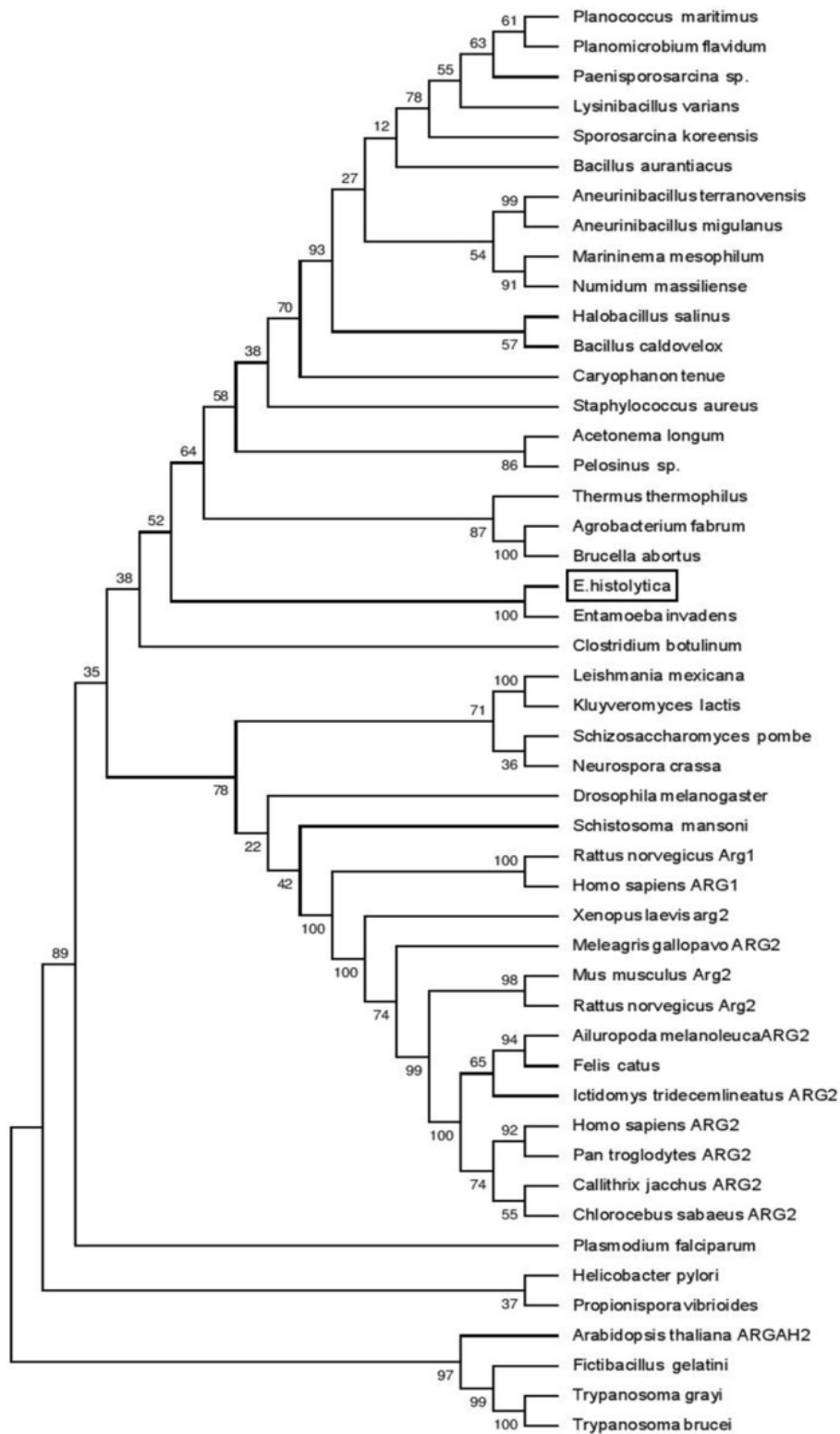


### Supplementary figure legends

**Fig. S1** Phylogenetic tree of arginase and related proteins. Arginases and related proteins present in PDB and NR database constructed by maximum likelihood method. The numbers below and above the branch points denote the confidence levels of the relationship of the paired sequences determined by boot strap statistical analysis. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site.

**Fig. S2** Determination of molecular mass by size exclusion chromatography. Standard curve Log of molecular weight Versus  $V_e/V_o$  was derived from the elution profile of standard protein on Superdex 200 gel filtration column.  $V_e$  is peak elution volume and  $V_o$  is the void volume of the column. The standards used were as follows: 1. Blue dextran (2000kDa) 2. Conalbumin (75kDa) 3. Bovine serum albumin (66kDa) 4. Ovalbumin (43kDa) 5. Lysozyme 14kDa).

Fig. S1



**Fig. S2**

