



Supplementary Materials: Recombinant Peptide Production Platform Coupled with Site-Specific Albumin Conjugation Enables a Convenient Production of Long-Acting Therapeutic Peptide

Mijeong Bak, Junyong Park, Kiyoon Min, Jinhwan Cho, Jihyoun Seong, Young S. Hahn, Giyoong Tae and Inchan Kwon

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Primer Name	Oligonucleotide Sequence (5'→3')	Generated Plasmid
V16AzF_F	AAGGCACCTTTACCAGCGATTAGAGTAGCTATCTGGAAGG	pQE80-sfGFP-
V16AzF_R	CCTTCCAGATAGCTACTCTAATCGCTGGTAAAGGTGCCTT	GLP1_16Amb
Y19AzF_F	GCGATGTGAGTAGCTAGCTGGAAGGTCAGGC	pQE80-sfGFP-
Y19AzF_R	GCCTGACCTTCCAGCTAGCTACTCACATCGC	GLP1_19Amb
F28AzF_F	GTCAGGCGGCCAAAGAATAGATTGCCTGGCTGGTGC	pQE80-sfGFP-
F28AzF_R	GCACCAGCCAGGCAATCTATTCTTTGGCCGCCTGAC	GLP1_28Amb
A8G_F	GCATCGAAGGTAGGCATGGTGAAGGCACCTTTACCAG	
A8G_R	CTGGTAAAGGTGCCTTCACCATGCCTACCTTCGATGC	

Table S1	Oligonucleotide	nrimers used	l in this study
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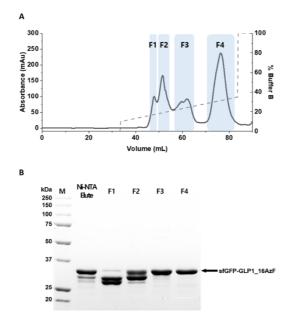


Figure S1. Purification of sfGFP-GLP1_16AzF. After nickel–nitrilotriacetic acid (Ni-NTA) purification of the cell lysates (the Ni-NTA elute in the gel image), further purification by anion exchange chromatography (**A**) was carried out to remove impurities from the sfGFP-GLP1_16AzF variant, as revealed by the gel image. Each fraction was investigated by sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS-PAGE). (**B**) The elution sample from the Ni-NTA purification was desalted with PD-10 and loaded onto a HiTrap Q HP column equilibrated with 20 mM Tris (pH 8.0), then eluted with an NaCl gradient. The dotted line represents the percentage of Buffer B (20 mM Tris with 1 M NaCl; pH 8.0). sfGFP-GLP1_16AzF (fractions 3 and 4; F3 and F4) was isolated from the impurities expected from the premature transition termination caused by the "amber" stop codon (fractions 1 and 2; F1 and F2), as revealed by the protein gel.

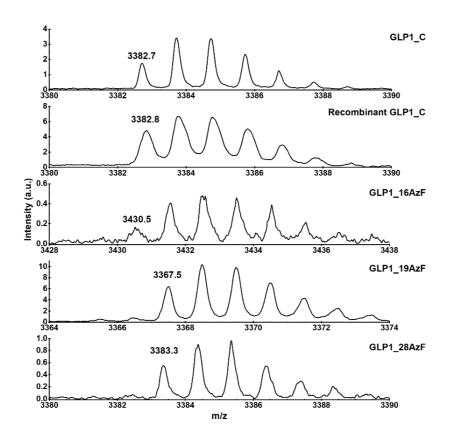


Figure S2. Monoisotopic mass confirmation by matrix-assisted laser desorption/ionization time-of-flight mass spectroscopy (MALDI-TOF MS) analysis of the chemically synthesized GLP1_C, recombinant GLP1_C, and GLP1_AzF variants. The monoisotopic masses of the chemically synthesized GLP1_C and recombinant GLP1_C were 3382.7 and 3382.8 m/z, respectively. The monoisotopic masses of GLP1_16AzF, GLP1_19AzF, and GLP1_28AzF were 3430.5, 3367.5, and 3383.3 m/z, respectively.

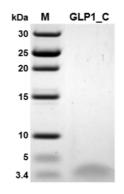


Figure S3. Confirmation of the molecular weight of GLP1_C on the 15% tricine gel stained with Coomassie brilliant blue. The band for GLP1_C located around 3.4-kDa band, which is consistent with its expected molecular weight, 3381.7 Da. M: protein molecular weight standards (Thermo Fisher Scientific, Inc., Waltham, MA, USA).

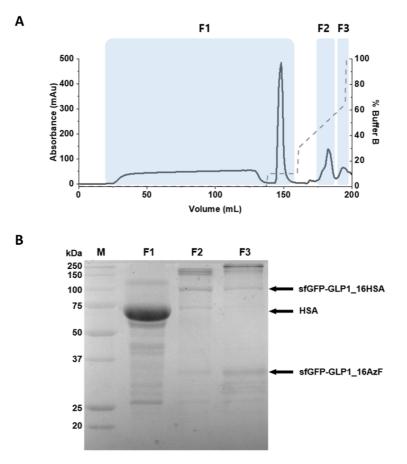


Figure S4. Purification of sfGFP-GLP1_16HSA after the conjugation of sfGFP-GLP1_16AzF and HSA-DBCO by strain-promoted azide–alkyne cycloaddition (SPAAC). After the conjugation of sfGFP-GLP1_16AzF and HSA-DBCO by SPAAC, cation exchange chromatography was carried out to purify the sfGFP-GLP1_16HSA. (**A**) The cation exchange chromatogram. The reacted conjugate was desalted with PD-10, loaded onto a HiTrap SP-HP column equilibrated with 20 mM sodium phosphate (pH 6.0), and eluted with an NaCl gradient. The fractions were collected and evaluated on protein gel (**B**). The dotted line represents the percentage of Buffer B (20 mM sodium phosphate with 1 M NaCl; pH 6.0). (**B**) Protein gel image associated with the cation exchange chromatogram. Protein molecular weight standards are shown in lane M. There was unreacted albumin-DBCO, which was not bound to the column (F1). The sfGFP-GLP1_16HSA conjugate was eluted in F2. The unreacted sfGFP-GLP1_16AzF was eluted in F3.

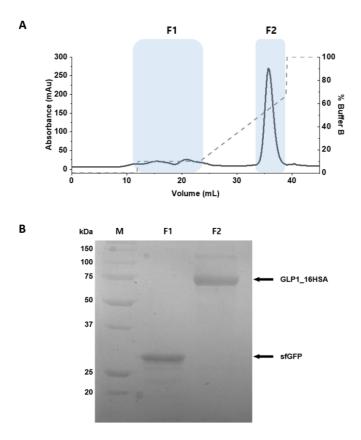


Figure S5. Purification of GLP1_16HSA after proteolytic cleavage by Factor Xa. After the proteolytic cleavage of sfGFP-GLP1_16HSA by Factor Xa, anion exchange chromatography was carried out to purify GLP1_16HSA. (**A**) The anion exchange chromatogram. The cleaved mixture of sfGFP and GLP1_16HSA was desalted with PD-10, loaded onto a HiTrap Q-HP column equilibrated with 20 mM Bis-Tris (pH 6.0), and eluted with an NaCl gradient. The fractions were collected and evaluated on protein gel (B). The dotted line represents the percentage of Buffer B (20 mM Bis-Tris with 1 M NaCl; pH 6.0). (**B**) Protein gel image associated with the anion exchange chromatogram. Protein molecular weight standards are shown in lane M. Cleaved sfGFP was observed in F1. GLP1_16HSA was observed in F2, as indicated in the gel image.

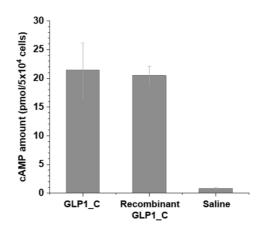


Figure S6. Comparative study of the biological activity of chemically synthesized GLP1_C (GLP1_C) and recombinant GLP1_C in GLP-1R-expressing cells. The cAMP production levels of GLP1_C and the recombinant GLP1_C in the GLP-1R-expressing cells were compared. The recombinant GLP1_C was obtained by processing sfGFP-GLP1_C with 1/500 (w/w) Factor Xa protease at room temperature for 12 h. There was no further purification. The concentration of both GLP1_C peptides was 10⁻⁷ M.

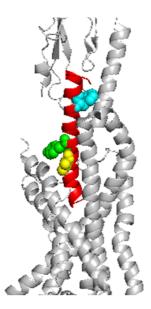


Figure S7. Location of V16, Y19 and F28 residues on Cryo-EM structure of the activated Glucagonlike peptide-1 receptor. The activated GLP-1R with bound GLP-1 is colored in gray, and the bound GLP-1 is colored in red. Each V16 residue, Y19 residue, and F28 residue (PDB ID: 5vai) is marked with yellow, green and cyan respectively. The difference on direction of side chain is observed on the image.