Title: **Energy flux couples sulfur isotope fractionation to electron transfer protein abundances in *Desulfovibrio vulgaris***

SUPPLEMENTAL FIGURES

Figure S1. Chemostat OD's vs. time.

Figure S2: Soluble and membrane associated electron and hydride carrier abundances.

Figure S3. Proteomics Summary.

Figure S4: S-isotope & energy protein shift co-plotted. & Energy Proteomic shifts summary re-plotted at scale.

SUPPLEMENTAL DATA AVAILABILITY

Proteomic data : Proteomic mass spectral data are available via proteomeXchange under accession PXD027511 and the MassIVE repository (massive.ucsd.edu) under accession MSV000087869.

Other Data: See https://doi.org/10.6084/m9.figshare.23989398.v1 for data.

Dataframe 1: Chemostat data; S isotopes & metabolites; cellular metabolites; cell counts.

Dataframe 2. Lipid H-isotopes.

Dataframe 3. Proteomics.

Figure S1.

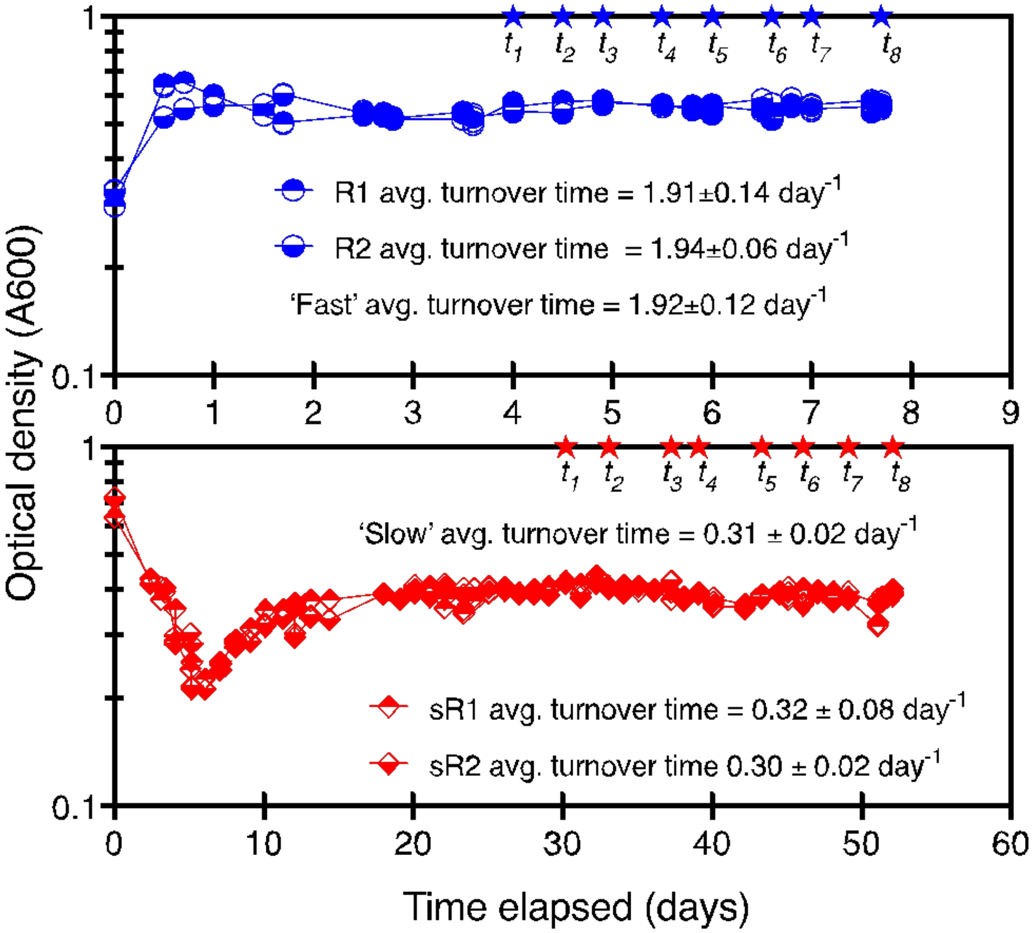
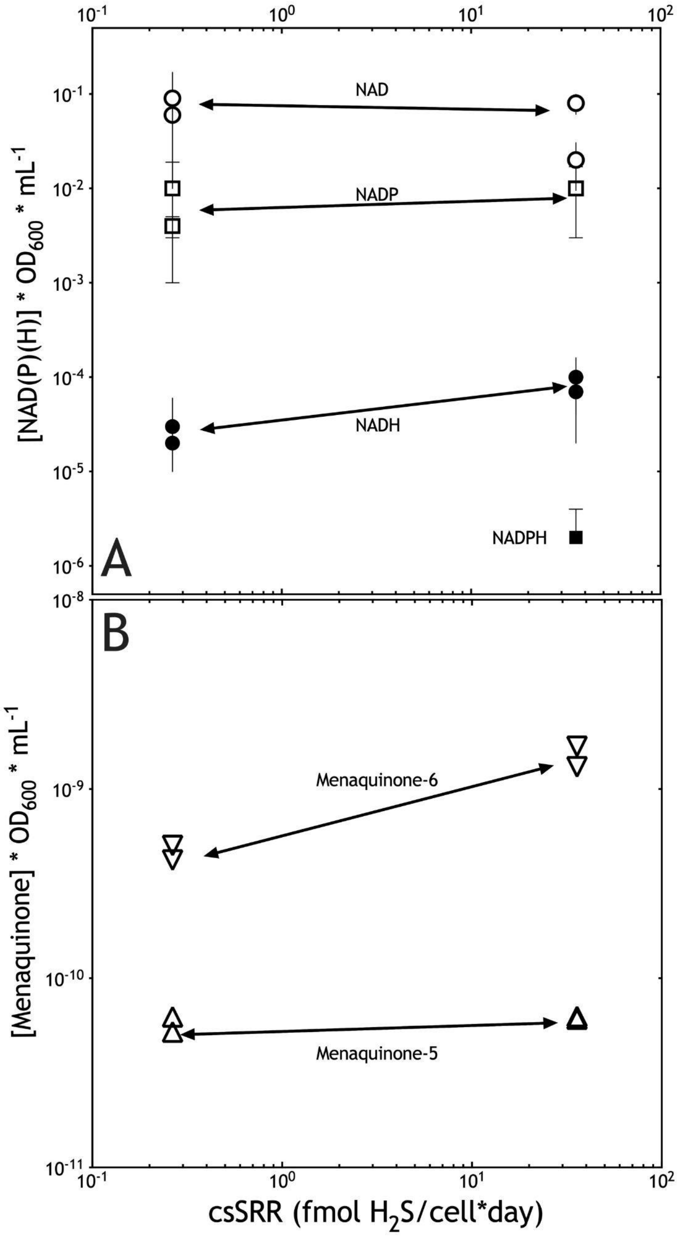


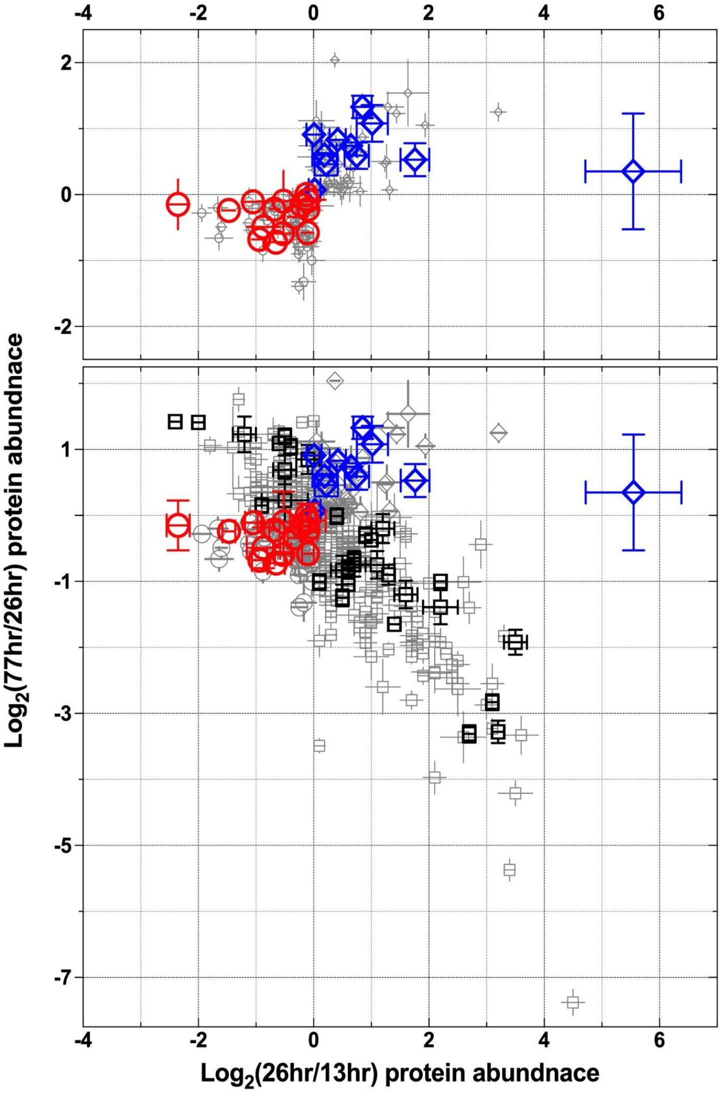
Figure S1. Visual display of steady-state experiments. Optical density of each bioreactor over the course of each chemostat experiment (circle and diamonds), with the eight sampled time points (stars). The top panel is from the fast reactors (~13 hr doubling time, proportional to 1.91 to 1.94 per day), whereas the bottom panel are from the slow turnover time reactors (~77 hr doubling time, proportional to 0.30 to 0.32 per day). The intermediate rate of ~26hr data is from Leavitt et al. 2019.

Figure S2.



Supplementary Figure S2. Cellular electron transfer intermediates from the slowest (77hr) and fastest (13hr) chemostat grown *Dv*H populations plotted versus csSRR. (A) soluble intracellular NAD(P)(H) hydride carriers, where each pool is normalized to a unit of biomass (OD600). (B) Membrane associated menaquinone's (MK's) 5 and 6, also normalized to biomass and measurements standards MK-4. These measurements were not collected in the Leavitt et al. (2019) study, and so are not available for 26hr *Dv*H chemostat population.

Figure S3.



Supplemental Figure S3. Proteomics Summary. COG-identified *energy proteins* from *Dv*H whose abundance scales positively with csSRR (red circles, most in 13hr) or inverse with csSRR (blue diamonds, most in 77hr), or outliers that are most or least abundant in the intermediate rate (black squares, most or least in 26hr). All other proteins whose abundance scaled significantly and positively with rate (gray circles), inverse to rate (gray diamonds), or most/lease in the intermediate rate (gray squares). The top panel only shows significantly different energy proteins (blue and red symbols are those featured in Figure 4 and S4), the bottom panel shows all proteins detected at all rates that showed statistically significant patterns. Symbols are the same across panels.

Figure S4.

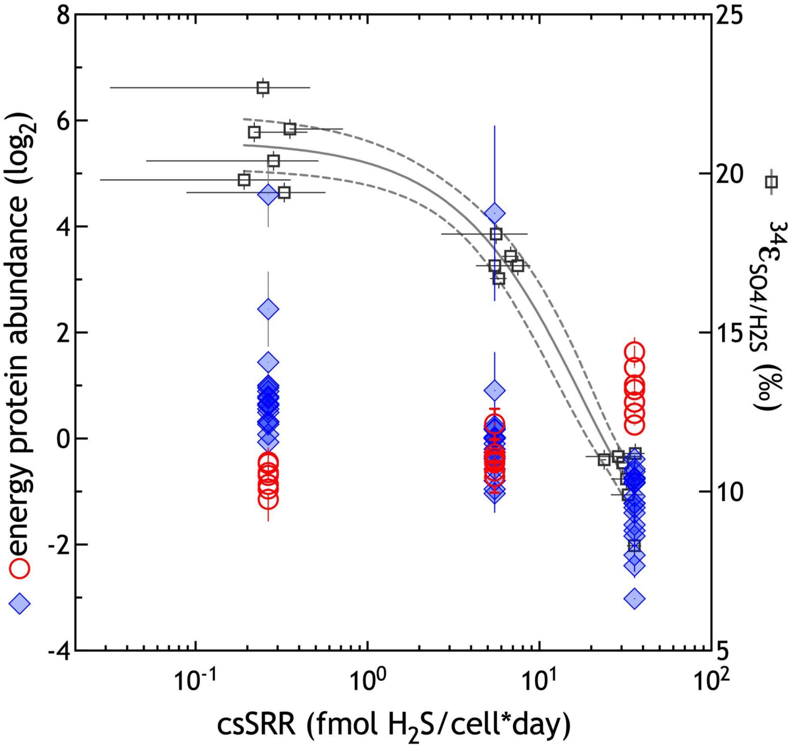


Figure S4. Chemostat S isotope fractionation and energy proteomics summary. These are the same data as in Figure 1B (black squares, right y-axis), and Figure 4A (blue diamonds) and 4B (red circles), here plotted with the same (left) y-axis scale.

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