

Multiple sequence alignment of the *SP* gene across various species. The alignment is presented in a grid format with species names on the left and amino acid sequences in the center. Red boxes highlight specific regions of the alignment, and a green box highlights a specific column. The alignment shows high conservation across many species, particularly in the regions highlighted by the red boxes.

Species listed include: *X. laevis*, *X. tropicalis*, *M. musculus*, *G. gallus*, *H. sapiens*, *B. Taurus*, *O. cuniculus*, *M. mulatta*, *C. sabaeus*, *O. afer*, *P. bivittatus*, *B. bubalis*, *C. mydas*, *P. tigris*, *P. maniculatus*, *P. catus*, *C. asiatica*, *E. edwardii*, *R. norvegicus*, *V. pacos*, *C. ferus*, *B. mutus*, *C. hircus*, *C. lupus*, *M. fascicularis*, *I. tridecemlineatus*, *M. ochrogaster*, *C. picta*, *M. undulatus*, *M. auratus*, *H. glaber*, *M. putorius*, *C. cristata*, *O. degus*, *J. jaculus*, *O. princeps*, *D. novemcinctus*, *C. simum*, *O. rosmarus*, *T. manatus*, *T. truncatus*, *N. leuca*, *O. orca*, *N. leucogenys*, *G. gorilla*, *S. boliviensis*, *P. anubis*, *O. garnettii*, *S. harrisii*, *P. abelii*, and *C. jacchus*.

The alignment shows a high degree of conservation across many species, particularly in the regions highlighted by the red boxes. The green box highlights a specific column, likely representing a conserved residue or a site of interest. The alignment is presented in a grid format with species names on the left and amino acid sequences in the center.