTCCTAATATTGTACAAAAAATAATTGATAGGACAGGGACGGAAACTAATTCATCATTCTTGAATATTTTTCTTTTGATGCTAGGAGCATGTATAATTGCATTTTTCGTGAGTTACTTATTTAAAGGAATAAAAATAATAGCCTTAAATGTGTTTTTAGGAAGAAAACTTGAAGCAAATACGTATAGACATCTCTTACAACTTCCATATAAGTTTTTTGAAACTAGATCAACTGGTGACTTGTTATATCGTATTCAAGGTACCACCAGTATTAAACAGATGTTGTCTACTCAGATTGTTGGAGGCGTAATTGATATTGGATCTGTTATTGCAATAATTTTTTATATGCAACAGAAGTCAGTGTTGCTTACAATTTGTGCTTTTGCCTTGTTCATGATAAATATTATAGTGATTTTAGTTATTCAACCTAAACTTACACAAGCTATTAATGGAGAGATTGTTGAACAGTCCAAATCTCAAACAGCTCAAATAGAATCATTATATTCAATTATTTCAATAAAGATTTCAGCTATGGAAGATTTGATCTATAAGAATTGGAGCAACATTTATGAGAGTGTTGTTGAAATGTTTCAAAAGAGGATGCTAATTTCAAATGCATATAGTGCTATTATGGCTGTACTTCAAAACTTTTCACCGATTTTAATATTGTGTTTAGGAATTAATGAGTATTATAAGGGAAACATTACCATAGGCGAAGTAATTGCGTTTCAAGCTATTTCTTCAACATTTTTTAATTTGGGAATGTCAATAGTAAATGTATACCCTCAATTTATTTCTGCATCACAATATTTAGATAGGATAGCAGATATTTGGAACAGGGAAGCTGAATTAGAGGATGAAAATGCAATTGTTAGAGAAATAAATGGTGATATAGAGTTAGAGGATGTATGTTTTTCATATTCAAAAAACTCAAAAAATGTACTTGAAAATATTTCAATGAATATTAAAAGAGGAACTAAAGTTGCAATTGTGGGGGCTTCTGGATCAGGAAAAAGTTCACTAAGTAAAATTTTAGTTGGGTTGTACAAGCCTACAAAAGGGACAATAAGATTTGATGGAATTCCTATTGAAAAATATGATAGGAAAGCTATCTGTAGGCAAATGGGAATCGTACCTCAGGATGCTATGTTATTTAATAAAAGTATATATGAAAATATAGTAATGGGAAATTTCAATATAACATTAGAACAGGTAGAAGAAATTACAAAGATTGCATGCATACATGATGAAATCAAAGCAATGCCCATGGGATACCATACAATAATATCTGAAATGGGTATGAATTTATCAGGAGGACAGAGACAGAGAATTTTATTAGCAAGATCAATGCTCTCGAATCCAAAGATTTTGGTGTTAGATGAAGCAACTAGTAGCTTAGATAATATTAATGAGAGAAAAATATCAAATTATTTATCTGGTATTGGATGCACAAGAATTATTATTGCGCATAGGTTGTCTACTATAGTTGATGCAGATGTTATATTCATAATGAAAAATGGACAAATTGCAGAATATGGTAAGCATGAAGAGTTGATAAGTAAGAATGGTGAATATAAAAAATTATATTATATCGGTAGAGATATAGATAATTTGAATGTTGTATAA

**Amino acid sequence CellPt**

MIKRSGIRIIKQLTETECGLCCCAMILRYYGSKESIRELQDYMDVGRDGISMFQIKHFLNEKGVSAKVYEVNEIDKLVHIDKPFICYWNQKHFVIVEKIKNNMFYIADPADGKVVLNREEFSKKFSKTILVSDVTEAFKPTKNRNYNPWITILQYLKENKILILEILILLGITYGITLEIPNIVQKIIDRTGTETNSSFLNIFLLMLGACIIAFFVSYLFKGIKIIALNVFLGRKLEANTYRHLLQLPYKFFETRSTGDLLYRIQGTTSIKQMLSTQIVGGVIDIGSVIAIIFYMQQKSVLLTICAFALFMINIIVILVIQPKLTQAINGEIVEQSKSQTAQIESLYSIISIKISAMEDLIYKNWSNIYESVVEMFQKRMLISNAYSAIMAVLQNFSPILILCLGINEYYKGNITIGEVIAFQAISSTFFNLGMSIVNVYPQFISASQYLDRIADIWNREAELEDENAIVREINGDIELEDVCFSYSKNSKNVLENISMNIKRGTKVAIVGASGSGKSSLSKILVGLYKPTKGTIRFDGIPIEKYDRKAICRQMGIVPQDAMLFNKSIYENIVMGNFNITLEQVEEITKIACIHDEIKAMPMGYHTIISEMGMNLSGGQRQRILLARSMLSNPKILVLDEATSSLDNINERKISNYLSGIGCTRIIIAHRLSTIVDADVIFIMKNGQIAEYGKHEELISKNGEYKKLYYIGRDIDNLNVV

**Nucleotide sequence cellM**

ATGGAAGATATGATAAGTTATTACGAAAAATGCTGGATGAAATTATATCCAGAAATGAAGAGTATAGAAGAGTTAAATACATATCTGAAAAAAGTATTTGGAAAGAGTCTTAAAGAAAAGTTGCAAAATGAAAGAGTAGAAAAAGTATCCGTAAAAGAGTACAACAGAAATTTAAAAATGTTTTTAGATGACAACATGCTAGAGAACATGAGATTTAGTAGGTTTTATGGACCAATTATGGTCGAATATATAGAGAATTTACCTAAATATATTGAAAAAACGATGATAGTGAAAAATATTAAACTGTTTATGGAAAGTATGATTCTTCAGCTATCTGACTTAATGTGTAGTATAGCTTTTCGTACAATGGTTTTTGAAATAAATAATGCGAAAAATAAAAATCTACTTAAAGGAGAGAGTCCTGAAGAGAGATATAAATATTTTAATAATGAATTGTTGGATGACTATCAATACCGAAAAAGTTTATATAGTGAGTATTGTTTTCTAGTTGAAACTTTAGATGAGTGTGCCAAAAATTTTGTGAAATACATTGAAGAAATACTTGTAAACACAAGTAAAAATATGTGTAGAATTCAAAGTGACGTTAATTCAAATATTGAATTAGGTAAACTCATAAATATTGAATTTGCTTTGGGAGATACTCATTGTAGAGGAAAAAGTGTAGCAAAACTGATTTTTGAAAATACAATAATTTATTATAAGCCTAGAAATAGTATAATTGATAACAAATTCCAATCAGTGCTTAATTTAATAAACGAAAAAGGTATACTTTCTGGTAGGAAATACAGAGTTATGAATATTCATGGAACAAGTGAATGTGGTTGGTTTGAAAATATTAAGTATGAAGAATGTAGAAGTATAGATAATGTTCATGATTATTATTTAAAGATAGGCGGCTTAATTGGCATTTTGTATTTCTTTAATGCAACAGATTTTCATCATGAAAATATTATAGCTTGTGCTGAAAATCCTATGTTAATAGATTTAGAATCAATATTTAGTGTAGAGATGAAAAGTAAAGTTTTTGATGAAAATAGTGCTTATAATAATGCAATTGAATATTTAAAATCAAGTGTACAATCGATTGGAATATTACCTAATAAGTTACATATTGGTGATTTAGATGACAAGTATGAAACAGGAGGTATTGTTTATAAAGAAAAACAAGTTGCACCAATAAAATCTTTAAAAGTTGTTAATGATGCATCTGATGGTATCCGTACGGAACTAGTAAATTCTATTATTGAAGGAAATCTTAATGCACCTAAATATAATGGCAATATTATAAACCCTAAAGAGTATGTTGAAGATATTAAGGAGGGATTTAGGTTAGTTTATAAATGGATTCTAGGCAACAAGAAAGAATTTATTGAATTTGTTGAAACGTCATTTAGTGAAACAAAAATAAGGATTATATTGAAGCCCACATTTATGTATGCACAAATAAATTCAATAGCAAAACATCCTAATTTTATGAGTAGCGAAGATGAGAATGAACTTATAAATGCAAGAATAGGTATATACGCAGATAATATCGATATTATTAAATCAGAAATAAGATCTTTAAAAAGATATGAGATACCTTATTTTTCAGCGTTATTTAACGAAGAAAAATTATTTGATGAAGATGAAAATGTATTAGAATCAAGATTAATTATTAGTCCCCAACTTTTATTTAGAAACAAAGTATGTAAAGCTACTGAAATAGATTTGAATAATCAAATAGATTTTATAAGTATTTCATTTTTAAGTAAAAATCCAGAAGAGCTTAGAACTGGAATTCATTATGTTGAAGATGCAGTTGAAATCATCAATACTGACAGTTATCTAAATGTTGCAAAAGAAATTGGTGATTATTTATATAGCATAGCAATTATCGGTGAAAATCAGCATGGCAAAAGTGATGCAACATGGATTGGAAGTGCTGTTTCAAAAATAGATGTTAATGATTGGACTTATAGTGTTTCAGATTTAGATTTATATAATGGAAATAGTGGTATAGCATTATTTCTATTAAATTTATGGAAAGTTACAAAGGATAAAAAATATCTTGATTTAGCAATACAGGCAGCAGAACTTATTATAAGCATAATTAAAAATAAGACATTTAATCATTCTACTCTTATAGGAGGGTTTAATGGTATCGGCTCTTATATTTACATAATTAGTAAATTAGTGGTGAATACCAATGATGAATATTTTTATAGTACGTTAATAGAATCTATTGACTTATTAGAAGAAAGAATTGAAGCCGCTTCAGAAATGGATTTAGTGGCTGGAGCAAGTGGAATGCTTGCAGTTTTATTGAATGTATATAGTGAAATTGATGATAAATTAATTAAAGAAAAAGTAAAACCACTTCTATATATGTTATTTTACAAGATCCAAGAGAATGTCAAAAGCGGTGGGAAACTAATTAGATATTCTGGTTTTGGACATGGAATTGCAGGGTGTATTCCATACTTGTACAAGTTGTATTTAATAGATGAAAATAGAGAAGTCTATCAGTTATTTAGTGAGTTATTGTCATATGAACGCGATCATTTCTATAGTAAGGAAGAAAAGGATTGGGTTATGTCTGATGATGAGGTCAATTATTCAAAAGCATGGTGTCATGGTGCACCAGGAATATTACTCGAAAAGATTATTCTAAAGGAATTAGGTTACGAGGATGAGTATTTGGATCAAGAGATCAAAGTGGCTTTAAATAATATTAAGAAAAAATGTATTGGTAATAATATAGTGTATTGTCATGGAGATATAGGAAACTTAGATATTATACAATATGCAGCAAAGATCAGCAAAGATGAAAAAATGATTAAGGAATGTAGTAACACATATGATAAGTTATTTCAACTACATATAAAAAATAACTGGAATAGTGAAGCGTCTGCATATAGTAAGTGTAAAGGGATAATGGTTGGAGTATCTGGTATTGGGCTATCATTACTGAGGATGATAAATAAGTATGATATAGATGATTTTCTTTGGCTAAGTTAA

**Amino Acid sequence CellM**

MEDMISYYEKCWMKLYPEMKSIEELNTYLKKVFGKSLKEKLQNERVEKVSVKEYNRNLKMFLDDNMLENMRFSRFYGPIMVEYIENLPKYIEKTMIVKNIKLFMESMILQLSDLMCSIAFRTMVFEINNAKNKNLLKGESPEERYKYFNNELLDDYQYRKSLYSEYCFLVETLDECAKNFVKYIEEILVNTSKNMCRIQSDVNSNIELGKLINIEFALGDTHCRGKSVAKLIFENTIIYYKPRNSIIDNKFQSVLNLINEKGILSGRKYRVMNIHGTSECGWFENIKYEECRSIDNVHDYYLKIGGLIGILYFFNATDFHHENIIACAENPMLIDLESIFSVEMKSKVFDENSAYNNAIEYLKSSVQSIGILPNKLHIGDLDDKYETGGIVYKEKQVAPIKSLKVVNDASDGIRTELVNSIIEGNLNAPKYNGNIINPKEYVEDIKEGFRLVYKWILGNKKEFIEFVETSFSETKIRIILKPTFMYAQINSIAKHPNFMSSEDENELINARIGIYADNIDIIKSEIRSLKRYEIPYFSALFNEEKLFDEDENVLESRLIISPQLLFRNKVCKATEIDLNNQIDFISISFLSKNPEELRTGIHYVEDAVEIINTDSYLNVAKEIGDYLYSIAIIGENQHGKSDATWIGSAVSKIDVNDWTYSVSDLDLYNGNSGIALFLLNLWKVTKDKKYLDLAIQAAELIISIIKNKTFNHSTLIGGFNGIGSYIYIISKLVVNTNDEYFYSTLIESIDLLEERIEAASEMDLVAGASGMLAVLLNVYSEIDDKLIKEKVKPLLYMLFYKIQENVKSGGKLIRYSGFGHGIAGCIPYLYKLYLIDENREVYQLFSELLSYERDHFYSKEEKDWVMSDDEVNYSKAWCHGAPGILLEKIILKELGYEDEYLDQEIKVALNNIKKKCIGNNIVYCHGDIGNLDIIQYAAKISKDEKMIKECSNTYDKLFQLHIKNNWNSEASAYSKCKGIMVGVSGIGLSLLRMINKYDIDDFLWLS

**Nucleotide sequence cellA**

ATGAAGAATTATGAAGAATTATTTAATGAAGTTAATGAAAATGCTTCATTACAAGCAGAATTAAACGGTGGTAGTATTGCAACTACTATAGTTTGCACAATTGCACAATCTCTTTTAGGTTGTGTTGGTAGCTATGTTCTTGGAAACAAGGGATATGGTTGTACAGTTACAAATGAATGTATGAGTAACTGTAGATAA

**Amino acid sequence pre-Cellulosin**

MKNYEELFNEVNENASLQAELNGGSIATTIVCTIAQSLLGCVGSYVLGNKGYGCTVTNECMSNCR

**Supplementary Table 1.** Precursor peptides identified and considered competent within the Clostridia clade. The table includes molecular weight (Mw), isoelectric point (IP), and grand average of hydropathicity (Gravy) values. These values were computed using the ProtParam tool for the core peptide, excluding any post-translational modifications. Additionally, it specifies the presence of Serine (S), Threonine (T), and Cysteine (C), and the predicted cycles by the RiPPMiner tool.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Bacteria** | **BGC Internal Code** | **Lanthipeptides** | **MW (Da)** | | **IP** | **GRAVY** | | **S+T** | | **C** | | **Cycles** | | |
| *Blautia wexlerae* DSM 19850 | AXVN01000112 | MKKNYRNPMTRPENFMNPAGNVMKEIKEADLNNFSAGAGEPRVSDGSQFCTSTKECNWGTIMFVCC | 3086.49 | 4.68 | | | -0.132 | | 6 | | 4 | | 3 |
| *Caldicellulosiruptor bescii* DSM 6725 | NC\_012034 | MKESTIIKNPVLRNKVNAKIYNPAGDIVKEIQEQNLPEQAGGGTPTVVVGVISAVTAVTNLAFSIDQAITKYYACSLVYTYSAECRSDGRSCRMR | 5696.53 | 8.61 | | | 0.323 | | 12 | | 3 | | 2 |
| *Caldicellulosiruptor kristjanssonii* 177R1B | NC\_014721 | MVETYKKNLYGITFEELEEGEMQELVGGGPEITTVIESIKAATAFSTLTCVGSAAASLIIATVITYIVTK | 4226.98 | 6.13 | | | 1.107 | | 12 | | 1 | | 1 |
| MNSTIESRIGICFEQLNEEEMLEAMGGNPWLGTPTTAALSTTVACGVVTGLVSAAVSVTVVITKKL | 3884.59 | 9.31 | | | 0.995 | | 11 | | 1 | | 1 |
| *Caldicellulosiruptor lactoaceticus* 6A | NZ\_AEKD0100002 | MNSTIESRIGICFEQLNEEEMLEAMGGNPWLGTPTTAALSTTFVCGVVSGLVSAAVSVTVVITKKL | 3946.66 | 9.31 | | | 1.018 | | 11 | | 1 | | 1 |
| *Caldicellulosiruptor sp.* Rt8.B8 | LACO01000001-R3 | MVETYKKNLYGITFEELEEGEMQELVGGGPEITTVIESIKAATAFSTLTCVGSAAASLIIATVITYIVTK | 4226.98 | 6.13 | | | 1.107 | | 12 | | 1 | | 1 |
| MNSTIESRIGICFEQLNEEEMLEAMGGNPWLGTPTTAALSTTVACGVVTGLVSAAVSVTVVITKKL | 3884.59 | 9.31 | | | 0.995 | | 11 | | 1 | | 1 |
| LACO01000001-R5 | MKESTIIKNPVLRNKVNAKIYNPAGDIVKEIQEQNLPEQAGGGTPTVVVGVISAVTAVTNLAFSIDQAITKYYACSLVYTYSAECRSDGRSCRMR | 5696.53 | 8.61 | | | 0.323 | | 12 | | 3 | | 2 |
| *Clostridium cellulovorans* 743B | NC\_014393 -R6 | MANYKIGAIFEQKNYEEMASSQMTGGDGFVTVTSPQYTLSCCITWTIPSIKLTV | 3131.65 | 5.82 | | | 0.614 | | 9 | | 2 | | 2 |
| *Clostridium cellulovorans* 743B | NC\_014393 -R18 | MQNYESKAGFISEMELDELVSNKTVGGATTVPCAIAIIGITLSAGICPTSACSKDCPWNN | 3349.90 | 5.81 | | | 0.676 | | 7 | | 4 | | 4 |
| MKNYEELFNEVNENASLQAELNGGSIATTIVCTIAQSLLGCVGSYVLGNKGYGCTVTNECMSNCR | 4288.97 | 7.82 | | | 0.526 | | 9 | | 5 | | 5 |
| *Clostridium scindens* ATCC 35704 | NZ\_DS499711 - R1 | LDIPAMDLFMGMLILGGCHSSATPFLSASSECLATFSNLEMQHSPIPVCNFR | 3870.36 | 6.00 | | | 0.075 | | 9 | | 3 | | 3 |
| *Clostridium* sp. BL8 | AUPA01000006 - R1 | MADYQKVTGFVSVQELEEVTEVDNGAIAWVSVLATAAFTVKLASAVVCETGACTGYCN | 3291.84 | 6.02 | | | 1.197 | | 6 | | 3 | | 3 |
| MKKYNDITGFVSVEELEEVSNEAQGGIALSAITFVTGTVIWIATRAVCETGACTSYCK | 3408.01 | 7.95 | | | 0.988 | | 8 | | 3 | | 3 |
| MQNNYNLSTGFVSIEELEEASNDIGVAGAFTTIACAAIGLSIAILTVAACPTESGACTGYCR | 3320.90 | 6.01 | | | 1.171 | | 7 | | 4 | | 4 |
| MKNIEMLKNPVLRTKYSVNEINPAGDLLTEVTEQDFTISVSGGYDSAKLGNQGSDCSWSRECQRICNWISYGSGGWFGC | 4079.44 | 6.09 | | | -0.619 | | 6 | | 4 | | 3 |
| *Clostridium* sp. KNHs209 | JPNB01000003 - R2 | MRNDILNLTNPMEEKELEQILGGGNGVIKTISHECAMNTWQFLFTCCS | 2791.22 | 6.72 | | | 0.292 | | 5 | | 3 | | 3 |
| *Dorea* sp. 5-2 | ASTD01000045 - R1 | MQQNSNLDYAGDLSVELGEIEKLIPKEEQVEGASTSTLMCGTYFTLICC | 1815.16 | 5.54 | | | 1.176 | | 6 | | 3 | | 3 |
| *Eubacterium plexicaudatum* ASF492 | AQFT01000101 - R1 | MRDENKKTNEVSGEAFEDLTISEMAEVQGAGDMEGELTTPVCVVIATASASVGLAKTFKGKC | 3255.81 | 6.21 | | | 0.539 | | 6 | | 2 | | 2 |
| *Lachnospiraceae bacterium* 2\_1\_58FAA | ACTO01000067 - R1 | MIDASILLYPIYGGVLMRSKRIPAEEQYRLIMECRQSGLTDHQWCVEHDIKPGTFYNWVKRLRQKGCVDLPASTG | 7233.35 | 8.99 | | | -0.640 | | 6 | | 3 | | 2 |
| *Lachnospiraceae bacterium* 3\_1\_57FAA\_CT1 | ACTP01000039 - R1 | LSGTKNRAGASKRRLTLCIRILYEMNGEKISGCSS | 2929.46 | 9.39 | | | -0.162 | | 5 | | 2 | | 2 |
| *Roseburia faecis* | CYXV01000003 - R1 | MEIKSILIKDTTREERIRIVQEGLNQCGGACDFCNGCDNLGGGSVDAFYEPYINGEKELREINEEYRSNSGLVK | 5034.45 | 4.25 | | | -0.674 | | 3 | | 3 | | 1 |
| MKDLRNPLTRTENFEHPSGNIMKELTEAELNSVAAGAGVARNSGGIACTLTGECNIGTHIKFCCYD | 3075.50 | 6.75 | | | 0.263 | | 4 | | 4 | | 3 |

**Supplementary Table 2**. RMSD values resulting from the structural alignments between PCAT1 and the Clostrisin and Cellulosin proteins models predicted by AlphaFold.

|  |  |  |
| --- | --- | --- |
| **PCAT1** | **Clostrisin** | **Cellulosin** |
| Protein domains | RMSD (Å) | RMSD (Å) |
| Complete protein | 3.211 | 2.924 |
| C39 peptidase | 0.982 | 0.86 |
| ABC membrane | 3.25 | 2.962 |
| ABC transport | 1.159 | 1.204 |

**Supplementary Table 3.** RMSD values resulting from the structural alignments between CylM and ClosM and CellM protein models.

|  |  |  |
| --- | --- | --- |
| **CylM** | **ClosM** | **CellM** |
| Domain | RMSD (Å) | RMSD (Å) |
| Complete protein | 4.652 | 6.261 |
| Dehydratase | 1.607 | 1.507 |
| N-Lobe | 1.186 | 1.244 |
| C-Lobe | 1.733 | 2.145 |
| KA | 0.568 | 0.901 |
| Ka11 | 0.96 | 0.602 |
| Cyclase | 4.888 | 3.532\* |

**Supplementary Table 4.** Expected masses to pre-Clostrisin Clostrisin, pre-Cellulosin and Cellulosin.

|  |  |  |  |
| --- | --- | --- | --- |
| **pre-Clostrisin (6XHis Tag)** | **MW** | **Clostrisin** | **MW** |
| MGSSHHHHHHSQDPNSSSARLQQNYESKAGFISEMELDELVSNKTVGGATTVPCAIAIIGITLSAGICPTSACSKDCPWNNC | **8680.64** | TTVPCAI AIIGITLSAG ICPTSACSKD CPWNNC | 3324.91 |
| Amino acid residues prone to dehydration, Numbering based on clostrisin: Ser15 (-OH), Ser23 (-OH), Ser26 (-OH), Thr1 (-OH-), Thr2 (-OH-),Thr14(-OH-).Thr22 (-OH-) | | | |
|
| 1(-OH) | 8662.64 | 1(-OH) | 3306.91 |
| 2(-OH) | 8644.64 | 2(-OH) | 3288.91 |
| 3(-OH) | 8626.64 | 3(-OH) | 3270.91 |
| 4(-OH) | 8608.64 | 4(-OH) | 3252.91 |
| 5(-OH) | 8590.64 | 5(-OH) | 3234.91 |
| 6(-OH) | 8572.64 | 6(-OH) | 3216.91 |
| 7(-OH) | **8554.64** | 7(-OH) | 3198.91 |
| **pre-Cellulosine (6XHis Tag)** | **MW** | **Cellulosina** | **MW** |
| MGSSHHHHHHSQDPNSSSARLQKNYEELFNEVNENASLQAELNGGSIATTIVCTIAQSLLGCVGSYVLGNKGYGCTVTNECMSNCRC | **9356.31** | SIATTIVCTI AQSLLGCVGS YVLGNKGYGC TVTNECMSNC RC | **4335.05** |
| Amino acid residues prone to dehydration, Numbering based on clostrisin: Ser1 (-OH), Ser13 (-OH),Ser20 (-OH),Ser38 (-OH),Thr4 (-OH-),Thr5 (-OH-),Thr9 (-OH-),Thr31 (-OH-),Thr33 (-OH-) | | | |
| 1(-OH) | 9339.31 | 1(-OH) | 4317.05 |
| 2(-OH) | 9322.31 | 2(-OH) | 4299.05 |
| 3(-OH) | 9305.31 | 3(-OH) | 4281.05 |
| 4(-OH) | 9288.31 | 4(-OH) | 4263.05 |
| 5(-OH) | 9271.31 | 5(-OH) | 4245.05 |
| 6(-OH) | 9254.31 | 6(-OH) | 4227.05 |
| 7(-OH) | 9237.31 | 7(-OH) | 4209.05 |
| 8(-OH) | 9220.31 | 8(-OH) | 4191.05 |
| 9(-OH) | **9203.31** | 9(-OH) | **4173.05** |

**Supplementary Table 5.** Resistance profile of all strains used in antimicrobial tests.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Antibiotic/  Bacteria | *S. aureus* ATCC 43300 | *S. epidermidis*MIQ43 | *P. aeruginosa* ATCC PA14 | *P. aeruginosa* MIQPA25 | *E. coli* K12 IM08B | *A. baumannii* 747 |
| Cephalothin | R | - | R | - | - | - |
| Cefazolin | R | - | R | - | - | - |
| Cefotaxime | R | - | S | R | - | S |
| Aztreonam | R | - | S | R | - | - |
| Penicillin G | R | R | R | - | - | I |
| Oxacillin | R | R | R | - | - | - |
| Ampicillin | M | R | R | - | - | R |
| Ticarcillin | M | - | S | - | - | - |
| Mezlocillin | M | - | S | - | - | - |
| Imipenem | S | - | - | S | - | S |
| Clindamycin | - | R | - | - | - | - |
| Erythromycin | R | R | - | - | - | - |
| TMT-SFM | R | R | - | - | - | - |
| Rifampicin | - | S | - | - | - | - |
| Vancomycin | S | S | - | - | - | S |
| Linezolid | - | S | - | - | - | - |
| Minocycline | - | S | - | - | - | - |
| Carbenicillin | - | - | - | R | - | - |
| Piperacillin | - | - | - | R | - | I |
| Ceftriaxone | - | - | - | R | - | - |
| Ceftazidime | - | - | - | M | - | R |
| Levofloxacin | - | - | - | M | - | S |
| Ofloxacin | - | - | - | M | - | S |
| Meropenem | - | - | - | S | - | S |
| Amikacin | - | - | - | S | - | S |
| Gentamicin | - | - | - | S | - | - |
| Ciprofloxacin | - | - | - | S | - | S |
| Norfloxacin | - | - | - | S | - | - |
| Colistin | - | - | - | S | - | S |
| Polymyxin | - | - | - | S | - | - |
| Streptomycin | - | - | - | - | R | - |

Diagrama

Descripción generada automáticamente

**Supplementary Figure 1. A** phylogenetic tree with the amino acid sequences closest to the c39 peptidase domains of ClosPt and CellPt, models **B** and **D** generated with alphafold 2.0, minimized with Chimera, figures **C** and **E**, Ramachandra plots of the models for ClosPt with favored Ramachandran of 96.85% and for CellpT with favored Ramachandran of 96.66%.

Gráfico de dispersión

Descripción generada automáticamente

**Supplementary Figure 2.** **A** Phylogenetic tree with the amino acid sequences closest to the total proteins ClosM and CellM, models **B** and **D** generated with Alphafold 2.0, minimized with Chimera, figures **C** and **E**, Ramachandra plots of the models for ClosM with favored Ramachandran of 96.93% and for CellPT with favored Ramachandran of 97.21%.

Esquemático

Descripción generada automáticamente con confianza media

**Supplementary Figure 3. A.** 20% SDS-PAGE gel of the Nickel affinity purification lanes showing the band enrichment corresponding to the protein products **A.1** pre-Cellulosin (8.3 kDa) **A.2** pre-Clostrisin (9.2 kDa) and **A.3** C39 peptidase domain (17.5 kDa). **C.** The proteolytic activity was monitored after 48h at 4 °C in the reaction mixtures of Clostrisin. **B.** Western Blot of heterologous expression of pre-Clostrisin, pre-Cellulosin and C39 peptidase domain, with a tagged His6X antibody. **C.** 15% tricine-SDS-PAGE gels of proteolysis reaction between pre-Clostrisin and C39 peptidase domain.

Una captura de pantalla de un celular

Descripción generada automáticamente con confianza media

**Supplementary material Figure 4.A** MALDI-TOF mass spectrophotometry of purified fractions of Cellulosin.

Gráfico, Histograma

Descripción generada automáticamente

**Supplementary material Figure 4.B** MALDI-TOF mass spectrophotometry of purified fractions of pre-Cellulosin.

Gráfico

Descripción generada automáticamente

**Supplementary Figure 4.C** MALDI-TOF mass spectrophotometry of purified fractions of Clostrisin.

Gráfico

Descripción generada automáticamente

**Supplementary Figure 4.D** MALDI-TOF mass spectrophotometry of purified fractions of pre-Clostrisin.