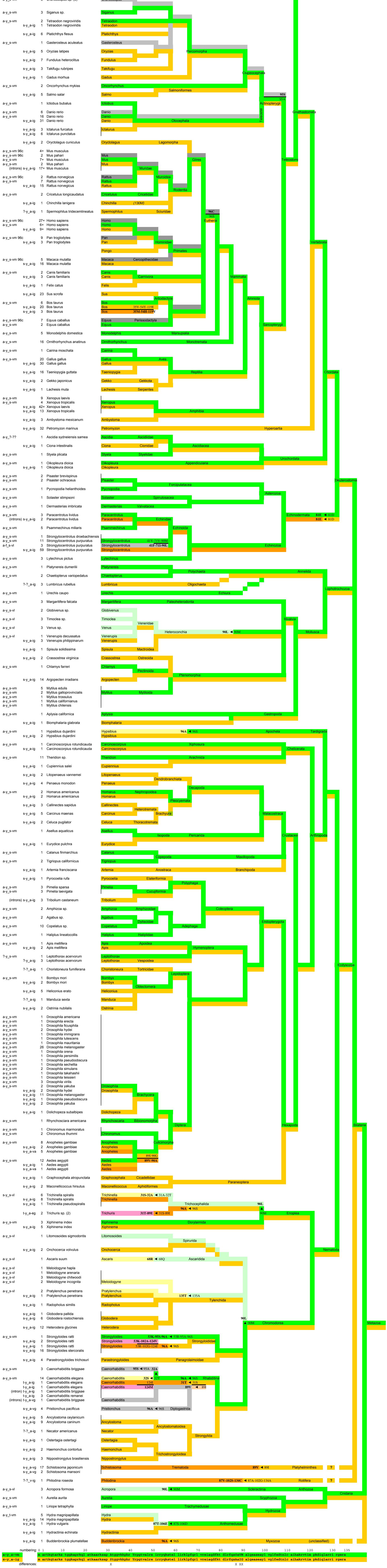


### Analysis of the evolution of metazoan histone H3 forms, based on Tree Of Life phylogenetic relationships

Full protein sequences are available in table format, arranged alphabetically and by location in the tree below.  
 A deduced single change is indicated by ▲ or ▼ (green for positive, red for negative), and the original residue (regular font) and the new residue (bold font).  
 Single-clade, single-residue variations without support by similar species are marked in bracketed italics.  
 Duplication-with-divergence of a functional H3 type, deduced as certain (or probable), is marked by a dark gray bar and a change of color, e.g. green-to-blue or gold-to-orange.

		Standard color use:
a-y_s-vm	■	a-y_h-vl
a-y_s-vm	■	a-y_q-vl
a-y_s-vl	■	a-y_q-vl
a-y_s-va	■	a-y_q-ig
a-f_s-vs	■	s-y_s-lg

GenBank et al.  
 [base record]  
 H3-idiotype # sequences Species Genus



Base sequences:

numbering: 0 1 10 20 30 40 50 60 70 80 90 100 110 120 130 135  
 a-y\_s-vm ■ artktgkarts tggkpkprgl atkaarasep atggvkkprp rrgptgvalve irryqgstei lirkgpgrl vrelaqslqif dlfrcfndadn algeasayi vgifiedthlc alahkrvtm pkdilqiarri rgera  
 a-y\_s-ig ■ artktgkarts tggkpkprgl atkaarasep atggvkkprp rrgptgvalve irryqgstei lirkgpgrl vrelaqslqif dlfrcfndadn algeasayi vgifiedthlc alahkrvtm pkdilqiarri rgera

differences:

x 10 x 20 x 30 x 40 x 50 x 60 x 70 x 80 x 90 x 100 x 110 x 120 x 130 x 135  
 x xx