Nucleotide sequence of human preprocathepsin H, a lysosomal cysteine proteinase

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The lysosomal cysteine proteinase cathepsin H is one of the most active proteinases in the human body. Until now only partial gene sequence information was available (1). A λ gt10 cDNA library constructed from a human U937 monocyte cell line was screened with a gene probe derived from a partial kidney cathepsin H clone (1) coding for the mature part of the protein. From 4.5 x 10⁵ plaques two full-length clones were isolated and characterized. The figure shows the previously unknown coding sequence of the prepro part of human preprocathepsin H and the derived protein sequence. Sequence comparison of the human preproregion with rat preprocathepsin H (2) indicated a very high degree of similarity with 82% identical nucleotide and 78% identical amino acid residues. In contrast, the human preprocathepsin H has two additional amino acid residues at the probable signal sequence cleavage site, compared to the rat enzyme. Similarity with preproregions of other related cysteine proteinases is rather low (20 - 30% identical amino acids).

| | -115 | | | | | | | | | -3 | 110 | | | | | | | | | | | | | | | |
|-----|---|---|---|---|---|---|---|-------|---|-----|-----|---|-----|------|-----|-----|---|-----|-----|---|---|---|---|---|---|----|
| | | | | | | | | | | | | M | W | A | т | L | ₽ | L | L | с | A | G | A | W | L | L |
| 1 | TTGCCGGCGCAAGAGCCAAGCCGCCAGCGCTGCTATGTGGGCCACGCTGCCGCCGCGCCCGGGGCCTGGCTCCTG | | | | | | | | | | | | | | | CTG | | | | | | | | | | |
| | -100 | | | | | t | | | | -90 | | | | | | | | -80 | | | | | | | | |
| | c | ; | v | Р | v | с | G | A | A | Е | L | s | v | N | s | L | Е | к | F | н | F | к | s | W | м | s |
| 80 | GGAGTCCCCGTCTGCGGTGCCGCCGAACTGTCCGTGAACTCCTTAGAGAAGTTTCACTTCAAGTCATGGATGTCT | | | | | | | | | | | | | | TCT | | | | | | | | | | | |
| | -70 -60 | | | | | | | | | | | | | | | | | | | | | | | | | |
| | F | : | H | R | к | т | Y | s | т | Е | Е | Y | н | н | R | L | Q | т | F | A | s | N | W | R | к | I |
| 155 | 5 AAGCACCGTAAGACCTACAGTACGGAGGAGTACCACCACAGGCTGCAGACGTTTGCCAGCAACTGGAG | | | | | | | | | | | | AGG | AAG | АТА | | | | | | | | | | | |
| | -50 | | | | | | * | | | | -40 | | | | | | | | -30 | | | | | | | |
| | 1 | I | A | н | N | N | G | N | н | т | F | ĸ | M. | A | L | N | Q | F | s | D | м | s | F | A | Е | I |
| 230 | A. | AACGCCCACAACAATGGGAACCACACATTTAAAATGGCACTGAACCAATTTTCAGACATGAGCTTTGCTGAAATA | | | | | | | | | | | | АТА | | | | | | | | | | | | |
| | | | | | | | | -20 ↓ | | | * | | | ↓-10 | | | | | | | | | | | | -1 |
| | F | C | н | к | Y | L | W | s | Е | P | Q | N | с | s | A | т | к | s | N | Y | L | R | G | т | G | P |
| 305 | A, | AAACACAAGTATCTCTGGTCAGAGCCTCAGAATTGCTCAGCCACCAAAAGTAACTACCTTCGAGGTACTGGTCCC | | | | | | | | | | | | | ccc | | | | | | | | | | | |

Fig: Nucleotide and derived protein sequence of human cathepsin H prepro region. Numbering of amino acid residues is according to (1). Asterisks indicate potential glycosylation sites. Putative protein cleavage sites are marked by arrows (see also 1).

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References:

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2. Ishidoh, H. et al. (1988) FEBS Letters 226, 33-37.