Supporting Information

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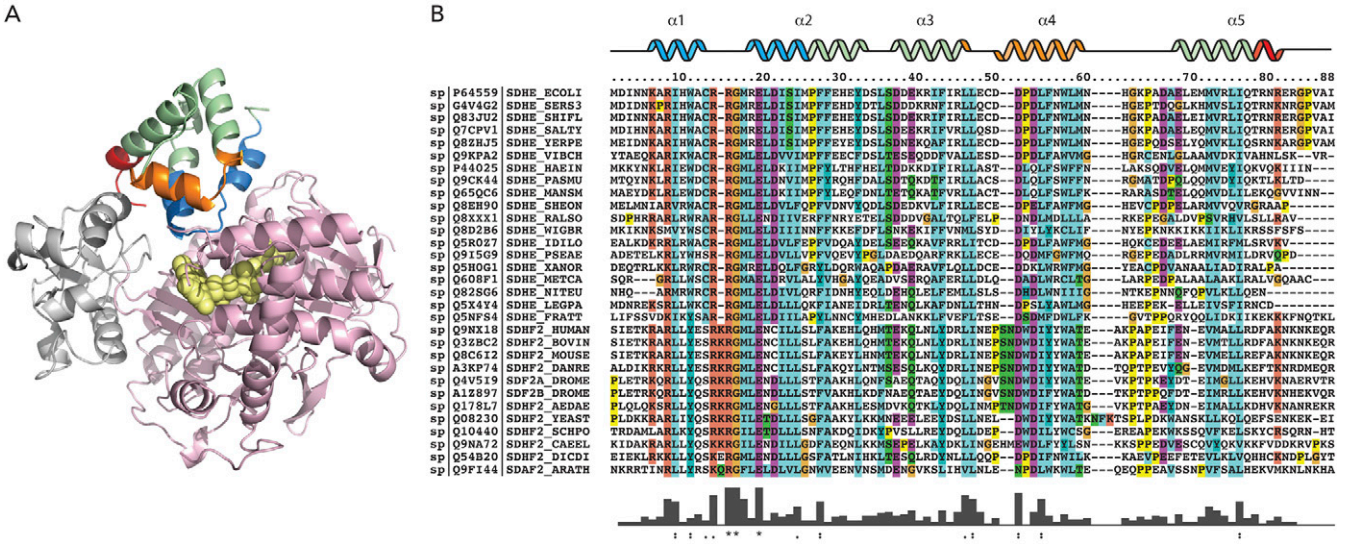

Fig. S1. Conserved residues in SdhE including the RGxxE motif form part of the interaction surface with SdhA. (*A*). Structure of *Escherichia coli* SdhAE complex highlighting regions of SdhE, colored blue, orange, and red, that contribute to the binding interface with SdhA. Noncontact regions of SdhE are colored green. (*B*). Entire primary sequence of *E. coli* SdhE aligned with the complete or core domain of homologous proteins from other bacteria, fungi, animals, and plants. Amino acid residue numbering is indicated for *E. coli* SdhE only, directly above the sequence. Secondary structure elements of SdhE are also shown above the alignment and are colored coded as defined in *A*: *E. coli* (P64559), *Serratia* spp. (G4V4G2), *Shigella flexneri* (Q83JU2), *Salmonella typhimurium* (Q7CPV1), *Yersinia pestis* (Q8ZHJ5), *Vibrio cholera* (Q9KPA2), *Haemophilus influenza* (P44025), *Pasteurella multocida* (Q9CK44), *Mannheimia succiniciproducens* (Q65QC6), *Shewanella oneidensis* (Q8EH90), *Ralstonia solanacearum* (Q8XXX1), *Wigglesworthia glossinidia brevipalpis* (Q8D2B6), *Idiomarina loihiensis* (Q5R0Z7), *Pseudomonas aeruginosa* (Q9I5G9), *Xanthomonas oryzae* (Q5H0G1), *Methylococcus capsulatus* (Q608F1), *Nitrosomonas europaea* (Q82SG6), *Legionella pneumophila* (Q5X4Y4), *Francisella tularensis* (Q5NFS4), *Homo sapiens* (Q9NX18), *Bos taurus* (Q3ZBC2), *Mus musculus* (Q8C6I2), *Danio rerio* (A3KP74), *Drosophila melanogaster* (Q4V5I9, A1Z897), *Aedes aegypti* (Q178L7), *Saccharomyces cerevisiae* (Q08230), *Schizosaccharomyces pombe* (Q10440), *Caenorhabditis elegans* (Q9NA72), *Dictyostelium discoideum* (Q54B20), and *Arabidopsis thaliana* (Q9FI44). The codes in parenthesis indicate primary accession numbers.

Table S1. Data collection and refinement statistics

Parameter	Value
Data collection	
Space group	$P2_12_12_1$
Cell dimensions	
a, *b*, *c*, Å	53.0, 100.0, 232.1
α, β, γ, °	90, 90, 90
X-ray source	AUS MX2
λ, Å	0.954
Detector	ADSC Quantum 315r
Resolution range, Å	50–2.15 (2.23–2.15)*
Observed reflections	284,545
Unique reflections	63,285
Completeness, %	93.0 (94.8)
Multiplicity	4.5 (4.4)
<I/σ(I)>	8.6 (1.6)
$R_{merge,}$ %	14.3 (80.0)
$R_{pim,}$ %	7.2 (41.1)
Refinement	
Reflections in working set†	47,878
Reflections in test set	2,561
Protomers (SdhAE complexes) per ASU	2
$R_{work,}$ %	19.9 (26.0)
$R_{free,}$ %	25.8 (28.0)
rmsd bond lengths, Å	0.009
rmsd bond angles, °	1.39
B factors, Å^2	
SdhA	15
SdhE	18
Ramachandran‡	
Favored, %	97.64
Allowed, %	2.20
Outliers, %	0.16
PDB ID code	6C12

*Values in parenthesis are for highest-resolution shell.
†Following anisotropic correction of data (1).
‡Calculated using MolProbity (2).

1. Strong M, et al. (2006) Toward the structural genomics of complexes: Crystal structure of a PE/PPE protein complex from Mycobacterium tuberculosis. *Proc Natl Acad Sci USA* 103:8060–8065.
2. Chen VB, et al. (2010) MolProbity: All-atom structure validation for macromolecular crystallography. *Acta Crystallogr D Biol Crystallogr* 66:12–21.

Table S2. Distances between the covalent FAD cofactor and structural elements putatively involved in covalent flavinylation

Protein	Base, Å (proton abstraction, C8 methyl group)	N1-C_2=O_2 stabilization	Amide near N5 (Å)
Bovine complex (II)*	His365 Nδ1-C8α (4.4)	Helix dipole (residues 415–429)	Gln62 NH (3.4)
SQR *E. coli*†	His354 Nδ1-C8α (4.0)	Helix dipole (residues 405–419)	Gln50 NH (3.1)
SdhAE complex‡	His354 Nδ1-C8α (4.2)	Helix dipole (residues 405–419)	Gln50 NH (4.4)

*PDB ID code 1ZOY (1).
†PDB ID code 2WDQ (2).
‡This work.

1. Sun F, et al. (2005) Crystal structure of mitochondrial respiratory membrane protein complex II. *Cell* 121:1043–1057.
2. Ruprecht J, Yankovskaya V, Maklashina E, Iwata S, Cecchini G (2009) Structure of Escherichia coli succinate:quinone oxidoreductase with an occupied and empty quinone-binding site. *J Biol Chem* 284:29836–29846.