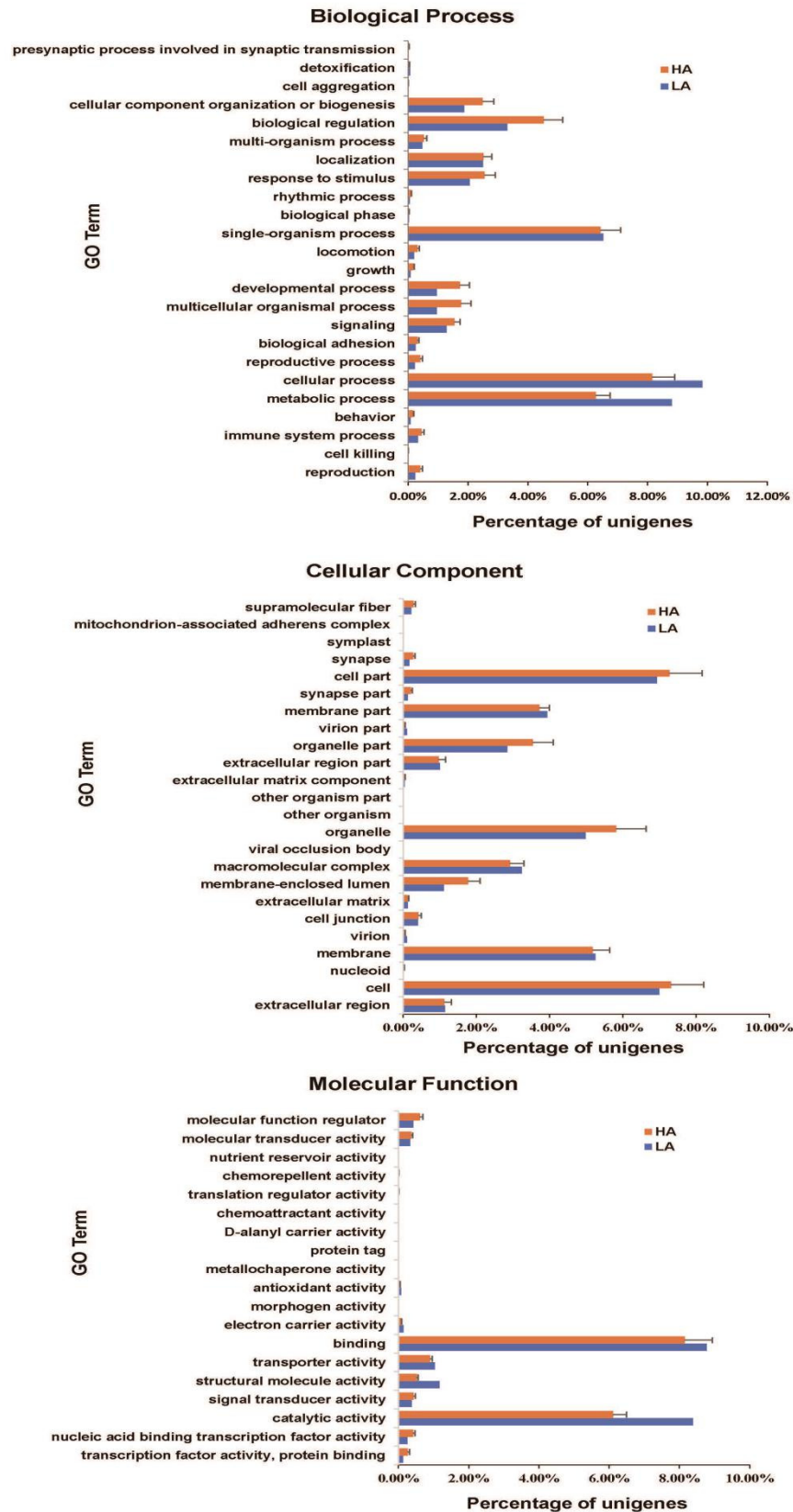
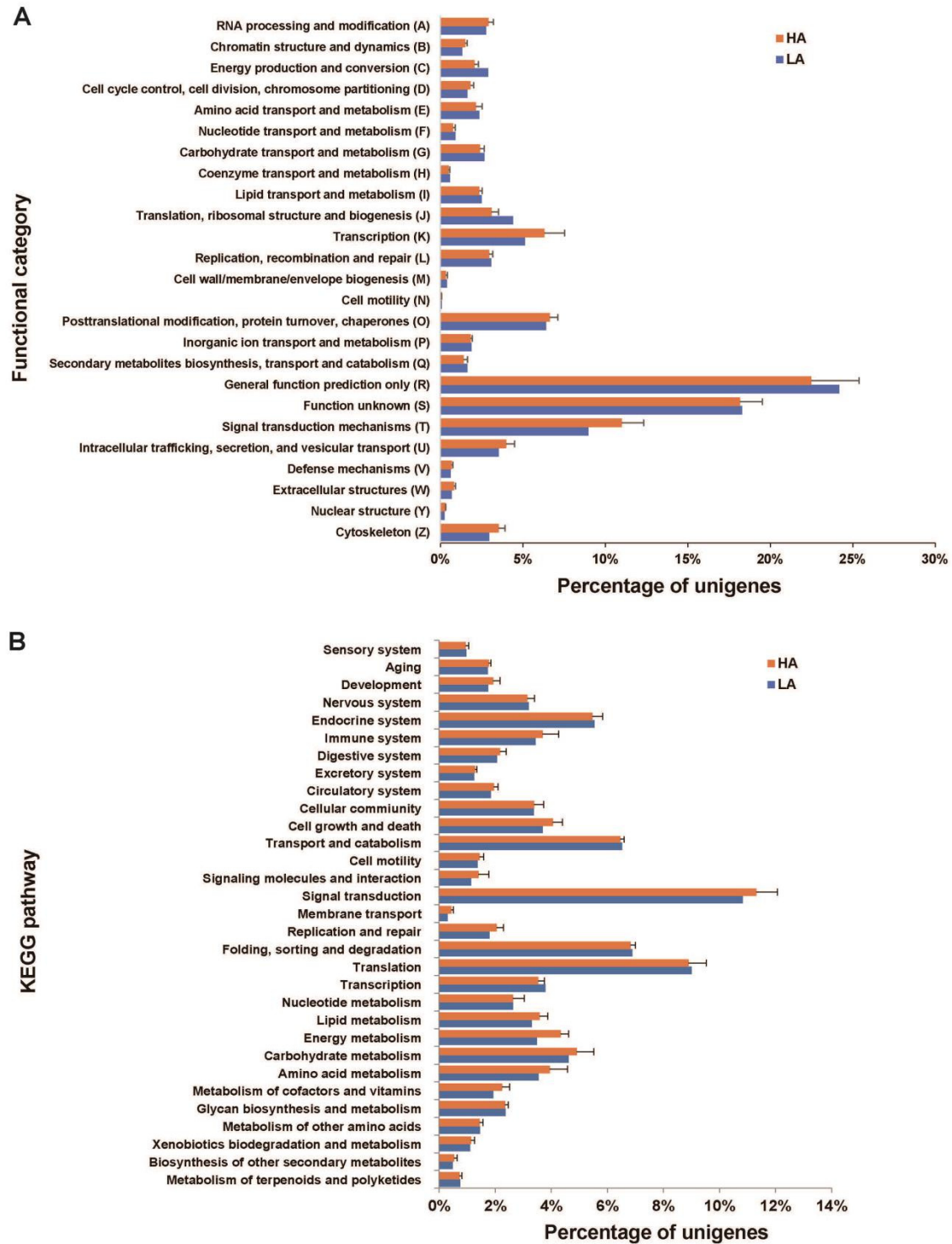


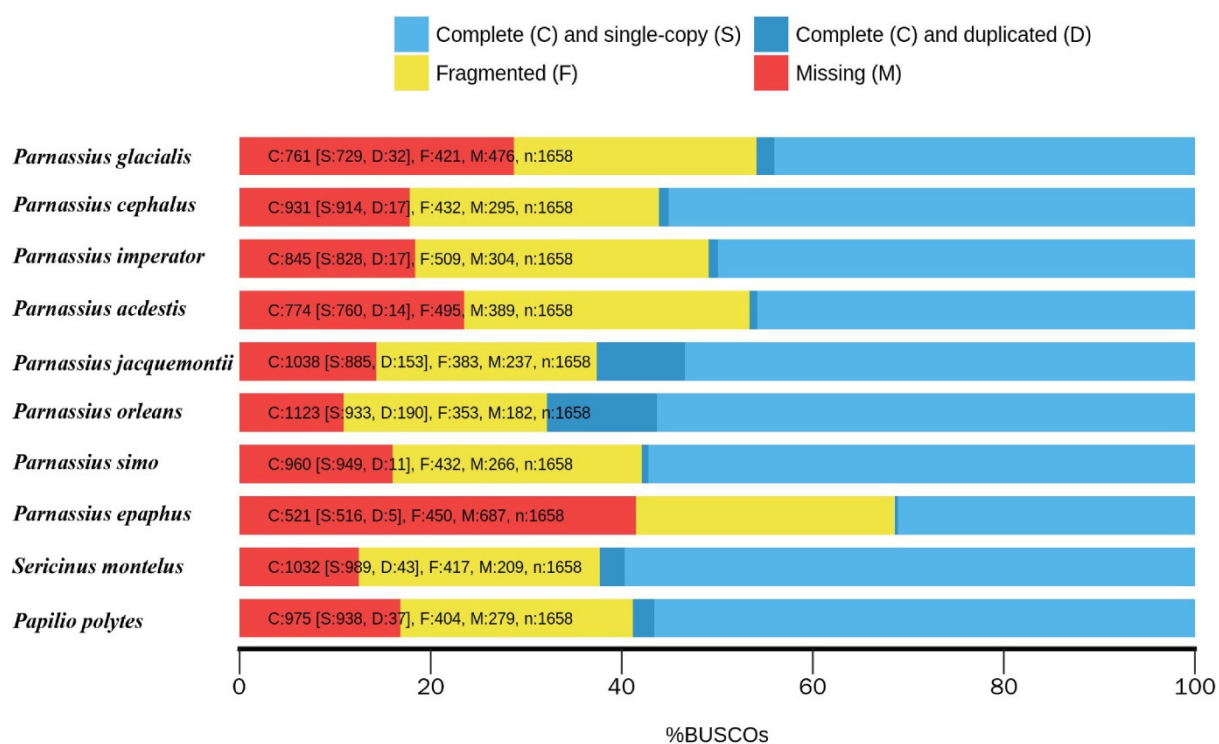
**Figure 1.** Results of annotation in the NR database for *Parnassius* species (*P. glacialis* (left) and *P. epaphus* (right) as examples).



**Figure 2.** Characteristics of GO term of biological process, cellular component and molecular function for *Parnassius* species (HA, *Parnassius* species colonized at high-altitude habitats except *Parnassius glacialis*; LA, *Parnassius glacialis* colonized at low-altitude habitats).

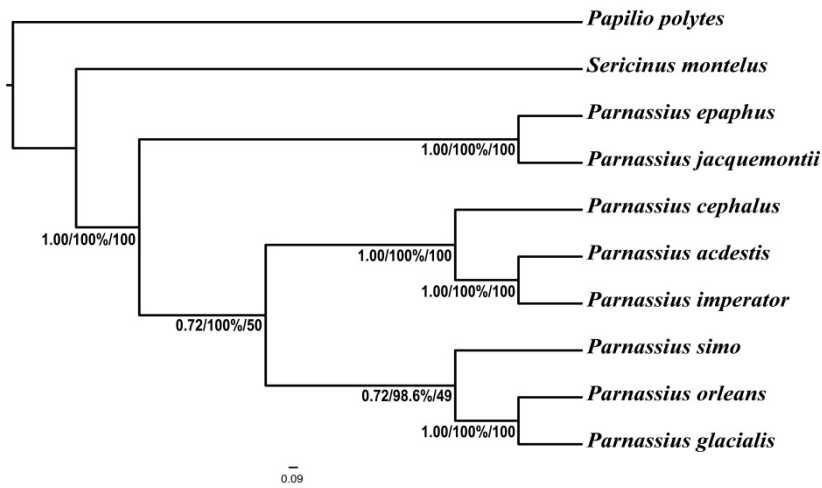


**Figure 3.** Characteristics of eggNOG functional category (A) and KEGG pathway classification (B) of unigenes for *Parnassius* species.

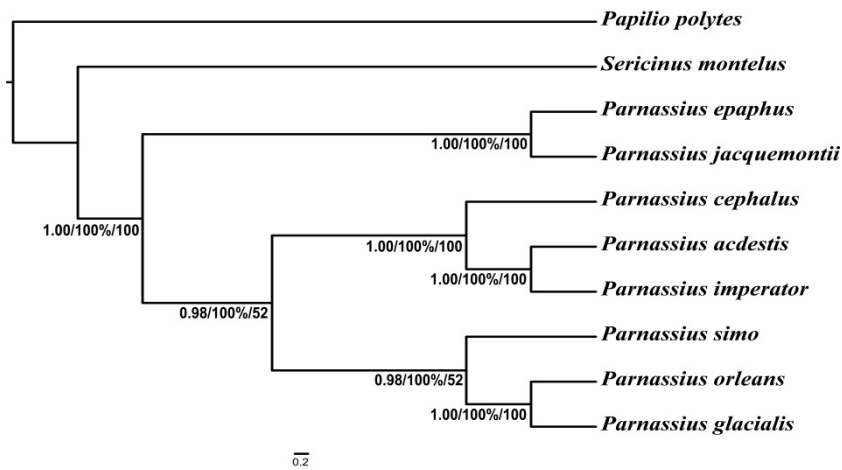


**Figure 4.** BUSCO analysis of transcriptome completeness. BUSCO v4.0.2 was run using insecta\_odb9 dataset.

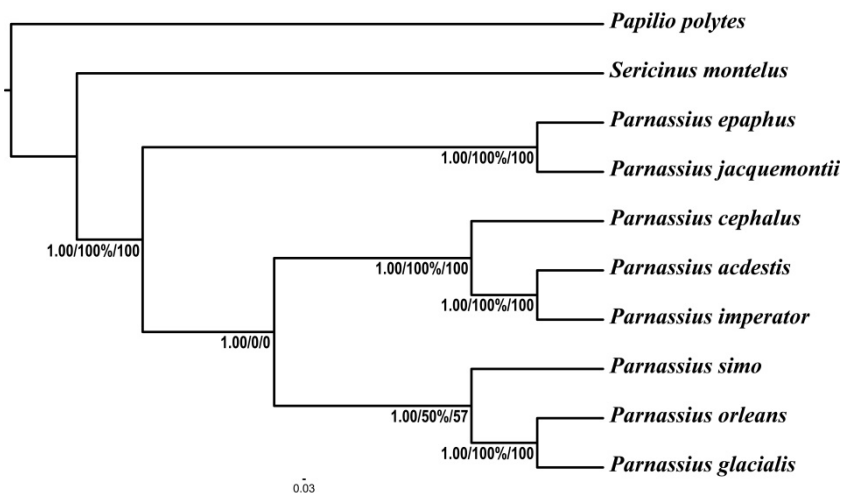
(a)



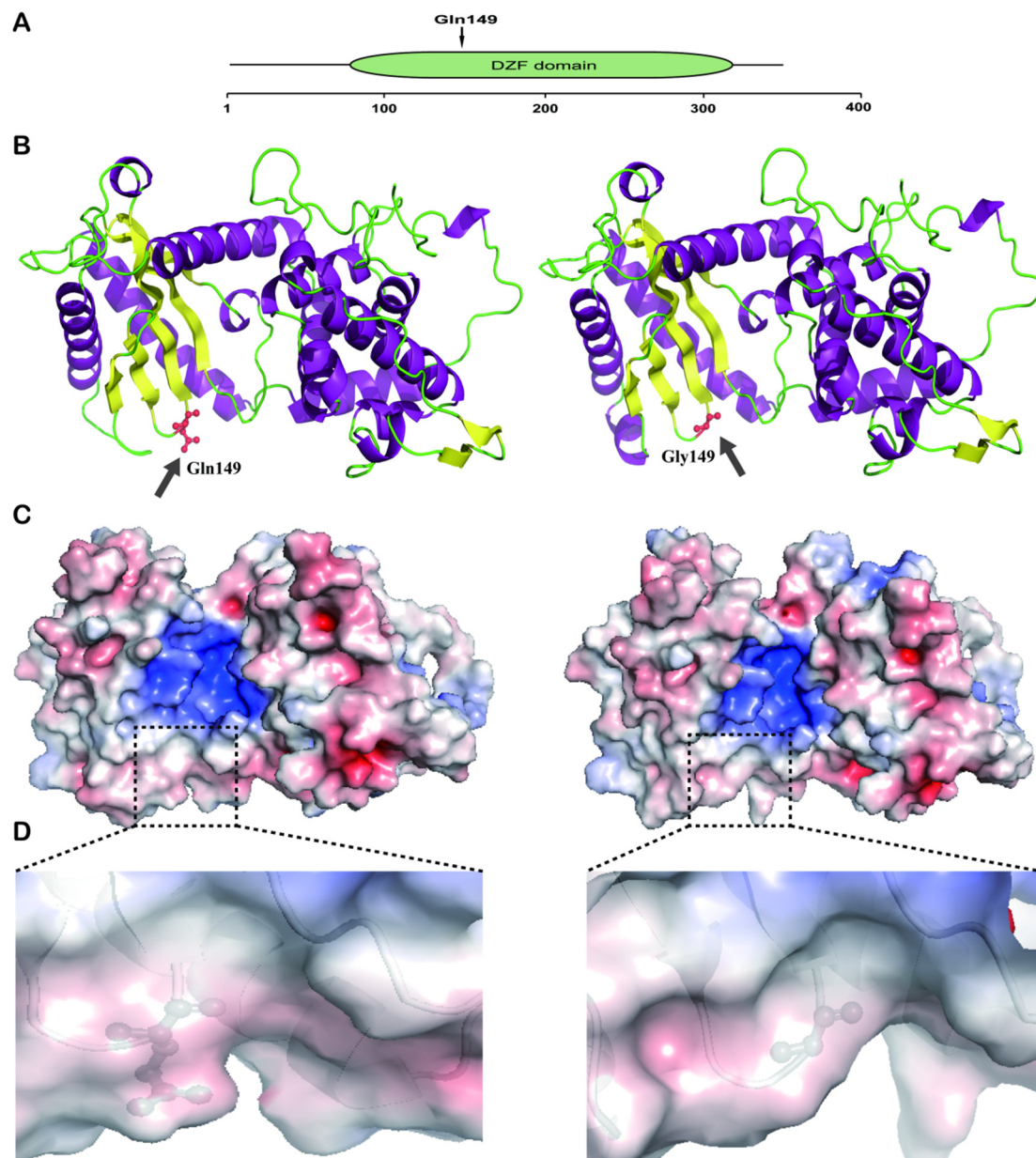
(b)



(c)

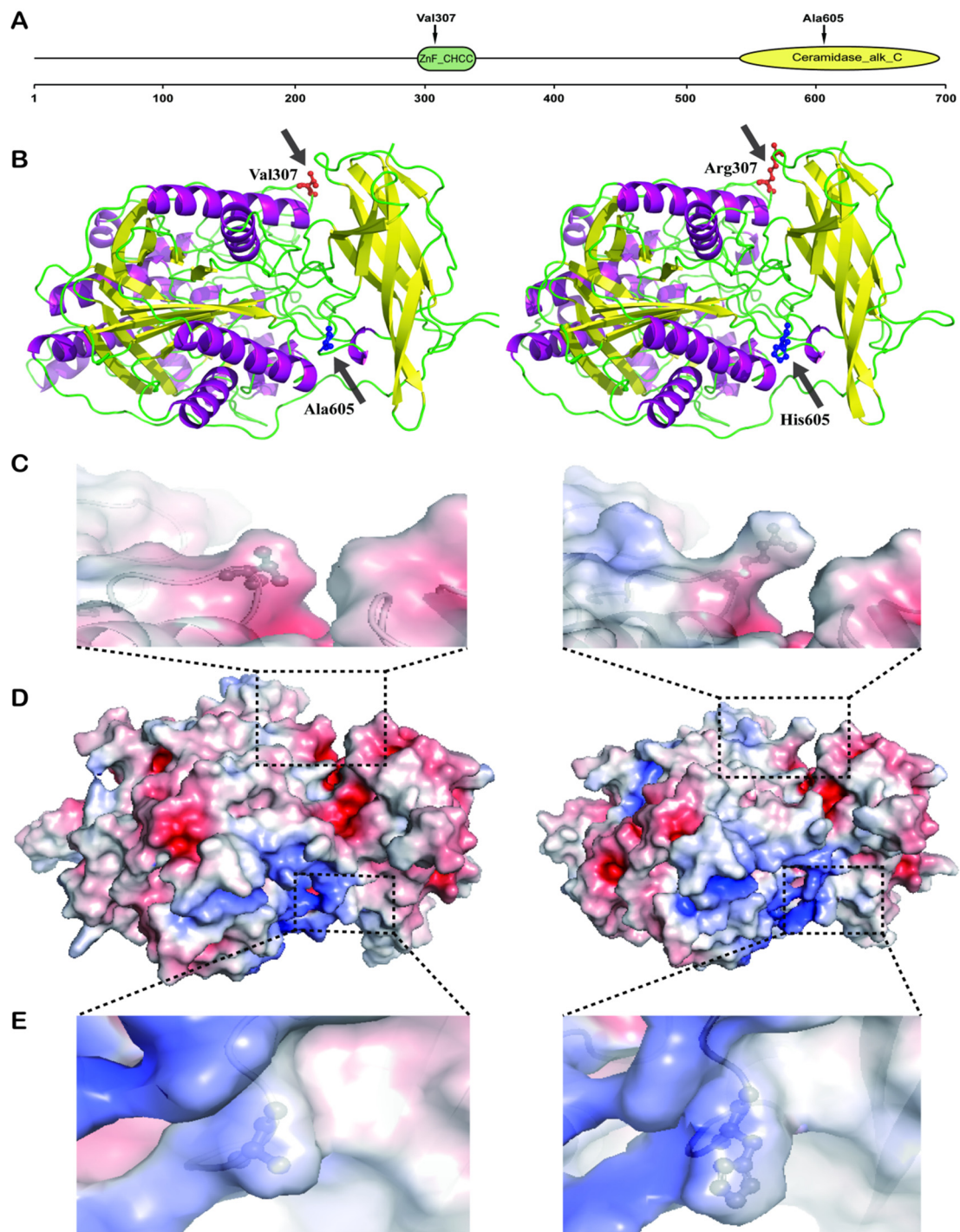


**Figure 5.** The species-level *Parnassius* phylogenetic relationships using maximum likelihood and Bayesian inference methods, (a) based on amino acid sequence and the best-fit amino acid model; (b) based on nucleotide sequence and the best-fit codon model; (c) based on nucleotide sequence and the best-fit nucleotide model. The PP (posterior probabilities), SH-aLRT and UFBoot support values are shown sequentially for each node.



**Figure 6.** Structure of ILF2 protein sequence of the *P. acdestis* (left) and *S. montelus* (right), respectively. A: The ILF2 protein domain with DZF domain; the candidate positively selected site is indicated by black arrow. B: the structures of helix, sheet and loop are shown in purple, yellow and green, respectively, with the positively selected residues shown with the red ball and stick representation. C: Electrostatic potential map of ILF2 domain; the range of electrostatic surface potential is shown from -7 kT/e (red color) to +7 kT/e (blue color). D: the zoomed-in picture of electrostatic potential around the positively selected residues. Template in the Protein Data Bank: 4atb.1.





**Figure 7.** Structure of CDASE protein sequence of the *P. acdestis* (left) and *S. montelus* (right), respectively. A: The CDASE protein domain with the ZnF\_CHCC domain and the highly conserved C-terminal tail (ceramidase\_alk\_C); two candidate positively selected sites are indicated by black arrows. B: the structures of helix, sheet and loop are shown in purple, yellow and green, respectively, with the positively selected residues shown with the red ball and stick representation. D: Electrostatic potential map of CDASE domain. C and E: the zoomed-in pictures of electrostatic potential around the positively selected residues. Template in the Protein Data Bank: 4wgk.1.