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Proteins as Solid-State Electronic Conductors

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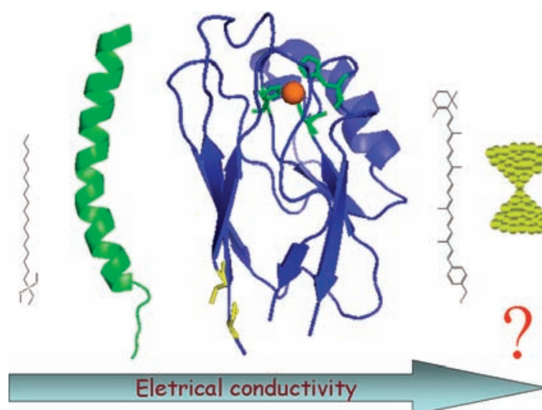
CONSPECTUS

Protein structures can facilitate long-range electron transfer in solution. But a fundamental question remains: can these structures also serve as solid-state electronic conductors? Answering this question requires methods for studying conductivity of the "dry" protein (which only contains tightly bound structured water molecules) sandwiched between two electronic conductors in a solid-state type configuration. If successful, such systems could serve as the basis for future, bioinspired electronic device technology.



In this Account, we survey, analyze, and compare macroscopic and nanoscopic (scanning probe) solid-state conductivities of proteins, noting the inherent constraints of each of these, and provide the first status report on this research area. This analysis shows convincing evidence that "dry" proteins pass orders of magnitude higher currents than saturated molecules with comparable thickness and that proteins with known electrical activity show electronic conductivity, nearly comparable to that of conjugated molecules ("wires"). These findings suggest that the structural features of proteins must have elements that facilitate electronic conductivity, even if they do not have a known electron transfer function.

As a result, proteins could serve not only as sensing, polar,or photoactive elements in devices (such as field-effect transistor configurations) but also as electronic conductors. Current knowledge of peptide synthesis and protein modification paves the way toward a greater understanding of how changes in a protein's structure affect its conductivity. Such an approach could minimize the need for biochemical cascades in systems such as enzyme-based circuits, which transduce the protein's response to electronic current. In addition, as precision and sensitivity of solid-state measurements increase, and as knowledge of the structure and function of "dry" proteins grows, electronic conductivity may become an additional approach to study electron transfer in proteins and solvent effects without the introduction of donor or acceptor moieties.

We are particularly interested in whether evolution might have prompted the electronic carrier transport capabilities of proteins for which no electrically active function is known in their native biological environment and anticipate that further research may help address this fascinating question.

1. Introduction

Electron transfer (ET) reactions are among the most fundamental processes in chemistry and biology.[1] Specifically, in biology ET is crucial for different energy conversion processes, from respiration to photosynthesis, and is prominent in diverse metabolic cycles. The work of Gray and co-workers that showed how several protein families support fast, long-range electron transfer (ET)[2,3] raises the question of whether they can be considered as potential electronic conductors, something that was proposed already by Szent-Gyoryi, Ladik, and others.[4,5] However, research on "*bio*-molecular electronics"[6] is still relatively rare, especially compared to work on "molecular electronics" with organic molecules. A major challenge to integrating proteins in a "solid-state" configuration (i.e., with only tightly bound, structured water

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retained within the protein) is the need to sandwich proteins between two solid electrodes.[7] There is also the further question of whether the proteins retain their structure (and, even more demanding, their activity) in such a configuration.

This research direction is motivated by the unique properties that have been acquired by proteins in their evolution toward carrying out complicated functions. Such properties may, based on our current understanding of the chemistry underlying molecular conductance, introduce proteins as a new type of conductive materials.

Most work on protein conductivity to date used scanning probe techniques, the results of which we also survey in this Account. Those measurements are carried out at the single (or few) molecule(s) level. We developed recently a strategy that permits large area protein monolayer junction preparation and measurement.[8] Building on our earlier work on electronic transport (ETp) across bacteriorhodopsin (bR) monolayers,[9] we could prepare and measure three distinct protein monolayers and an organic molecular monolayer, as a first comparison between current−voltage characteristics of junctions with only the protein as variable. Taken together, these data allow us to provide a critical account of solid-state ETp of proteins on the nanoscopic (single molecule) and macroscopic (monolayers) levels.

2. Protein Monolayer Solid-State Junctions[8−11]

We will focus mainly on two proteins, that is, azurin (Az) and bacteriorhodopsin (bR), which have been studied in various configurations. Indications for the robustness of these proteins that allows them to remain intact in a solid-state configuration was found not only in their morphological properties as observed by atomic force microscopy (AFM) but also in their UV−visible absorption (bR, Az) and fluorescence emission (Az) spectra, probes that are extremely sensitive to major protein conformational changes[10−13] and are used to rule out protein denaturation.

Azurin (Az) is a soluble small, type I blue copper protein, functioning as an electron carrier in bacteria. It serves as a model for studying long-range ET in proteins.[14,15] Az was studied by *electrochemical* scanning tunneling microscopy (EC-STM)[16,17] and as a component integrated in electronic devices.[13,18] Bacteriorhodopsin functions as a light-driven proton pump in the halophilic archea *Halobacterium salinarum*.[19] It is a membrane protein, embedded in a 2D crystalline matrix of protein and lipids in a defined ratio. Neither bR nor its related rhodopsins are known to be involved in any ET reac-

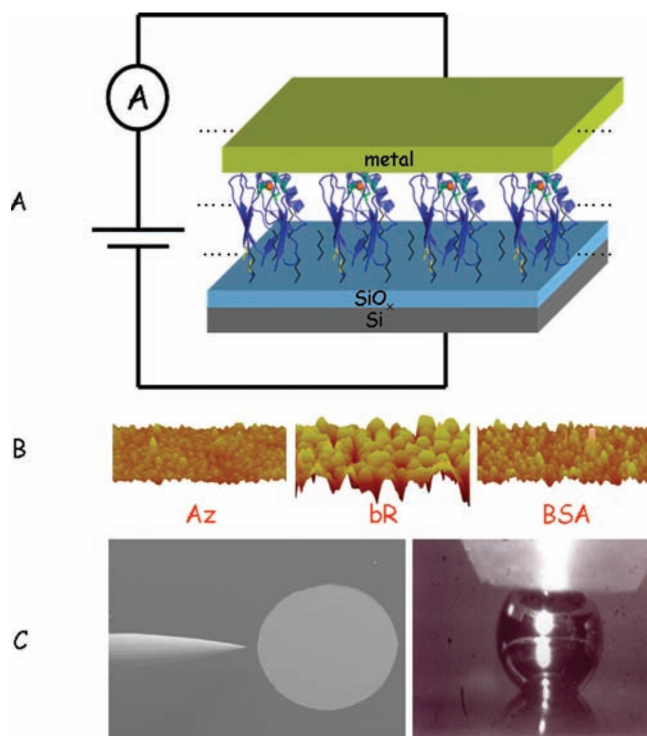

FIGURE 1. (A) Schematic of protein monolayer junction (of Az protein molecules in this example). The monolayer is self-assembled on a chemically modified oxidized Si surface. A large area top metal electrode is then deposited to complete the junction. This cartoon, not drawn to scale, shows only a few Az molecules; the top electrodes for monolayer junction measurements (see (C)) cover $\sim 10^{10}$ Az molecules. (B) AFM images (500×500 nm^2, *z* scale = 5 nm) of Az, bR, and BSA monolayers, showing homogeneous protein coverage of the surface (over the entire ~ 1 cm^2 area). (C) Two methods for making top contacts to monolayers: a ready-made, 60 nm thick, 0.05 cm diameter Au film, deposited from water and contacted by a thin probe (left) and a 0.05 cm diameter Hg drop (right).

tions. We used also monolayers of bovine serum albumin (BSA), a plasma protein, and of octadecyltrimethoxysilane (OTMS), an 18-carbon long saturated hydrocarbon chain. All monolayers were assembled on a chemically modified, thin SiO_x layer, grown on top of a Si wafer, and resulted in homogeneous, smooth layers, indicating dense packing of the proteins (80−90% coverage by AFM). The junction configuration with the top metal electrodes used for these measurements is shown in Figure 1.

The salient features of our ETp measurements are the similarities in current magnitudes between Az and bR, and those between currents through BSA and octadecyltrimethoxysilane (OTMS; Figure 2), which are around 2 orders of magnitude lower than the first couple. The similarity in measured currents for BSA and OTMS is misleading, though, because BSA presents an ~ 2 fold thicker barrier than OTMS; that is, also BSA, a protein which is not known to be electrically active, is

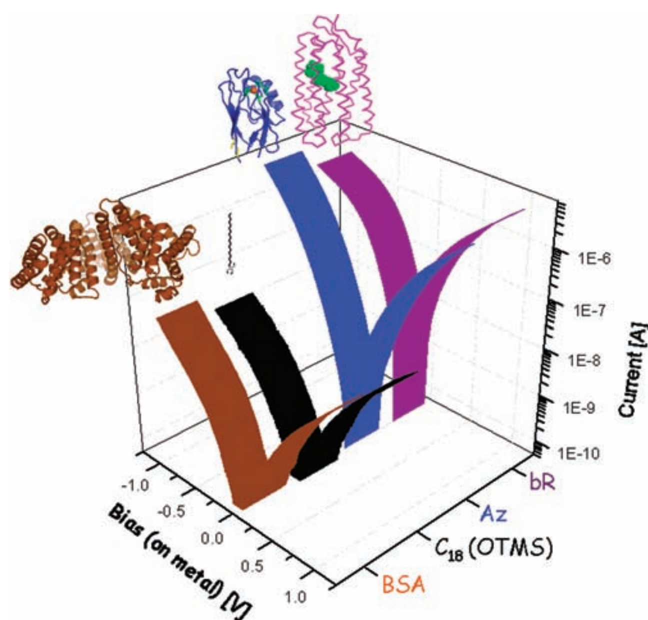

FIGURE 2. Current−voltage ($I-V$) characteristics of protein monolayer junctions (bR, Az, BSA) and an organic monolayer junction (OTMS). Structures of the four species are shown on top of the curves, drawn to scale with respect to one another. Az and bR coordinates are from the Protein Data Bank (PDB), code 1AZU for Az (Cu in orange, disulfide bridge in yellow), code 1R2N for bR (retinal in green); the BSA model was obtained from ModBase.

much more efficient an electron transport medium than a saturated alkyl chain.[20]

By measuring currents through our junctions *before* and *after* protein adsorption (at 1 V, which makes the result equivalent to conductance), we can fit them to an exponential dependence on barrier width.[21−23]

$$I = I_0 \exp(-\beta l) \qquad (1)$$

using the currents through the junction without the protein as I_0 and the protein length (from X-ray structure dimensions in the proposed orientations, as supported by our monolayer characterization) as the width, l (36, 50, 40, and 25 Å for Az, bR, BSA, and OTMS respectively). We use simple tunneling as a first approximation, even though single step tunneling is a very unlikely scenario with such barrier widths, in order to evaluate β from relation 1 as an effective tunneling decay constant. Relation 1 assumes that the current between the two electrodes flows because of direct, *nonresonant* tunneling, a common approximation in molecular electronics (cf. ref 24). We then use the β value to decide which mechanism may better describe our junctions' behavior (single- or multistep tunneling), because, even though many quantities are lumped together in β, its evaluation is useful to categorize molecular species into groups of different ET (and ETp) efficiency.

The β values, obtained from eq 1, are 0.12 $Å^{-1}$ for bR, 0.18 $Å^{-1}$, for Az and 0.27 $Å^{-1}$ for BSA, well below the 0.5−1 $Å^{-1}$ values that fit simple tunneling across organic monolayer junctions,[24] as shown by the $\beta = 0.68$ $Å^{-1}$ OTMS monolayer result. These low β values suggest that a mechanism different from direct tunneling will describe these observations better, as will be discussed later (see also the Supporting Information).

To explain the higher ETp efficiency through Az and bR than through BSA, we refer to the chemical composition of the first two systems that allows them to carry out their specific function, as known from wet measurements.[25] The retinal chromophore that lies at a 20−25° angle to the membrane surface (Figure 2) may facilitate ETp across bR, as it consists of a polyene chain, a derivative of the family of carotenes known to play a role in ET processes. Studies on carotenes revealed low decay constants,[26] and much higher conductivity than that through alkanes.[27] In general, transport across conjugated molecules yields lower decay constants than those across aliphatic ones.[28] We also suggest that the natural ability of bR to transport protons provides an electrically screened pathway, which can be employed by electrons.[9] This can be understood by considering the effective dielectric constant of the groups surrounding the sites that are involved in proton pumping, where the dielectric constant is derived from polarization of these specific groups.

In Az, redox activity is carried out by the Cu center, a property which may well be relevant for ETp across solid-state junctions. In addition, both Az and bR contain tryptophan residues, which have been suggested to contribute to ET in proteins.[14,29] Still, in the solid-state configuration, even BSA is more efficient a conductor than a simple saturated hydrocarbon chain, an issue that will be discussed later.

3. Conductive Probe AFM Studies[30−38]

As mentioned earlier, much of the protein conductivity work to date used scanning probe techniques, mainly conductive probe atomic force microscopy (CP-AFM). In CP-AFM, the protein molecule(s) can be adsorbed to the substrate or to the tip. In any case, only one or few molecules will form the electrical junction (Figure 3). Both Az and bR were studied by CP-AFM. For Az, we focus on studies of Davis and co-workers,[30] who adsorbed Az on a Au-coated AFM tip. The (tip + protein) then approached a conducting substrate, and, upon contact, $I-V$ curves were recorded under varying forces. We extract values of $\sim 3 \times 10^{-10}$ A/junction under a force of 6 nN (at an applied bias of 1 V) from their results. For bR, fragments of

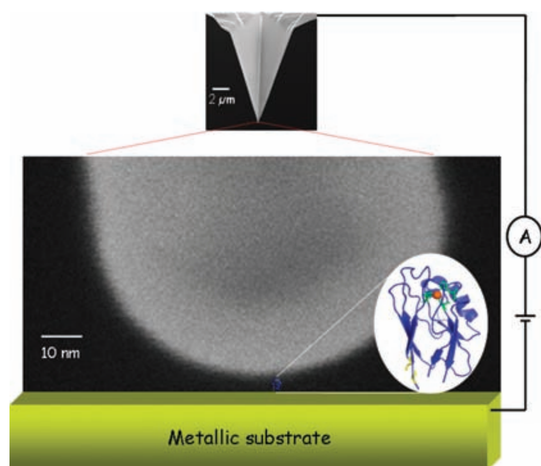

FIGURE 3. CP-AFM configuration: a conducting (metal-coated in this figure) tip is used to contact a molecule that is adsorbed either directly to it or to the underlying metallic substrate. The enlarged electron micrograph of the tip apex is scaled to the size of a protein molecule, Az in this case (shown enlarged on the right), to show the actual dimensions of this junction. In practice, several molecules can be contacted by a tip of this size. Top: low magnification electron micrograph of the tip.

purple membranes (from *H. salinarum* that was also used in the earlier mentioned study on bR monolayers) were adsorbed on a Au substrate, and *I*−*V* curves recorded, when a Au-coated tip was parked over the membrane surface.[31] The current density, extracted from these measurements, is 50 pA/bR trimer (25 nm^2 area, at 1 V bias).

To put these results in perspective, we summarized the reported data on electronic conduction through protein systems, using CP-AFM, in such metal−protein−metal (MPM) configuration, in Table 1. This summary, which gives the raw data for MPM junctions with a single protein layer (although an unknown number of molecules in most studies; see below),[30−38] shows several aspects that are important for interpreting the behavior of this kind of junctions:

(1) Applied force. While the studies of Davis and co-workers include the (stress-induced) effect of protein mechanics on CP-AFM current transport,[30,35] such information is missing in most other CP-AFM studies, which complicates assessing effects of differences in exerted forces. The actual length of the protein layer and the surface area of the substrate that is contacted by it change with applied force. However, every protein system will be affected in its own way, because the biomolecular mechanics differ from protein to protein. One possibly related example for such an effect is the large difference (at 0.5 V) between the current measured through the RC complex in its soluble form[37] and that measured through the RC complex that is reconstituted into a lipid bilayer.[33] The latter may well present a more robust configuration for the protein.

(2) Contact area. Although all studies, included in Table 1, use the same basic method and similar apparatus, the actual geometric contact area can differ between experiments, due to differences in tip diameter and geometry and the type of molecules, which dictate the adhesive forces. This uncertainty makes it impossible, in most cases, to estimate the number of molecules involved in the measurement and, thus, to extract current/molecule values.

Since all the tips that are used in these experiments have 20−50 nm diameter, we estimate that the contact areas of different junctions differ by no more than a factor of 5−6, and we will use current density to compare data.

(3) Electrode materials. The difference between metals that make up the electrode for the junctions may affect the tunneling characteristics of molecular junctions because of the difference in work functions[39] (see also the Supporting Information). Such an effect can be detected for the Cyt-C-modified Au-coated AFM tip, for which two different measurements are given, on a Au and Highly Oriented Pyrolytic Graphite (HOPG) surface.[32] We note that while the two experiments (compared at a given force) yield different currents, this may be due to the difference in, for example, adhesion forces between the molecules and the different surfaces, rather than the difference between the work functions of the metals.

(4) Protein orientation. The effect of protein orientation (the direction in which the protein is positioned between the electrodes) on the measured current was observed previously for reaction centers in a *wet* electrochemical experiment, that is, one involving a liquid electrolyte.[40,41] Table 1 indicates that *solid-state conductivity* changes dramatically between opposite orientations of both YCC[32] and (soluble) RC,[37] while the electrodes remain the same. We can suggest two possible reasons for this result. A trivial reason could be that the number of molecules participating in the current transport process is not the same, depending on if adsorption is onto the substrate or onto the tip. Alternatively, orientation may affect the polarity of the protein donor and acceptor groups, with respect to the biased electrodes. The change in polarity can affect the preferred conduction path(s) for electrons, namely a donor group may be located in one orientation closer to the substrate and in another orientation closer to the tip. In such a case, the shape of the *I*−*V* characteristic will be different, likely in terms of asymmetry (rectification). The last option emphasizes the possibility that in a solid-state configuration the electrical behavior can actually be controlled by the protein's

TABLE 1. Raw Data Values for Various CP-AFM Junctions[a]

protein	junction	molecular length (from X-ray structure)	applied force	current/junction	ref
yeast cytochrome *c* (YCC)	Au//**YCC**-Au coated tip (cys → haem)	38 Å	2−10 nN	$< -10^4$ pA (−1 V) (>6 nN)	32
yeast cytochrome *c* (YCC)	HOPG-**YCC**//Au coated tip (haem → cys)	38 Å	30−86 nN	−600 pA (−1 V) (30 nN)	32
yeast cytochrome *c* (YCC)	Au-**YCC**//Au coated tip (haem → cys)	38 Å	13−27 nN	-10^4 pA (−1 V) (27 nN)	32
light harvesting 2 complex (reconstituted in lipid bilayer) (LH2)	HOPG/**LH2**-Pt\Ir coated tip	56 Å	2 nN	∼250 pA (0.5 V)	33
reaction center (reconstituted in lipid bilayer) (RC)	HOPG/**RC**-Pt\Ir coated tip	73 Å	2 nN	−30 pA (−0.5 V)	33
cytochrome *c* (Cyt C)	SAM modified Au// **Cyt C**-SAM modified Au coated tip	38 Å	N.A.	∼500 pA (1 V)	34
plastocyanin (PC)	Au//**PC**-Au coated tip	30 Å	4−9 nN	∼2. 10^3 pA (1 V)	36
bacteriorhodopsin (bR)[b]	Au/**bR**-diamond tip (Boron-doped)	50 Å	N.A.	2 pA/nm^2 (1 V)	31
azurin (*Pseudomonas Aeroguinosa*) (Az)	HOPG-**Az**//Au coated tip	36 Å	6−32 nN	∼300 pA (6 nN); ∼10^4 pA (32 nN) (1 V)	30
yeast cytochrome *c* (YCC)	Au/**YCC**-Pt coated tip	38 Å	40 nN	∼3 × 10^3 pA (1 V)	35
reaction center (RC)	Au//**RC**-Cr\Au coated tip (donor → acceptor)	73 Å	10−15 nN	∼45 × 10^3 pA (1 V)	37
reaction center (RC)	Au//**RC**-Cr\Au coated tip (acceptor → donor)	73 Å	10−15 nN	∼2 × 10^3 pA (1 V)	37
reaction center (RC)	SAM modified Au/**RC**-Au/Cr coated tip	73 Å	1 nN	570pA (1 V)	38

[a] All currents are given in pA. Junction order: substrate−**protein**−tip. // = Chemisorption; / = physisorption; \ = tip coating composition; - = controlled mechanical approach. [b] Normalized to nm^2.

chemical structure; that is, the proteins can function as more than just a dielectric.

4. Comparative Analysis

To compare between the different samples, and between monolayer junction and CP-AFM studies, we extracted currents per unit area (nm^2) for different junctions, using a calculated contact size at a bias voltage of +1 V (or −1 V, in cases of higher currents at negative applied bias) for the monolayer results and at 0.5 V (or −0.5 V) bias for CP-AFM studies. We choose these moderate applied potentials because effects such as electrical breakdown or field emission transport are then unlikely.

To extract current/nm^2 from protein monolayer junctions, the currents are divided by 1.5×10^{11} (the geometrical contact area, in nm^2, of the macroscopic contacts). In addition, the monolayer results should be corrected for the presence of the oxide and organic linker layers.[42] To normalize the CP-AFM currents, we divide the observed currents by the calculated contact area, based on the dimensions of a single molecule in the cases of Az (3 nm diameter), the carotenoid and peptide (1 nm^2 area), on those of a bR trimer in the case of bR, and on the size of the tip in the cases of RC, and the organic layers that will be described later. The normalized currents as function of molecular dimension, taken to be the crystallographically determined dimensions of the proteins in the proposed orientations, in agreement with AFM characterizations, are shown in Figure 4.

Figure 4a illustrates the above-discussed trends between the conductivities of the different monolayers. In addition, it can be seen that CP-AFM values are higher than those deduced from macroscopic measurements. The values cannot be compared directly because a given external bias across a junction yields a much higher electric field between nanometer sized electrodes (an AFM tip, here) than between the presumably smoother macroscopic electrodes, and the potential profile at the contacts will be different. Furthermore, as macroscopic monolayers have defects, the junction's *effective* contact area (how many molecules actually carry the current) is unknown and the calculated current *densities* may be underestimated. A similar discrepancy exists for organic molecules.[24]

Figure 4b summarizes CP-AFM currents through alkanethiols with 6 (∼7.6 Å) and 10 (∼12.6 Å) carbons,[39] and oligophenyleneimine (OPI 6, 47 Å; OPI 10, 73 Å),[28] a thiolated-carotenoid molecule (∼28 Å),[27] which are conjugated "molecular wires", as well as Az,[30] bR,[31] Cyt C,[35] and RC[33] as exemplary protein systems, and a 25 Å long helical peptide, measured in an STM junction.[43] Normalizing these currents (per nm^2) (see the Supporting Information for details) shows that

(i) the currents through Az and Cyt C are higher than those measured through (the much shorter) decanethiol and comparable to that through the comparably sized carotenoid;

(ii) the current through bR is similar to that measured through a conjugated system of similar length (47 Å) or through decanethiol;

(iii) the current through RC is comparable to that through a conjugated system of similar length;

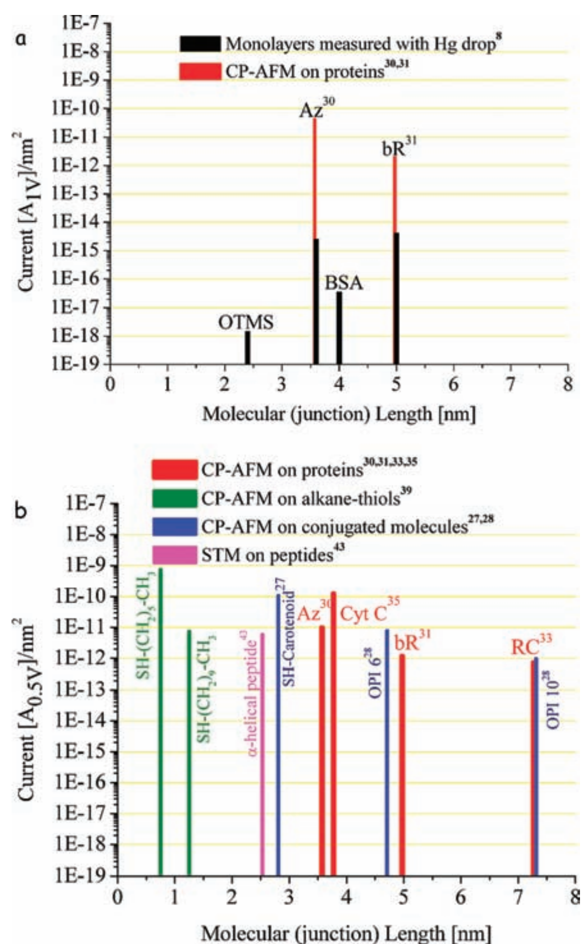

FIGURE 4. (a) Current densities, under 1 V applied bias, measured through protein monolayer junctions (black) and through proteins in CP-AFM configurations (red). (b) Current densities, under 0.5 V applied bias, measured by CP-AFM through saturated molecules (green), conjugated molecules (blue), peptides (magenta), and proteins (red). Estimated errors: molecular lengths can be up to 25% smaller; current densities can be up to 5× smaller, due to uncertainty about number of molecules in a junction (see the Supporting Information for more details).

(iv) the current through a helical peptide is comparable to that through an alkanethiol, half the size.

While saturated hydrocarbon chains are commonly viewed as molecular electronic "insulators", conjugated chain molecules are usually considered as "molecular wires", electrically conducting elements. Figure 4b suggests that *proteins can act more akin to conducting than to insulating elements*.

5. Possible Mechanisms of ET in Proteins

The remarkable ET efficiency of certain proteins is well-known,[1,3,44] and we shall now consider how we can interpret the solid-state results that we summarized here, with the guidance of common ET models. For ET, proteins can be viewed either as a uniform medium for tunneling between separated cofactors[45] or as a complex molecular medium with several tunneling pathways.[46]

ET through proteins can be treated in a donor—bridge—acceptor configuration,[47] a configuration that was reformulated to fit also molecular conductors in a solid-state configuration allowing a connection between ET rates and bridge conduction.[48] Tunneling across a molecular bridge can be described by *superexchange* (coherent tunneling)[49] or by charge *hopping*,[50,51] two mechanisms with fundamentally different dependence on temperature (hopping is a thermally activated process) and on bridge length (coherent tunneling decays much stronger with distance than hopping).

The two mechanisms can be distinguished by studying the length dependence and from analysis of the temperature dependence of ET rates. One relevant system where ET can be studied with the bridge length as the main variable is that of synthetic and modified polypeptides. These will, in our view, become important to help understand the factors that help proteins to conduct current (especially in light of the above-mentioned results with BSA that has no cofactors). The role of covalent polypeptides in ET can be by way of robust mechanical support for the redox sites, as well as via additional electronic states that can facilitate tunneling between the redox cofactors.[52] In (solution) peptide studies, *hopping* was proposed to dominate if small decay coefficients are calculated. Amide groups were considered as hopping sites,[53] and the resulting hydrogen-bonded network was suggested to contribute to the electronic coupling.[54] Aromatic amino acid side chains were also shown to facilitate electron hopping.[55,56] *Superexchange* was proposed to contribute partially or dominate if midrange decay constants were observed.[57]

Interestingly, the observed distance dependence of the ET rate was found to be anomalous in some of those studies. For short peptides, a large decay coefficient was found, while, as the peptide bridge became longer, the decay coefficient decreased dramatically, probably due to a transition from superexchange to hopping, as was demonstrated for oligoproline and later for oligoglycine junctions (two systems that form a well-defined structure which allows reliable estimates of the ET pathway length).[58–60] Changes in decay coefficients from 1.4 to 0.18 $Å^{-1}$ were observed experimentally, and the coexistence of superexchange and hopping was also supported theoretically.[61,62]

These observations may shed light on the results obtained so far with ETp of proteins. Based on their size, the proteins discussed here belong to the weak distance dependence regime of the complex dependence scheme, shown in Figure 5 (to the right of the transition point, for peptides, at ~25

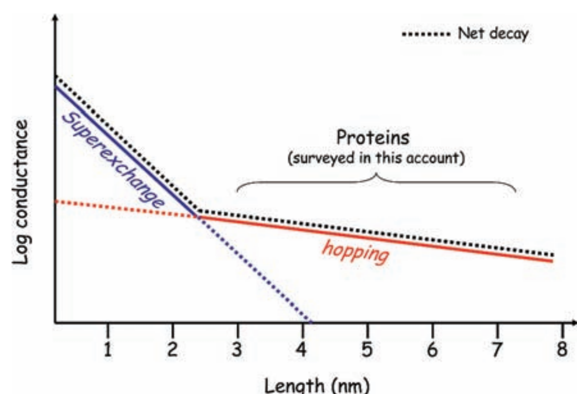

FIGURE 5. Schematic description of the distance-dependence of molecular conductance and the two main mechanisms that are involved. The distance at which the transition from superexchange (strong decay) to hopping (weak decay) occurs is taken from studies on peptides of varying lengths. The length range, spanned by the proteins that are mentioned in this Account, is marked (3−7.3 nm).

Å).[15,29,45,63] Therefore, we suggest that the observed ETp in proteins may be dominated by hopping, because the direct tunneling efficiency becomes negligibly small across bridges of such lengths. We stress that tunneling does not involve the electron−protein interaction that can lead to redox chemistry, while in the injection hopping regime electrons that are injected from the electrodes and pass through the protein bridge will reside on protein electronic energy levels. However, modern organic electronics teaches that the critical parameter is the residence time of electrons on the bridge. If this time is less than that required for a redox reaction, the protein can bear and even use carrier injection. The stability of our own measurements and characterizations provide clear evidence that no irreversible chemical changes of the proteins take place during electronic transport. It should also be noted that features that are common in protein electrochemistry (e.g., redox peaks in cyclic voltammograms) will not be observed in the solid-state measurements discussed here.[25]

Finally, we note that calculating the rate of ET from observed conductances yields rates that are 4−6 orders of magnitude higher than those observed in solution studies, possibly indicating further differences between the solid-state and solution ET processes (cf. ref 38 and the Supporting Information).

6. Conclusions and Outlook

The study of solid-state electronic transport across proteins should develop as more data acquired under well-defined conditions accumulate, for example, current at a given applied voltage or conductance. In many cases, it is difficult to compare the data (currents, conductance) to those obtained from measurements of *ET rates* in solution.

There are several reasons why solid-state measurements should be distinguished from those in solution.[25] The former includes applying bias voltage, perturbation of molecular orbitals by metallic electrodes, and an additional source of charges from the electrodes. Modification of the protein, which is still required for measuring ET rates in solution, is *not* needed for solid-state ETp measurements. Analysis of liquid-state ET data is far more mature than that of solid-state ETp data, which presently neglects thermal fluctuations and considers position and occupation of states within the protein bridge only in a cursory manner (see the Supporting Information).

One of the most critical points concerns the role played by the water molecules[64] still present in the solid-state junctions. Tightly bound water molecules within the proteins as well as hydration shells on the proteins/protein monolayers may contribute to the overall electrical properties,[65] and this issue requires thorough investigation through, for example, measurements under varying relative humidity conditions (see the Supporting Information).

Future progress and better understanding of ETp will require that data, acquired for different systems with different instrumentation, are presented in a common way so as to make comparisons easier and more reliable (e.g., as we tried to compare between CP-AFM and monolayers results). Experiments should involve proteins where minimal changes are introduced by utilizing single site mutations and modifications of critical groups: Az having none or other metal ions (Zn, Au etc.), artificial bR retinal-derived pigments, and single amino acid mutants (e.g., Trp) of both proteins (and the involvement of other types of proteins, e.g., Cyt C). This approach, which was already initiated for Az[63] and bR,[9] should shed light on the sensitivity of ETp to structural changes and point out the potential of using proteins as electronic conductors with structure−(electrical) function relation. In addition, analysis of the physics underlying the above MPM junctions should aim at evaluating interface energetics and density of states and at studying the ETp activation energy to assess the contribution of injection hopping. In this respect, temperature-dependent electrical measurements will be important to shed light on the contribution of charge hopping to the electron transport processes.

Finally, the idea that proteins can act as electronic transport media on the nanometer scale may be rationalized intuitively by considering the special features that proteins have to offer, leaving only their size as an obstacle to make them more conducting. Why for many types of protein (apart from specialized proteins) this efficiency for electronic

transport is not reflected in their function remains an intriguing question.

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Supporting Information Available. Addendum to section 5, discussion of the ET mechanisms and methods to distinguish between them; addendum to section 3 and conclusions-discussion on the role of surface states and water molecules; calculation of the current densities of Figure 4; discussion on the relation between ET rates and conductivity. This material is available free of charge via the Internet at http://pubs.acs.org.

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