Fig. S4 (3 of 4)
Sequence alignment of prokaryotic and eukaryotic DHNA-CoA thioesterases and related proteins. Proteins highlighted in red have been shown to bear DHNA-CoA thioesterase activity in vitro and in vivo (Slr0204; DHNAT1-2) or in vitro (EscCo 1VH9). 2HX5, 2FS2, and 1VH9 indicate PDB numbers of reference tri-dimensional structures used to adjust the alignment. Corresponding secondary structures are shown on top. Identical residues are shaded in black, similar ones in grey. The TE (Thioester-active Enzymes) nomenclature and classification is from (Cantu et al., 2010). The blue and red arrows point to the conserved catalytic residue in the Slr0204-type (TE12) and 4HBT-Il (TE11) subfamilies, respectively. The red and yellow boxes indicate the 4HBT-II and Paal motifs, respectively, as defined in (Dillon and Bateman, 2004). Full names and taxonomic origin of species, and protein accession numbers are listed in Table S2.