Factor B and the Mitochondrial ATP Synthase Complex*

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Factor B is a subunit of the mammalian ATP synthase complex, whose existence has been controversial. This paper describes the molecular and functional properties of a recombinant human factor B, which when added to bovine submitochondrial particles depleted of their factor B restores the energy coupling activity of the ATP synthase complexes. The mature human factor B has 175 amino acids and a molecular mass of 20,341 Da. The preparation is water-soluble, monomeric, and is inactivated by monothiol- and especially dithiol-modifying reagents, probably reacting at its cysteine residues Cys-92 and Cys-94. A likely factor B gene composed of 5 exons has been identified on chromosome 14q21.3, and the functional role of factor B in the mammalian ATP synthase complex has been discussed.

It is generally considered that the mammalian mitochondrial ATP synthase complex is composed of 16 unlike subunits (1–3). These subunits are α, β, γ, δ, ε, and ϵ in the catalytic F₁ domain; OSCP, α, b, c, d, e, f, g, F₆, and A6l in F₀ and stator; and the ATPase inhibitor protein, IF₃, which binds reversibly to F₁ to inhibit ATP hydrolysis. In 1967, Sanadi and co-workers (4) showed that sub mitochondrial particles prepared by sonication from bovine mitochondria suspended in 0.25 M sucrose and 0.6 mM EDTA and adjusted to pH 9.0 with ammonium hydroxide lost considerable activity for respiration-driven ATP synthesis and ATP hydrolysis-driven electron transfer from succinate to NAD. Addition to the ammonia-EDTA-treated particles (AE-SMP) of a partially purified soluble protein extracted from mitochondrial acetone powders partially restored these activities (4, 5). Sucrose density gradient centrifugation suggested a molecular mass of 32 kDa for the active peak of the soluble preparation, which was designated factor B (4, 5). By using bovine mitochondrial acetone powder extracts, we isolated a pure and monodisperse protein, which restored ATP synthase-coupled activities to AE-SMP (6). Its molecular mass as estimated from sedimentation equilibrium and gel filtration experiments was 11–12 kDa, and it was immunoprecipitated by Sanadi’s anti-factor B antiserum in an Ouchterlony double diffusion experiment (7). Sanadi and co-workers (5, 8) revised the molecular mass of their preparation to 29.2 kDa and suggested that it is a dimer of monomer molecular mass of 14.6 kDa. They also obtained preparations of relative molecular mass of 13–15 and 47 kDa, which exhibited factor B-like activity (5, 9, 10), and in 1990 (11) they published the sequence of the 55 amino-terminal amino acids of a factor B preparation with a relative molecular mass of 22 kDa.

The existence of factor B as a component of the ATP synthase complex remained controversial, however. Although Sanadi (5, 12) claimed that the ATP synthase complex prepared in his laboratory contained factor B, a thorough analysis of the polypeptide composition of an ATPase complex prepared in Walker’s laboratory demonstrated the existence of the 16 unlike polypeptides mentioned above but no factor B (1, 2). The multiplicity of Sanadi’s factor B-like preparations with relative molecular masses ranging from 13–15 to 47 kDa, the small yield of our preparation, which precluded antibody production and chemical analyses, and the compelling extensive data of Walker’s laboratory discouraged further interest in the pursuit of factor B.

More recently, two nucleotide sequences corresponding in part to Sanadi’s 55-amino acid sequence of the factor B amino terminus were detected by our colleagues in the human genome. The shorter frame corresponding to 96 amino acid residues was expressed with a histidine tag. The expressed protein was found in inclusion bodies, and when extracted with 8 M urea and dialyzed the protein exhibited no factor B-like activity. The longer frame corresponding to 175 amino acid residues was expressed once with a histidine tag and a second time fused to thioredoxin. Both were recognized after purification by polyclonal antibodies raised to the shorter polypeptide. The histidine-tagged preparation was also inactive, but the other, after removal of thioredoxin, exhibited all the functional features described previously by Sanadi and co-workers (4, 5) and by ourselves (6, 7) for factor B. This paper describes the molecular and functional properties of this human factor B preparation.

EXPERIMENTAL PROCEDURES

Materials—NAD, NADH, ATP, oligomycin, and 2,4-dithiothreitol were obtained from Calbiochem; DCCD, venturicidin, FCCP, tributyltin chloride, NEM, p-chloromercuribenzoate, sodium succinate, and 2-mercaptoethanol were from Sigma; DEAE-Sepharose was from Amersham Biosciences; polyacrylamide was from Bio-Rad; Tris was from ICN; and oxonol VI was from Molecular Probes. All other chemicals were reagent grade. AE-SMP were prepared from heavy beef heart mitochondria (13) according to Ref. 14. After a final wash with 0.25 M sucrose containing 10 mM Tris-HCl, pH 7.8, the particles were suspended in the same medium at 17 mg of protein/ml and stored at –80 °C in small aliquots. F₆-ATPase was prepared according to Senior and Brooks (15) and stored in 50% saturated ammonium sulfate at 4 °C. The catalytic activity of the enzyme was in the range of 90–100 μmol of ATP hydrolyzed...
resulted in 0.02% final concentration. The incubation was continued for 4 h, and the culture was harvested by centrifugation and stored at 10 °C for 2 days to ensure total reduction of the NADP. The supernatant was used for the preparation of the fusion protein. The fusion protein was eluted with 50 mM imidazole in the above buffer. The purified recombinant human factor B was assayed for reconstitution of the ATP-driven reverse electron transfer activity of AE-SMP in the absence of diothiothreitol. The ATPase activities of F1-ATPase and AE-SMP were measured spectrophotometrically by the coupled pyruvate kinase/lactate dehydrogenase method as before (17).

RESULTS

Molecular Properties of Factor B—The predicted amino acid sequence of human factor B is shown in Fig. 1. In the amino-terminal 55 residues, there are three differences between the mature human factor B shown in Fig. 1 and the sequence published by Sanadi and co-workers for the bovine protein (11). The human amino acid residues Tyr-4, Cys-33, and Gln-43 are, respectively, His, Gly, and Gln in the bovine protein (11). Therefore, it was assumed that extraction conditions ATP synthesis and energy-linked reactions driven by ATP hydrolysis. Therefore, it was assumed that extraction


do not hallucinate.
of mitochondria with ammonia-EDTA partially removed one or more factor B-like molecules from the mitochondrial ATP synthase complexes. However, the effectiveness and the specificity of this extraction procedure for factor B removal were unclear. Fig. 3 depicts immunoblots of mitochondria (column A), SMP (column B), and AE-SMP (column C) blotted with subunit-specific polyclonal antibodies to recombinant human factor B (row 1), a subunit of bovine F_{1} (row 2), bovine OSCP (row 3), and bovine ATPase inhibitor protein IF_{1} (row 4). For other details, see “Experimental Procedures.”

The nucleotide and the deduced amino acid sequences of human factor B. Arrow indicates the start of the sequence of the mature human factor B shown in boldface letters and numbered on the right. Asterisk indicates the termination codon. For details see “Experimental Procedures.” This nucleotide sequence has been submitted to the GenBank™/EBI Data Bank with accession number AY052377.

The levels of F_{1} as represented by its H_{9251} subunit, and OSCP, which is not anchored to the membrane, were essentially unchanged by the extraction. The level of IF_{1} was decreased in AE-SMP (Fig. 3, bottom row) which was understandable, because of the alkaline pH of the extraction medium (24). Consistent with these results, the ATPase activity of AE-SMP was shown to be about 40% higher than that of SMP.

Fig. 4 shows on the ordinate the activity of AE-SMP for ATP hydrolysis-driven electron transfer from succinate to NAD as affected by addition of increasing amounts of recombinant human factor B (row 1), a subunit of bovine F_{1} (row 2), bovine OSCP (row 3), and bovine ATPase inhibitor protein IF_{1} (row 4).
electron transfer activity (10–12% as compared with 87% when factor B was added), indicating in agreement with the data of Fig. 3 that the poor coupling activity of AE-SMP was not due to the loss of F₁ and/or OSCP.

It has long been known that addition of low concentrations of oligomycin to SMP treated with EDTA or ammonia-EDTA partially restores their energy-coupled activities. Apparently, when added at low concentrations oligomycin preferentially reacts with and seals the proton leakiness of the fraction of the ATP synthase complexes that have been rendered defective, thereby allowing the remaining intact ATP synthases to function normally (26). Further addition of oligomycin would then begin to inhibit the intact ATP synthases, resulting in a decrease of the ATP synthase-coupled activity tested. Similar results are shown in Fig. 5. It is seen that addition to AE-SMP of oligomycin up to about 150 ng (0.3 nmol/mg protein) increased the ATP-driven reverse electron transfer activity of the particles from about 5 to about 54 nmol of NADH formed (min·mg protein)⁻¹, and that further increase in oligomycin concentration resulted in inhibition. As was shown previously (6), addition of low concentrations of oligomycin (<120 ng/mg protein) to factor B-replenished AE-SMP caused no activation but only partial inhibition of ATP-driven reverse electron transfer activity. We have examined the effect of other F₀ inhibitors with regard to activation of ATP-driven electron transfer from succinate to NAD. At concentrations that caused inhibition of ATPase activity of AE-SMP from 10 to 70%, venturicidin and tributyltin chloride had no stimulating effect on its reverse electron transfer activity. Incubation of AE-SMP at 0°C with 6 μM DCCD caused a time-dependent inhibition of its ATPase activity, as expected. At 10 and 20 min of incubation, when ATPase activity was inhibited by 30 and 43%, respectively, ATP-driven reverse electron transfer activity of the particles was increased from 4 nmol of NADH formed (min·mg)⁻¹ to 18 at 10 min and to 27 at 20 min of incubation. Further incubation of AE-SMP with 6 μM DCCD lowered this stimulated activity to 22 at 30 min and to 7 at 50 min. Previous preparations of bovine factor B were shown to be inhibited by thiol and dithiol modifiers (5–7). The effects of these modifiers on recombinant human factor B are shown in Fig. 6. It is seen that factor B was inhibited when treated with the compounds shown, with the dithiol modifiers phenylarsine oxide and Cd²⁺ causing 50% inhibition at <10 μM concentration. As seen in Fig. 1, human factor B contains 6 cysteine residues, two of which are located at positions 92 and 94. The strong inhibitory effects of phenylarsine oxide and Cd²⁺ suggest that these dithiol modifiers bind to cysteine residues 92 and 94 of factor B.

Effect of Factor B on Membrane Potential—Fig. 7 shows the formation of a membrane potential in SMP (traces A and B), AE-SMP (traces C and D), and AE-SMP plus factor B (traces E and F) as monitored by the absorbance change of oxonol VI at 630 minus 603 nm. Traces A and B are controls with SMP, showing membrane energization upon addition of ATP or NADH and deenergization by inhibition of ATP hydrolysis by oligomycin, inhibition of NADH oxidation by rotenone, or by uncoupling with FCCP. Traces C and D show that AE-SMP could not develop a high membrane potential upon addition of either ATP or NADH but that addition of oligomycin repaired this defect and allowed high membrane potential formation upon subsequent addition of NADH. Similar results were obtained when oligomycin was replaced with venturicidin or tributyltin chloride or when the AE-SMP was treated for 60 min at 0°C with 10 μM DCCD. Like oligomycin, these reagents inhibited ATP hydrolysis but allowed membrane potential formation, as in Fig. 7C, upon addition of NADH (data not shown). These results suggested, therefore, that removal of factor B created a proton leak in the F₀ of AE-SMP, which could be blocked by the specific F₀ inhibitors mentioned. Traces E and F show that the addition of factor B to AE-SMP repaired the defect shown in traces C and D and made it possible for the particles to develop a high membrane potential upon addition of either ATP or NADH. As seen in traces E and F, the development of the membrane potential to a static head level in
factor B-supplemented AE-SMP was a slow process as compared with the results shown in traces A and B for SMP. It is possible that factor B binding to AE-SMP requires an energized conformation of FO-F1, apparently best achieved with the addition of ATP. This possibility would be somewhat analogous to the binding of IF1 to F1, which occurs during ATP hydrolysis by the enzyme (24).

**DISCUSSION**

**Molecular Properties of Factor B**—According to the data reported here, mature human factor B is composed of 175 amino acid residues with a molecular mass of 20,341 Da and the amino acid sequence shown in Fig. 1. The active, recombinant human factor B purified and used in the studies reported here contained an extra LAL tripeptide at its amino terminus. It was water-soluble, monomeric, and stable when stored at −80 °C in a pH 8.0 buffer containing 5 mM 2-mercaptoethanol. In its amino-terminal 55 residues and molecular mass, this recombinant human factor B is similar to the latest of a number of bovine mitochondrial factor B preparations reported previously by Sanadi and co-workers (11). Because rigorous data on the purity and the amino-terminal sequences of the other factor B-like preparations of Sanadi and co-workers are not available, it is not possible to discuss them further, nor can we compare our pure protein of molecular mass 11–12 kDa, which was isolated from bovine heart mitochondria and exhibited a factor B-like activity (6, 7), with the recombinant factor B described here. Its low yield precluded in 1976 any attempts at amino-terminal sequencing, but its sensitivity to thiol and dithiol modifiers suggests that it might have been an active proteolytic fragment of the bovine factor B. This possibility is supported by the fact that immunoblots of bovine heart mitochondria with our polyclonal antibody used in the present work recognized only a single protein band corresponding in mobility on SDS gels to that of our recombinant human factor B.

**Factor B Gene**—Fig. 8 shows a segment of the human genome on chromosome 14q21.3. This segment spans −13 kb and contains 5 exons, of which the nucleotide sequences of the areas depicted in Fig. 8 by the filled boxes from ATG in exon 1 to TAA in exon 5 correspond to the sequence of the human factor B cDNA shown in Fig. 1, except that in the draft sequence of the Human Genome Project (27) the nucleotide T-168 is given as C, which would result in the substitution of Pro for Leu in the corresponding position of the presequence of factor B. As seen in Fig. 8, there are 2 stop codons and 2 polyadenylation signals in this DNA segment. An mRNA transcript arising from the processing of pre-mRNA at poly(A) site ATTAAA would encode a hypothetical protein HSU79253 (Locus identification number 27109). Reverse transcription PCR, using multiple tissue cDNA panels I and II (CLONTECH), showed that mRNAs corresponding to both the short (exons 1–3) and the long (exons 1–5) sequences were present in 16 different human tissues that we examined. As mentioned above, the short polypeptide con-

**Fig. 6.** Inhibition of factor B with NEM, p-chloromercuribenzoate (pCMB), phenylarsine oxide (PAO), and CdSO4. Factor B was preincubated with the indicated reagents as described under “Experimental Procedures” and then was added to the reaction mixture for reconstitution of the ATP-driven reverse electron transfer activity of AE-SMP. The factor B concentration in the reaction mixture was 17.6 µg of factor B/mg of AE-SMP. 100% activity was 160 nmol of NADH formed (min/mg AE-SMP) Thompson.

**Fig. 7.** Effects of factor B and oligomycin on membrane potential formation by AE-SMP. The reaction mixture at 30 °C contained 0.25 M sucrose, 50 mM Tris-HCl, pH 7.5, 2 mM MgCl2, 2 µM oxonol VI, and 0.1 mg of SMP (traces A and B) or AE-SMP (traces C–F) per ml. Where indicated 4.5 mM ATP, 0.25 mM NADH, 5 µg of oligomycin/ml, 5 µM rotenone, and 5 µM FCCP were added. In experiments E and F, the reaction mixtures contained 6 µg of factor B. Trace D, oligomycin was added 7.5 min after the addition of NADH (see the 4-min gap) to allow NADH to become completely oxidized. Membrane potential formation was monitored by the absorbance change of oxonol VI at 630 minus 603 nm in an SLM DW-2000 dual wavelength spectrophotometer.
taining a His tag was expressed in our laboratory as inclusion bodies and was used to raise polyclonal antibodies. This antibody preparation recognized in bovine heart mitochondria a single protein with a mass of 22 kDa, which could be extracted from SMP by the procedures used to remove factor B (Fig. 3). The short polypeptide, expected to have a mass of ~11 kDa, was not detected in bovine heart mitochondria. This consideration suggests that this short “isof orm” of factor B, if translated, either does not enter mitochondria or is degraded after entering this organelle.

A second human homologue, the hypothetical protein FLJ10241 (Locus identification number 55101) encoded by a gene located on chromosome 1q21.2, with sequence similarity of 49% to human factor B, was identified by BLASTP (28) search of the GenBank™ data base. This search also revealed the existence of two mouse orthologues (GenBank™ accession numbers NP_080812 and BAB26107) with sequence similarities of 83 and 47%, respectively, as well as two gene products in Drosophila melanogaster (GenBank™ accession numbers AA58055 and AA51634) and Caenorhabditis elegans (GenBank™ accession numbers AA95868 and AA58941) exhibiting 44–52% sequence similarity to human factor B. Neither a prokaryotic homologue nor a counterpart in Saccharomyces cerevisiae has been identified.

Role of Factor B—The results presented here clearly show that factor B is necessary for the energy transduction activity of the ATP synthase complex. Treatment of well coupled SMP with ammonia-EDTA at pH 8.8 resulted in the specific removal of a protein of 22 kDa and in the inability of the AE-SMP to develop and maintain a membrane potential as a result of ATP hydrolysis or NADH oxidation (Fig. 7). This defect could be repaired by addition to the AE-SMP of a recombinant human protein of 22 kDa at a molar concentration nearly stoichiometric to the ATP synthases of the particles. The recombinant human protein was homologous in molecular mass and amino-terminal sequence to the purified bovine factor B of Sanadi and co-workers (11), and like all factor B preparations was sensitive to treatment with monothiol and especially dithiol modifiers.

The bovine ATP synthase complex contains at least 7 subunits of totally unknown function, namely subunits e, Fα, A6L, d, e, f, and g. This complexity makes it difficult to employ the E. coli ATP synthase with only 8 unlike subunits (29) as a model into which to build a role for factor B. However, the basic operational design of the E. coli ATP synthase, which is composed of a catalytic, a rotor, and a stator domain (30, 31), applies to the more complicated ATP synthases (32, 33), and we will discuss the role of factor B in the light of this basic design. The fact that factor B is not a component of the catalytic domain is clear and needs no further consideration. It cannot be a necessary component of the stator either, because unlike the systems lacking OSCP the ATPase activity of AE-SMP (5 μmol/min/mg) is completely inhibited by F0 inhibitors, including DCCD whose mechanism of inhibition is well known. The sensitivity of the ATPase activity of AE-SMP to F0 inhibitors also indicates that in these particles the rotating part of F0, i.e. γ and δ, is not disengaged from F0. These considerations allow the conclusion, therefore, that factor B is a component of F0.

As seen in Fig. 7, AE-SMP is uncoupled and incapable of forming a membrane potential as a result of respiration or ATP hydrolysis. This defect can be repaired by addition of factor B or by addition of F0 inhibitors at concentrations that these reagents inhibit ATP hydrolysis. Repair by factor B allows membrane potential formation as a result of ATP hydrolysis or respiration. Repair by F0 inhibitors allows only respiration-dependent membrane potential formation, which indicates that the proton leak of AE-SMP involves, at least in part, the normal proton channel of F0. This leads to the following important question. Because the proton leak of AE-SMP can be blocked by F0 inhibitors, especially DCCD, does the proton leak from the cytosolic (positive) side to the matrix (negative) side of the membranes in respiring AE-SMP require the rotation of the c ring? Based on the generally accepted basic design and operation of the ATP synthase complex, the answer to this question is no. This is because in respiring AE-SMP the proton leak, which can be blocked by DCCD, occurs in the absence of F1 substrates. These considerations allow the conclusion that the F0 of mammalian ATP synthase is capable of uncoupled transmembrane proton translocation via a second path that involves, at least in part, its normal proton channel, possibly including Glu-58 of subunit c. Proton translocation via this second path does not require the operation of the rotor of the ATP synthase and can be blocked by the water-soluble factor B that appears to bind to F0 on the matrix side.

Whether the F0 subunits Fα, A6L, d, e, f, and g, which like factor B do not have prokaryotic counterparts, are involved in this second proton path remains to be seen. Another mammalian F0-F1 subunit that does not have a prokaryotic counterpart is the ATPase inhibitor protein, IF1, that binds to F1 β subunits and prevents futile ATP hydrolysis when the proton-motive force is low (34–36). The fact that factor B can also be easily and reversibly removed from F0-F1 and the fact that its displacement results in dissipation of membrane potential may be indicative of a regulatory function for factor B as well. It is generally assumed that the state 4 rate of respiration is due to a slow proton leak through the mitochondrial inner membrane at high proton-motive force. However, it is well known that proteoliposomes of sonicated phospholipids plus a proton pump such as cytochrome oxidase or nicotinamide nucleotide transhydrogenase are not as leaky as high proton-motive force as SMP. Therefore, considering that over-reduction of the respiratory chain results in an increased rate of superoxide anion production, which leads to the formation of toxic H2O2 and hydroxyl radicals (37, 38), it is possible that factor B acts as a pressure valve for maintaining the proton-motive force (hence the reduced level of the respiratory chain) below a damaging threshold (see also the concept of “mild uncoupling” in Ref. 38).

Finally, another point that deserves consideration is the designation “factor B” for the protein discussed here. More than 2 decades ago, the word “factor” was correctly replaced by “subunit,” and already there are among the ATP synthase subunits a β subunit and a b subunit. Continuing the alphabetical sequence beyond e, f, and g would result in confusion with the yeast ATP synthase subunit designations. Therefore, it may be appropriate to designate the protein under consideration here as subunit s, after its original discoverer.

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REFERENCES

1. Walker, J. E., Lutter, R., Dupuis, A., and Runswick, M. J. (1991) Biochemistry 30, 5369–5378
2. Collinson, I. R., Runswick, M. J., Buchanan, S. K., Fearnley, I. M., Skehel, J. M., Van Ranj, M. J., Griffiths, D. E., and Walker, J. E. (1994) Biochemistry 33, 7791–7798
3. Belogrudov, G. I., Tomich, J. M., and Hatefi, Y. (1996) J. Biol. Chem. 271, 20340–20345
4. Lam, K. W., Swann, D., and Elzinga, M. (1969) Arch. Biochem. Biophys. 119, 477–484
5. Sanadi, D. R. (1982) Biochim. Biophys. Acta 683, 39–56
6. You, K.-S., and Hatefi, Y. (1976) Biochim. Biophys. Acta 423, 398–412
7. Stiggall, D. L., Galante, Y. M., Kiehl, R., and Hatefi, Y. (1997) Arch. Biochem. Biophys. 196, 638–644
8. Lam, K. W., Swann, D., and Elzinga, M. (1969) Arch. Biochem. Biophys. 130, 175–182
9. Joshi, S., Hughes, J. B., Shaikh, F., and Sanadi, D. R. (1979) J. Biol. Chem. 254, 10145–10152
10. Shanksar, R., Suri, B. P., and Sanadi, D. R. (1975) Arch. Biochem. Biophys. 168, 394–402
11. Kantham, L., Rajchowdhury, R., Ogata, K. K., Javed, A., Rice, J., and Sanadi, D. R. (1990) FEBS Lett. 277, 105–108
12. Joshi, S., Kantham, L., Kaplay, S., and Sanadi, D. R. (1985) FEBS Lett. 179, 143–147
13. Hatefi, Y., and Lester, R. L. (1958) Biochim. Biophys. Acta 27, 83–88
14. Joshi, S., and Sanadi, D. R. (1979) Methods Enzymol. 55, 384–391
15. Senior, A. E., and Brooks, J. B. (1979) Arch. Biochem. Biophys. 140, 257–266
16. Matsuno-Yagi, A., and Hatefi, Y. (1984) Biochemistry 23, 3508–3514
17. Stiggall, D. L., Galante, Y. M., and Hatefi, Y. (1979) Methods Enzymol. 55, 388–389
18. Belogrudov, G., and Hatefi, Y. (1994) Biochemistry 33, 4571–4576
19. Ausubel, F. M., Brent, R., Kingston, R. E., Moore, D. D., Seidman, J. C., Smith, J. A., Struhl, K., Allbritton, L. M., Geen, D. M., Varki, A., and Chanda, V. R. (eds) (1997) Current Protocols in Molecular Biology, Wiley Interscience, New York
20. Tzagoloff, A., Luttington, K. H., and MacLennan, D. H. (1968) J. Biol. Chem. 243, 2405–2412
21. Lutter, R., Saraste, M., van Walraven, H. S., Runswick, M. J., Finel, M., Deatherage, J. F., and Walker, J. E. (1993) Biochem. J. 285, 799–806
22. Groth, G., and Walker, J. E. (1996) Biochem. J. 318, 351–357
23. McEnery, M. W., Buhle, E. L., Aebi, U., and Pedersen, P. L. (1984) J. Biol. Chem. 259, 4642–4651
24. Galante, Y. M., Wong, S.-Y., and Hatefi, Y. (1981) Biochemistry 20, 2671–2678
25. Matsuno-Yagi, A., and Hatefi, Y. (1988) Biochemistry 27, 335–340
26. Lee, C.-P., and Ernst, L. (1965) Biochem. Biophys. Res. Commun. 18, 523–529
27. International Human Genome Sequencing Consortium (2001) Nature 409, 860–921
28. Altschul, S. F., Madden, T. L., Schaffer, A. A., Zhang, J., Zhang, Z., Miller, W., and Lipman, D. J. (1997) Nucleic Acids Res. 25, 3389–3402
29. Fillingame, R. H. (1990) in The Bacteria (Kruvilch, T. A., ed) Vol. 12, pp. 345–391, Academic Press, New York
30. Hutcheon, M. L., Duncan, T. M., Ngai, H., and Cross, R. L. (2001) Proc. Natl. Acad. Sci. U. S. A. 98, 8519–8524
31. Junge, W., Panke, O., Cherepanov, D. A., Gumbiowski, K., Mubler, M., and Engelbrecht, S. (2001) FEBS Lett. 504, 152–160
32. Stock, D., Leslie, A. G. W., and Walker, J. E. (1999) Science 286, 1700–1705
33. Stock, D., Gibbons, C., Arechaga, I., Leslie, A. G. W., and Walker, J. E. (2001) Curr. Opin. Struct. Biol. 10, 672–679
34. Schwerzmann, K., and Pedersen, P. L. (1986) Arch. Biochem. Biophys. 250, 1–18
35. Hashimoto, T., Yoshida, Y., and Tagawa, K. (1990) J. Bioenerg. Biomembr. 22, 27–38
36. Ichikawa, N., Yoshida, Y., Hashimoto, T., Ogasawara, N., Yashikawa, H., Imamoto, F., and Tagawa, K. (1990) J. Biol. Chem. 265, 6274–6278
37. Chance, B., Sies, H., and Rovires, A. (1979) Physiol. Rev. 59, 827–865
38. Papa, S., and Skulachev, V. P. (1997) Mol. Cell. Biochem. 174, 305–319
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