Supplemental information

Peptide sequence-driven direct electron transfer properties and binding behaviors of gold-binding peptide-fused glucose dehydrogenase on electrode Hyeryeong Lee, Eun Mi Lee, Stacy Simai Reginald, and In Seop Chang

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: Figure S1-S8 and Table S1 and S2

Before TEV protease treatment After TEV protease treatment GDHγα GDHγα GDHγα GDH $\gamma\alpha$ GDHγα $GDHy\alpha$ GDHγα GDH ya M GDH $\gamma\alpha$ $GDH\gamma\alpha$ (kDa) $-M_{GBP}$ $-V_{GBP}$ -T_{GBP} $\hbox{-}M_{GBP}$ $-V_{GBP}$ -L_{GBP} -L_{GBP} -T_{GBP} 72 60.0 61.3 61.4 60.7 61.1 55_ 43 -▶28.0 23.5 20.7 17 ____

Figure S1. SDS-PAGE analysis of GDHγα proteins (native GDHγα and GDHγα- X_{GBP} ; X = L, M, T, and V) before and after TEV protease treatments. SDS-PAGE gel (12%); band near 60 kDa: GDHα or GBP-tagged GDHα; band at 23.5 kDa: GDHγ before TEV protease treatment; band at 20.7 kDa: GDHγ after TEV protease treatment; band at 28 kDa: TEV protease. M: marker, related to Figure 1.

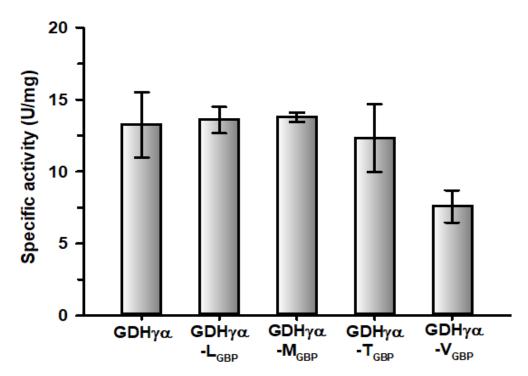


Figure S2. Comparison of enzyme activity of native GDH $\gamma\alpha$ and mutants (GDH $\gamma\alpha$ -X_{GBP}; X = L, M, T, and V) according to glucose oxidation rate. Reaction mixture consisted of 0.05 mg/mL protein, 100 mM glucose, 0.5 mM DCIP, and 6 mM PMS in 10 mM phosphate buffer (pH 7.4), related to Figure 1.

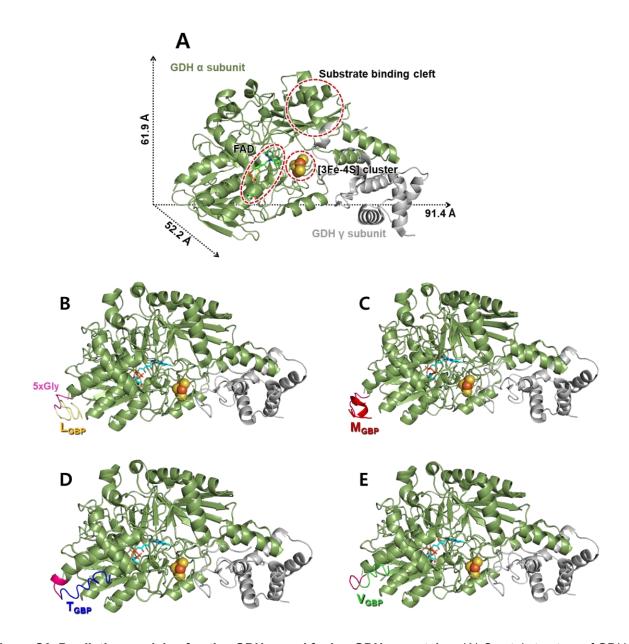


Figure S3. Prediction models of native GDHγα and fusion GDHγα proteins. (A) Crystal structure of GDHγα complex reported previously (PDB ID: 6A2U). Herein, the protein structure is visualized with PyMOL program, and the dimensions were analyzed in the same program. Structural models of (B) GDHγα-L_{GBP}, (C) GDHγα-M_{GBP}, (D) GDHγα-T_{GBP}, and (E) GDHγα-V_{GBP}. The structures of the GDH α subunit fused with different GBPs, which presented highest C-value predicted by the I-TASSER, was aligned on PyMOL using previously determined crystal structures for native FAD-dependent glucose dehydrogenase from *Burkholderia cepacia* (PDB ID: 6A2U), related to Figure 2.

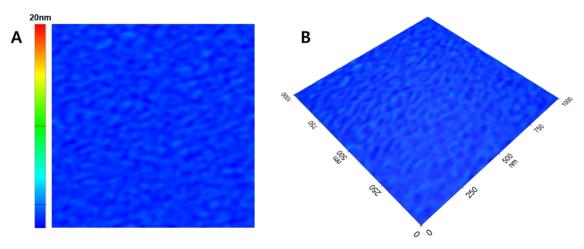


Figure S4. AFM images for bare Au surface used for enzyme binding studies. (A) 2-D topography and (B) 3-D topography; scanned area is 1 μ m × 1 μ m related to Figure 4.

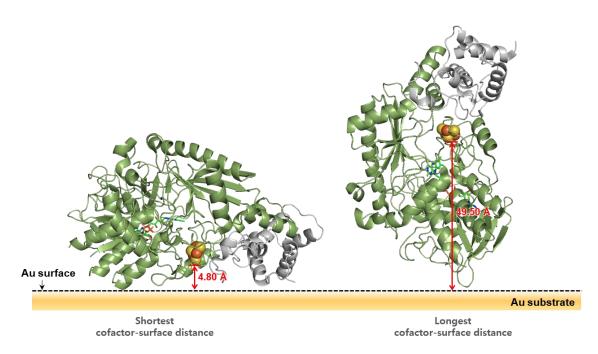


Figure S5. Schematic depiction of GDH $\gamma\alpha$ -bound gold substrate, and shortest and longest distance between [3Fe-4S] cluster and electrode surface available according to enzyme binding orientation on electrode, related to Figure 5.

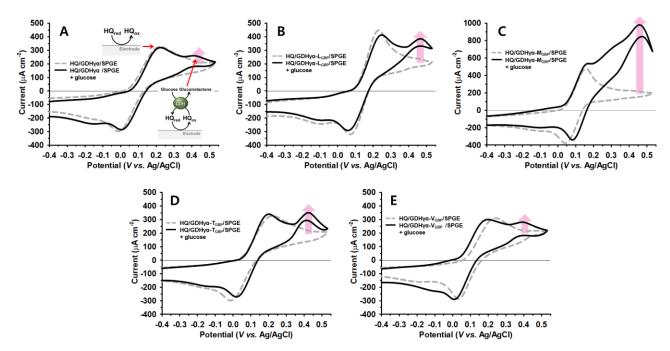


Figure S6. CV of mediated electron transfer systems. The CV profiles of (A) HQ/GDHγα/SPGE, (B) HQ/GDHγα-L_{GBP}/SPGE, (C) HQ/GDHγα-M_{GBP}/SPGE, (D) HQ/GDHγα-T_{GBP}/SPGE, and (E) HQ/GDHγα-V_{GBP}/SPGE in the absence and presence of glucose 100 mM in PBS buffer (pH 7.4) (scan rate: 100 mV s⁻¹). The inset within the (A) is schematic description of reaction mechanism corresponding with anodic peaks, related to Figure 6.

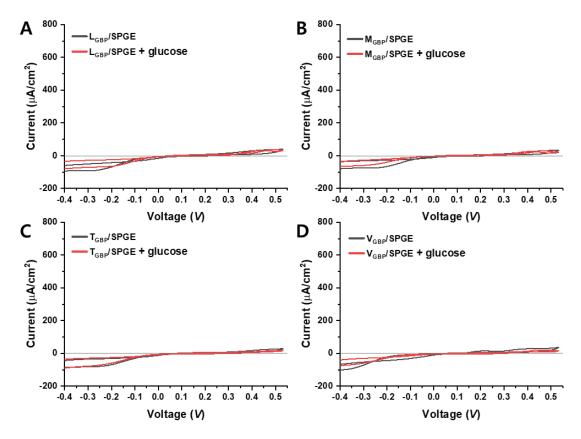


Figure S7. CV at the GBP-only conditions. The CV profiles of (A) L_{GBP}/SPGE, (B) M_{GBP}/SPGE, (C) T_{GBP}/SPGE, (D) V_{GBP}/SPGE in the absence and presence of glucose 100 mM in PBS buffer (pH 7.4) (scan rate: 100 mV s⁻¹). Each peptide was immobilized on electrode surface by immersing the SPGEs in the 50 μ M peptide for 2hrs, with mild shaking, related to Figure 6.

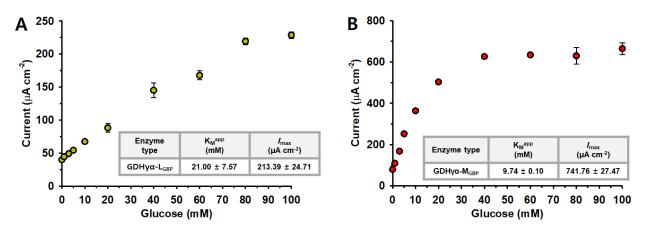


Figure S8. Plot of anodic peak current (*I*_{peak}) from cyclic voltammetry. The *I*_{peak} of (A) GDHγα-L_{GBP}/SPGE and (B) GDHγα-M_{GBP}/SPGE was obtained during successive glucose injections (1, 3, 5, 7, 10, 20, 40, 60, 80, and 100 mM). Inset: apparent electrochemical parameters (K_M^{app} and *I*_{max}) of GDHγα-L_{GBP}/SPGE or GDHγα-M_{GBP}/SPGE, related to Figure 6.

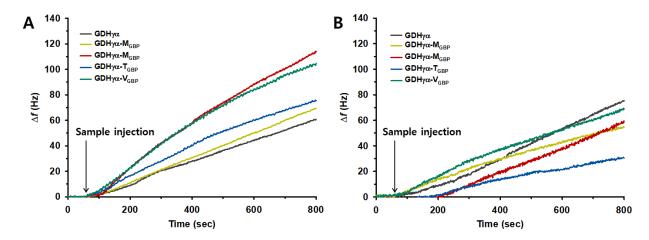


Figure S9. QCM frequency changes after injection of wild type GDH $\gamma\alpha$ and GDH $\gamma\alpha$ -X_{GBP} (X = L, M, T, and V) on (A) Au and (B) Si surfaces, related to Figure 9 and Figure 10.

Table S1. Gold-binding peptides and peptide properties, related to Figure 1.

GBP types	Sequence	Molecular	Isoelectric pointReferences	
		weight (Da)		
L _{GBP}	LKAHLPPSRLPS	1,315.58	11.41	Nam <i>et al.</i> , 2006
М _{GBP}	MHGKTQATSGTIQS	1,446.60	9.88	Brown, 1997
T _{GBP}	TGTSVLIATPGV	1,115.29	6.02	Huang <i>et al.</i> , 2005
V_{GBP}	VSGSSPDS	734.72	3.75	Kim <i>et al.</i> , 2010

Table S2. Onset and peak potentials in cyclic voltammogram of native GDHγα/SPGE or GDHγα-

X_{GBP}/SPGE (X = L, M, T, or V), related to Figure 6.

Types of enzyme-electrodes	E _{on} ^a (V vs. Ag/AgCl)	E _p ^b (V vs. Ag/AgCl)	
GDHγα/SPGE	0.364 ± 0.006	0.420 ± 0.006	
GDHγα-L _{GBP} /SPGE	0.036 ± 0.009	0.359 ± 0.011	
GDHγα-M _{GBP} /SPGE	-0.304 ± 0.003	-0.091 ± 0.005	
GDHγα-T _{GBP} /SPGE	N.M.°	N.M.	
GDHγα-V _{GBP} /SPGE	0.191 ± 0.004	0.310 ± 0.004	

^aonset potential; ^bpeak potential; ^cnot measurable

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