Supplementary material

GeoFold: Topology-based protein unfolding pathways capture the effects of engineered disulfides on kinetic stability.

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Guide to GeoFold DAGs

In each of the directed acyclic graphs (DAG) presented here, node 1 is the natively folded state. Circles denote intermediates of unfolding as defined by the GetCuts algorithm. Lines with diamonds are bifurcating directed edges, connected one node to two. Black diamonds are hinges, red diamonds are pivots and white diamonds are breaks, as described in the main paper. The green pathway is the one with the highest traffic in an UnfoldSim simulation. Conditions for the simulation are written on each slide (additional setting can be found in Table 1 of the main paper). Only the edges with at least 10% of the maximum UnfoldSim traffic are plotted.

DAGs can be interpreted in terms of the narrowness of the unfolding pathway. If only the green pathway is present, then GeoFold predicts the folding ensemble to be very tight (and probably more susceptible to mutation). On the other hand, if the DAG contains many pathways, then GeoFold predicts that the pathway is maleable, and probably insensitive to mutation.

Note that some proteins split in the middle at the beginning of unfolding (towards the top of the DAG), while others unfold from the ends, a single linear pathway. Other proteins have several required steps before splitting into multiple pathways -- a bottleneck.







Geofold DAG for PDBid:1BNG Barnase 95-102 mutant. Oxidized ω =40































