Currently no data are available. Subfamilies (a) and (b) are both found in *A. thaliana* and *O. sativa*.

(a) *H. sapiens*: EPC1, a component of the p400/NuA4 and TIP60 H4/H2A histone acetyltransferase (HAT) complexes.

* S. cerevisiae*: EPL1, knockout is homozygous lethal. Component of the NuA4 H4/H2A HAT complex, the only essential HAT in yeast.

(b) *D. melanogaster* only [E(Pc)]. Heterozygous mutations are enhancers of mutations in polycomb genes and suppressors of position effect variegation. Homozygous mutations are lethal. (a) is also found in *D. melanogaster*.

*H. sapiens*: BR140, implicated in somatic cell development. BRL, expressed in germline tissue.

* C. elegans*: LIN-49, implicated in somatic cell development and homeotic gene expression. Genetic and regulatory interactions with homeobox transcription factors including mab-5, egl-5, lim-6, cog-1. RNAi phenotype: post-embryonic growth defect, sterile progeny, uncoordinated movement defect.

*D. melanogaster*: CG1845, strong 2-hybrid interaction with CG16838, an AAA-ATPase protein complex formation chaperone.


* S. cerevisiae*: NTO1, knockout is viable. Strong 2-hybrid interactions with (i) SAS3, the catalytic subunit of the NuA3 H3 HAT complex, which is implicated in gene silencing, (ii) UMP1, a protein complex formation chaperone, and (iii) SLM6, a protein of unknown function.

* C. elegans*: Y53G8AR.2, RNAi phenotype: WT.

*D. melanogaster*: RHINOCEROS, nuclear protein that regulates Ras pathway genes to restrict epidermal growth factor signaling in the eye.