



Figure S2. Multiple sequence alignment of *T. gondii* ATrx1, mouse nucleoredoxin (MmNrx1), *Trypanosoma brucei* tryparedoxin (TbTryX), and related *Babesia bovis* protein (Bbov). The tryparedoxin domains, which represent a subfamily of Trxs, are marked (TryX) and the predicted location of the WCPPC active site is shaded red. TryX domain 1 is predicted to be inactive as is that the TryX domain 2 of *B. bovis*. The hydrophobic region of the putative signal anchor region of ATrx1 and the predicted signal sequence of the *B. bovis* protein are shaded yellow. The core of the ATrx1 TMD that is predicted by some but not all transmembrane prediction programs, is underlined. The region that is absent in the predicted ATrx1 protein resulting from alternative splicing is shaded blue. Numbers above the alignment mark residues at the boundaries of deletion constructs discussed in the text. The sequences were aligned using Clustal except that the N-terminal half of tryparedoxin was aligned based on similarity to NCBI conserved domain cd03009. Residues in the aligned sequences that are identical to ATrx1 are shaded black and those that are similar are shaded gray. Gaps are indicated by dashes. Accession numbers are ATrx1, EU555314; *Mus musculus* nucleoredoxin, X92750; *T. brucei* tryparedoxin CAA07003, and *B. bovis*, BBOV_II002190 (systematic gene name). *Eimeria tenella* also possesses an apparent orthologue of ATrx1; it is not shown since the various gene models differ significantly from one another.