

# Presequence protease 1, chloroplastic/mitochondrial (PREP1), Recombinant Protein

Cat *RP05095*

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## Species

*Arabidopsis thaliana* (Mouse-ear cress)

## Full Product Name

Recombinant *Arabidopsis thaliana* Presequence protease 1, chloroplastic/mitochondrial (PREP1) , partial

## Product Gene Name

PREP1 recombinant protein

## Product Synonym Gene Name

PREP1

## Purity

Greater or equal to 85% purity as determined by SDS-PAGE. (lot specific)

## Format

Lyophilized or liquid (Format to be determined during the manufacturing process)

## Host

E Coli or Yeast or Baculovirus or Mammalian Cell

## Molecular Weight

121,015 Da

## Storage

Store at -20°C. For long-term storage, store at -20°C or -80°C. Store working aliquots at 4°C for up to one week. Repeated freezing and thawing is not recommended.

## Protein Family

Presequence protease

## NCBI Accession #

NP\_188548.2

## NCBI GI #

22331173

## NCBI GenBank Nucleotide #

NM\_112804.5

## NCBI GeneID

821451

## NCBI Official Full Name

presequence protease 1

## NCBI Official Symbol

PREP1

**FOR RESEARCH OR FURTHER MANUFACTURING USE ONLY**

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# Presequence protease 1, chloroplastic/mitochondrial (PREP1), Recombinant Protein

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## NCBI Official Synonym Symbols

ATPREP1; ATZNMP; presequence protease 1

## NCBI Protein Information

presequence protease 1

## NCBI Summary

Zinc metalloprotease pitrilysin subfamily A. Signal peptide degrading enzyme targeted to mitochondria and chloroplasts. Expressed only in siliques and flowers

## UniProt Gene Name

PREP1

## UniProt Synonym Gene Names

ZNMP1; AtPreP1; PreP 1; AtZnMP1

## UniProt Protein Name

Presequence protease 1, chloroplastic/mitochondrial

## UniProt Synonym Protein Names

Zinc metalloprotease 1; AtZnMP1

## UniProt Primary Accession #

Q9LJL3

## UniProt Secondary Accession #

Q8RUN6

## UniProt Related Accession #

Q9LJL3

## UniProt Comments

ATP-independent protease that degrades both mitochondrial and chloroplastic transit peptides after their cleavage. Also degrades other unstructured peptides. Specific for peptides in the range of 10 to 65 residues. Shows a preference for cleavage after small polar residues and before basic residues, with a bias for positively charged amino acid residues.

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