

Multiple sequence alignment of representative SET-domain sequences. The CLUSTAL X (1.83) multiple alignment of 113 representative SET-domain sequences used to reconstruct the maximum likelihood (Fig. 1) and maximum parsimony (Additional file 9) phylogenies.

SET3

SET4

E(2)

SET1

ashl

Su(var)-3-9

pr-set7

SET5

SET6

SET7