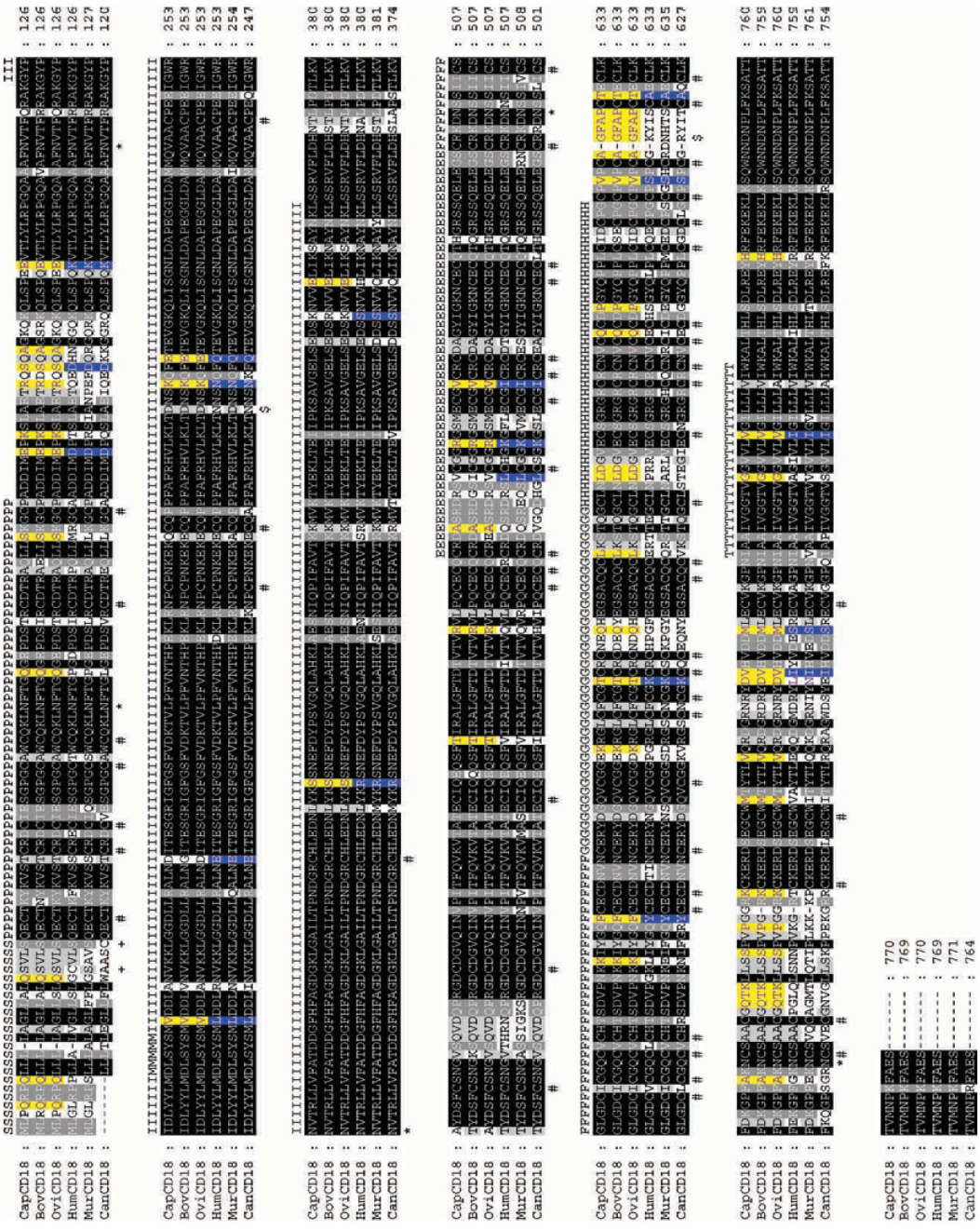

Figure 2. Comparison of the caprine (Cap-), bovine (Bov-), ovine (Ovi-), human (Hum-), murine (Mur-) and Canine (Can-) β_2 sub-units (CD18) amino acid sequences. The letters in the top row identify the constitutive blocks: putative signale peptide (S), plexin-semaphorin-integrin domain (P), I-like domain (I), MIDAS-like stretch (M), EGF domains 1 (E), 2 (F), 3 (G), 4 (H) and transmembrane region (T). Black, dark grey, light grey, yellow and blue columns represents identity among 6, 5, 4, ruminants and non-ruminants species, respectively. Conserved (#) and additional (+) cysteine residues, along with conserved (*) and additional ($) potential N-glycosylation sites are marked at the bottom of the alignment.