

Supplementary Materials

Table S1. Classification of human cathepsins according to the MEROPS database of proteolytic enzymes. The data was retrieved from the MEROPS database [39].

File S1. Sequence alignment of the UniProt and PDB sequences of human procathepsin B. The sequence alignment between human procathepsin B [76] 1D (UniProtKB ID P07858 [52] (upper panel) and 3D (PDB ID: 3pbh:A, [77]) (lower panel) was retrieved from the PDBSum web server [78]. The differences between the PDB and UniProt sequences are indicated with a black cross (X).

File S2. Sequence alignment of the UniProt and PDB sequences of human procathepsin H. The sequence alignment between human procathepsin H [79] 1D (UniProtKB ID P09668 [52] (upper panel) and 3D (PDB ID: 6czk:A, [60]) (lower panel) was retrieved from the PDBSum web server [78]. An amino residue difference between the PDB and UniProt sequences is indicated with a black cross (X).

File S3. Sequence alignment of the UniProt and PDB sequences of human procathepsin X. **(A)** The sequence alignment between human procathepsin X [50, 51] 1D (UniProtKB ID Q9UBR2 [52] (upper panel) and 3D (PDB ID: 1deu:A, [75]) (lower panel) was retrieved from the PDBSum web server [78]. An amino residue difference between the PDB and UniProt sequences is indicated with a black cross (X). **(B)** The sequence alignment between human procathepsin X [50, 51] 1D (UniProtKB ID Q9UBR2 [52] (upper panel) and 3D (PDB ID: 1deu:B, [75]) (lower panel) was retrieved from the PDBSum web server [78]. The differences between the PDB and UniProt sequences are indicated with a black cross (X).

File S4. Sequence alignment of the UniProt and PDB sequences of human procathepsin C. The sequence alignment between human procathepsin C [80] 1D (UniProtKB ID P53634 [52] (upper panel) and 3D (PDB ID: 3pdf:A, [81]) (lower panel) was retrieved from the PDBSum web server [78]. The differences between the PDB and UniProt sequences are indicated with a black cross (X).

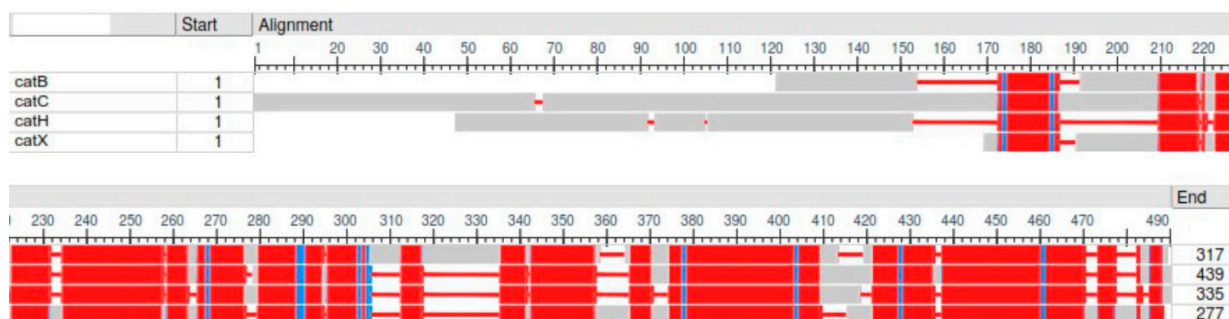


Figure S1. Schematic representation of the multiple sequence alignment of human procathepsins B, C, H, and X. The multiple sequence alignment of human procathepsin B (catB; 1pbh:A [82]), human 8 procathepsin C (catC; P53634|25-463; [80]), human procathepsin H (catH; 6czk:A; [60]), and human procathepsin X (catX; 1deu:A; [75]) was performed using a constrained-based multiple alignment tool (COBALT) [Papadopoulos, J. S.; Agarwala, R., *Bioinformatics*. 2007, 23, (9), 1073-9].

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