

This image displays a multiple sequence alignment of CAPN1 and CAPN2 protein isoforms across various species, including CAPN3, CAPN5, CAPN6, CAPN7, CAPN8, CAPN9, CAPN10, CAPN11, CAPN12, CAPN13, CAPN14, CAPN15, and CAPN16 [demi-calp]. The alignment is organized into several conserved domains and regions, indicated by arrows and labels at the top and between blocks: NS, anchor helix, PC1, CBS-1, CBS-2, IS1, PC2, C2L, IS2, and PEF, C2, or C2L.

Species and accession numbers are listed on the right side of the alignment, such as CAPN1 [μCL], CAPN2 [mCL], CAPN3 [p94], CAPN5 [hTRA-3], CAPN6 [p94], CAPN7 [Pa|BH], CAPN8 [nCL-2], CAPN9 [nCL-4], CAPN10 [p94], CAPN11 [p94], CAPN12 [p94], CAPN13 [p94], CAPN14 [p94], CAPN15 [SOLH], and CAPN16 [demi-calp].

Conserved residues are highlighted in yellow (e.g., ITPVYCTGVS, AGIAAKLAKDREAEG, LGRHERAIKYL, LFRDEAFP, PVPQSGLYKDL, GNPSKTYG, WKRPTELL, SN-PQ, FIVDGTATRD, 106: CAPN1 [μCL]). Conserved residues are highlighted in red (e.g., GCSID, WMSF, RDFMREF, TRLE, ICNLT, PDALK, SRTI, RK, WNTTYEGTWR, RSTAGGCRN, YPATFWVNPF, KIRL, DE, TDDPDDYGD, 412: CAPN1 [μCL]).

The alignment shows high sequence conservation across the different isoforms, particularly in the CBS-1 and CBS-2 domains. The sequence ends with residues such as ELFSANEHL, 130: CAPN16 [demi-calp] at the bottom.