Table S2. Structural alignment of the SQR to the known structures deposited on the PDB performed with the server DALI (www.ebi.ac.uk/dali)

Target	rmsd, Å	No. of aligned residues	Identity, %
1fcd_A	2.4	362	21
2yvf_A	2.8	321	18
2gmh_A	3.1	143	17
1dx1_C	3.1	329	14
1nda_B	3.2	325	16
2qcu_B	3.2	148	15
4gr1	3.2	328	15
1zk7_A	3.3	322	14
2cfy_F	3.4	327	15
1qla_A	4.5	190	13

Root-mean-square deviations are indicated in ångströms; identities indicate the percentage of structurally aligned residues that are identical in the SQR and in the respective aligned partner. PDB codes correspond to the following: 1fcd, flavocytochrome *c*:sulfide dehydrogenase; 2yvf, ferredoxin reductase; 2gmh, electron transfer flavoprotein (ETF):ubiquinone reductase; 1dxl, dihydrolipoamide dehydrogenase; 1nda, trypanothione oxidoreductase; 2qcu, glycerol-3-phosphate dehydrogenase; 4gr1, glutathione reductase; 1zk7, mercuric reductase; 2cfy, thioredoxin reductase; 1qla (2bs2), quinol:fumarate reductase.