

Table S2. Completeness of proteomic data estimated using 303 BUSCO gene families that are evolutionarily conserved in eukaryotes. The two taxa with significantly lower hits to BUSCO gene families are highlighted in the yellow field.

Protein data	Full-length	Proportion	Fragmented	Proportion	Missing	Proportion
<i>C. merolae</i>	283	93.4%	10	3.3%	10	3.3%
<i>G. phlegrea</i>	280	92.4%	6	2.0%	17	5.6%
<i>G. sulphuraria</i>	276	91.1%	7	2.3%	20	6.6%
<i>P. purpureum</i> + <i>aerugineum</i>	276	91.0%	9	3.0%	18	6.0%
<i>R. marinus</i>	274	90.4%	8	2.6%	21	7.0%
<i>G. chorda</i>	272	89.8%	7	2.3%	24	7.9%
<i>C. crispus</i>	231	76.2%	23	7.6%	49	16.2%
<i>P. umbilicalis</i>+<i>P. yezoensis</i>	171	56.5%	75	24.8%	57	18.7%