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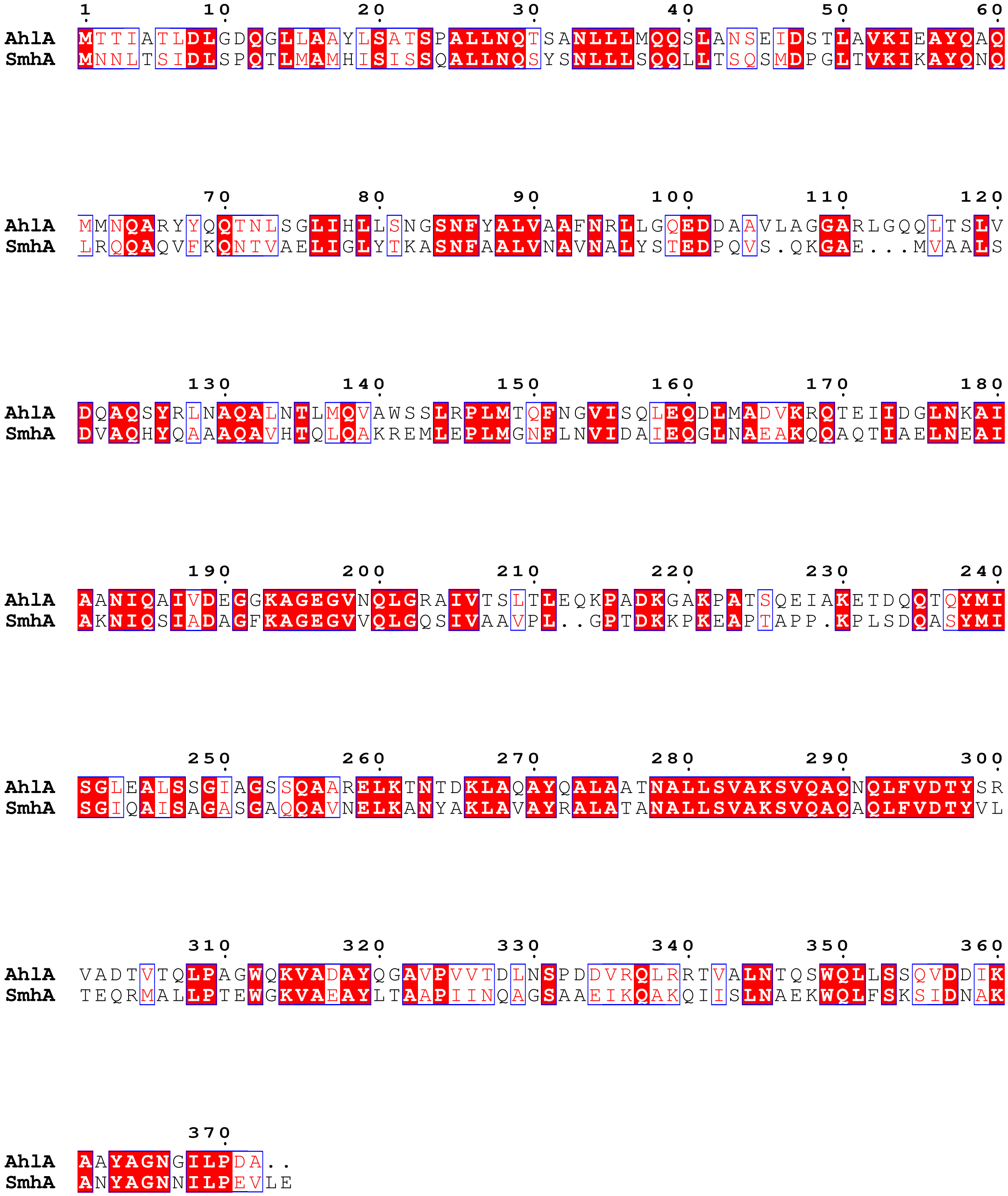
Supporting information for article:

The A component (SmhA) of a tripartite pore-forming toxin from *Serratia marcescens*: expression, purification and crystallographic analysis

Alicia M. Churchill-Angus, Svetlana E. Sedelnikova, Thomas H. B. Schofield and Patrick J. Baker



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         1        10        20        30        40        50        60
AhlA     MTTIATLDLGDQGLLAAYLSATSPALLNQTSANLLLMQQSLANSEIDSTLAVKIEAYQAQ
SmhA     MNNLTSIDLSPQTLMAMHISISSQALLNQSYSNLLLSQQLLTSQSMDPGLTVKIKAYQNQ

                  70        80        90       100       110       120
AhlA     MMNQARYYQQTNLSGLIHLLSNGSNFYALVAAFNRLLGQEDDAAVLAGGARLGQQLTSLV
SmhA     LRQQAQVFKQNTVAELIGLYTKASNFAALVNAVNALYSTEDPQVS.QKGAE...MVAALS

                 130       140       150       160       170       180
AhlA     DQAQSYRLNAQALNTLMQVAWSSLRPLMTQFNGVISQLEQDLMADVKRQTEIIDGLNKAI
SmhA     DVAQHYQAAAQAVHTQLQAKREMLEPLMGNFLNVIDAIEQGLNAEAKQQAQTIAELNEAI

                 190       200       210       220       230       240
AhlA     AANIQAIVDEGGKAGEGVNQLGRAIVTSLTLEQKPADKGAKPATSQEIAKETDQQTQYMI
SmhA     AKNIQSIADAGFKAGEGVVQLGQSIVAAVPL..GPTDKKPKEAPTAPP.KPLSDQASYMI

                 250       260       270       280       290       300
AhlA     SGLEALSSGIAGSSQAARELKTNTDKLAQAYQALAATNALLSVAKSVQAQNQLFVDTYSR
SmhA     SGIQAISAGASGAQQAVNELKANYAKLAVAYRALATANALLSVAKSVQAQAQLFVDTYVL

                 310       320       330       340       350       360
AhlA     VADTVTQLPAGWQKVADAYQGAVPVVTDLNSPDDVRQLRRTVALNTQSWQLLSSQVDDIK
SmhA     TEQRMALLPTEWGKVAEAYLTAAPIINQAGSAAEIKQAKQIISLNAEKWQLFSKSIDNAK

                 370
AhlA     AAYAGNGILPDA..
SmhA     ANYAGNNILPEVLE
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Supplementary figure S1. Pairwise sequence alignment of AhlA and SmhA. Red boxes with white text shows identical residues, while white boxes with red text shows similar residues.

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Optimized      4    ATGAACAACCTGACCAGCATCGACCTGAGCCCGCAAACCCTGATGGCGATGCACATCAGC
Original       4    ATGAATAACTTGACGAGTATTGATTTAAGCCCGCAAACACTAATGGCAATGCATATTTCC

Optimized     64    ATTAGCAGCCAAGCGCTGCTGAACCAGAGCTACAGCAACCTGCTGCTGAGCCAGCAACTG
Original      64    ATTTCATCACAGGCATTGCTTAATCAAAGCTATAGTAATTTGTTGCTCAGCCAGCAATTA

Optimized    124    CTGACCAGCCAGAGCATGGACCCGGGTCTGACCGTGAAGATTAAAGCGTATCAGAACCAA
Original     124    TTAACGTCACAAAGTATGGACCCTGGCCTGACCGTTAAAATCAAGGCGTACCAAAATCAA

Optimized    184    CTGCGTCAGCAAGCGCAAGTGTTCAAACAGAACACCGTTGCGGAGCTGATCGGCCTGTAC
Original     184    CTGCGGCAGCAGGCGCAAGTATTCAAACAAAATACGGTCGCAGAATTGATCGGGTTATAT

Optimized    244    ACCAAGGCGAGCAACTTTGCGGCGCTGGTGAACGCGGTTAACGCGCTGTATAGCACCGAG
Original     244    ACCAAAGCGTCAAATTTCGCCGCCCTGGTCAACGCCGTCAATGCGCTGTATTCCACCGAG

Optimized    304    GACCCGCAAGTTAGCCAGAAGGGTGCGGAAATGGTGGCGGCGCTGAGCGATGTTGCGCAA
Original     304    GATCCTCAGGTGTCGCAGAAAGGCGCAGAAATGGTGGCTGCGCTTTCCGATGTCGCGCAA

Optimized    364    CACTATCAAGCGGCGGCGCAGGCGGTGCACACCCAGCTGCAAGCGAAACGTGAGATGCTG
Original     364    CACTACCAGGCCGCAGCACAAGCCGTCCACACGCAGTTGCAGGCGAAACGCGAAATGCTG

Optimized    424    GAACCGCTGATGGGTAACTTCCTGAACGTTATCGACGCGATTGAGCAAGGCCTGAACGCG
Original     424    GAGCCTTTGATGGGCAATTTCCTTAACGTCATTGACGCCATCGAACAAGGGCTGAACGCC

Optimized    484    GAAGCGAAGCAGCAAGCGCAGACCATTGCGGAGCTGAACGAAGCGATCGCGAAAAACATC
Original     484    GAGGCGAAACAACAGGCGCAAACCATCGCTGAGCTCAACGAAGCGATCGCCAAAAATATC

Optimized    544    CAGAGCATTGCGGATGCGGGTTTTAAGGCGGGCGAGGGCGTGGTTCAACTGGGTCAGAGC
Original     544    CAAAGCATCGCAGATGCGGGTTTCAAAGCGGGTGAAGGGGTTGTGCAGCTTGGACAATCC

Optimized    604    ATTGTTGCGGCGGTTCCGCTGGGTCCGACCGACAAGAAACCGAAAGAAGCGCCGACCGCT
Original     604    ATCGTCGCCGCCGTGCCGCTCGGCCCGACGGATAAAAAACCGAAAGAAGCGCCAACCGCG

Optimized    664    CCGCCGAAGCCGCTGAGCGATCAAGCGAGCTATATGATCAGCGGCATTCAGGCGATCAGC
Original     664    CCTCCGAAGCCGCTTAGCGACCAGGCCAGCTATATGATCTCCGGCATTCAGGCGATCTCG

Optimized    724    GCGGGTGCGAGCGGTGCGCAGCAAGCGGTGAACGAGCTGAAGGCGAACTACGCGAAACTG
Original     724    GCGGGCGCTTCCGGTGCACAACAGGCCGTTAATGAACTGAAGGCAAACTACGCCAAATTG
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Optimized    724    GCGGGTGCGAGCGGTGCGCAGCAAGCGGTGAACGAGCTGAAGGCGAACTACGCGAAACTG
Original     724    GCGGGCGCTTCCGGTGCACAACAGGCCGTTAATGAACTGAAGGCAAACTACGCCAAATTG

Optimized    784    GCGGTTGCGTACCGTGCGCTGGCGACCGCGAACGCGCTGCTGAGCGTGGCGAAAAGCGTT
Original     784    GCCGTGGCCTATCGGGCTTTGGCAACCGCCAATGCGCTGCTCTCCGTCGCCAAGTCCGTG

Optimized    844    CAGGCGCAAGCGCAGCTGTTCGTGGACACCTACGTTCTGACCGAACAACGTATGGCGCTG
Original     844    CAAGCCCAGGCCCAATTATTTGTCGACACCTATGTTCTCACCGAGCAGCGCATGGCGTTA

Optimized    904    CTGCCGACCGAGTGGGGTAAAGTGGCGGAAGCGTATCTGACCGCGGCGCCGATCATTAAC
Original     904    CTGCCGACAGAATGGGGCAAGGTGGCGGAAGCCTATCTGACGGCTGCGCCCATCATTAAC

Optimized    964    CAAGCGGGCAGCGCGGCGGAGATCAAGCAAGCGAAACAGATCATTAGCCTGAACGCGGAA
Original     964    CAAGCCGGCAGCGCAGCGGAAATTAAACAAGCCAAACAAATCATTTCGCTCAATGCGGAA

Optimized   1024    AAGTGGCAGCTGTTTAGCAAAAGCATTGATAACGCGAAGGCGAACTACGCGGGCAACAAC
Original    1024    AAATGGCAGCTGTTTTCAAAGTCTATTGATAACGCCAAAGCTAACTATGCAGGAAACAAC

Optimized   1084    ATCCTGCCGGAAGTT
Original    1084    ATCCTGCCGGAAGTT
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Supplementary figure S2. Optimized and unoptimized nucleotide sequence for SmhA. Altered nucleotides are highlighted in red.