

Sequence-structure-function relationships in the microbial protein universe

Supplementary Data 2

Visualization of novel fold clusters

cluster 161 – 87 different sequences

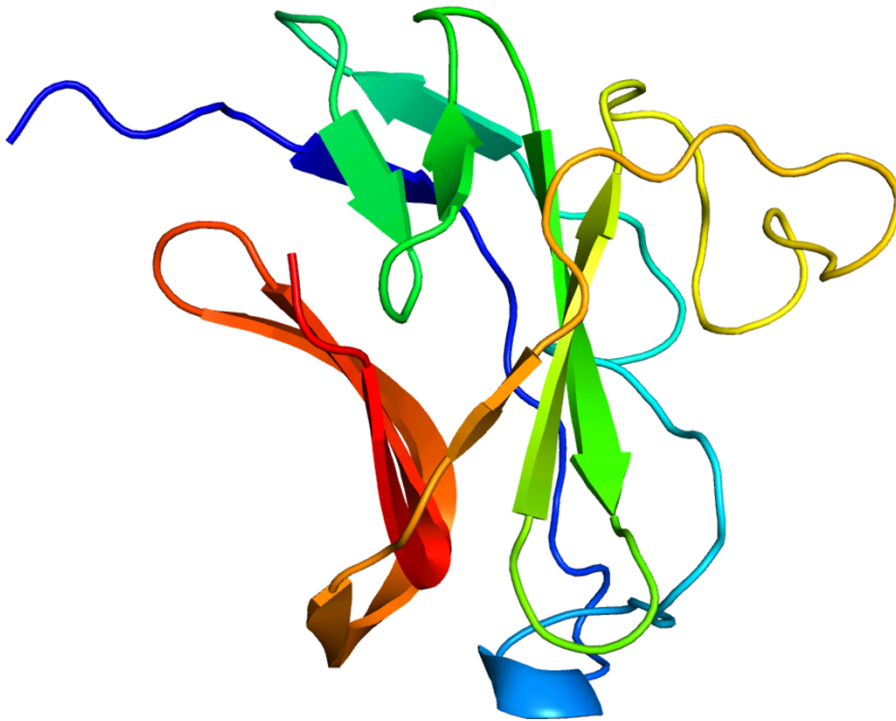


Fig. 1: Representative Rosetta models for all novel fold clusters (numbered). Figures with red background are hard false positives and with yellow background are soft false positives.

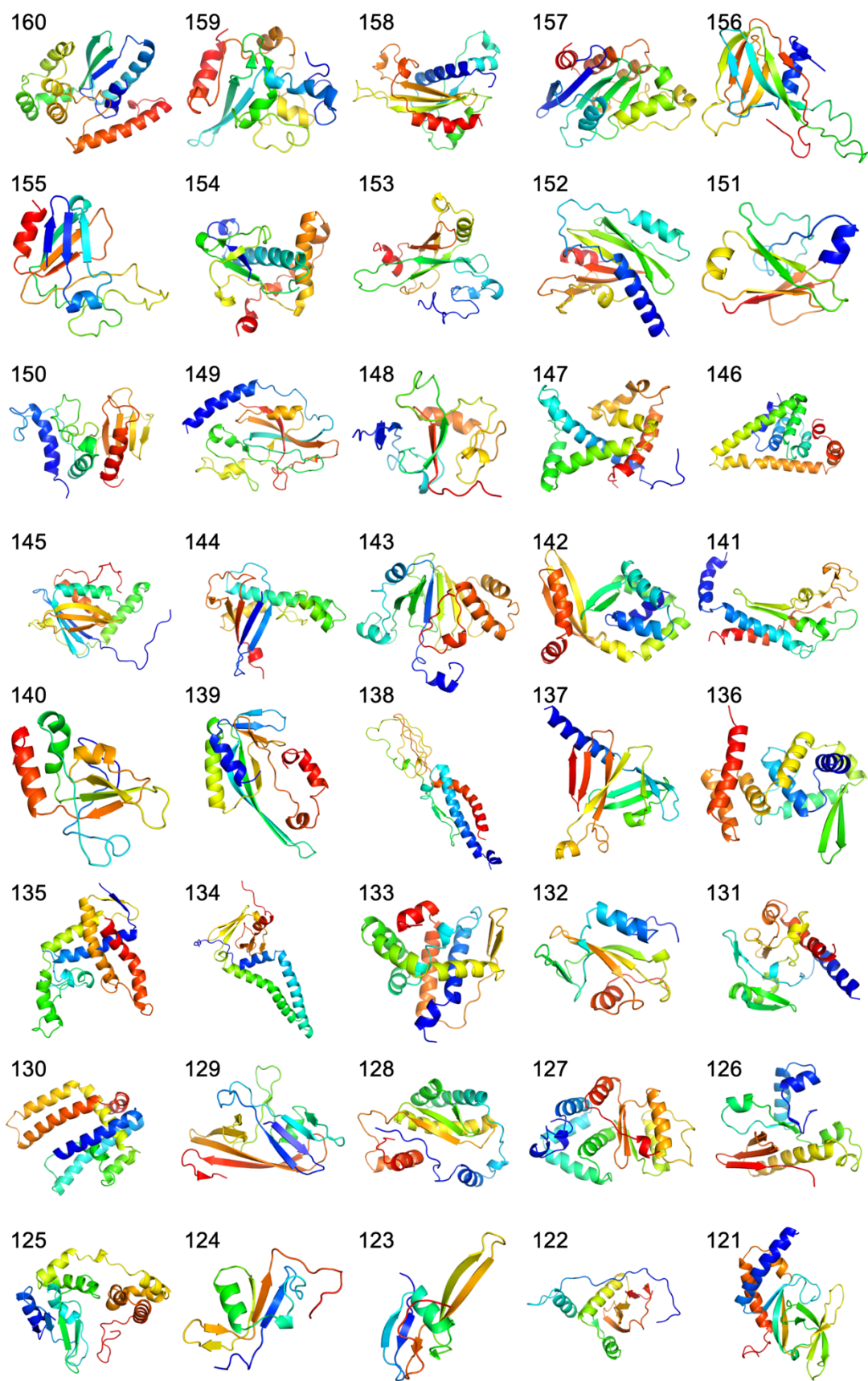


Fig. 1 continued

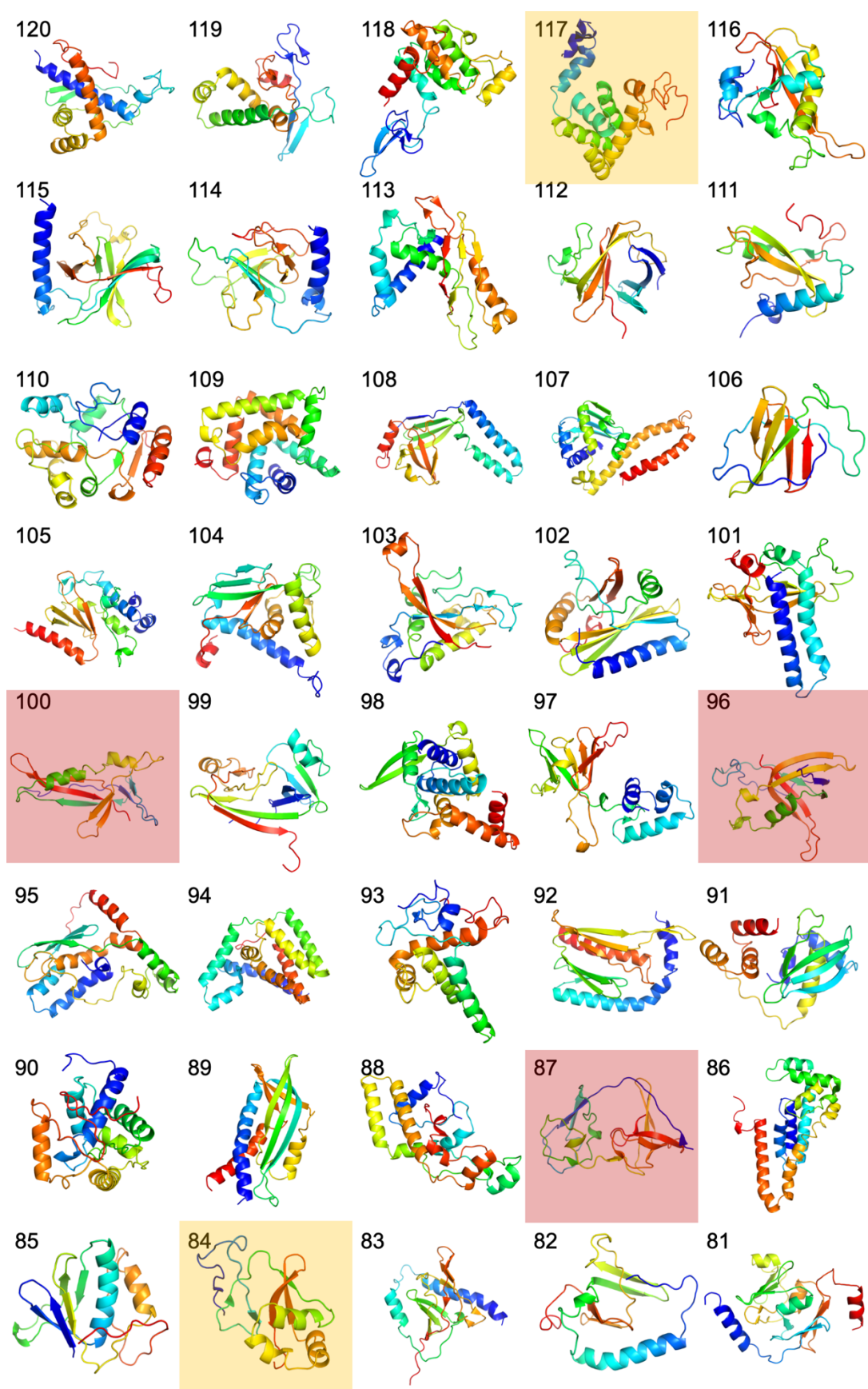


Fig. 1 continued

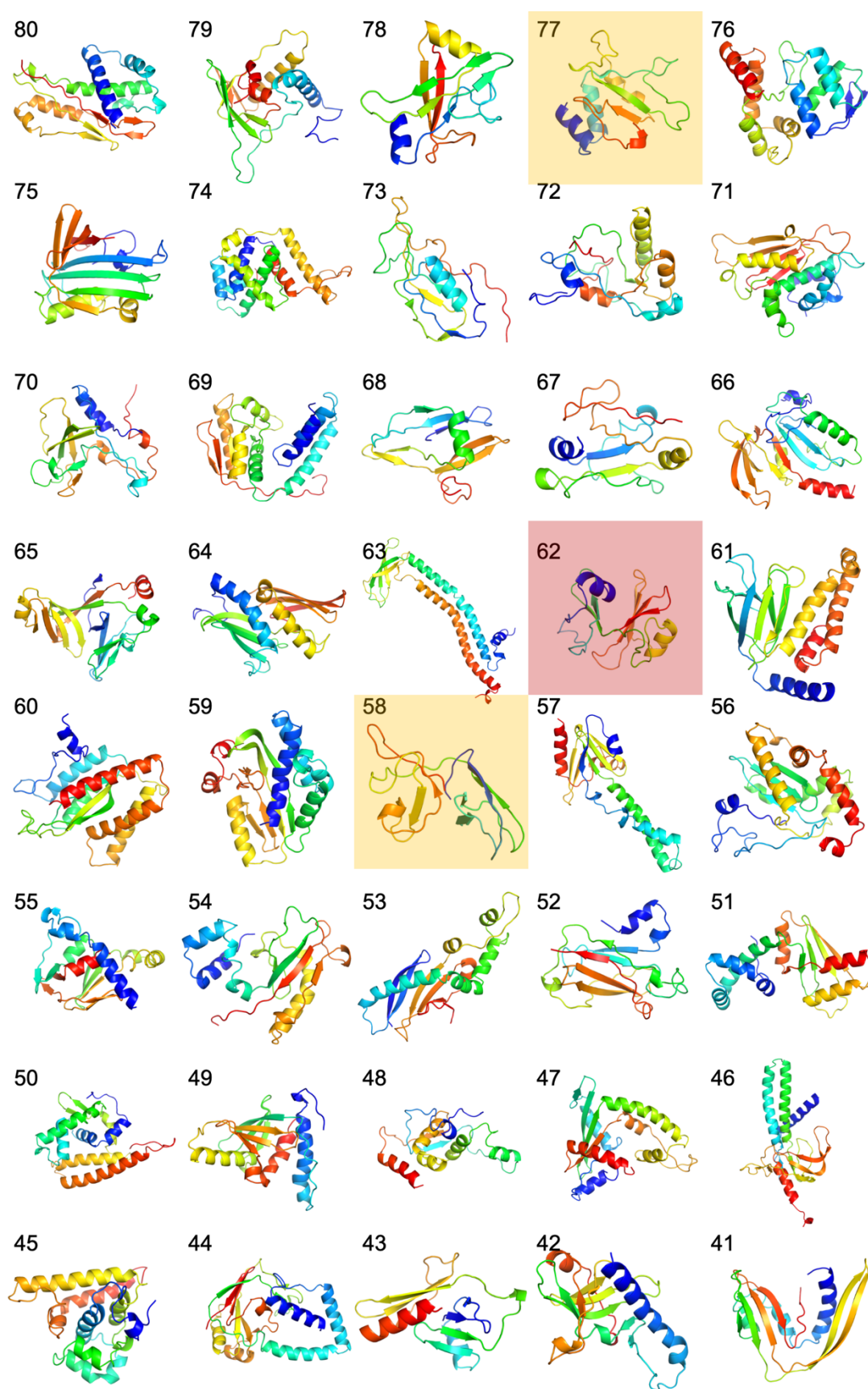


Fig. 1 continued

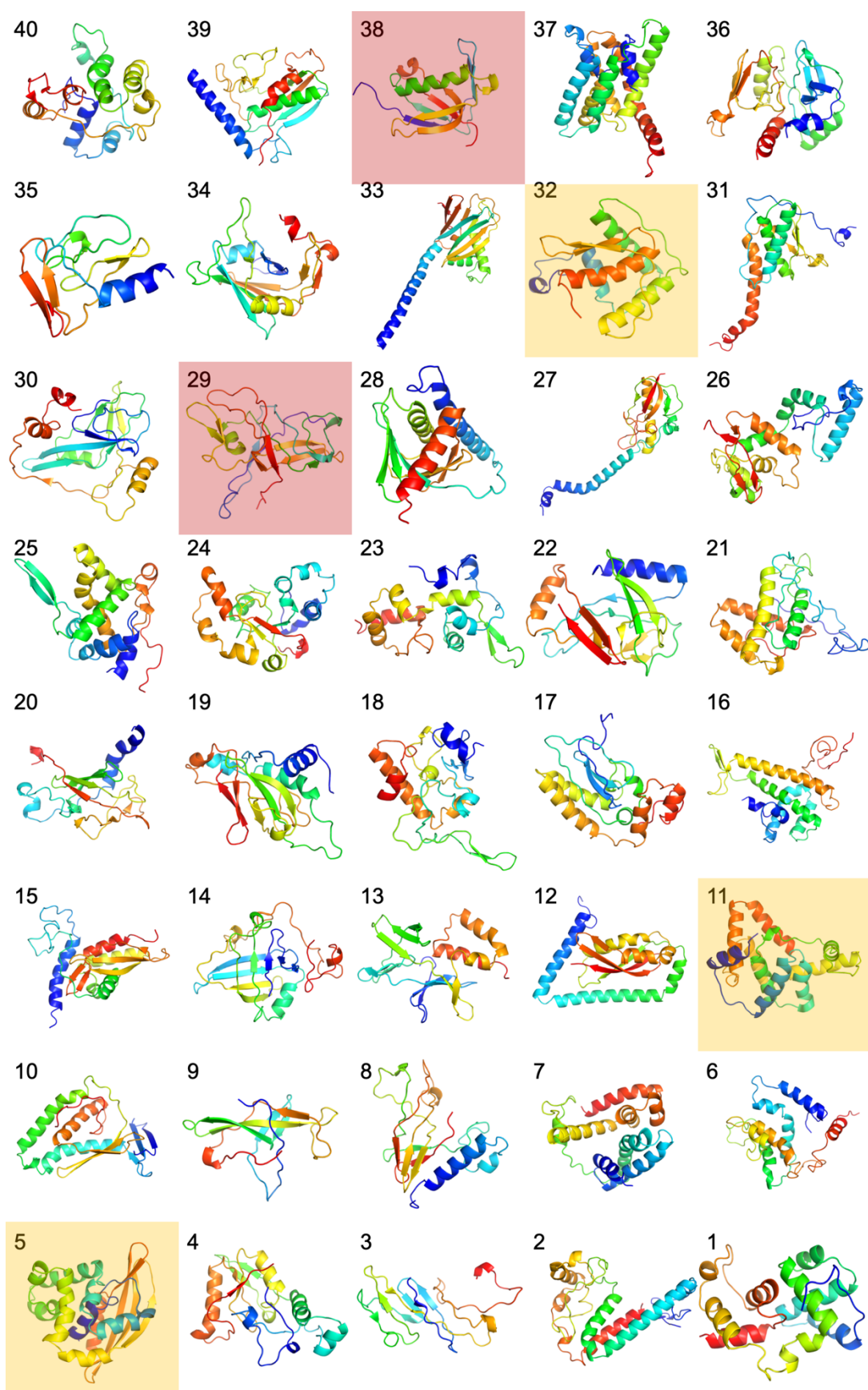


Fig. 1 continued

