Electronic Supplementary Information:

Tuning the electron transport band gap of bovine serum albumin by doping with Vb12

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1. Molecular docking

We performed the molecular docking for intermolecular interactions between Vb12 and BSA. The molecular docking was performed using the Discovery Studio 2.5 (DS 2.5) software package (Accelerys).[1] The crystal structure of the three-dimensional structure of BSA used in the calculations was obtained from the protein data bank (PDB, code: 3V03). For docking study, The DFT/B3LYP method with the 6-31G(d,p) basis set was employed to perform the geometry optimization and vibration analysis of Vb12. The quantum chemistry calculations were carried out with the use of the Gaussian 03 program package with the default convergence criteria.[2] The flexible docking between Vb12 and BSA molecules was carried out with Vb12 (with optimized structure) as a ligand and BSA molecule as a receptor to obtain the ligand (Vb12)-protein (BSA) energy minimized docked conformation. During the docking study, all crystallographic water molecules and heteroatoms were removed from BSA and hydrogen atoms were added. The potential of the 3D structure of the protein was assigned according to the CHARMM force field. The minimum binding energy conformer was searched out of 10 different conformers for the docking simulation by considering the values of Libdockscore, Cdocker energy, Cdocker interaction energy, and hydrogen bonds and the resultant one was used for further analysis.

2. Experimental section

Preparation and characterization of the Vb12–BSA: For preparation of the Vb12–BSA, BSA (5 μM, Sigma-Aldrich) was allowed to interact with Vb12 (5 μM) in phosphate buffer solution (PBS, 10 mM, pH 7.4) for more than 4 h. The formation of the Vb12–BSA was characterized with fluorescence spectra, which were recorded on a Cary Eclipse fluorescence spectrophotometer (Varian) using a 1 × 1 cm path length quartz cuvette at ambient temperature. BSA was exited at 295 nm in order to minimize the contribution from tyrosine. The fluorescence emission spectra were collected with an integration time of 0.1 s. The emission and the excitation slits were kept at 5 and 1.5 nm, respectively. Each spectrum was an average of five scans. Appropriate blanks corresponding to the buffer were subtracted to correct the fluorescence background. To evaluate the structural and conformational changes of BSA caused by

doping with Vb12, circular dichroism (CD) measurements were performed on a circular dichroism spectropolarimeter (Chriascan, Applied Photophysics). The results were analyzed based on the CDNN program (version 2.0) and compared with those of free BSA, i.e., without Vb12 doping.

Immobilization of the Vb12–BSA onto silicon substrate: To measure the *I–V* response, the Vb12–BSA was immobilized on a semiconductor substrate. We chose a doped n-type silicon (111) as the substrate (resistivity < 5 mΩ·cm). Prior to immobilization, the Si wafer was first treated according to previously reported procedures.[3,4] The Si wafer was first cleaned sequentially by ultrasonication in ethyl acetate, acetone, and ethanol (5 min in each), followed by 30 min of piranha treatment (7:3 v/v of H_2SO_4/H_2O_2) at 80 °C. Then, a SiO_2 layer (~10 Å in thickness) was grown onto the Si surface, as required for subsequent modification with organosilanes, by HF etching for 90 s, followed by dipping in piranha solution again for 5 s. After thoroughly rinsed in water and dried under N_2 flow, a monolayer of 3-aminopropyl trimethoxysilane (3-APTMS), an NH_2-terminated linker, was grown on the SiO_2-covered Si wafer by immersing it into a 3-APTMS solution (10% v/v, in methanol) for 4 h, followed by ultrasonication in methanol for 3 min. This procedure can yield a layer of 3-APTMS on Si wafer with thickness of ~5–6 Å. Finally, the 3-APTMS-modified Si wafer was immersed into a Vb12–BSA solution (5 μM, in a sealed vial) for 4 h for the Vb12–BSA immobilization, which proceeds via the reaction of the –COOH on the surface of BSA and the $–NH_2$ of the 3-APTMS, yielding a protein layer with a thickness of ~30 to 35 Å. The immobilization processes and the morphology of the protein on the Si surface were observed by atomic force microscopy (AFM) with a Nanoscope IIIa scanning probe microscope (Digital Instruments) in tapping mode.

***I–V* response measurements:** *I–V* responses were recorded with a hanging Hg drop as a top-contact electrode using an Autolab PGSTAT302N electrochemical station (Metrohm) at an ambient temperature by employing a two-electrode system in the bias range of –2.5 V to +2.5 V. The Hg drop was formed by placing an Hg drop on the top of the Vb12–BSA layer using a controlled-growth hanging mercury drop

(HMD) electrode apparatus. *I–V* curves were measured on at least three separate samples. The Hg drop was used to contact five points on each sample. *I–V* characteristics that are shown are the average of at least 15 different measurements. The standard error of this averaging is less than 10%. Short circuit measurements were observed in less than 5% of the measurements.

References

1 Discovery Studio, version 2.1, Accelrys Inc., San Diego, CA, 2008.

2 M. J. Frisch, G. W. Trucks, H. B. Schlegel, G. E. Scuseria, M. A. Robb, J. R. Cheeseman, J. A. Montgomery Jr., T. Vreven, N. Kudin, J. C. Burant, J. M. Millam, S. S. Iyengar, J. Tomasi, V. Barone, B. Mennucci, M. Cossi, G. Scalmani, N. Rega, G. A. Petersson, H. Nakatsuji, M. Hada, M. Ehara, K. Toyota, R. Fukuda, J. Hasegawa, M. Ishida, T. Nakajima, Y. Honda, O. Kitao, H. Nakai, M. Klene, X. Li, J. E. Knox, H. P. Hratchian, J. B. Cross, C. Adamo, J. Jaramillo, R. Gomperts, R. E. Stratmann, O. Yazyev, A. J. Austin, R. Cammi, C. Pomelli, J. W. Ochterski, P. Y. Ayala, K. Morokuma, G. A. Voth, P. Salvador, J. J. Dannenberg, V. G. Zakrzewski, S. Dapprich, A. D. Daniels, M. C. Strain, O. Farkas, D. K. Malick, A. D. Rabuck, K. Raghavachari, J. B. Foresman, J. V. Ortiz, Q. Cui, A. G. Baboul, S. Clifford, J. Cioslowski, B. B. Stefanov, G. Liu, A. Liashenko, P. Piskorz, I. Komaromi, R. L. Martin, D. J. Fox, T. Keith, M. A. Al-Laham, C. Y. Peng, A. Nanayakkara, M. Challacombe, P. M. W. Gill, B. Johnson, W. Chen, M. W. Wong, C. Gonzalez, J. A. Pople, Gaussian 03, revision B.03, Gaussian Inc., Pittsburgh, PA, 2003.

3 I. Ron, L. Sepunaru, S. Itzhakov, T. Belenkova, N. Friedman, I. Pecht, M. Sheves, D. Cahen, *J. Am. Chem. Soc.*, 2010, **132**, 4131.

4 S. Bera, J. Kolay, S. Banerjee, R. Mukhopadhyay, *Langmuir*, 2017, **33**, 1951.

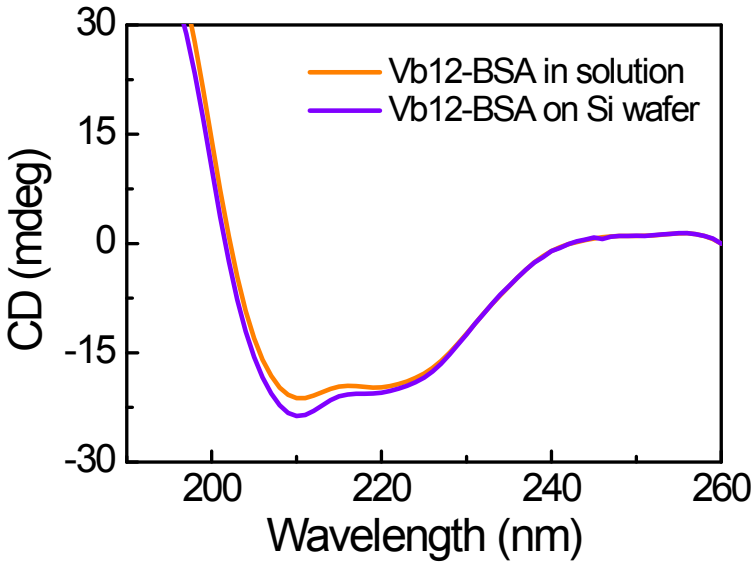

Fig. S1. CD spectra of Vb12–BSA (1 μM) dissolved in PBS and immobilized on the 3-APTMS-modified Si wafer surface.