Cathepsin G is in humans encoded by the CTSG gene. It is one of the three serine proteases of the chymotrypsin family that are stored in the azurophil granules, and also a member of the peptidase S1 protein family, Cathepsin G plays an important role in eliminating intracellular pathogens and breaking down tissues at inflammatory sites, as well as in anti-inflammatory response.

The CTSG gene is located at chromosome 14q11.2, consisting of 5 exons. Each residue of the catalytic triad is located on a separate exon. Five polymorphisms have been identified by scanning the entire coding region.

Cathepsin G is one of those homologous protease that evolved from a common ancestor by gene duplication.

Cathepsin G is a 255-amino-acid-residue protein including an 18-residue signal peptide, a two-residue activation peptide at the N-terminus and a carboxy terminal extension.

The activity of cathepsin G depends on a catalytic triad composed of aspartate, histidine and serine residues which are widely separated in the primary sequence but close to each other at the active site of the enzyme in the tertiary structure.

Cathepsin G has a specificity similar to that of chymotrypsin C, but it is most closely related to other immune serine proteases, such as neutrophil elastase and the granzymes.

As a neutrophil serine protease, was first identified as degradative enzyme that acts intracellularly to degrade ingested host pathogens and extracellularly in the breakdown of ECM components at inflammatory sites.

It localizes to Neutrophil extracellular traps (NETs), via its high affinity for DNA, an unusual property for serine proteases.

Transcript variants utilizing alternative polyadenylation signals exist for this gene.

Cathepsin G was also found to exert broad-spectrum antibacterial action against Gram-negtive and –positive bacteria independent of the function mentioned above.[14] Other functions of cathepsin G have been reported, including cleavage fo receptors, conversion of angiotensin Ito angiotensin Ⅱ, platelet activation, and induction of airway submucosal gland secretion.

Cathepsin G has been reported to play an important role in a variety of diseases, including rheumatoid arthritis, coronary artery disease, periodontitis, ischemic reperfusion injury, and bone metastasis.

It is also implicated in a variety of infectious inflammatory diseases, including chronic obstructive pulmonary disease, acute respiratory distress syndrome, and cystic fibrosis.

A recent study shows that patients with CTSG gene polymorphisms have higher risk of chronic postsurgical pain, suggesting cathepsin G may serve as a novel target for pain control and a potential marker to predict chronic postsurgical pain.

An upregulation of cathepsin G was reported in studies of keratoconus.

Giese et al., identified CatG, and to a higher extend CatG and lactoferrin (LF), as an exogenous regulator of cell surface Major histocompatibility complex (MHC) I expression of immune cells and

glioblastoma stem cells. In addition, levels of MHC I molecules are reduced on dendritic cells from CatG deficient mice compared to their wild type counterparts. Furthermore, cell surface CatG on immune cells, including T cells, B cells, and NK cells triggers MHC I on THP-1 monocytes suggesting a novel mechanism for CatG to facilitate intercellular communication between infiltrating cells and the respective target cell. Subsequently, our findings highlight the pivotal role of CatG as a checkpoint protease which might force target cells to display their intracellular MHC I:antigen repertoire [1)].

1)
Giese M, Turiello N, Molenda N, Palesch D, Meid A, Schroeder R, Basilico P, Benarafa C, Halatsch ME, Zimecki M, Westhoff MA, Wirtz CR, Burster T. Exogenous cathepsin G upregulates cell surface MHC class I molecules on immune and glioblastoma cells. Oncotarget. 2016 Oct 28. doi: 10.18632/oncotarget.12980. [Epub ahead of print] PubMed PMID: 27806341.