

O15729 4 PKVFFDITIG.[2].KAGRIVMELFNDIVPKTAENFRCLCTGE.[6].YKGCGFHHRVIKDFMIQGGDFTRHNGTGG 77 *E. histolytica*
AAQ94596 11 PIVFFDVSIG.[2].EVGRMKIELFADIVPKTAENFRQFCTGE.[9].YKGCFFHHRVIKDFMIQGGDFVNGDGTGI 87 Zebrafish
NP_610224 17 PVVFFDI AVG.[2].EIGRMIFELFADTVPRTAENFRQFCTGE.[9].YKGASFHHRVIKDFMIQGGDFVQGDGTGV 93 Fruit fly
B53522 179 PRVFFDISID.[2].PAGRIEFELFADVVPKTAENFRALCTGE.[11].YKGCFFHRIIPQFMCQGGDFTRMNGTGG 257 *T. gondii*
AAR11779 4 PRVFFDVTAN.[2].PVGRIMMELRGDVVPKTAENFRALCTGE.[4].YKGSPPFHRVIPSFMCQGGDFTRQNGTGG 75 *C. farreri*
AAC05639 4 PIVFFDITAD.[2].PVGRIEMELYADDVPKTAENFRALCTGE.[11].FKGSTFHRVIPNFMCQGGDFTRNGTGG 82 *C. reinhardtii*
EAA42921 7 DKVFFDITIG.[2].PLGRITMGLFGSIVPKTAENFKKLCTGE.[4].YKGSTFHRVIPKFMQGGDFTNHNGTGG 78 *G. lamblia*
1AK4_A 4 PTVFFDIAVD.[2].PLGRVSFELFADKVPKTAENFRALSTGE.[4].YKGSCHFRIIPGFMCQGGDFTRHNGTGG 75 Human
CAE76450 12 PLVFFDITLG.[2].PLGRITFELFKDVVPKTAENFRQFCTGE.[10].YKGSKFHRIIPFMCQGGDFLNGDGTGS 89 *N. crassa*

O15729 78 KSIYGTKEADEAFTVKH.[1].KPGMLSMANAGPNTNGSQFFITITVPCPWL DKGHVVFVGQVVEGYDVVKMIENN 147 *E. histolytica*
AAQ94596 88 CSIYRGFFADENFRMKH.[1].GPGLLSMANSGPNTNGSQFFITCTKCDWLDKGHVVFVGKVVDGLLMRKIENV 157 Zebrafish
NP_610224 94 TSIYGNTFGDENFTLKH.[1].SPGLLSMANSGKETNGSQFFITCAKNFLDKGHVVFGRVLDGLLMRKIENV 163 Fruit fly
B53522 258 ESIYGEKFADENFSYKH.[1].EPFLLSMANAGPNTNGSQFFITITVPCPWL DKGHVVFVGKVVAQGEVVKMMEAE 327 *T. gondii*
AAR11779 76 KSIYGEKFADENFTLKH.[1].GPGVLSMANAGPNTNGSQFFLCTARTEWLDKGHVVFVGSGMDVVKKIESY 145 *C. farreri*
AAC05639 83 ESIYGEKFADENFKHRH.[1].GPGVLSMANAGPNTNGSQFFLCTVETAWLDKGHVVFVGKVCKGMDVVKVKEGY 152 *C. reinhardtii*
EAA42921 79 KSIYGAKEPDENFEIKH FVGCLSMANAGPNTNGSQFFLTVADTAWLDKGHVVFGRVLDGMDVVKAIETT 147 *G. lamblia*
1AK4_A 76 KSIYGEKFEDENFILKH.[1].GPGILSMANAGPNTNGSQFFICTAKTEWLDKGHVVFVGKVKEGMNIVEAMERF 145 Human
CAE76450 90 .[1].CIYGTKEFADENFILKH.[1].TPGLLSMANAGPNTNGSQFFITITVPTPFLDKGHVVFVGKVVDGMDVVKKMENT 160 *N. crassa*

O15729 148 .[7].PKKAVVIADCG 165 *E. histolytica*
AAQ94596 158 .[7].PKLPVVVSQCG 175 Zebrafish
NP_610224 164 .[7].PKLPVTISQCG 181 Fruit fly
B53522 328 .[6].PKCAVEISSCG 344 *T. gondii*
AAR11779 146 .[6].TSEKIIVADCG 162 *C. farreri*
AAC05639 153 .[6].TRATFAIADCA 169 *C. reinhardtii*
EAA42921 148 .[7].PVEKVVVADCG 165 *G. lamblia*
1AK4_A 146 .[6].TSKKITIADCG 162 Human
CAE76450 161 .[9].PNLDVVVIAQCG 180 *N. crassa*

Figure S3. Sequence alignment for the most similar members of the PPIase CyP-type and the 18 kDa CyP from *Entamoeba histolytica*. All proteins are identified with NCBI Accession number, and the alignment was carried out in CDD data base [45]. Amino acids in the active site are in yellow boxes and conserved residues are in gray boxes.