

Table S3 Evolutionary pressures in the phylogenetic groups. For each protein group, calculated selective pressure and positive selection sites ascertained using PAML (ver. 4.9) are also displayed (Yang, 2007; Xu and Yang, 2013).

Query ^a	Domain	Number of sequences	Global d _N /d _S estimated in PAML (M0)
group1	fungi	5	0.13437
group2	fungi	2	0.00365
group3	fungi	3	0.00373
group4	fungi	3	0.19951
group5	fungi	7	0.05046
group6	fungi	2	0.12459
group7	amoeba & bacteria	5	0.00782
group8	bacteria	11	0.20365
group9	bacteria	4	0.00924
group10	bacteria	2	0.08421
group11	fungi	4	0.02745
group12	fungi	7	0.05325
group13	fungi	5	0.14272
group14	fungi	4	0.12259
group15	fungi	10	0.13256
group16	fungi	5	0.03671
group17	fungi	4	0.13805
group18	fungi	6	0.13668
group19	fungi	6	0.16407
group20	bacteria	4	0.00641
group21	fungi	2	0.11683

^aIn this study, the classification of groups was performed based on the phylogenetic tree, protein domains, and specific sites.