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Supporting information for article:

Crystallization and preliminary X-ray crystallographic studies of dipeptidyl peptidase 11 from *Porphyromonas gingivalis*

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AA seq.   1 M K K R L L L P L F A A L C L S Q I A H A D E G M W L M Q Q L G R K
Native   1 ATGAAAAAAAGACTATTGCTCCCCCTCTTTGCAGCTCTCTGCCTGAGCCAGATAGCTCATGCGGACGAGGGTATGTGGCTGATGCAACAGCTCGGACGGA
Optimized 1 ATGAAAAAACGCCTGCTGCTGCCGCTGTTCGCCGCTCTGTGCCTGTCCAAATCGCCCATGCCGATGAAGGTATGTGGCTGATGCAACAGCTCGGCCGTA

AA seq.   35 Y A Q M K E R G L K M K E Y D L Y N P N G T S L K D A V V L F D G
Native   101 AGTATGGCAGATGAAAGAACGCGGCCTTAAGATGAAGGAATACGACCTTTATAATCCCAACGGCACATCGCTGAAAGATGCCGTAGTGCTATTCGACGG
Optimized 101 AATATGGCCAGATGAAAGAACGCGGTCTGAAAATGAAAGAATACGATCTGTATAATCCGAATGGCACCTCACTGAAAGACGCCGTTGTTCTGTTTGATGG

AA seq.   68 G C T G E V V S D R G L V L T N H H C G Y D M I Q A H S T L E H N
Native   201 AGGATGTACGGGCGAGGTCGTTTCCGATCGCGGACTGGTACTGACCAATCACCACTGCGGATACGATATGATCCAGGCTCACAGCACGCTCGAGCATAAC
Optimized 201 CGGTTGCACCGGCGAAGTCGTGTCGGATCGGGTCTGTCTGACCAACCATCACTGTGGCTATGACATGATTCAGGCCCATAGCACCCTGGAACACAAC

AA seq. 101 Y L E N G F W A M R E A D E L P N K D I S V V F I D K I E D V T D Y
Native   301 TATCTCGAAAATGGATTTTGGGCGATGAGAGAAGCGGATGAATTACCGAACAAGGATATTTCCGTGGTATTCATCGACAAGATCGAAGATGTCACAGACT
Optimized 301 TACCTGGAAAATGGTTTTTGGGCAATGCGCGAAGCTGACGAACTGCCGAACAAAGATATTTCTGTTGTCTTCATCGATAAAATCGAAGATGTCACCGATT

AA seq. 135 V K K E L K A I K D P N S M D Y L S P K Y L Q K L A D K K A G K N
Native   401 ACGTCAAGAAAGAACTCAAAGCCATCAAAGATCCCAACAGCATGGACTACCTTCTCTCCGAAGTACCTGCAAAGTTGGCTGACAAGAAAGCCGGCAAGAAA
Optimized 401 ATGTGAAAAAAGAACTGAAAGCCATCAAAGACCCGAATAGTATGGATTATCTGTCCCCGAAATACCTGCAGAAACTGGCGGATAAAAAAGCCGGCAAAAA

AA seq. 168 F S A K N P G L S V E I K A F Y G G N L Y L M F T K K T Y T D V R
Native   501 CTTTTCTGCCAAAAATCCGGGACTTTCCGTAGAGATCAAAGCCTTCTACGGGGGCAATCTCTACCTGATGTTTACCAAAAAAACTTATACGGATGTTCGA
Optimized 501 CTTTAGCGCAAAAAATCCGGGTCTGTCTGTTGAAATTAAAGCTTTTTATGGCGGTAATCTGTACCTGATGTTCACCAAGAAAACCTATACGGATGTTCGT

AA seq. 201 L V G A P P S S I G K F G A D T D N W I W P R H T G D F S I F R I Y
Native   601 CTGGTGGGAGCACCTCCCAGCAGCATAGGCAAATTCGGTGCCGATACGGACAACTGGATCTGGCCTCGTCATACTGGCGACTTCTCCATCTTCCGTATCT
Optimized 601 CTGGTCGGCGCACCGCCCAGCTCTATTGGCAAATTCGGTGCCGATACCGACAACTGGATCTGGCCGCGTCATACGGGCGACTTTAGCATTTTCCGCATCT

AA seq. 235 A D K N G N P A P Y S E D N V P L K P K R F F N I S L G G V Q E N
Native   701 ATGCGGACAAGAATGGCAATCCCGCACCATACTCTGAAGATAATGTTCCGCTCAAGCCGAAGCCGTTTCTTCAATATCTCCCTTGGTGGAGTACAAGACGAA
Optimized 701 ATGCAGATAAAAACGGTAATCCGGCTCCGTACAGCGAAGATAATGTCCCGCTCAAACCGAAACGCTTTTTCAACATTTCTCTCGGCGGTGTGCAGGAAAA

AA seq. 268 D Y A M I M G F P G T T H R Y F T A S E V D E W K S I D N D I R I
Native   801 CGACTATGCCATGATAATGGGTTTCCCCGGTACTACGCACCGCTATTTCACGGCTTCCGAAGTAGACGAATGGAAAAGCATCGACAACGATATTCGCATC
Optimized 801 TGATTATGCGGATGATCATGGGCTTTCCGGGTACCACGCACCGCTACTTCACCGCCAGTGAAGTGGATGAATGGAAATCCATTGATAACGACATTCGCATC

AA seq. 301 R M R D I R Q G V M L R E M L A D P Q I K I M Y S A K Y A A S Q N A
Native   901 CGCATGCGTGATATTCGTCAGGGTGTGCATGCTTAGGGAAATGCTGGCCGATCCTCAGATCAAAATCATGTATTCAGCTAAATATGCCGCTTCGCAGAATG
Optimized 901 CGTATGCGCGATATCCGTCAGGGTGTTATGCTGCGCGAAATGCTGGCGGACCCGCAGATTAAAATCATGTATTCAGCGAAATACGCGGCCTCGCAAAACG

AA seq. 335 Y K R A I G A N W A I K T R G L R Q N K Q A M Q D R L I A W G A K
Native 1001 CTTACAAACGTGCTATAGGTGCCAACTGGGCGATCAAGACACGCGGCCTGCGTCAAAACAAACAGGCGATGCAGGACAGACTGATCGCATGGGGAGCGAA
Optimized 1001 CCTATAAACGCGCGATTGGCGCCAATTGGGCAATCAAGACCCGTGGTCTGCGCCAGAATAAACAAGCAATGCAGGATCGTCTGATTGCGTGGGGCGCGAA

AA seq. 368 Q G T P R Y E E A V H E I D A T V A K R A D L R R R Y W M I E E G
Native 1101 GCAGGGTACTCCTCGATATGAAGAGGCCGTACACGAAATCGATGCTACGGTAGCCAAACGTGCGGATCTGCGCCGTCGTTATTGGATGATAGAAGAGGGT
Optimized 1101 ACAGGGTACCCCGCGCTATGAAGAAGCGGTTCATGAAATTGACGCCACGGTCGCAAAACGTGCTGATCTGCGTCGCCGTTACTGGATGATCGAAGAAGGC

AA seq. 401 I I R G I E F A R S P I P T E D E T K A L Q G N D A S A R K E A I D
Native 1201 ATCATCCGTGGGATCGAGTTTGCCCGTTCTCCTATCCCCACCGAAGATGAGACGAAAGCTCTGCAAGGCAATGATGCTTCGGCTCGCAAGGAGCGCCATCG
Optimized 1201 ATTATCCGTGGTATTGAATTTGCACGCAGTCCGATCCCGACCGAAGACGAAACGAAAGCTCTGCAGGGTAACGATGCGTCCGCCGCAAGAGCGCATTG

AA seq. 435 K I R T R Y S K F A N K D Y S A E V D K K V A V A M L T E Y L K E
Native 1301 ATTAAGATTCGTACACGCTACAGCAAATTTGCCAACAAGGACTATAGTGCAGAGGTGGACAAGAAAGTGGCCGTAGCCATGCTGACGGAATACCTCAAGGA
Optimized 1301 ACAAAATCCGTACCCGCTATTCAAAATTCGCAAATAAAGACTACTCGGCTGAAGTGGATAAAAAAGTCGCAGTGGCTATGCTGACGGAATATCTGAAAGA

AA seq. 468 I P Y E N L P L H L R L V K D R F A G D V Q A Y V D D I F A R S V
Native 1401 AATACCCTATGAGAATCTGCCCTCTCCATTTGCGTCTCTGTGAAAGACCGCTTTGCCGGAGACGTTCAGGCCTATGTGGACGACATATTCGCTCGCTCCGTT
Optimized 1401 AATTCCGTACGAAAACCTGCCGCTGCACCTTGCGTCTGGTGAAAGACCGCTTTGCGGGCGATGTTCAAGCCTATGTCGATGACATCTTTGCCCGTAGCGTT

AA seq. 501 F G S E A Q F D A F A A V P S V E K L A E D P M V L F A S S V F D E
Native 1501 TTCGGTAGCGAAGCACAGTTCGATGCCTTTGCGGCAGTACCTTCTGTAGAAAAGCTTGCCGAAGATCCTATGGTACTCTTCGCCTCTTGGTTTTCGACG
Optimized 1501 TTCGGTTCTGAAGCACAGTTTGATGCTTTCGCAGCTGTGCCGTCCGTTGAAAAACTGGCAGAAGATCCGATGGTCCTGTTTGCTAGTTCCGTGTTCGACG

AA seq. 535 Y R K L Y N E L R P Y D D P I L R A Q R T Y I A G L L E M D G D Q
Native 1601 AATACCGCAAACTCTACAACGAACTTCGTCCCTATGACGATCCTATTCTAAGGGCGCAACGCACCTACATTGCAGGTCTCTTGGAAATGGATGGCGATCA
Optimized 1601 AATATCGTAAACTGTACAATGAACTGCGCCCGATGATGACCCGATTCTGCGCGCGCCAGCGTACCTACATTGCGGGTCTGCTGGAAATGGATGGTGACCA

AA seq. 568 D Q F P D A N L T L R F T Y G Q V K G Y S P R D N V Y Y G H Q T T
Native 1701 GGATCAATTCCCCGGATGCTAACCTGACACTTCGTTTCACCTATGGTTCAAGTGAAGGGCTATTCACCCCGTGACAATGTTTACTACGGACATCAAACCAC
Optimized 1701 GGATCAATTTCCGGATGCGAACCTGACCCTGCGTTTCACGTATGGCCAAGTGAAAGGTACAGTCCGCGCGATAATGTTTATTACGGCCATCAGACCACG

AA seq. 601 L D G V M E K E D P D N W E F V V D P K L K A V Y E R K D F G R Y A
Native 1801 TTGGATGGTGTGATGGAAAAAGAAGATCCCGATAATTTGGGAATTTGTAGTCGATCCCAAGCTGAAAGCCGTATACGACGTAAAGACTTCGGCCGTTATG
Optimized 1801 CTGGACGGTGTGATGGAAAAAGAAGACCCGGATAACTGGGAATTTGTCGTTGATCCGAAACTGAAAGCGGTTTATGAACGTAAAGACTTTGGCCGCTACG

AA seq. 635 D R S G R M P V A F C A T T H T T G G N S G S P V M N A N G E L I
Native 1901 CCGATCGCAGCGGTCGCATGCCTGTCGCCTTTTGTGCCACCACACATACAACCGGCGGCCAACTCAGGCAGTCCGGTCATGAATGCCAACGGCGAACTGAT
Optimized 1901 CCGATCGCTAGCGGTCGCATGCCGGTTGCCTTTTGTGCAACCACCCACACCACCGGCGGTAATTCAGGCTCGCCGGTCATGAACGCCAATGGCGAACTGAT

AA seq. 668 G L N F D R N W E G V G G D I Q Y L A D Y Q R S I I V D I R Y V L
Native 2001 CGGTCTCAACTTCGATCGTAACTGGGAGGGAGTCGGTGGCGACATCCAGTATCTGGCCGACTACCAGCGCAGCATCATTGTGGATATTCGCTACGTCCTG
Optimized 2001 TGGTCTGAACTTTGATCGCAATTGGGAGGGTGTGGGCGGTGACATTCAATATCTGGCAGATTACCAGCGTTCTATTATCGTGGATATCCGCTATGTTCTG

AA seq. 701 L V I D K V G G C Q R L L D E M N I V P *
Native 2101 CTTGTGATAGACAAAGTAGGCGGTTGCCAACGCCTGTTGGATGAAATGAATATCGTTCCCTAA
Optimized 2101 CTGGTGATTGATAAAGTCGGTGGTTGTCAGCGTCTGCTGGATGAAATGAACATCGTGCCGTGA

Figure S1. Optimization of PgDPP11 DNA sequence. AA seq., amino acid sequence of PgDPP11 (UniProt accession number: B2RID1); Native, native DNA sequence of PgDPP11 from *Porphyromonas gingivalis* ATCC 33277 (GenBank accession number: AP009380); Optimized, codon-optimized DNA sequence of PgDPP11 used in this study.