

Article

# Optical Fluorescence Imaging of Native Proteins Using a Fluorescent Probe With a Cell Membrane-Permeable Carboxyl Group

Jung Min Kim <sup>1\*</sup>, Young-Mi Kang<sup>2</sup>

<sup>1\*</sup> BK21 FOUR R&E Center for Environmental Science and Ecological Engineering, Korea University,  
Anam-ro145, Seongbuk-gu, Seoul 02842, Republic of Korea

<sup>2</sup> Department of Orthopaedic surgery, Yonsei University college of medicine, 50-1 Yonsei-ro Seodaemun-  
gu Seoul 03722, Republic of Korea

\*Correspondence: Tel; +82-2-3290-4778, [erine7.kim@gmail.com](mailto:erine7.kim@gmail.com).

**Supplementary Figure S1:** The construction of N-terminus-tagged HIV-1 Tat protein.

**Supplementary Figure S2:** Analysis of R-phycoerythrin (PE)-labeled streptavidin by SEC-HPLC with PE labeled streptavidin as the control group.

**Supplementary Figure S3:** Analysis of biotin ligase (BirA) by SEC-HPLC. The analytical SEC-HPLC profiles of BirA as the control group.

**Supplementary Figure S4:** Comparative analysis of BirA enzyme-dependent labeling of FAM 56 with a carboxyl group structure and biotin.

**Supplementary Figure S5:** LC-MS spectrum of the purified fluorescein (FAM 56)-labeled Tat.

**Supplementary Figure S6:** Mass spectrum profile of predigested fluorescein (FAM 56)-labeled Tat protein.

## Supplementary Figure Legends

### Figure S1. The construction of N-terminus-tagged HIV-1 Tat protein.

Schematic description of the HIV Tat protein labeled with free carboxyl group fluorescent dyes at the N-terminus. The hexahistidine (6×His)-tag was introduced in the C-terminus for Ni-affinity chromatography and carrying Avi-tag at the C-terminus for biotin labeling.

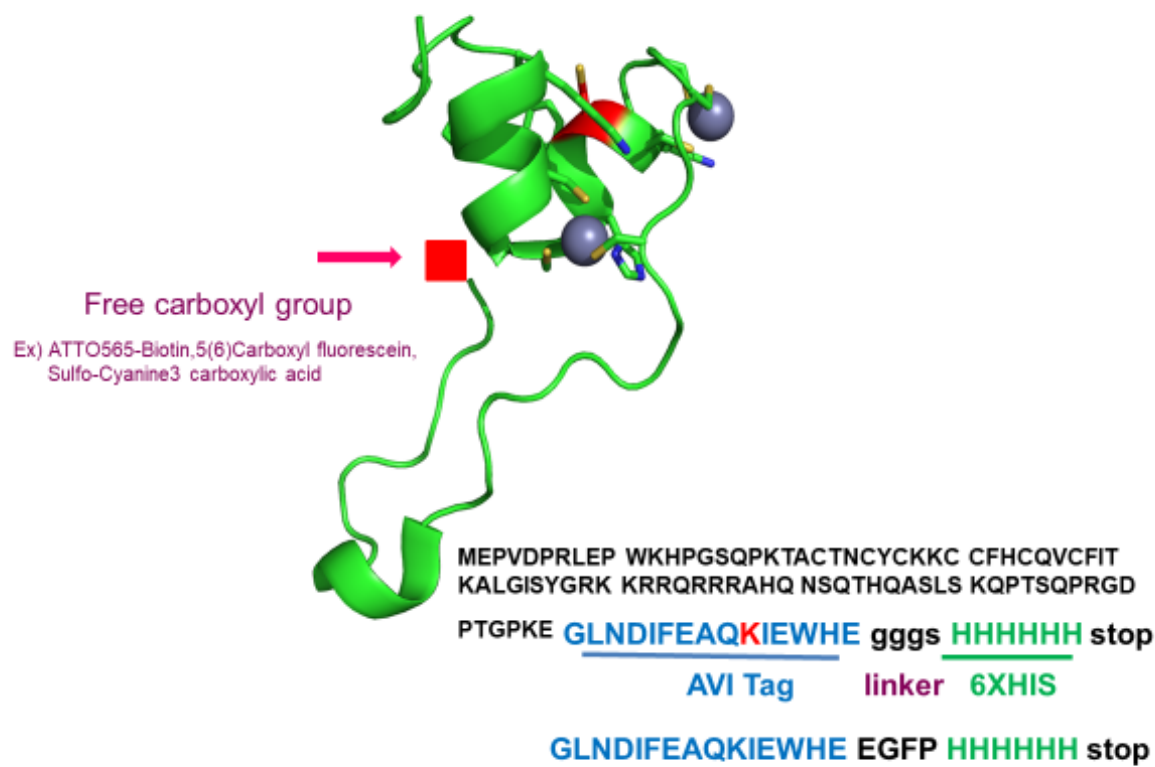
**Figure S2. Analysis of R-phycoerythrin (PE)-labeled streptavidin by SEC-HPLC with PE-labeled streptavidin as the control group.** Compared to the peaks of PE-labeled streptavidin alone, UV (280 nm, black line) detection at 5.576 min, PE-labeled streptavidin is shown with the highest peak at 5.547 min (8 L.U.) (FLD, Ex: 488 nm/Em: 575 nm, blue line). PE emissions are given in relative light units (LU).

**Figure S3. Analysis of biotin ligase (BirA) by SEC-HPLC. The analytical SEC-HPLC profiles of BirA as the control group.** SEC-HPLC of N-terminally fluorescence-labeled Tat peaks at 10.565 min (UV 280 nm, blue line, black line) and 11.388 min (FLD, Ex: 492 nm/Em: 517 nm, red line), respectively.

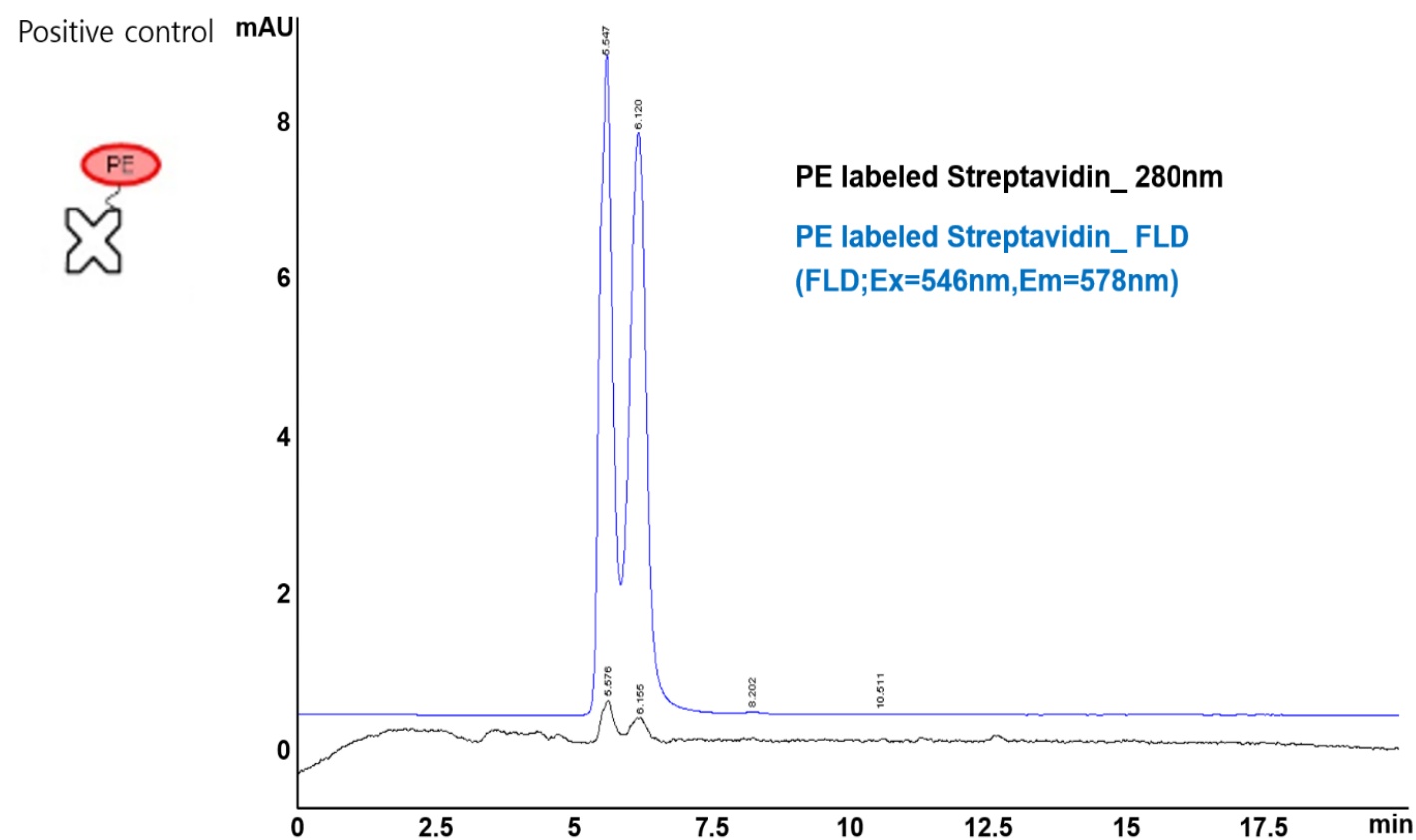
**Figure S4. Comparative analysis of BirA enzyme-dependent labeling of FAM 56 with a carboxyl group structure and biotin.** Detection of the N-terminally biotin-labeled Tat protein as the control was performed using R-phycoerythrin (PE)-labeled streptavidin alone. Positive control PE-labeled streptavidin with BirA spectrum (FLD, Ex: 488 nm/Em: 532 nm, blue line) from FAM 56-labeled Tat without BirA as negative control (FLD, Ex: 492 nm/Em: 517 nm, red line).

**Figure S5. LC-MS spectrum of the purified fluorescein (FAM 56)-labeled Tat.** HPLC-MS of purified FAM 56-labeled Tat alone (The highest peak corresponding to the retention time (RT) of 17.87 min; 751.49  $m/z$  detected) was further analyzed by comparison with the HPLC-MS chemical matching database.

**Figure S6. Mass spectrum profile of predigested fluorescein (FAM 56)-labeled Tat protein.** The purified FAM 56-labeled Tat protein (The highest peak corresponding to the retention time of 7.21 min in Figure 4) from HeLa cells was further analyzed by LC-MS and western blot. Identification of Tat protein using LC-MS data relies on the peptide map from a Tat sequence target matching database. The following peptide sequences in the Tat protein match with the spectrum measurement. (a) RAHQNSQTHQASLSK, (b) AHQNSQTHQASLSK, and (c) LEPWKHPGSQPK, respectively.

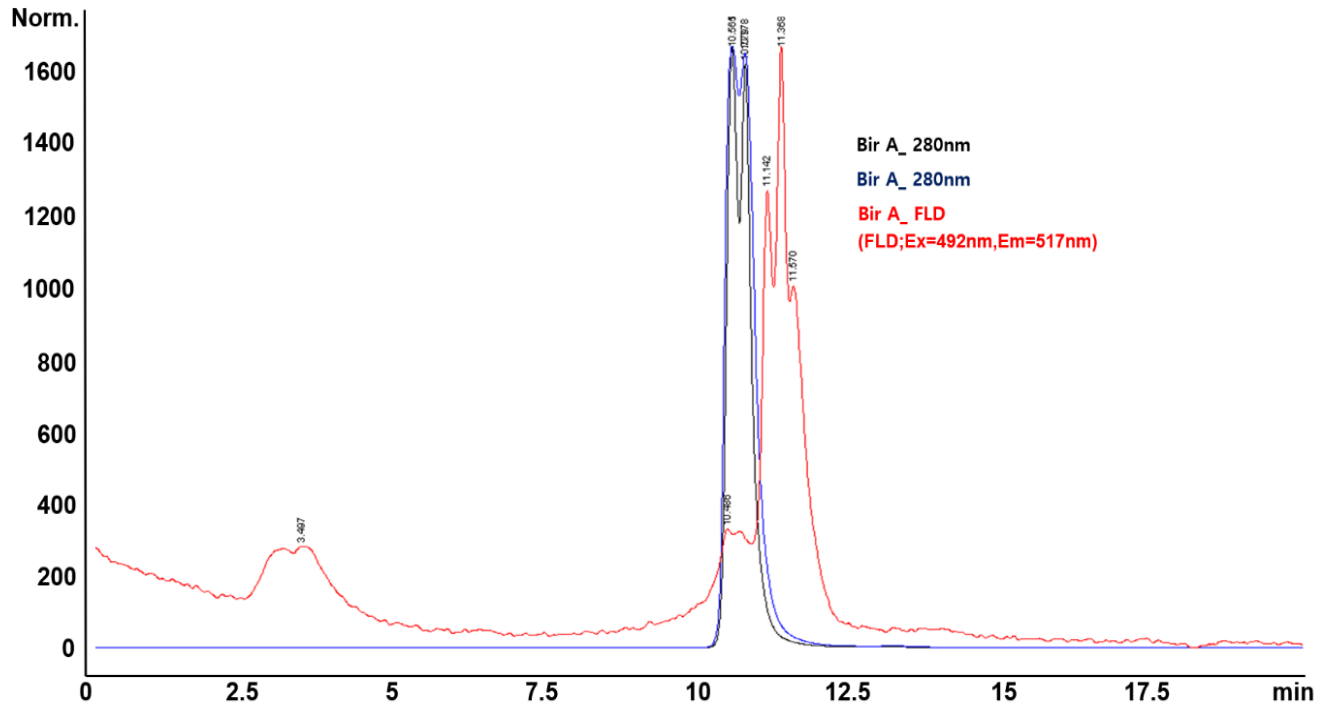


**Figure S1.** The construction of N-terminus-tagged HIV-1 Tat protein. Schematic description of the HIV Tat protein labeled with free carboxyl group fluorescent dyes at the N-terminus. The hexahistidine (6×His)-tag was introduced in the C-terminus for Ni-affinity chromatography and carrying Avi-tag at the 8-terminus for biotin labeling.

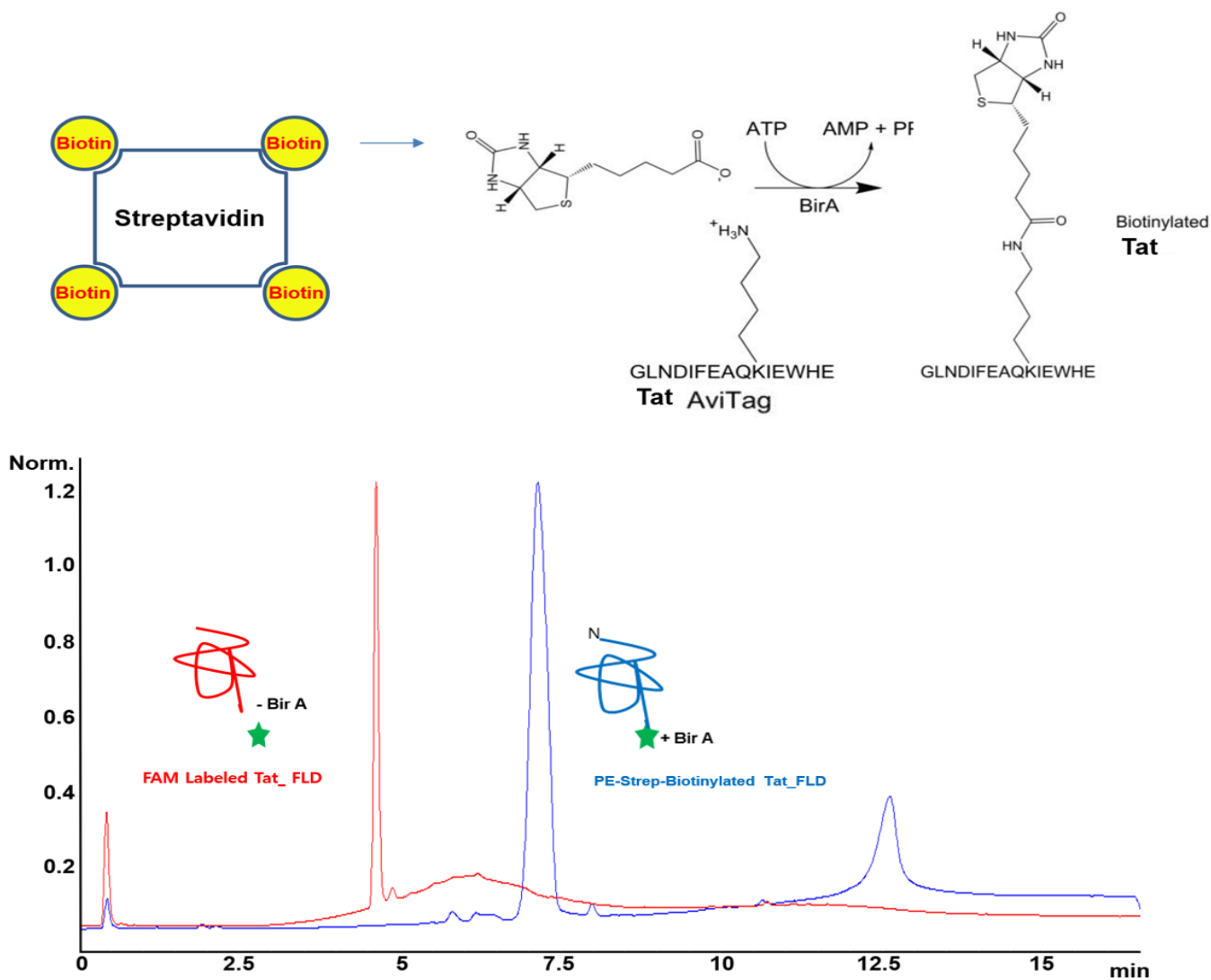


**Figure S2.** Analysis of R-phycoerythrin (PE)-labeled streptavidin by SEC-HPLC with PE-labeled streptavidin as the control group. Compared to the peaks of PE-labeled streptavidin alone, UV (280 nm, black line) detection at 5.576 min, 1PE-labeled streptavidin is shown with the highest peak at 5.547 min (8 L.U.) (FLD, Ex: 488 nm/Em: 575 nm, blue line). PE emissions are given in relative light units (LU).

## Bir A only

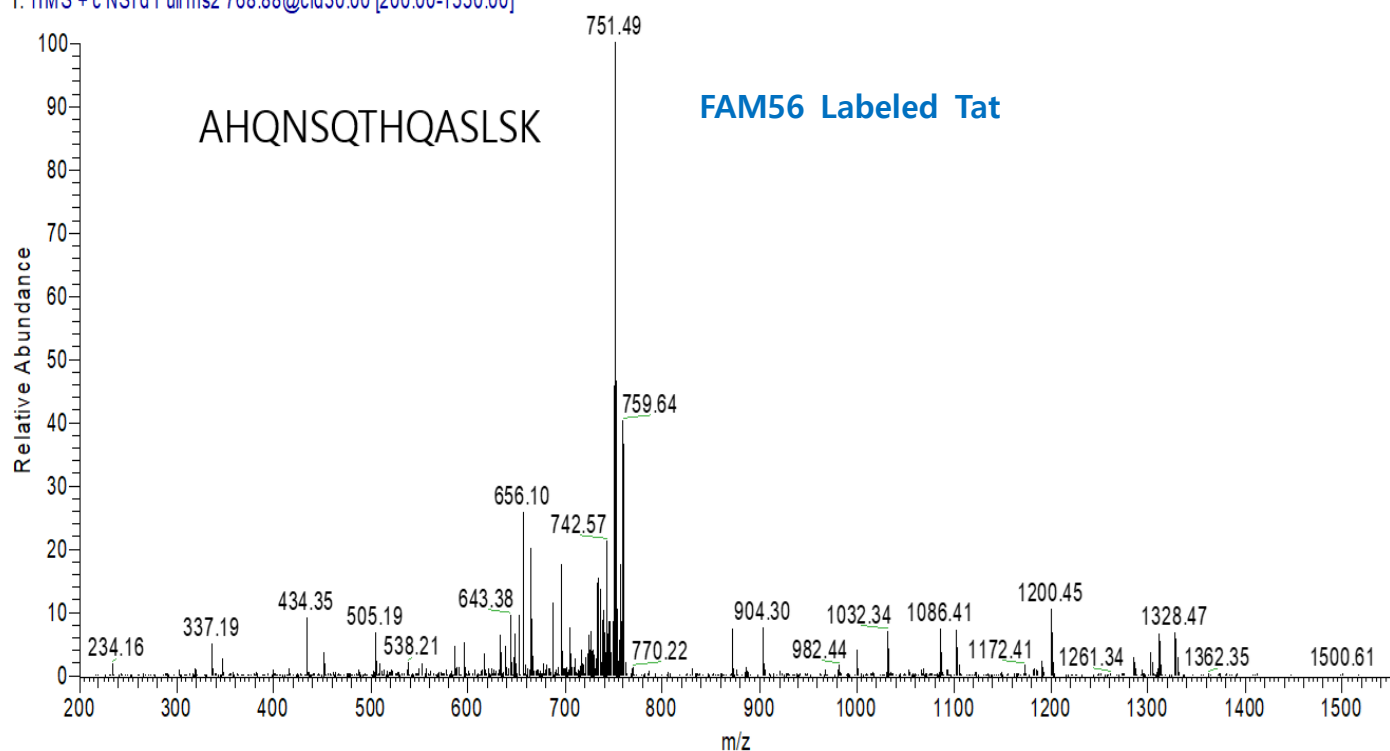


**Figure S3.** Analysis of biotin ligase (BirA) by SEC-HPLC. The analytical SEC-HPLC profiles of BirA as the control group. SEC-HPLC of N-terminally fluorescence-labeled Tat peaks at 10.565 min (UV 280 nm, blue line, black line) and 11.388 min (FLD, Ex: 492 nm/Em: 517 nm, red line), respectively.



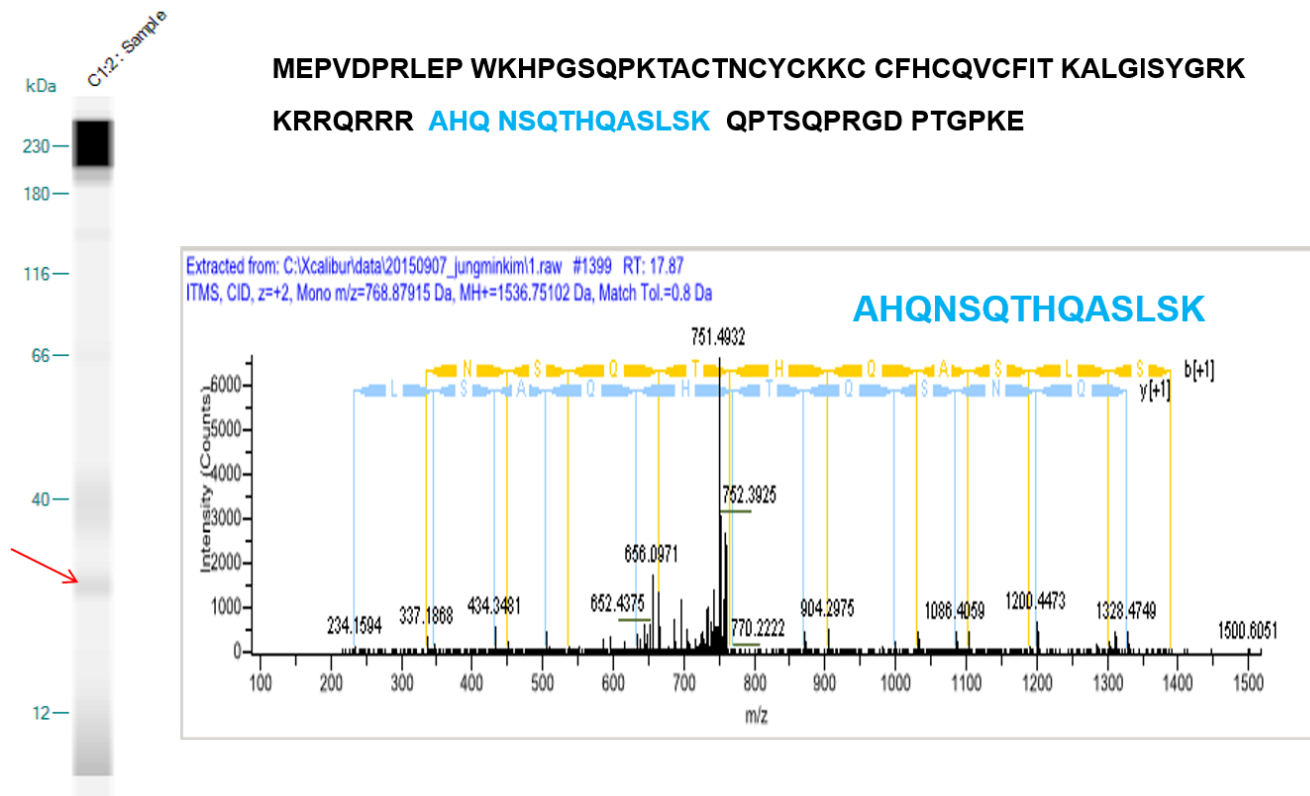
**Figure S4.** Comparative analysis of BirA enzyme-dependent labeling of FAM 56 with a carboxyl group structure and biotin. Detection of the N-terminally biotin-labeled Tat protein as the control was performed using R-phycoerythrin (PE)-labeled streptavidin alone. Positive control PE-labeled streptavidin with BirA spectrum (FLD, Ex: 488 nm/Em: 532 nm, blue line) from FAM 56-labeled Tat without BirA as negative control (FLD, Ex: 492 nm/Em: 517 nm, red line).

1#1399 RT: 17.87 AV: 1 NL: 6.62E3  
T: ITMS + c NSI d Full ms2 768.88@cid30.00 [200.00-1550.00]



**Figure S5.** LC-MS spectrum of the purified fluorescein (FAM 56)-labeled Tat. HPLC-MS of purified FAM 56-labeled Tat alone (The highest peak corresponding to the retention time (RT) of 17.87 min; 751.49 *m/z* detected) was further analyzed by comparison with the HPLC-MS chemical matching database.

## Sequence of HIV Tat protein.



**Figure S6.** Mass spectrum profile of predigested fluorescein (FAM 56)-labeled Tat protein. The purified FAM 56-labeled Tat protein (The highest peak corresponding to the retention time of 7.21 min in Figure 4) from HeLa cells was further analyzed by LC-MS and western blot. Identification of Tat protein using LC-MS data relies on the peptide map from a Tat sequence target matching database. The following peptide sequences in the Tat protein match with the spectrum measurement. (a) RAHQNSQTHQASLSK, (b) AHQNSQTHQASLSK, and (c) LEPWKHPGSQPK, respectively.