

## Supporting Information

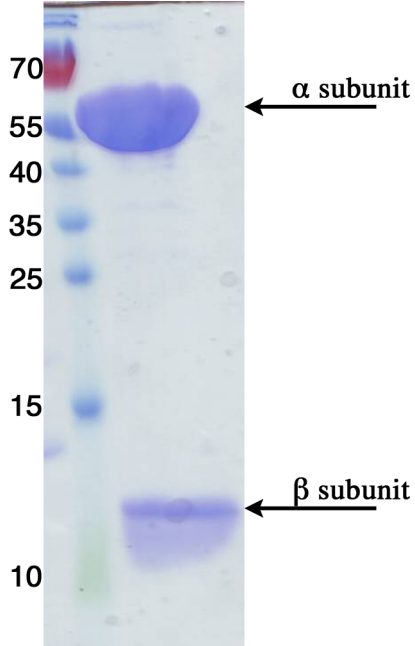
### Structure and protein-protein interactions of methanol dehydrogenase from *Methylococcus capsulatus* (Bath)

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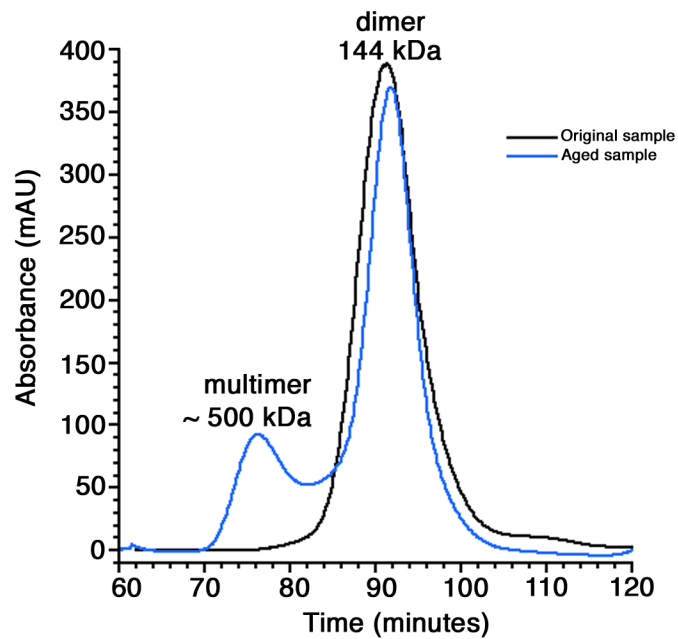
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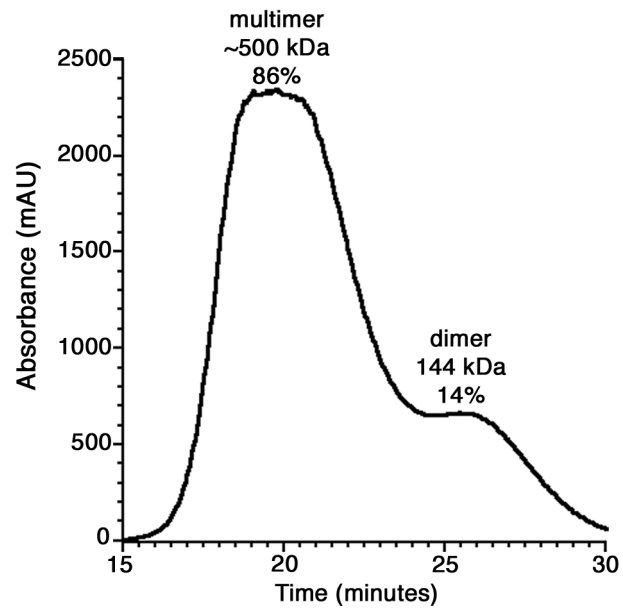
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**Figure S1.** SDS-PAGE gel of MDH isolated from *M. capsulatus* (Bath) after final purification step on a Superdex 200 column equilibrated with 25 mM PIPES pH 7.2, 150 mM NaCl, 0.03 % DDM, 1 mM benzamidine. The sample is > 90 % pure after the size exclusion column with yields of ~ 30 mg per liter of *M. capsulatus* (Bath) culture.



**Figure S2.** Superdex 200 size exclusion traces of MDH showing the formation of higher order oligomers over time, with freezing and concentrating. A prep grade Superdex 200 16/600 column, total column volume 120 mL, was used. The initial trace (black) shows only a single, homogeneous peak. After freezing and concentrating, a second peak appears (blue), indicative of high order oligomers. Crystallization samples were prepared with the dimeric protein (black trace).



**Figure S3.** The oligomerization state of *M. capsulatus* (Bath) MDH is affected by the protein concentration. SEC trace of concentrated MDH protein (120 mg/mL) run on a Superdex 200 10/300 column, total column volume 24 mL. The predominant form of MDH is the multimer at concentrations > 100 mg/mL.