

Structural and functional diversity of EF-hand proteins: Evolutionary perspectives

Supplemental Figures

Hiroshi Kawasaki,* and Robert H. Kretsinger#

* Department of Medical Life Science, Graduate School of Medical Life Science,
Yokohama City University, Suehiro-cho 1-7-29, Tsurumi-Ku, Yokohama, Kanagawa
230-0045, JAPAN

Department of Biology, University of Virginia, Charlottesville, VA, 22904, USA

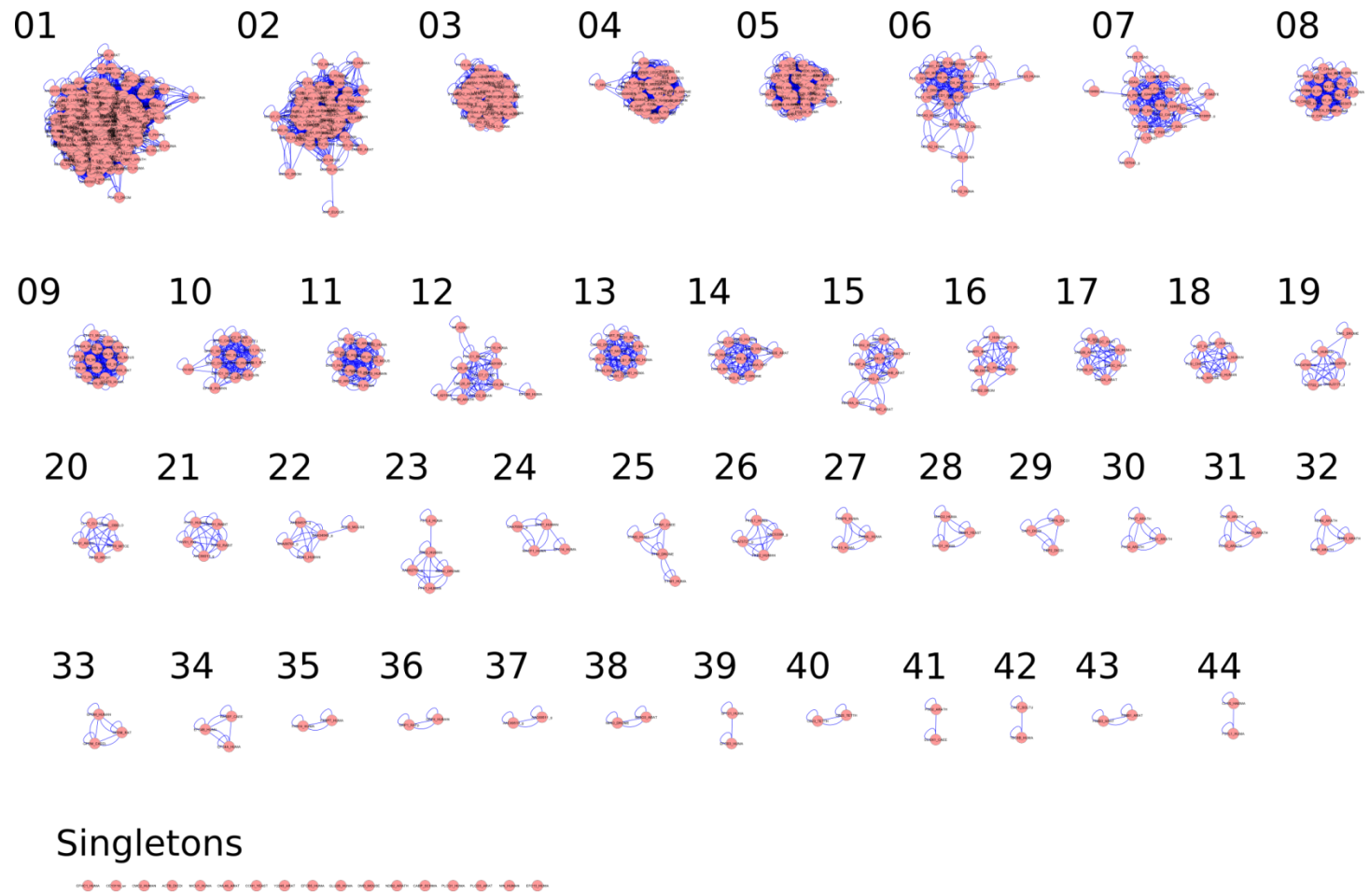
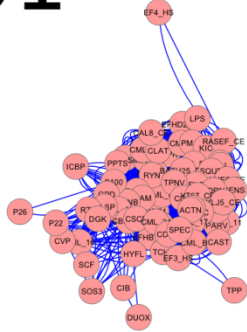


Figure S1

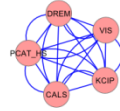
Clusters of EF-hand proteins

There were 905 sequences for EF-hand database. These sequences were analyzed by FASTA with all by all search selecting top 100 sequences of similarity. We made pairs of sequence by selecting with >50 % similarity (counts identical or conservative replacements) for over a 50 residue-span. Some sequences do not show this similarity with any other members of database. We did not analyze these sequences further. We got 50951 pairs, which made a network with 884 nodes. MCL clustering with similarity (Granularity parameter = 2.0, cut off of similarity = 0.5) gave 44 clusters and 17 singletons (cluster maker MCL v1.11). We removed these 17 singletons for further analysis. The subfamilies in each cluster are shown in Table 1 (see Cluster_Fig1 column).

01



02



03



04



05



06



07



Singletons



Figure S2

Simplified Relationship among subfamilies

The network shown in Figure 2 was converted to a simplified network, in which each pair of subfamilies is directly connected with an edge of the shared number of homologs; self loops were removed.

Subfamilies were classified by MCL clustering (granularity parameter = 2.0, cut-off of the numbers of shared homologs = 5.0) using Cytoscape.

The subfamilies in each cluster and singletons are shown in Table 1 (see Cluster_FigS2 column).