Supplemental Data

Structure of the redox sensor domain of *Methylococcus capsulatus* (Bath) MmoS

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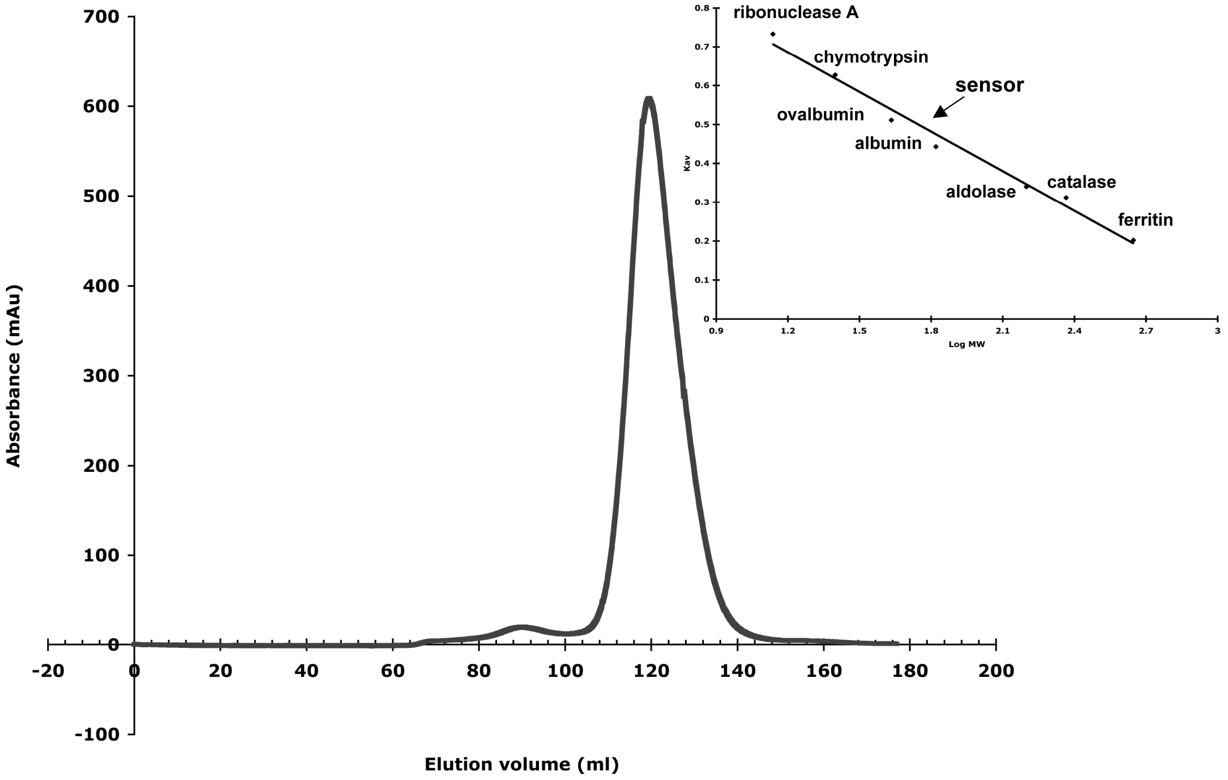

Figure S1: Oligomeric state of the MmoS sensor domain determined by gel filtration on Superdex 200. The sensor domain elutes between albumin (67 kDa) and ovalbumin (43 kDa), consistent with a dimer.

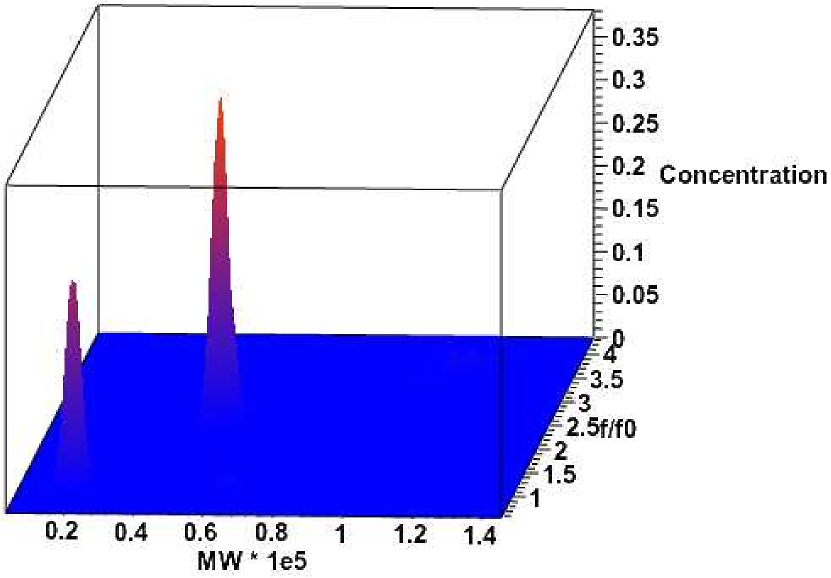

Figure S2: Three-dimensional plot showing results from Genetic - Monte Carlo Ultrascan Analysis. X-axis, MW in Daltons; y-axis, frictional ratio: f/f_0; z-axis; % concentration. The lower MW peak corresponds to the monomer; the higher MW peak corresponds to the dimer.

Table S1: Sedimentation velocity analysis of the sensor domain: results from the genetic algorithm -Monte Carlo analysis with 95% confidence intervals

	Solute 1 (Dimer) Confidence Interval (Min, Max)	Solute 2 (Monomer) Confidence Interval (Min, Max)
Molecular weight (kDa)	54.6 (50.5, 57.0)	22.8 (19.9, 29.3)
Sedimentation Coefficient (10^{-13})	2.10 (2.07, 2.10)	2.44 (2.30, 2.48)
Diffusion Coefficient (10^{-7})	3.53 (3.36, 3.70)	1.12 (1.13, 1.20)
Frictional Ratio, f/f_0	2.50 (2.39, 2.56)	1.09 (1.03, 1.15)
Cumulative percentage of total concentration (%)	61.3	33.7
Remaining 5.1% comes from one or more species with a molecular weight of 105-132 kDa		