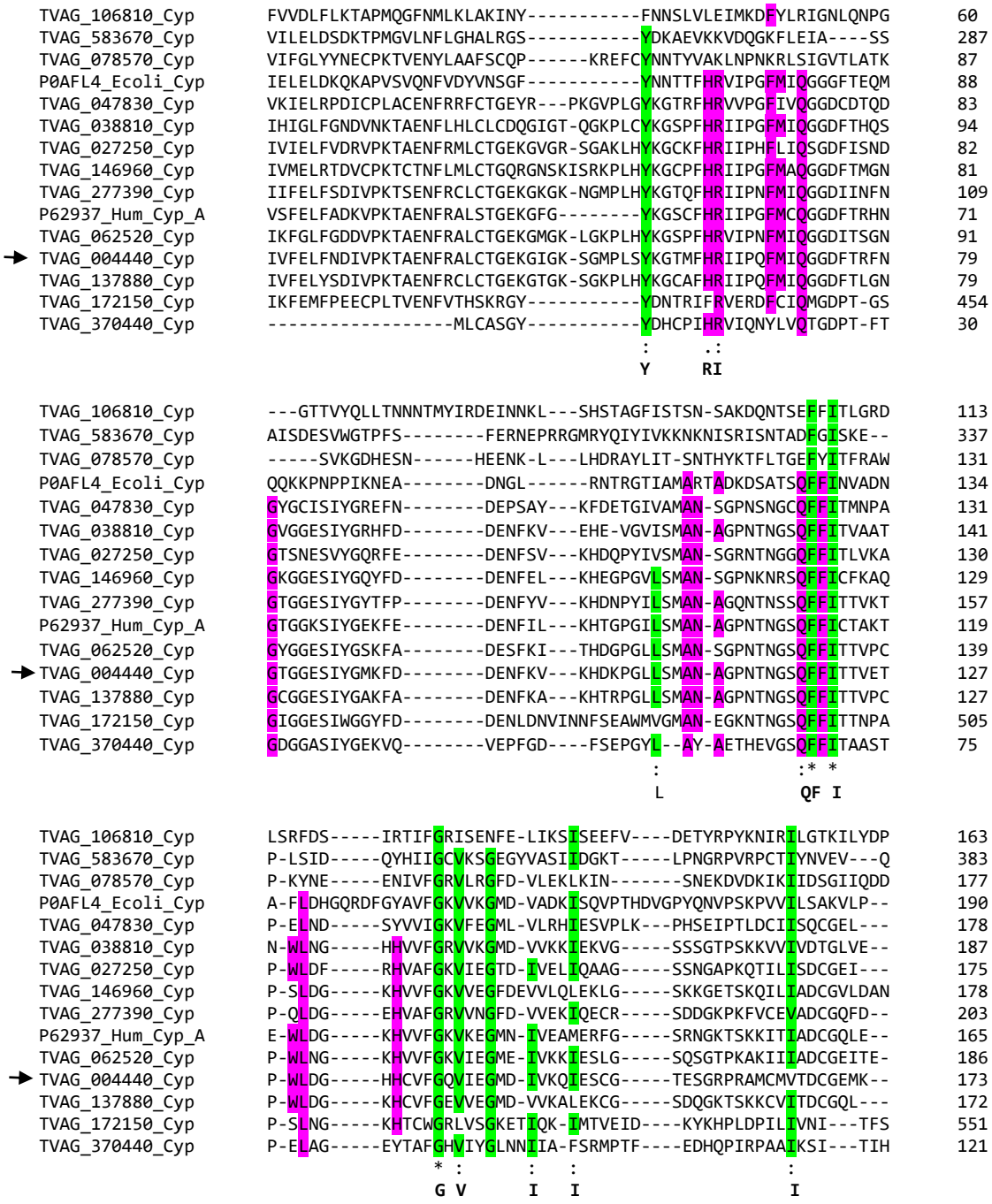

Figure S2. Sequence alignments of the CLD of *T. vaginalis* cyclophilins. Alignments were run with ClustalW2 tool embedded in EMBOSS-Needle[42]. Amino acids of the catalytic site in CLD in pink, conserved amino acids of CyPs from *T. vaginalis* in green. "**:**" Indicates strong groups fully conserved, "*****" Indicates a single fully conserved residue. Arrows indicate TvCyP19 sequence. Sequences were retrieved from UniProt database[25] (https://www.uniprot.org/, Release 2023_02).