CNT 結合アプタマー選択と炭素材料吸着能

CNT-bonded aptamer selection and carbon material adsorption capacity

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We proposed a novel CNT/protein/CNT junction for nanodevices. Outer-surface of cage shaped protein could be genetically modified to bind a CNT and make a heterojunction which improves the thermoelectric properties of CNT composites. We used the Ph.D.-12 phage display system for the aptamer SELEX (Systematic evolution of ligands by exponential enrichment) and panning out high-affinity CNT aptamers. We got 223 sequences from 2 different CNT materials, Meijo D and Tuball. We analyzed the hydrophobicity of candidate aptamers with ECS score. In general, the score showed pulsation, suggested aptamers might be displayed the hydrophilic and hydrophobic amino acid on the opposite side of a helix. The 3D structure of top 4 aptamer sequences were predicted using PEP-FOLD3 (Paris University). The calculated 3D models showed alfa helical structures, which was consistent with hydrophobicity score distribution (Figure 1). The DNA-binding protein from starved cells protein (Dps) is member of cage shaped protein which composed of 12 self-assembled 18 kDa subunits that could display N and C terminal at outer shell surface. The aptamer modified Dps protein was produced with protein expression method. The highest scored aptamer MY1 was linked with Dps using pET20b plasmid with mutagenesis kit. The fusion protein MY1-Dps was purified with two steps of HPLC (ion exchange & gel filtration) and confirmed with SDS-PAGE. The adsorption specificity of the purified MY1-Dps protein to carbonaceous material was measured by electrochemical impedance spectroscopy (EIS). The measuring solution was PBS, after equilibration, we added 0.01 mg/mL and 0.1 mg/mL Dps to PBS sequentially. The results showed that MY1-Dps adsorbed carbonaceous electrode much more than wild-type Dps (wDPs). We could use this phage display to get CNT binding aptamer. This research is partially supported by CREST (Grant No. JPMJCR18I3) from JST.

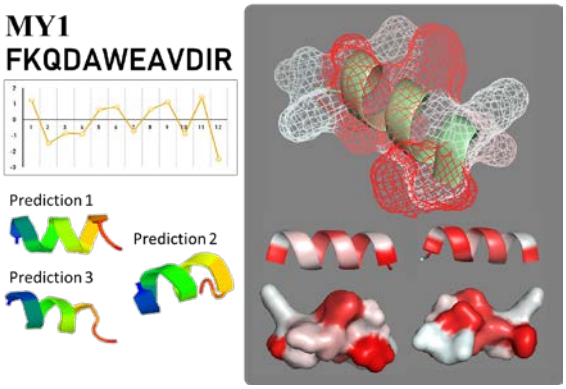

Figure 1. The ESC score and 3D prediction of the aptamer MY1. The rainbow models were the best 3 probable models for MY1 in PEP-FOLD3. We used the prediction 1 to drawn the distribution of ESC surface by PyMol. It shows that hydrophobic and hydrophilic amino acid were displayed on different side.

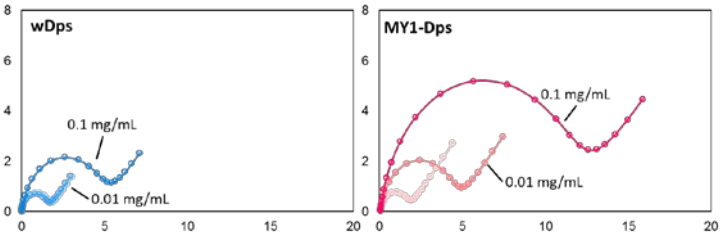

Figure 2. The EIS results of MY1-Dps and wild-Dps.