

Fig S1. Network distances are similar between the Organic and Cytoscape force-directed layout weighted by E-value.

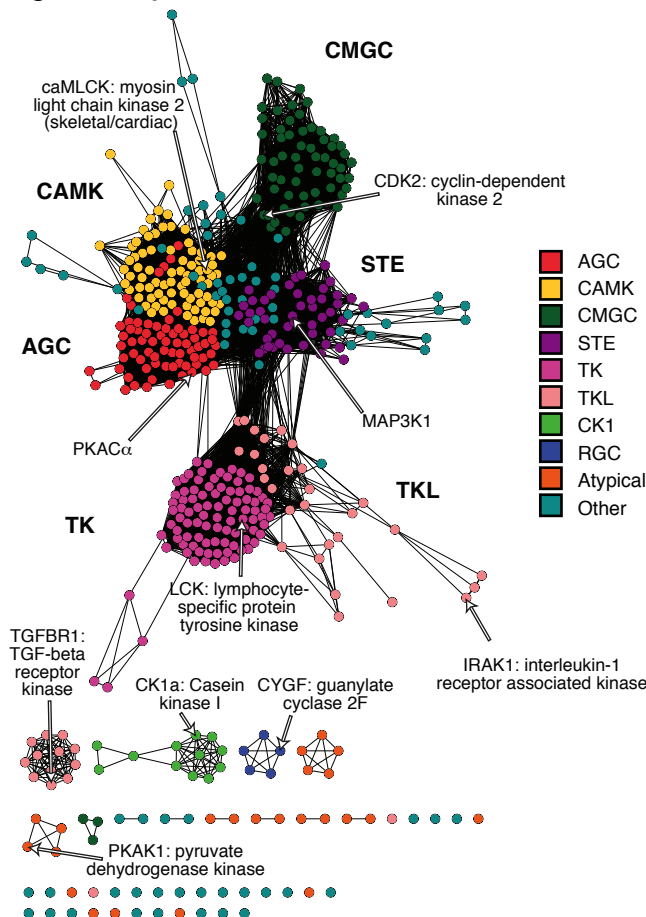
This page: Statistics (A) describing the comparison of the kinase network from Fig. 3 laid out using the Organic layout (B) or the Cytoscape force-directed layout weighted by edge E-value (C).

Following page: Statistics (D) describing the comparison of the amine GPCR network from Fig. 2B laid out using the Organic layout (E) or the Cytoscape force-directed layout weighted by edge E-value (F).

A. BLAST E-values	A. BLAST E-values	
B. Organic layout	R: 0.934 ± 0.003 Z: 41.2 P: 0.0	B. Organic layout
C. Cytoscape force-directed layout weighted by E-value	R: 0.895 ± 0.003 Z: 35.3 P: 7.02×10^{-273}	R: 0.900 ± 0.003 Z: 36.8 P: 2.92×10^{-297}

Pearson's correlations (R) and associated Z-scores (Z) and P-values (P) describing the similarity between the relative pairwise distances between 419 human kinase domain sequences in common as assessed by (A) all shortest paths between $-\log_{10}(\text{BLAST E-values})$, (B) the shortest paths between sequences as displayed by the Organic two-dimensional graph layout algorithm, and (C) the shortest paths between sequences in the two dimensional Cytoscape force-directed layout, weighted by BLAST E-value. The pairwise BLAST E-values and the graph layout algorithm correspond to a network thresholded at an E-value of 1×10^{-25} .

B. Organic Layout



C. Force-directed layout weighted by E-value

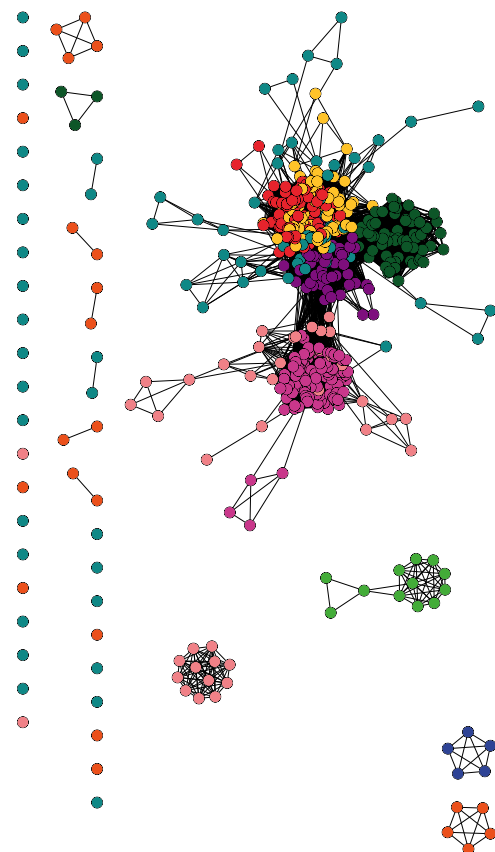


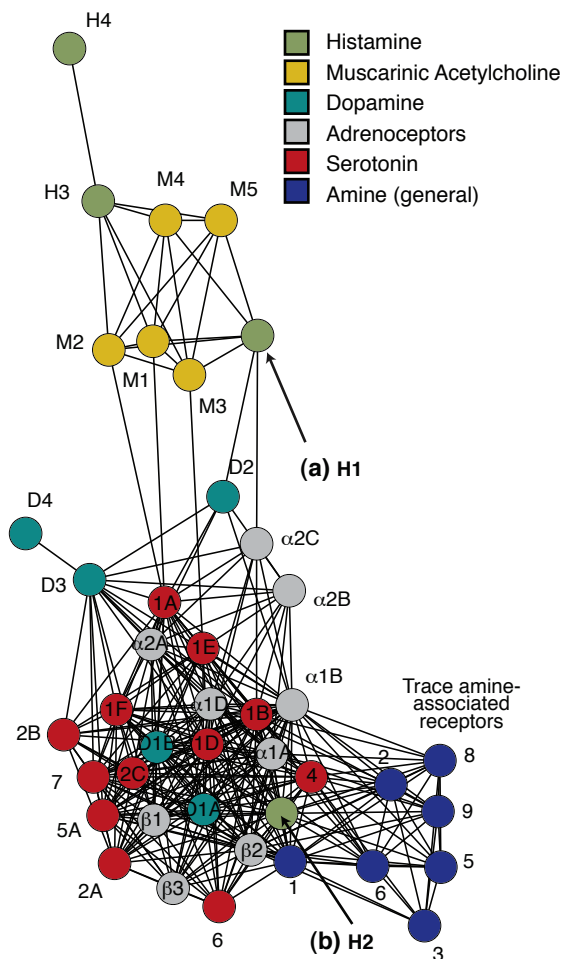
Fig S1. Continued

D.

A. BLAST E-values	A. BLAST E-values	
B. Organic layout	R: 0.906 ± 0.034 Z: 11.87 P: 8.04×10^{-33}	B. Organic layout
C. Cytoscape force-directed layout weighted by E-value	R: 0.850 ± 0.034 Z: 9.52 P: 8.78×10^{-22}	R: 0.877 ± 0.035 Z: 10.16 P: 1.47×10^{-24}

Pearson's correlations (R) and associated Z-scores (Z) and P-values (P) describing the similarity between the relative pairwise distances between 42 amine GPCR domain sequences in common as assessed by (A) all shortest paths between $-\log_{10}(\text{BLAST E-values})$, (B) the shortest paths between sequences as displayed by the Organic two-dimensional graph layout algorithm, and (C) the shortest paths between sequences in the two dimensional Cytoscape force-directed layout, weighted by BLAST E-value. The pairwise BLAST E-values and the graph layout algorithm correspond to a network thresholded at an E-value of 1×10^{-33} .

E. Organic Layout



F. Force-directed layout weighted by E-value

