SUPPORTING INFORMATION

Impact of quaternary structure upon bacterial cytochrome c peroxidases: does homodimerization matter?

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Organism of origin (oxidation state)	Interfacial residues	Number of charged interfacial residues	Total area (Å^2) of interface	Charged pairs across the dimer	PDB code
Shewanella oneidensis (fully reduced)	50	7	1930	6	3O5C
Pseudomonas aeruginosa (oxidized)	35	11	1207	7	1EB7
Pseudomonas aeruginosa (semi-reduced)	46	10	1591	N/A	2VHD
Pseudomonas nautica (oxidized)	34	8	1204	N/A	1RZ6
Pseudomonas nautica (semi-reduced)	44	8	1563	N/A	1RZ5
Geobacter sulfurreducens (oxidized)	38	8	1333	2	3HQ6
Geobacter sulfurreducens S134P/V135K (oxidized)	45	8	1714	2	3HQ8
Rhodobacter capsulatus (oxidized)	37	12	1231	8	1ZZH
Paracoccus pantotrophus (oxidized)	39	5	1342	4	2C1U
Paracoccus pantotrophus (semi-reduced)	46	6	1706	2	2C1V
Nitrosomonas europaea (oxidized)	51	10	1987	6	1IQC

Table S1. Details of PisaPSE server analysis on the dimeric interfaces of structurally characterized bC*c*P enzymes

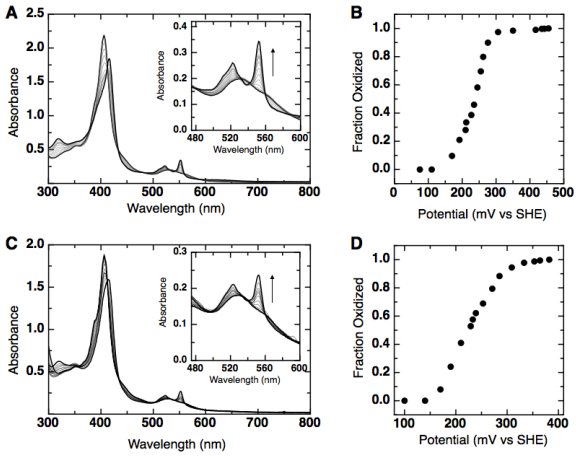

Figure S1. Potentiometric redox titrations of Shewanella oneidensis cytochrome c peroxidase (A/B) wild-type and (C/D) E258K charge reversal mutant. Plots A and C show the optical changes associated with the electrochemical reduction of the high potential heme. Plots B and D show te curves which give Nernst plots of 1 electron redox centers and the midpoint potential of the high potential heme centers.