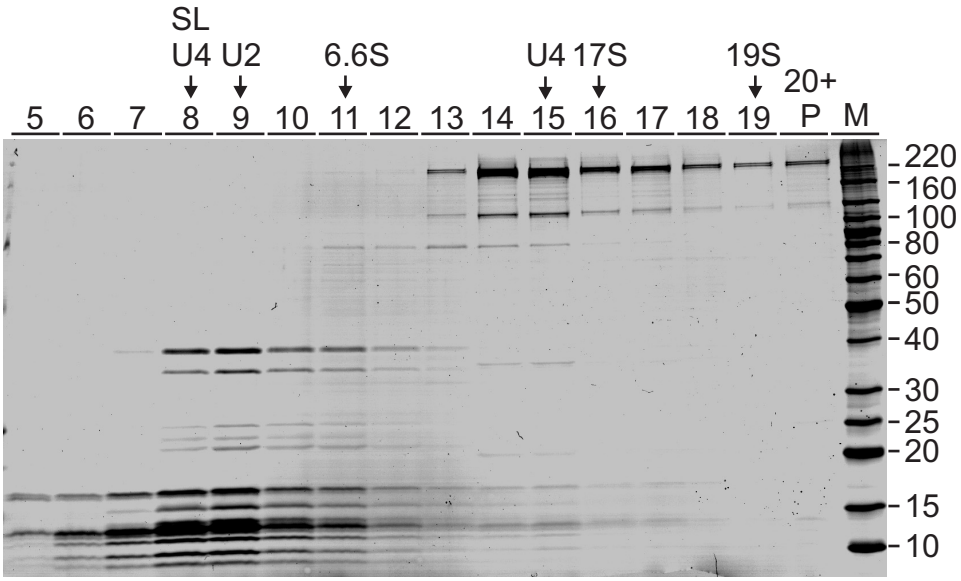

FIG. S1. Sedimentation analysis of SmD1-P-copurified proteins. An eluate of a standard SmD1-PTP purification was sedimented through a linear 10-40% sucrose gradient which was fractionated from top to bottom. Fraction 20 was combined with the resuspension of pelleted material (20 + P). Proteins from each fraction were separated by SDS-PAGE and stained with Sypro ruby as described in Schimanski *et al.* (2005, Mol. Cell. Biol. 25:7303-7313). Marker proteins with known S-values were analyzed in parallel gradients. Total RNA was prepared from aliquots of the gradient fractions and analyzed by the primer extension assays specified in the methods section. Since the RNAs were only partially stable during the run of the experiment, peak abundances could only be determined for the SL RNA (SL) and the U2 and U4 snRNAs. Sizes of marker (M) proteins are specified on the right.

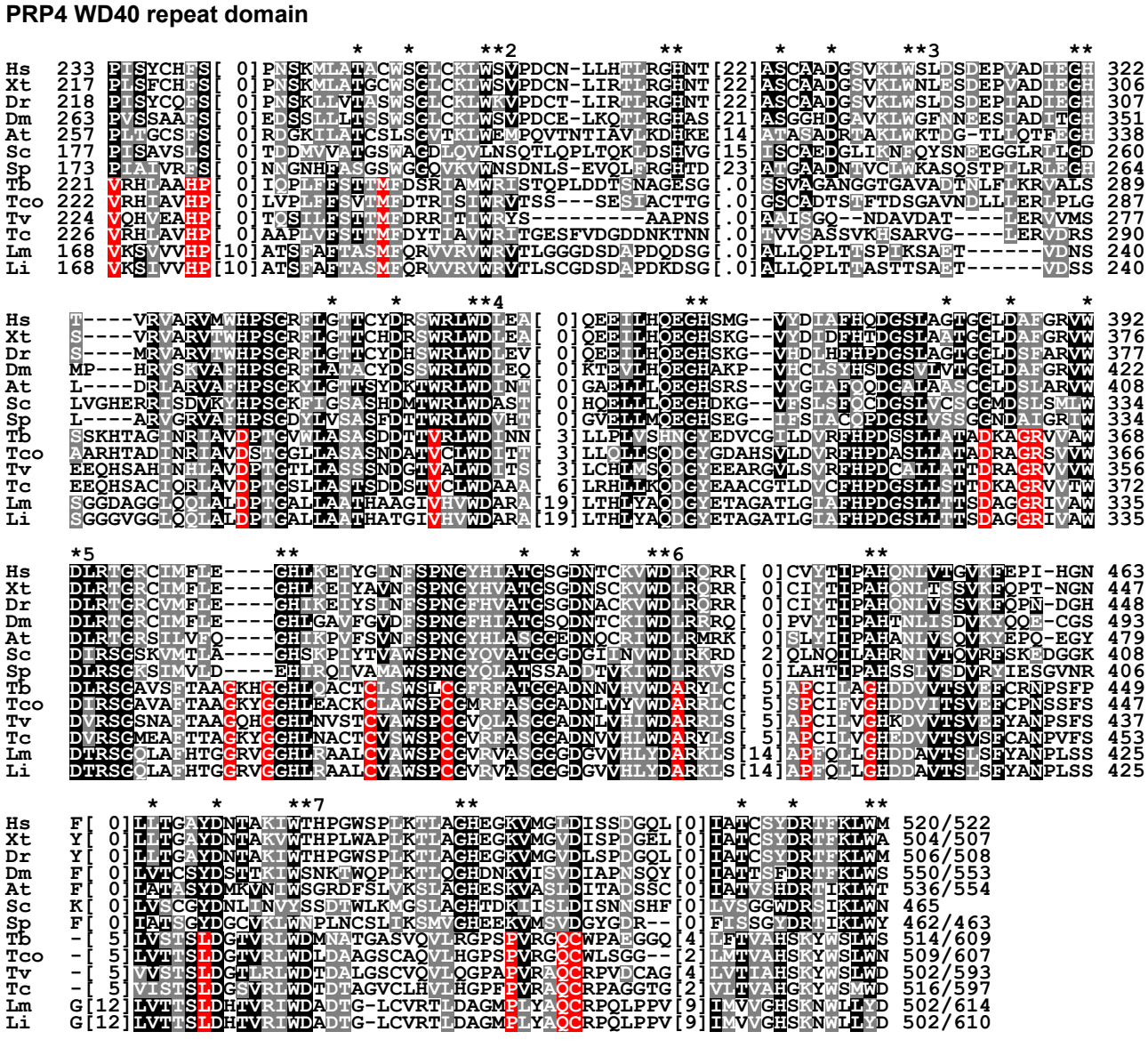

FIG. S2. ClustalW sequence alignment of the PRP4 WD repeat domains from *H. sapiens* (Hs, NP_004688), *X. tropicalis* (Xt, AAH61324), *D. rerio* (Dr, NP_956049), *D. melanogaster* (Dm, NP_648990), *A. thaliana* (At, AAM14969), *S. cerevisiae* (Sc, YPR178W), *S. pombe* (Sp, SPAC227.12), *T. brucei* (Tb, Tb10.70.7190), *T. congolense* (Tco, congo928f05.p1k_5), *T. vivax* (Tv, Tviv89a04.p1k_1), *T. cruzi* (Tc, Tc00.1047053506855.340), *L. major* (Lm, LmjF21.1120), and *L. infantum* (Li, LinJ21_V3.1360). Numbers above the sequences indicate the beginning of a WD40 repeat and asterisks mark key residues of the WD40 motif. Numbers at the beginning and at the end of each row indicate the sequence positions. Positions with more than 50% similarity or identity are shaded in gray and black, respectively. Parasite-specific identities without similar residues in the sequences of other eukaryotes are shaded in red. Numbers of amino acids in stretches of limited or no sequence conservation are denoted in parentheses.

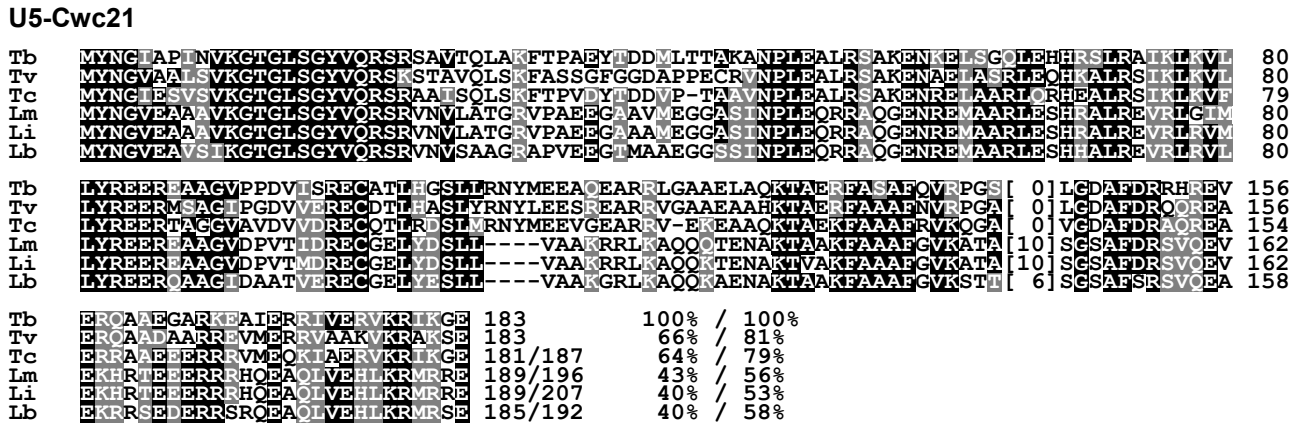

FIG. S3. ClustalW sequence alignment of trypanosomatid U5-Cwc21 orthologues from *T. brucei* (Tb09.160.2110), *T. vivax* (Tviv1778d04.q1k_1), *T. cruzi* (Tc00.1047053504797.130), *L. major* (LmjF01.0190), *L. infantum* (LinJ01_V3.0190), and *L. brasiliensis* (Lb, LbrM01_V2.0220). Positions with more than 50% similarity or identity are shaded in gray and black, respectively. Numbers of amino acids in stretches of limited or no sequence conservation are specified in parentheses. The identity/similarity values specified at the end of each sequence were derived from pair-wise comparisons with the *T. brucei* sequence using the EMBOSS program (http://www.ebi.ac.uk/Tools/emboss/align/) at default parameters.