

Tetrahymena Toxoplasma	MREVISIHVGQGGI QVGNACWELFCLE HGIQPDGQMP SDKTIGGGDDA FNTFFSETGAGK 60 MREVISIHVGQAGI QIGNACWELFCLE HGIQPDGQMP SDKTIGGGDDA FNTFFSETGAGK 60 *****:*****
Tetrahymena Toxoplasma	HVPRAVFLDLEPTV IDEVRTGTYR QLFHPEQL ISGKEDAANNFARGH YTIGKEIVDLCLD 120 HVPRCVFLDLEPTV IDEVRTGTYR HLFHPEQL ISGKEDAANNFARGH YTIGKEIVDLSDL 120 *****:*****
Tetrahymena Toxoplasma	L136F RIRKLADNCTGLQGFL VFNSVGGGTGSG LGSLLLERILSVDY GKKS KLGFTIYPSPVSTA 180 RIRKLADNCTGLQGFL MFNAVGGGTGSG LGCLLLERILSVDY GKKS KLNFCSWPSPVSTA 180 *****:*****
Tetrahymena Toxoplasma	T239I VVEPYNSILSTHSIL LEHTDVAVMLDNEAIY DICRRNLDIERPTY TNILNR LIAQVISSLTA 240 VVEPYNSVLSTHSIL LEHTDVAVMLDNEAIY DICRRNLDIERPTY TNILNR LIAQVISSLTA 240 *****:*****
Tetrahymena Toxoplasma	R243C/S I252L SLREDGALNVDT ITEFQTNLVPYPRIH FMLSSYAPI ISAEKAYHEQL SVAEITNSAFE PAN 300 SLREDGALNVDT ITEFQTNLVPYPRIH FMLSSYAPI ISAEKAYHEQL SVAEITNSAFE PAS 300 *****:*****
Tetrahymena Toxoplasma	MMAKCDPRHGKYMAC SMYRGDVVPKDVN ASIAITIKTKRTIQF VWDWCPTGFKV GINYQPP 360 MMAKCDPRHGKYMAC CLMYRGDVVPKDVN AAVATIKTKRTIQF VWDWCPTGFK CGINYQPP 360 *****:*****
Tetrahymena Toxoplasma	TVVPGGDLAKVMRAV CMISNSTAIAEVFSR LDHKFDL MYAKRAFVHWYVGEG MEEGEFSE 420 TVVPGGDLAKVMRAV CMISNSTAIAEVFSRM DHKF LYAKRAFVHWYVGEG MEEGEFSE 420 *****:*****
Tetrahymena Toxoplasma	AREDLAALEKDYEEVG IETAEEGEGEE GY ----- 449 AREDLAALEKDYEEVG IETAEEGEGEE GYGDEY 453 *****:*****

Supplemental Figure S1: A clustal alignment of the amino acid sequence of *T. gondii* α 1-tubulin and *T. thermophila* α -tubulin. Residues that differ between the two proteins are highlighted in yellow. Locations of the point mutations H28Q, L136F, R243S, T239I and I252L that were introduced into *T. thermophila* α -tubulin are boxed. Individual amino acids are colored to reflect their chemical properties: blue: acidic; green: hydroxyl/amine/basic/Q; magenta: basic; and red: small, hydrophobic (including aliphatic Y).