Figure 7. The phylogenetic tree of human bromodomains. Sequence similarity–based dendrogram of the human bromodomains was generated using the neighbor-joining method with MEGA (Kumar et al. 2004). Sequences of the human bromodomains were obtained from the SMART database (Letunic et al. 2004) and aligned with SMART bromodomains' hidden Markov models using Hmmalign (Sonnhammer et al. 1997). (Modified from Zhang et al. 2010.)

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