



PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM Books
 Search PubMed for

[Limits](#) [Preview/Index](#) [History](#) [Clipboard](#) [Details](#)

Entrez PubMed

1: Protein Eng 1994
 Jan;7(1):57-64

[Related Articles, Protein, Structure, Books, LinkOut](#)

Evolutionary divergence and conservation of trypsin.

Rypniewski WR, Perrakis A, Vorgias CE, Wilson KS.

PubMed Services

European Molecular Biology Laboratory (EMBL), Hamburg, Germany.

Related Resources

The trypsin sequences currently available in the data banks have been collected and aligned using first the amino acid sequence homology and, subsequently, the superposed crystal structures of trypsins from the cow, the bacterium *Streptomyces griseus* and the fungus *Fusarium oxysporum*. The phylogenetic tree constructed according to this multiple alignment is consistent with a continuous evolutionary divergence of trypsin from a common ancestor of both prokaryotes and eukaryotes. Comparison of crystal structures reveals a strict conservation of secondary structure. Similarly, in the alignment of all the sequences, insertions and deletions occur only in regions corresponding to loops between the secondary structure elements in the known crystal structures. The conserved residues cluster around the active site. Almost all conserved residues can be associated with one of the basic functional features of the protein: zymogen activation, catalysis and substrate specificity. In contrast, the residues of the hydrophobic core of the protein and the calcium ion binding sites are generally not conserved. The conserved features of trypsin and the nature of the conservation are discussed in detail.

PMID: 8140095 [PubMed - indexed for MEDLINE]

[Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)
[Department of Health & Human Services](#)
[Freedom of Information Act](#) | [Disclaimer](#)

i686-pc-linux-gnu Jul 16 2002 16:34:53