Study of conformational changes in dynamic multidomain enzymes

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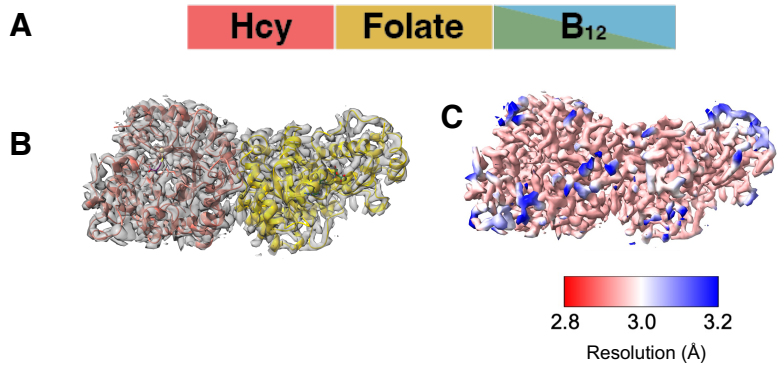

Figure 1. (A) Topology of 3-domain Ec MetH and Tm MetH from N- to C-terminus: homocysteine (Hcy) binding domain, folate binding domain and cobalamin (B_{12}) binding domain. Ec MetH is a monomer, while Tm MetH is a dimer. (B) EM map solved by co-freezing 3-domain Ec MetH with apoferritin. The model was built in ModelAngelo, and substrates were docked in. Only the first two domains are visible. (C) Local resolution estimation for the map.

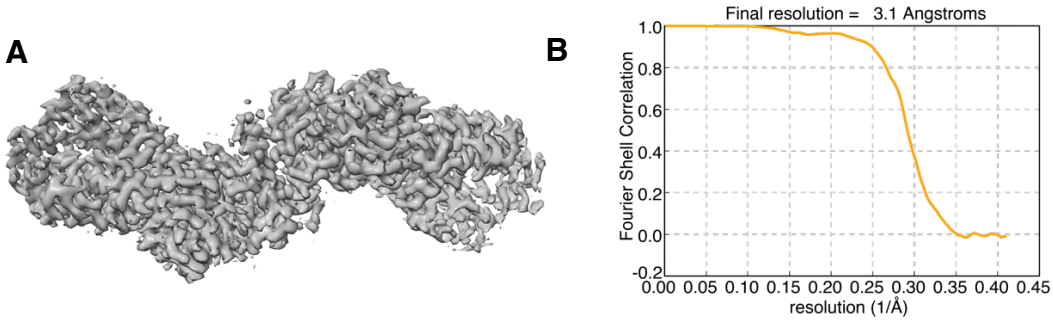

Figure 2. (A) EM map solved by freezing Tm MetH with detergent reveals a dimer. Again, the cobalamin-binding domain is missing from both the 2D classes and the 3D map. (B) Fourier shell correlation and resolution estimated by relion with masked half maps.

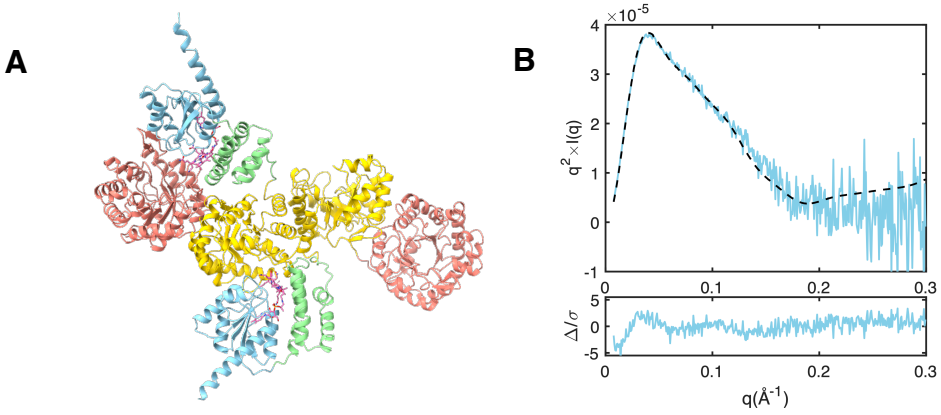

Figure 2. (A) AlphaFold Model of resting-state Tm MetH depicts the cobalamin domain (blue/green) associating with different parts of the Hcy (pink) and folate (yellow) domains. (B) SAXS profile (blue) and theoretical scattering from model (dashed line) show good agreement indicating that the enzyme remains intact in solution.