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ERRATUM

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# Cytochrome *c* oxidase assembly factors with a thioredoxin fold are conserved among prokaryotes and eukaryotes

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The figure reprinted on the next page should have been printed in color instead of black and white (Fig. 1).

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## References

14. Corpet F (1988) Multiple sequence alignment with hierarchical clustering. Nucleic Acids Res 16:10881–10890
16. Jones DT (1999) Protein secondary structure prediction based on position-specific scoring matrices. J Mol Biol 292:195–202
17. Choi HJ, Kang SW, Yang CH, Rhee SG, Ryu SE (1998) Crystallization and preliminary X-ray studies of hORF6, a novel human antioxidant enzyme. Acta Crystallogr D Biol Crystallogr 54:436–437
18. Hirotsu S, Abe Y, Okada K, Nagahara N, Hori H, Nishino T, Hakoshima T (1999) Crystal structure of a multifunctional 2-Cys peroxiredoxin heme-binding protein 23 kDa/proliferation-associated gene product. Proc Natl Acad Sci USA 96:12333–12338
23. Papadopoulou LC, Sue CM, Davidson MM, Tanji K, Nishino I, Sadlock JE, Krishna S, Walker W, Selby J, Glerum DM, Coster RV, Lyon G, Scalais E, Lebel R, Kaplan P, Shanske S, De Vivo DC, Bonilla E, Hirano M, DiMauro S, Schon EA (1999) Fatal infantile cardioencephalomyopathy with COX deficiency and mutations in SCO2, a COX assembly gene. Nat Genet 23:333–337
31. Nicholas KB, Nicholas HB Jr, Deerfield DWI (1997) GeneDoc: Analysis and Visualisation of Genetic Variation. http://www.cris.com/~Ketchup/genedoc.shtml

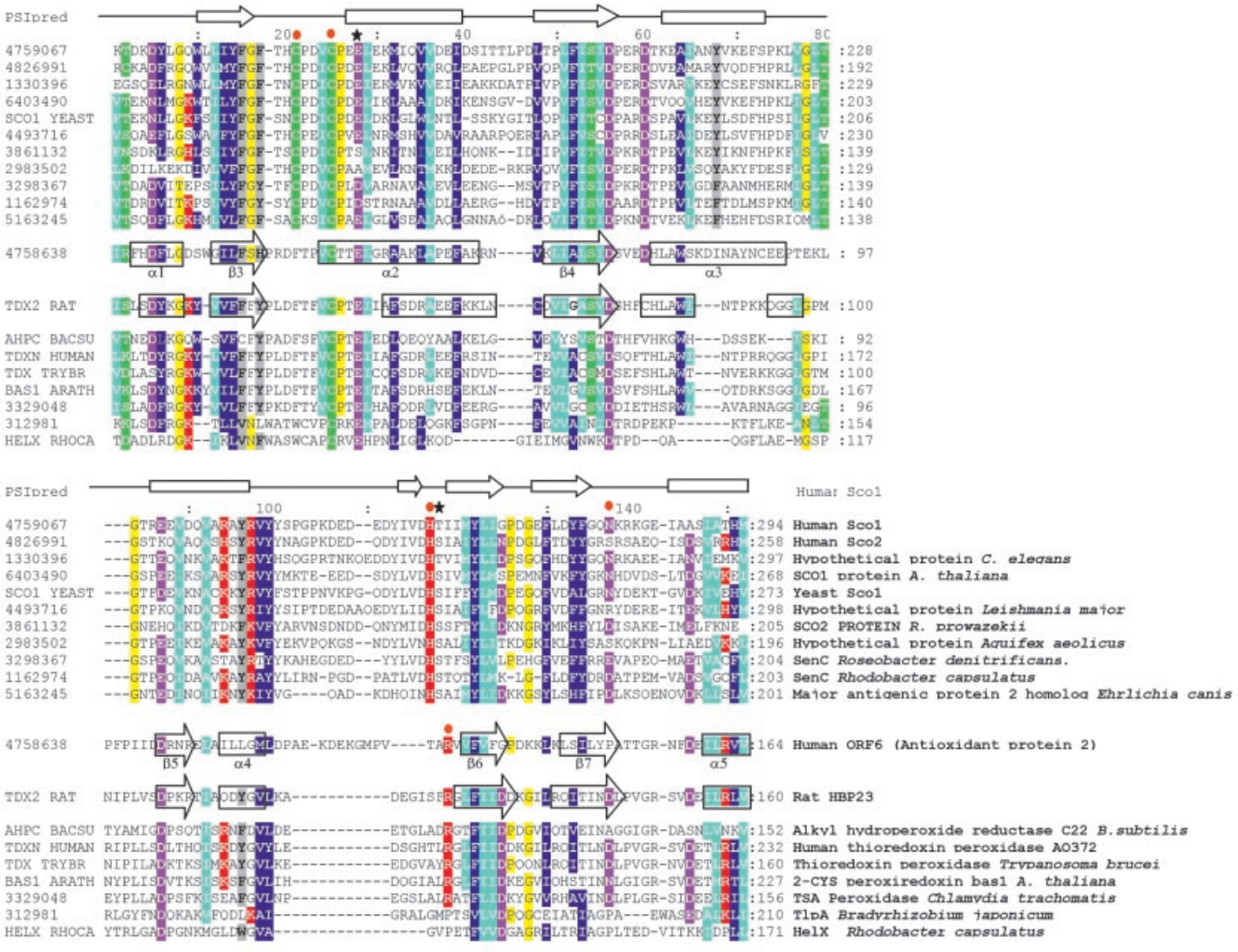


**Fig. 1** Multiple alignment of Sco1-related proteins. A PSI BLAST search (E-value=0.001) of NCBI nonredundant protein database with the C-terminal portion of *Saccharomyces cerevisae* Sco1p revealed similarity to peroxiredoxins after the second iteration and bacterial thiol:disulfide oxidoreductases after the third iteration. Representative members of these groups were aligned using MULTALIN [14] with the following settings: symbol comparison table – BLOSUM 62, gap penalty 8, gap penalty at extension 0.05. Aligned sequences were prepared for publication using GenDoc [31]. Conserved amino acids were colored according to the following scheme: *dark blue* hydrophobic residues (ACFGHIKLMVWY); *light blue* aliphatic residues (ILV); *gray* aromatic residues (FHWY); *red* positively charged residues (KRH); *purple* DENQ; *green* polar (CDEHKNQRST); *yellow* small (ACDGNPSTV). *Left column* SwissProt protein names or GenBank identifier codes; *right column* amino acid positions are indicated for each protein; *on the top of the alignment* amino acid positions of aligned proteins; *above the alignment with open rectangles* secondary structure predicted with PSIpred [16], α-helixes; *open arrows* β-strands. Secondary structure of human AOP2 (ORF6) and rat HBP23 is assigned from respective crystal structures and is shown as following: *black rectangles* α-helices; *black arrows* β-strands. The annotation of secondary structure elements is as in crystal structure of ORF6 [17, 18]. *Orange circles* residues of the putative active center and Arg-119 of the ORF6 active center; *black stars above the alignment* amino acid residues in the proposed Sco active center that are mutated in patients with infantile cardioencephalomyopathy [23]