Supplementary Fig. S1: Phylogenetic relationship among established and novel antizyme proteins. The dendrogram was constructed using ClustalW's built-in neighbour-joining algorithm [Higgins DG, Thompson JD, Gibson TJ (1996) Methods Enzymol. 266: 383-402]. Before tree calculation from the antizyme multiple alignment, all columns containing gaps were removed. A red rectangle indicates novel antizymes from the *Hemiascomycetes*. Major taxa are indicated on the right. The species abbreviations are as follows: SCER = *Saccharomyces cerevisiae*; SPAR = *S. paradoxus*; SMIK = *S. mikatae*; SBAY = *S. bayanus*; SKUD = *S. kudriavzevii*; SCAS = *S. castellii*; SKLU = *S. kluyveromyces*; KWAL = *Kluyveromces lactis*; AGOS = *Ashbya gossypii*; NEUCR = *Neurospora crassa*; BOTRY = *Botrytis cinerea*; EMENI = *Emericella nidulans*; SCHPO = *S. pombe*; PNEUMO = *Pneumocystis carinii*; CHICK = *Gallus gallus*; XENLA = *Xenopus laevis*; FUGU = *Takifugu rubripes*; TORMA = *Torpedo marmorata*; DROME = *Drosophila melanogaster*; AEDES = *Aedes aegypti*; ANOPHE = *Anopheles gambiae*; BOMBYX = *Bombyx mori*; CAEEL = *C. elegans*; PRIPA = *Pristionchus pacificus*; ONCVO = *Onchocerca volvulus*