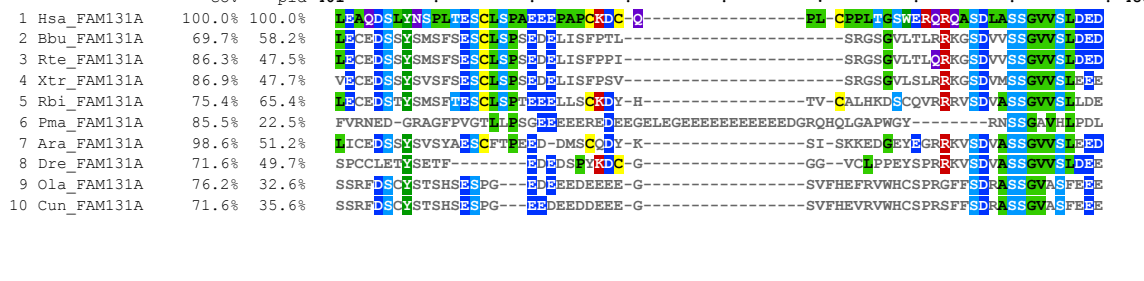
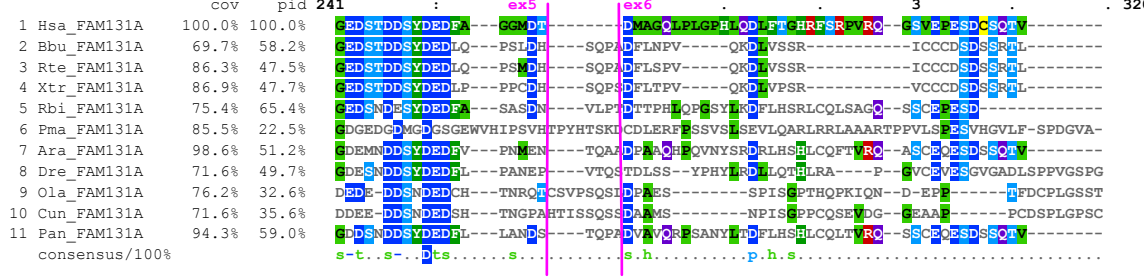
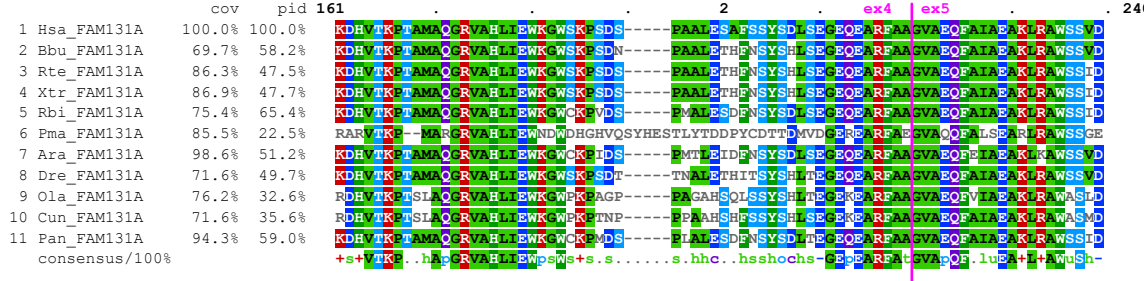
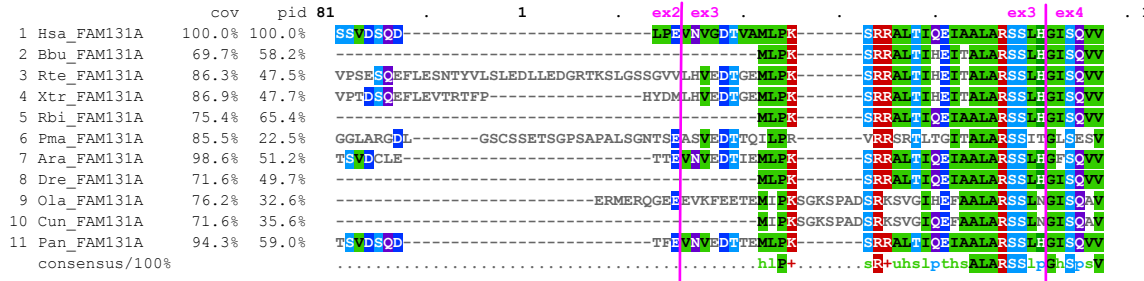
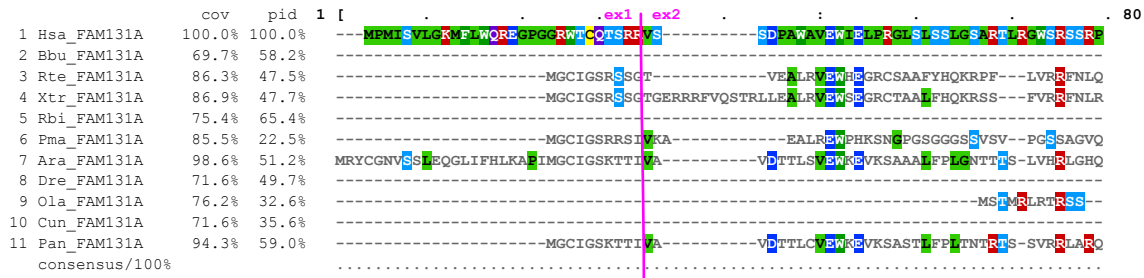


Multiple Sequence Alignment of Distant Orthologs



11 Pan_FAM131A	94.3%	59.0%	LICESSVSVVWESCFSEED-DLEKDY-Q-----TV-CAEQEVGYEGRRKVSDFSSGLVSEEN
consensus/100%			..t..p.hp.sh.....t.....h..SSghph.-.
	cov	pid	481 .] 494
1 Hsa_FAM131A	100.0%	100.0%	EAEAEQ-----
2 Bbu_FAM131A	69.7%	58.2%	EEDQP-----
3 Rte_FAM131A	86.3%	47.5%	EEDQP-----
4 Xtr_FAM131A	86.9%	47.7%	EDDQP-----
5 Rbi_FAM131A	75.4%	65.4%	EDEAEAEQ-----
6 Pma_FAM131A	85.5%	22.5%	KAEVAPT-----
7 Ara_FAM131A	98.6%	51.2%	EAEQ-----
8 Dre_FAM131A	71.6%	49.7%	DVDEEREAEQ----
9 Ola_FAM131A	76.2%	32.6%	EEDQEKKDDK---
10 Cun_FAM131A	71.6%	35.6%	ERDEDEVKKEFLM
11 Pan_FAM131A	94.3%	59.0%	EAEAEAEVE---
consensus/100%			c.....