

Supplementary Information for Simmons et al.

I. Primary amino acid sequences of PlyCP390 and PlyCP26F

PlyCP390:

MKIALRGGHSPNCK***GANVLRDEQSCMWALADEVEKVLTSHGHTVVR****CETTL****SNEREDVR***QGAKKGYNCDFISLHMNASDGRGNGT
EAWVARSARSSIKEIASRLCKNYATLGLQNRGVKEKNYWEMTDNCPNIIFETMFCDDKHDIWASTSWDKLARLIANAIDPNIPLEKEQ
*DYYR*VCVQRFTNKEDA EKAQQRISNELGYCFAEKIHHHHHHH

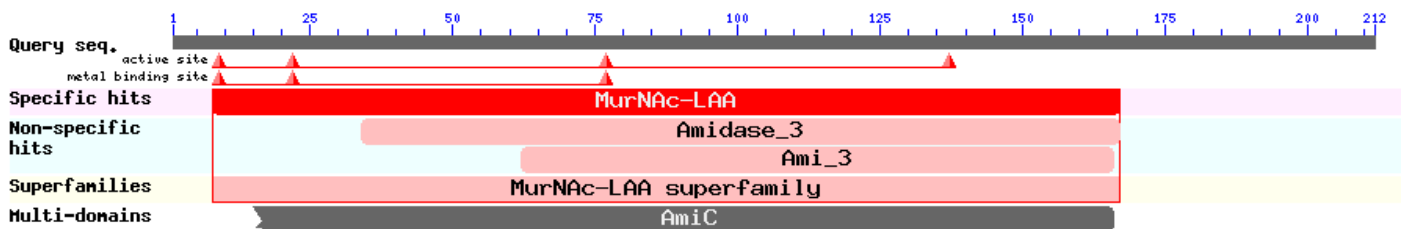
Bold italic sequences are those identified by mass spectrometry. Underlined sequences are those peptides identified that were juxtaposed to one another although identified separately while the outlined sequence EQDYR was a smaller peptide also detected within the larger fragment. The first twelve amino acids were identified by direct Edman degradation amino acid sequencing of the purified recombinant protein.

PlyCP26F:

MIIGSRYGHSNCRGAK***GLRDEVDAMKPLHFEFK****IMEQYGH****TIDCCSNANTQNGELSEGARKANAQILD***FISWHGNGKGGGQGCEA
WIANNSRAPYAERMCK***NFSSLGFK***NRGVK***YSDKYEMRNINAPNIIFETLFLDSEKDISI***WSPPIYEVMARYLANAIDPNIPLEKEQDYR
VCVQRFTNKEDA EKAQQRISNELGYCFAEKIHHHHHHH

Bold italic sequences are those identified by mass spectrometry. Underlined sequences are those peptides identified that were juxtaposed to one another although identified separately while the sequence EQDYR was detected individually in PlyCP26F. The first ten amino acids were identified by direct Edman degradation amino acid sequencing of the purified recombinant protein.

II. Results of BLAST analysis and PFAM identification of the PlyCP390 and PlyCP26F:



N-acetylmuramoyl-L-alanine amidase or MurNac-LAA (also known as peptidoglycan aminohydrolase, NAMLA amidase, NAMLAA, Amidase 3, and peptidoglycan amidase; EC 3.5.1.28) is an autolysin that hydrolyzes the amide bond between N-acetylmuramoyl and L-amino acids in certain cell wall glycopeptides. MurNac-LAA in this family is one of several peptidoglycan hydrolases (PGHs) found in bacterial and bacteriophage or prophage genomes that are involved in the degradation of the peptidoglycan. The bacteriophage MurNac-LAAs are endolysins since these phage-encoded enzymes break down bacterial peptidoglycan at the terminal stage of the phage reproduction cycle. As opposed to autolysins, almost all endolysins have no signal peptides and their translocation through the cytoplasmic membrane is thought to proceed with the help of phage-encoded holin proteins. The amidase catalytic module is fused to another functional module (cell wall binding module or CWBM) either at the N- or C-terminus, which is responsible for high affinity binding of the protein to the cell wall (Vollmer W et al. FEMS Microbiol Rev 32:259, 2008).