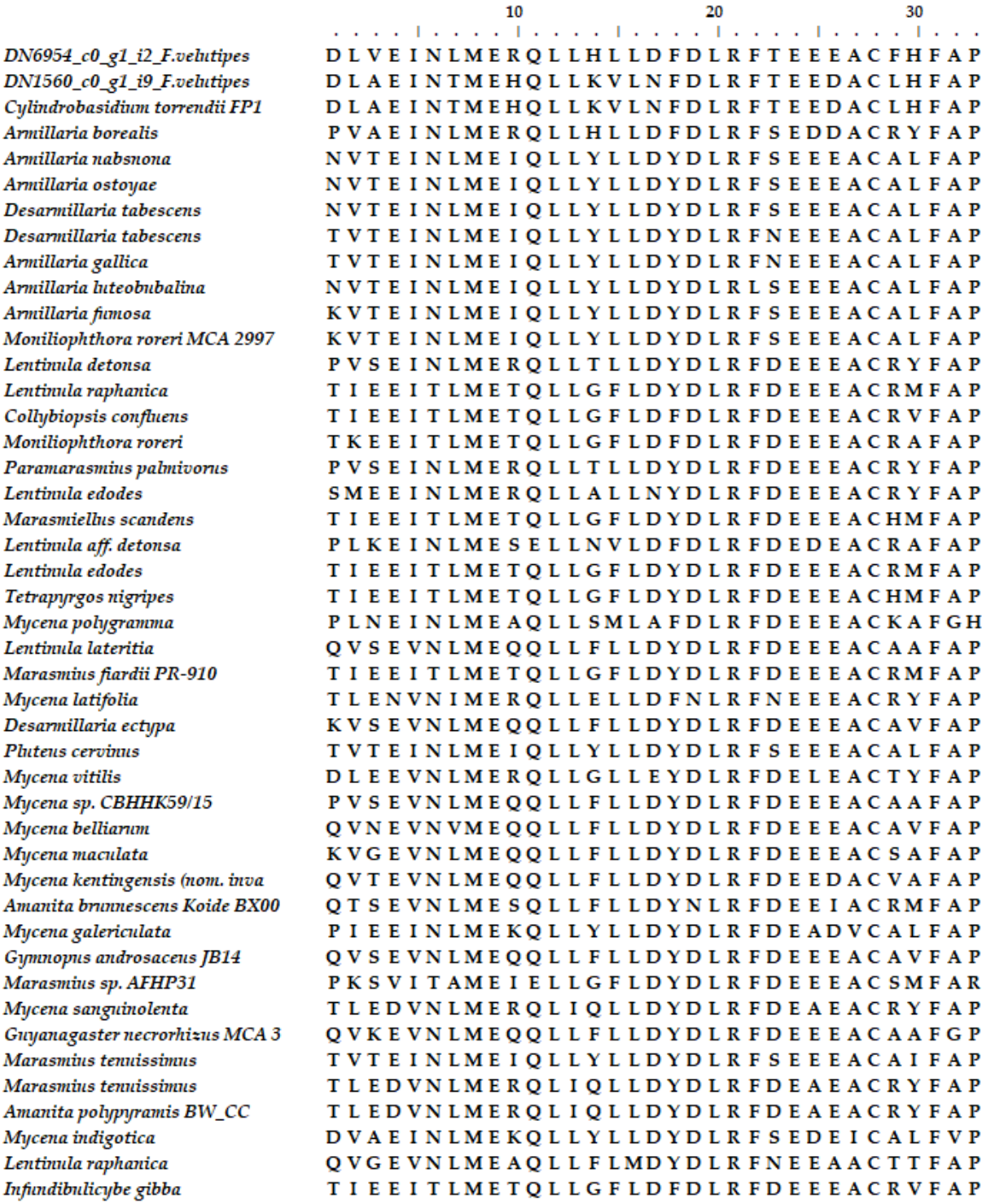


Figure S2. Multiple sequence alignment of conserved amino acid regions outside the canonical cyclin_N domain in cyclin homologs identified by PSI-BLAST. Sequences were aligned using PSI-BLAST hits from *F. velutipes* cyclin genes and representative basidiomycete species.

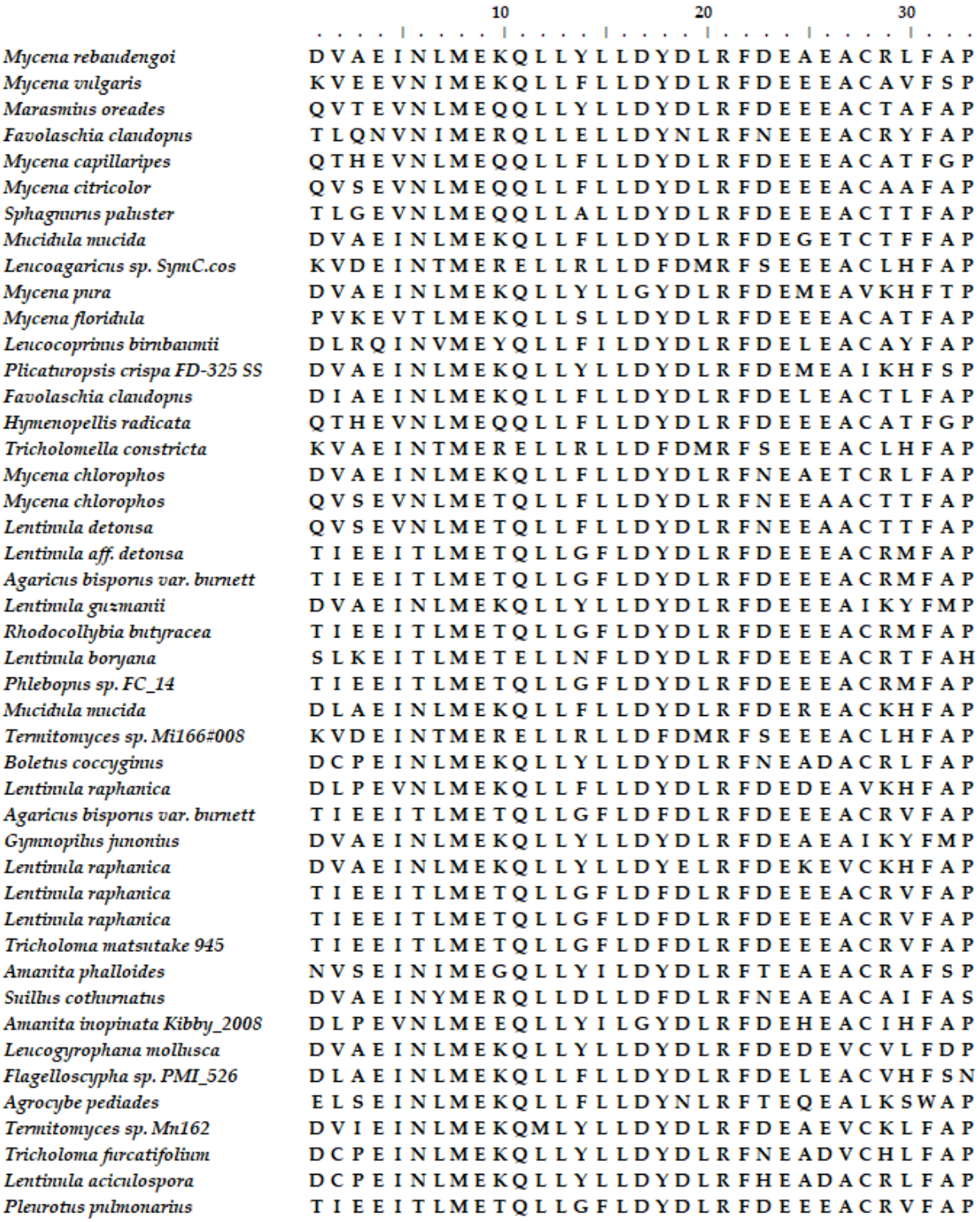


Figure S2. Continued.

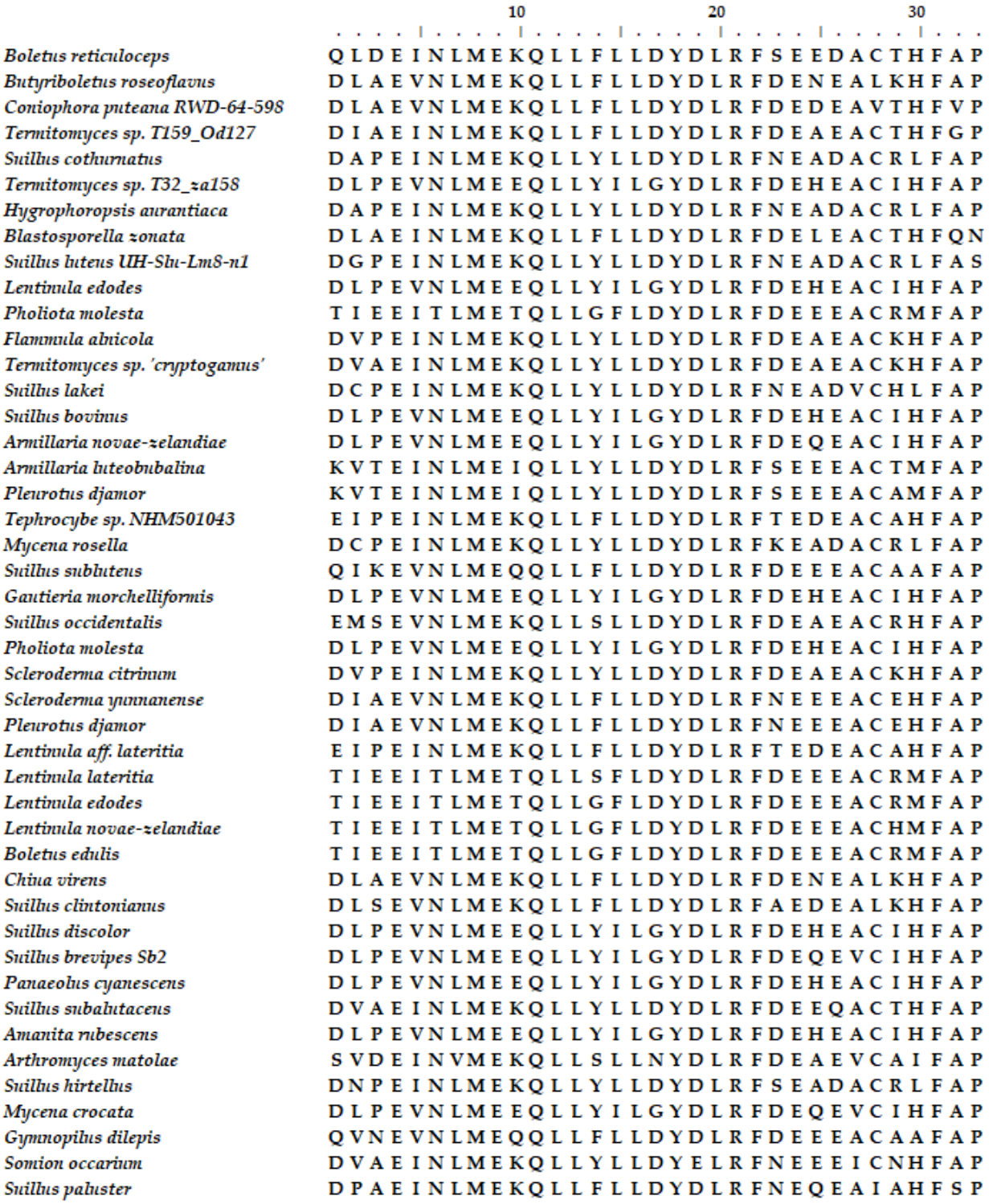


Figure S2. Continued.

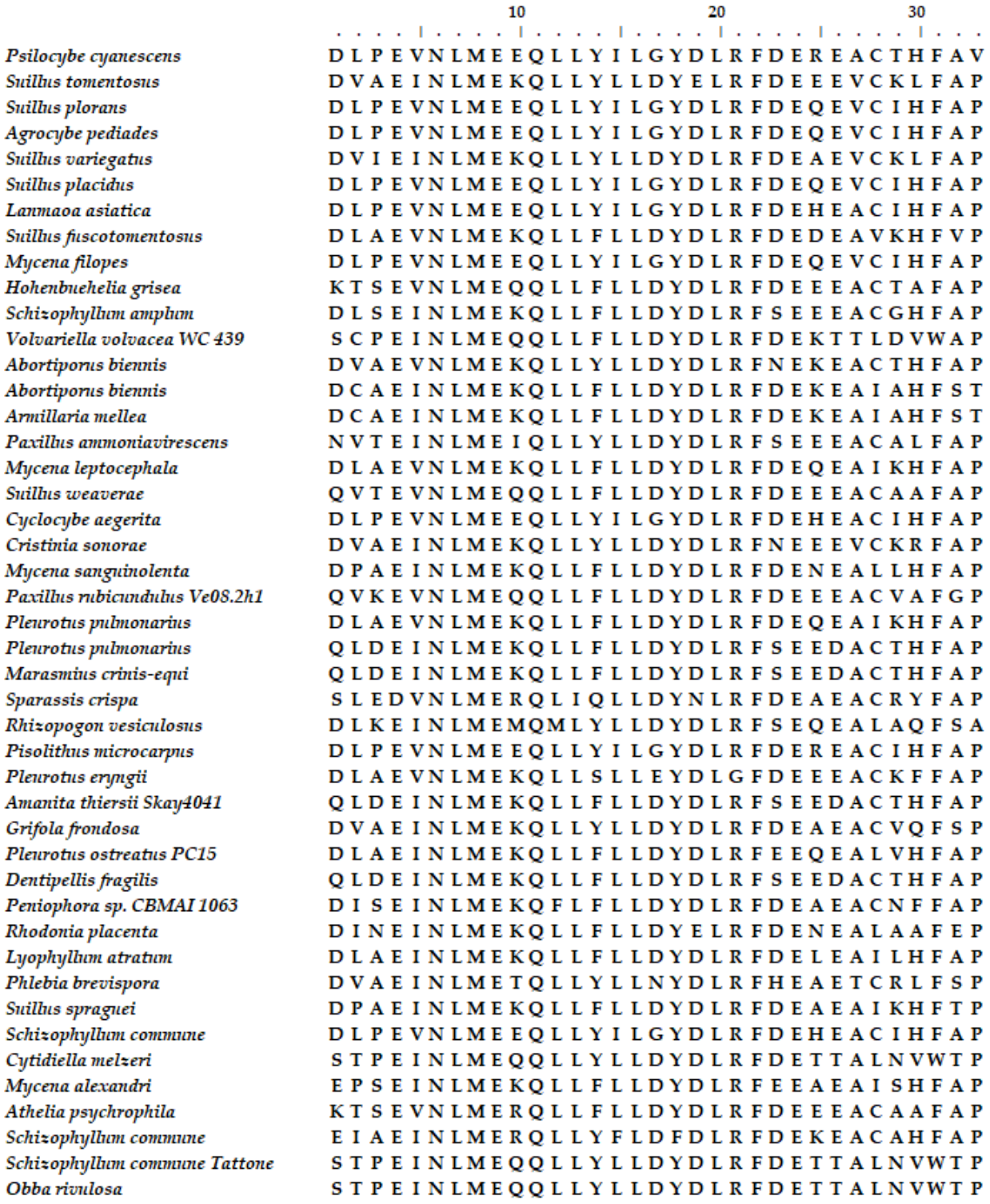


Figure S2. Continued.

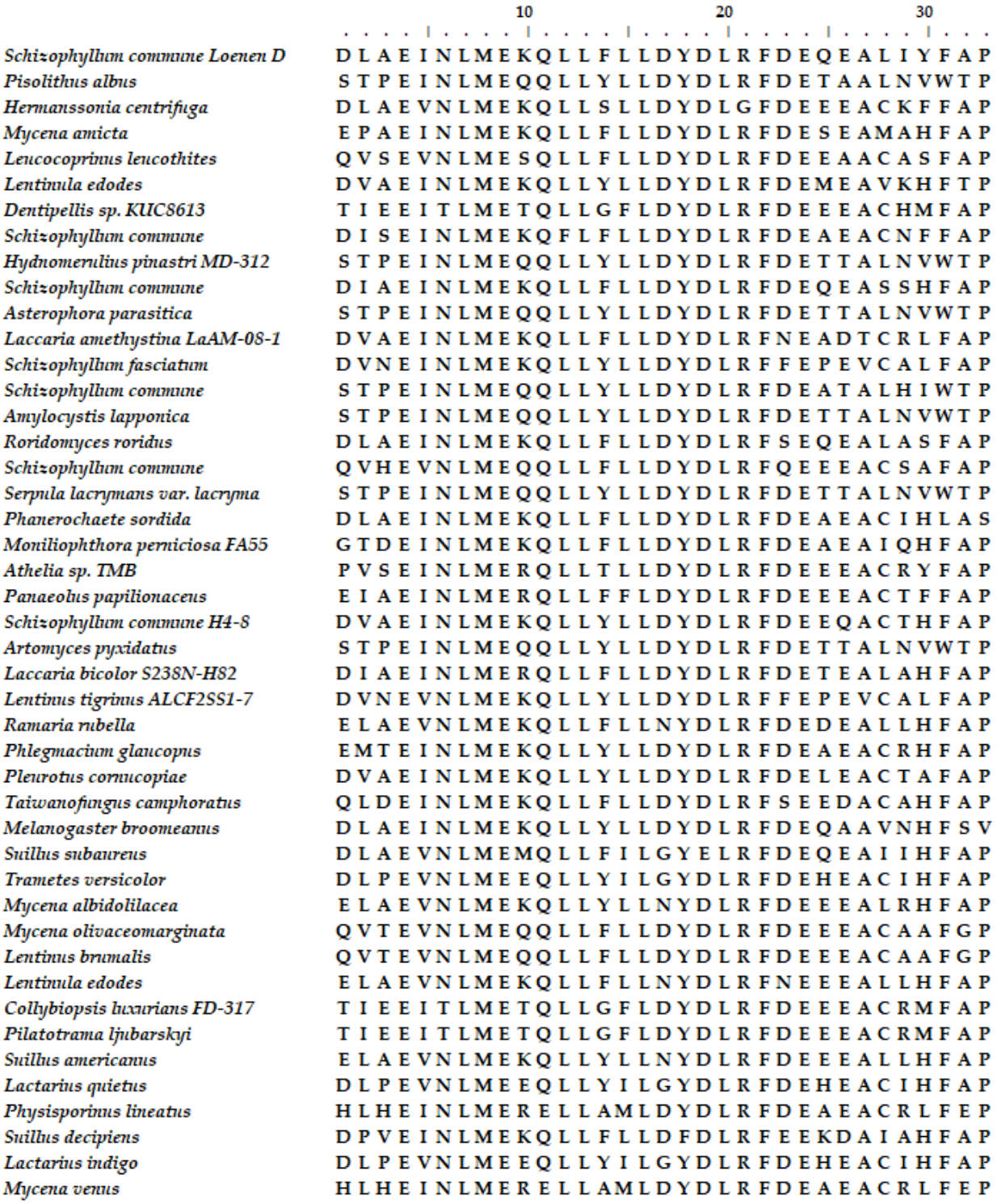


Figure S2. Continued.

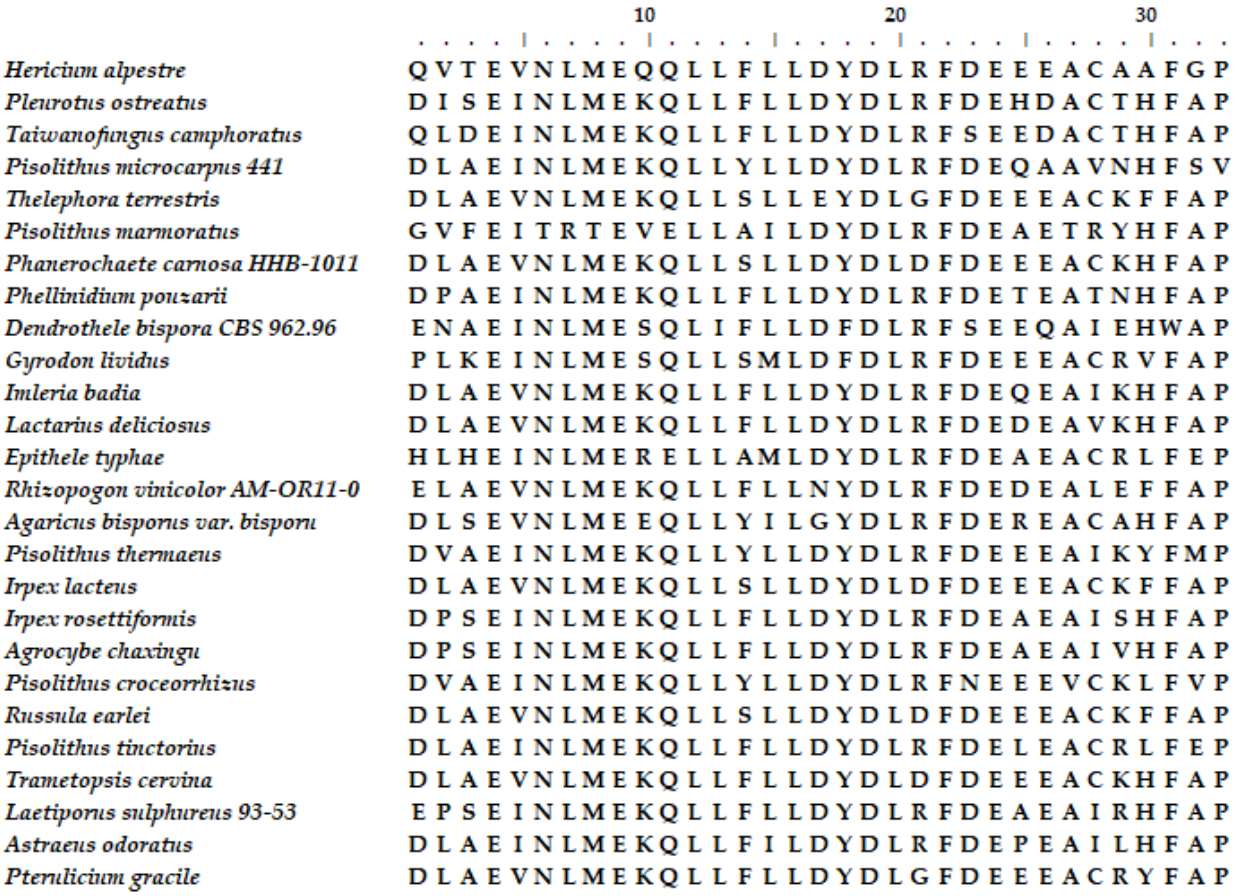


Figure S2. Continued.