Proteomes (Gene3D) HMMs Structural census Character normalization $G_{xy_norm} = Round \left[\frac{Ln (G_{xy} + 1)}{Ln (G_{xy_max} + 1)} \times 20 \right]$ Character coding Character argumentation Data matrices $\begin{vmatrix} g_{x_{i},y_{i}} & g_{....} & g_{x_{v},y_{i}} \\ g_{x_{i},y_{2}} & g_{....} & g_{x_{v},y_{2}} \\ g_{x_{i},y_{m}} & g_{....} & g_{x_{v},y_{m}} \end{vmatrix} \longleftrightarrow \begin{vmatrix} g_{x_{i},y_{i}} & g_{....} & g_{x_{v},y_{i}} \\ g_{x_{i},y_{i}} & g_{x_{v},y_{i}} & g_{x_{v},y_{i}} \\ g_{x_{i},y_{m}} & g_{x_{v},y_{m}} & g_{x_{v},y_{m}} \end{vmatrix}$ Phylogenetic analysis Tree of *n* architectures Tree of *m* proteomes p5 p4 p3 p2 **p1 Evolutionary timeline**

Figure S1 A methodological flowchart illustrating the reconstruction of phylogenies of proteomes and protein architectures using protein domain census data.