# Recombinant Rat Insulin Degrading Enzyme, His-tagged

**Cat. No.** Ide-761R **Lot. No.** (See product label)

## SPECIFICATION

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| **Product Overview** | Recombinant rat insulin degrading enzyme was fused to a His•Tag sequence and expressed in*S. frugiperda*insect cells.MW = 110 kDa. |
| **Species** | Rat |
| **Source** | S.frugiperda |
| **Description** | Insulin Degrading Enzyme (IDE) is a large zinc-binding protease of the M16A metalloprotease subfamily known to cleave multiple short polypeptides that vary considerably in sequence. IDE was first identified by its ability to degrade the B chain of the hormone insulin. This activity was observed over fifty years ago, though the enzyme specifically responsible for B chain cleavage was identified more recently. This discovery revealed considerable amino acid sequence homology between IDE and the previously characterized bacterial protease pitrilysin, suggesting a common proteolytic mechanism. |
| **Purity** | ≥90% by SDS-PAGE. |
| **Form** | Liquid. In 100 mM potassium phosphate buffer, 20% glycerol, pH 7.3. |
| **Specific Activity** | ≥3 U/mg protein. |
| **Unit Definition** | One unit is defined as the amount of the enzyme that will catalyze the hydrolysis of 1 μmol iodinated insulin per h at 37°C, pH 7.3. |

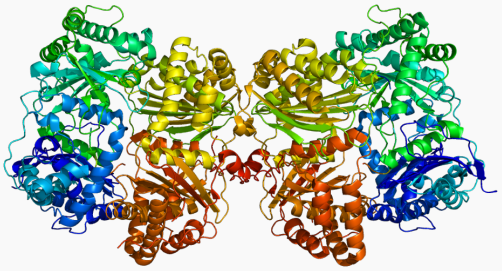
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| **Specificity** | ≥4 units/mg protein. |
| **Storage** | ≤ -70℃. Avoid freeze/thaw. |

## GENE INFORMATION

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| **Gene Name** | Ide insulin degrading enzyme [ Rattus norvegicus ] |
| **Synonyms** | Ide; insulin degrading enzyme; INSDEGM; insulin-degrading enzyme; insulysin; insulinase; insulin protease; EC 3.4.24.56 |
| **Gene ID** | 25700 |
| **mRNA Refseq** | NM_013159 |
| **Protein Refseq** | NP_037291 |
| **UniProt ID** | P35559 |
| **Chromosome Location** | 1q53 |
| **Pathway** | Alzheimer"s disease |
| **Function** | ATP binding; ATPase activity; beta-amyloid binding; beta-endorphin binding; insulin binding; metal ion binding; metalloendopeptidase activity; peptidase activity; nucleotide binding; peptide hormone binding; protein binding; protein homodimerization activity; zinc ion binding |

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| **PDB rendering based on 2g47.** |  |

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