

Discovery of new genetic variants of Methionine Aminopeptidases

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Methionine Aminopeptidases (MetAPs) are the enzymes that specifically remove the initiator methionine during protein synthesis. MetAPs are classified into Type1 and Type2 MetAPs, based on a 60 amino acid insert in the catalytic region of Type2 MetAP. Type1 MetAPs further classified into Type1a, Type1b, Type1c and Type1d based on the N-terminal extensions. MetAPs are considered as potential pharmaceutical targets to treat various diseases like cancer, rheumatoid arthritis, obesity and various microbial infections etc. as the knocking out of map gene which codes for MetAPs is shown to be lethal to cell. Even though MetAPs are potential drug targets the main problem associated with MetAPs is specificity as the active site where the competitive inhibition is targeted is very much conserved in different isoforms across all organisms. In a recent discovery from our lab showed a molecule specifically targeting *Streptococcus pneumoniae* MetAP without affecting human Type1 MetAP. This discovery encouraged us to find more MetAPs with extra insertions in the catalytic site of MetAPs. In the present study, exclusive genome wide search has resulted in new MetAPs in the species of *Vibrio*. MetAPs with either no insert or two inserts or three inserts were identified. One each from three classes of MetAPs (no insert, two inserts, and three inserts) were cloned expressed and purified for further biochemical and structural characterization.

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