

Figure 8. Phylogeny of LAR and other PIP-family enzymes across land plant lineages. Protein sequences were retrieved as a single orthogroup containing the *Vitis vinifera* LAR from the 1KP orthogroup database2 (Ka-Shu Wong et al., 2019), sub-sampled, and supplemented with guide and *A. filiculoides* LAR-like sequences. The 785 sequences were aligned with MAFFT-linsi (Katoh et al., 2019), then trimmed using trimAL (Capella-Gutiérrez et al., 2009) and, using iQtree (Nguyen et al.,2015), the phylogenetic tree computed with the resulting 305 parsimony informative sites. The best-fit substitution model was LG+R7 and bootstrap support was determined via SH-aLRT (Kalyaanamoorthy et al., 2017). The tree was annotated in iTOL; highlighting characterized enzymes and sequences of particular interest (Letunic and Bork, 2019). Nodes with bootstrap support equal or greater than 80% SH-aLRT are indicated by circles (a full inventory of the sequences in this tree is in **Fig. S7**). EGS and IGS clustered in two groups: IGS/EGS-I and IGS/EGS-II. PLR, pinoresinol-lariciresinol reductase; IFR, isoflavone reductase; PCBER, phenylcoumaran benzylic ether reductase; EGS, eugenol synthase; IGS, isoeugenol synthase; LAR, leucoanthocyanidin reductase; WLAR, fern specific LAR-like.