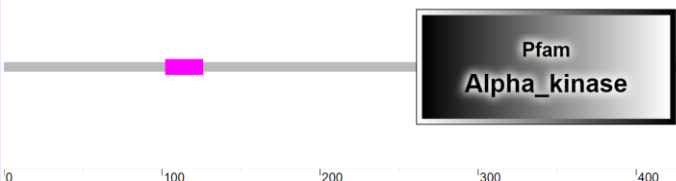


# Characterization of p53 family homologs in evolutionary remote branches of Holozoa

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**Supplementary material 7: Phmmer of the putative p53 family DBD sequence from *Entamoeba histolytica* (Q868M8). Results with E-value lower than 1 are reported. The red line depicts E-value lower than 0.01. The analysis identifies only the sequence itself and two mutant versions of the same protein, compared to the thousands of significant hits including human p53, p63 and p73 for our novel characterized p53 family homologs in Supplementary material 2. The lower part of the table shows the most significant domain found in *E. histolytica* Q868M8 by SMART, which is highly similar to the alpha kinase Pfam domain. No similarities with the p53 family DBD by contemporary validated methods were identified.**

Phmmer of putative DBD from <i>Entamoeba histolytica</i> (Reference Proteomes database)			
Target	Description	Species	E-value
Q868M8_ENTHI	<i>Q868M8, annotated as “p53-like protein”</i>	<i>Entamoeba histolytica</i>	5.30E-129
B1N3R5_ENTHI	<i>Uncharacterized protein (mutant of Q868M8)</i>	<i>Entamoeba histolytica</i>	8.30E-129
C4MBK2_ENTHI	<i>p53-like protein (mutant of Q868M8)</i>	<i>Entamoeba histolytica</i>	4.00E-128
A0A0N5AEU6_9BILA	Uncharacterized protein	<i>Syphacia muris</i>	0.075
A0A080K1V4_9NEIS	Transcriptional regulator	<i>Snodgrassella alvi</i> SCGC AB-598-O02	0.083
C4LWZ0_ENTHI	Elongation factor 2 kinase putative	<i>Entamoeba histolytica</i>	0.11
A0A0A1UFE6_ENTIV	Elongation factor 2 kinase, putative	<i>Entamoeba invadens</i> IP1	0.19
A0A183EY03_9BILA	Uncharacterized protein	<i>Gongylonema pulchrum</i>	0.46
The most significant Pfam domain found in <i>Entamoeba histolytica</i> (Q868M8) by SMART			
		Domain	E-value
		Low_complexity (102 – 126 aa)	NA
		Pfam: alpha_kinase (261 – 425 aa)	2.5E-8