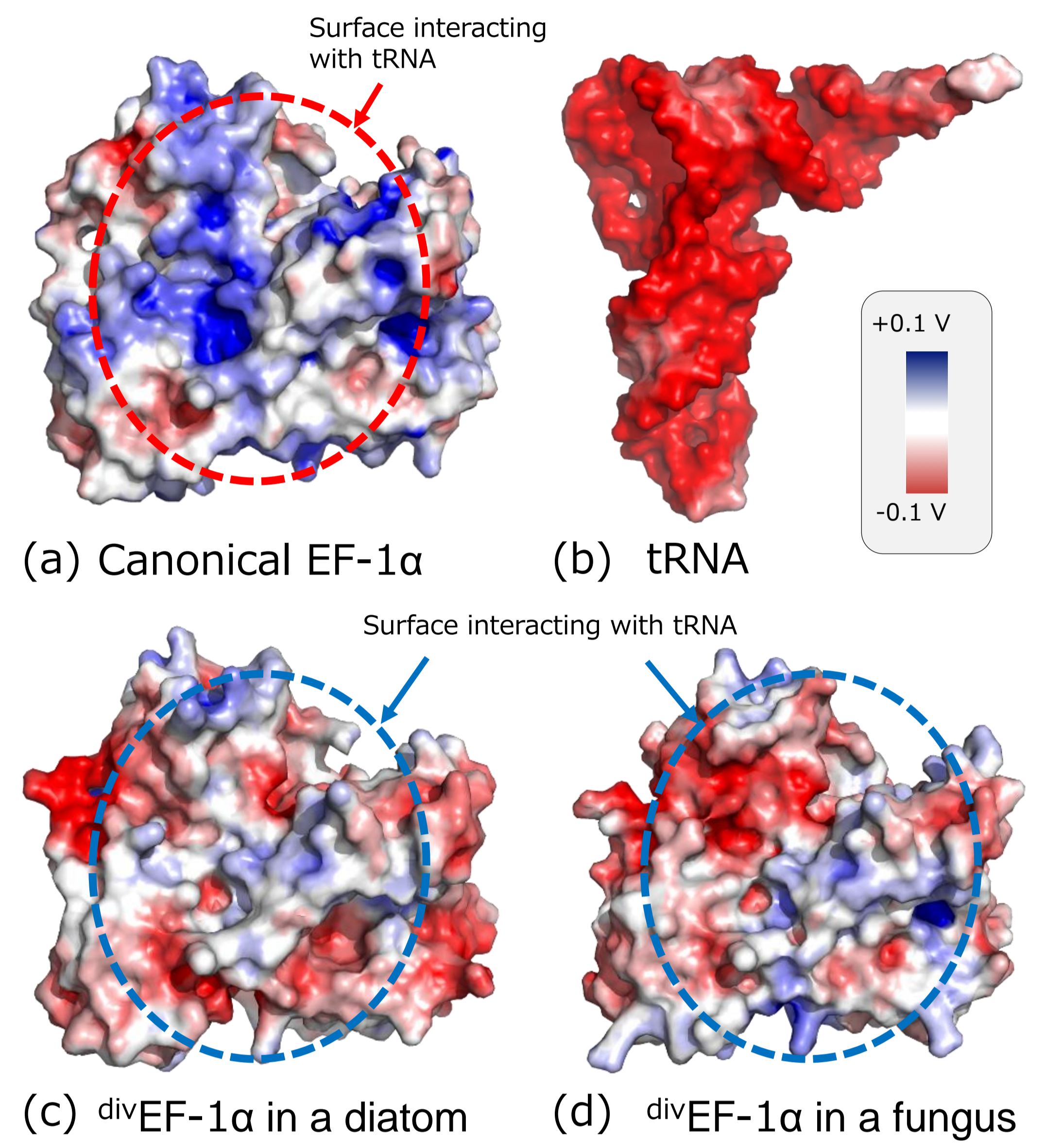


## Biological Sciences

### *In silico* structural modeling and analysis of translation elongation factor 1 $\alpha$ proteins

Translation elongation factor-1 $\alpha$  (EF-1 $\alpha$ ) interacts with tRNA during protein synthesis. Some eukaryotes appeared to possess highly divergent EF-1 $\alpha$  ( $^{div}$ EF-1 $\alpha$ ), implying that these proteins lack the ability to interact with tRNA. We modelled the tertiary structures of  $^{div}$ EF-1 $\alpha$  and validated their model structures by molecular dynamics simulations. We found that the molecular surfaces of  $^{div}$ EF-1 $\alpha$  are negatively charged partly, suggesting that they may not interact with negatively charged tRNA as strongly as the canonical EF-1 $\alpha$  with the positively charged surfaces.

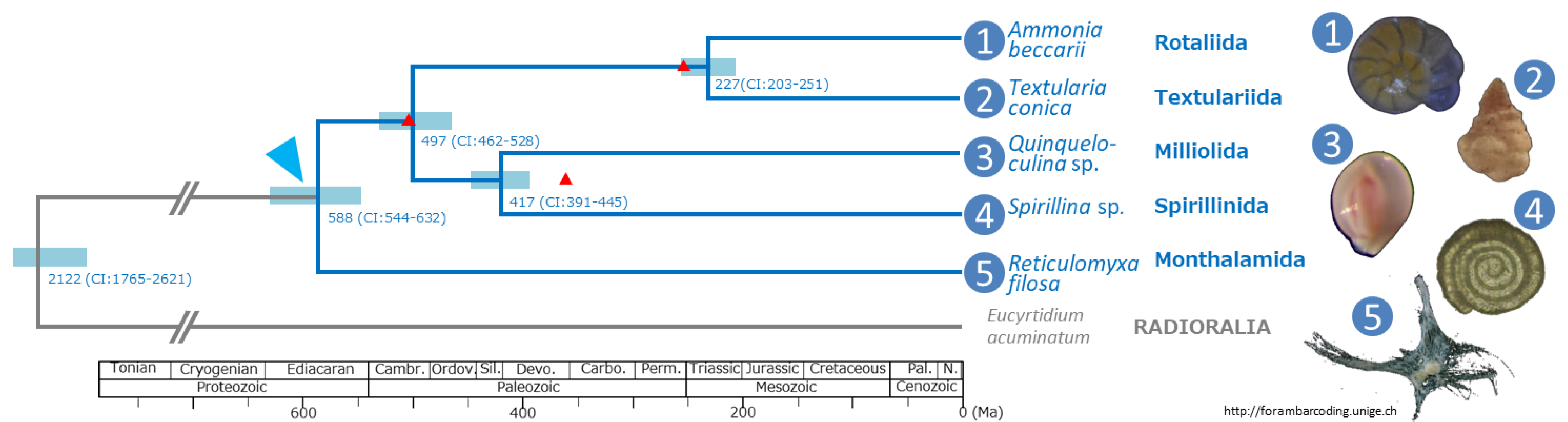
**Fig. 1: EF-1 $\alpha$  and tRNA structures and surface electrostatic distribution.** (a) EF-1 $\alpha$  structure of an archaeon (PDB ID: 3WXM). (b) tRNA structure (PDB ID: 1EHZ). (c & d)  $^{div}$ EF-1 $\alpha$  models. Dotted lines in (a), (c) and (d) indicate the surfaces interacting with tRNA.



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### Robust estimations of the phylogenetic relationship and divergence time among five major orders in Foraminifera

Prior to this study, the major branching order in Foraminifera has not been resolved with confidence. We obtained the RNA-seq data (~0.7-1.2 Gb) from the species representing orders Textulariida, Spirillinida, Milliolida and Rotalliida, and assembled a 157-protein alignments (41,365 positions). Our phylogenomic analyses recovered the robust relationship among the five orders, and estimated ~588 Mya for the divergence of Foraminifera (highlighted by a blue arrowhead) with a 95% confidence of ~544-632 Mya in the Ediacaran.



**Fig. 2: Chronogram of five foram species representing the five major orders.** The foram clade was shown in blue. We generated the sequence data from the species labelled as ①-④. Node ages were inferred using Bayesian inference with an uncorrelated relaxed clock model. Values at nodes indicate ages estimated by median heights of clade, blue bars at nodes represent 95% confidence intervals and red triangles correspond to the lower constraints based on fossil records.