Content

Titles	Pages
Emission spectra of BODIPY ₁ -Pep ₄ in mixture solvent of water and DMSO	S2
Photophysical properties of BODIPY-peptide conjugates	S 3
Distribution of signal of BODIPY ₁ -Pep ₄ and nuclear blue in cell lines	S 4
Chemical experiments	S5–S12
Biological experiments	S13-S14
NMR spectra of products	S15–S31
HPLC chromatographs and MALID-TOF HRMS spectra of products	S32–S76





Fig. S1. Comparison of emission spectrum of **BODIPY₁-Pep₄** (1.2 uM) in solvents with different ratios of PBS7.4 and DMSO.



Fig. S2. Comparison of fluorescent intensity of **BODIPY₁-Pep₄** (1.2 uM) at 512 nm in solvents with different ratios of PBS7.4 and DMSO.

Photophysical properties of BODIPY-peptide conjugates

	λ absorption (nm)	ε (× 10 ⁴ M ⁻¹ cm ⁻¹)	λ _{excitation} (nm)	λ emission (nm)	τ (ns)	Φ (%) ^b
BODIPY ₁ -Pep ₁	503	5.81	501	515	3.18	50.1
BODIPY ₃ -Pep ₁	526	5.10	526	542	5.23	34.0
BODIPY9-Pep1	560	4.07	557	599	0.991	5.58

	Table. S1. F	Photophysical	property of]	BODIPY _n -Pep ₁ .	a
--	--------------	---------------	---------------	---	---

^{a.} all data are recorded in DMSO

^{b.} the quantum yields are measured by comparative method with reference rhodamine 6G in water ($\Phi = 95\%$).



Fig. S3. Absorption (A), excitation (B) and emission (C) spectra of BODIPY₁-Pep₁.



Fig. S4. Absorption (A), excitation (B) and emission (C) spectra of BODIPY₃-Pep₁.



Fig. S5. Absorption (A), excitation (B) and emission (C) spectra of BODIPY₉-Pep₁.



Distribution of signal of BODIPY₁-Pep₄ and nuclear blue in the cell lines

Fig. S6. Profiles of the emission intensity of the **BODIPY₁-Pep₄** and nuclear blue were plotted along the red arrow A. C666, B. HeLa. The signal of **BODIPY₁-Pep₄** and nuclear blue overlapped well in C666 cell line (EBNA+) but not in HeLa cell line (EBNA-).

Chemical Experiments

Reagents: All amino acid building blocks for Fmoc-strategy SPPS were purchased from Bidepharm. For synthesizing **Pep₁~Pep₁₀**, Fmoc-Ala-OH, Fmoc-Val-OH, Fmoc-Ile-OH, Fmoc-Leu-OH, Fmoc-Met-OH, Fmoc-Phe-OH, Fmoc-Tyr(tBu)-OH, Fmoc-Tyr(PO₃(MDPSE)₂)-OH, Fmoc-Trp(Boc)-OH, Fmoc-Ser(tBu)-OH, Fmoc-Thr(tBu)-OH, Fmoc-Asn(Trt)-OH, Fmoc-Gln(Trt)-OH, Fmoc-Cys(Trt)-OH, Fmoc-Gly-OH, Fmoc-Pro-OH, Fmoc-Arg(Pdf)-OH, Fmoc-His(Boc)-OH, Fmoc-Lys(Boc)-OH, Fmoc-Asp(tBu)-OH, Fmoc-Glu(tBu)-OH, Fmoc-Glu(tBu)-OH, Fmoc-6-Ahx-OH, Fmoc-2-Nal-OH, Fmoc-4-Cpa-OH, Fmoc-3-Pal-OH, Fmoc-Cit-OH. For **Pep₁₁**, Fmoc-Lys(Alloc)-OH was used to take place Fmoc-Lys(Boc)-OH as building block of lysine. The Rink Amide resin (100-200 mesh) and Wang resin (100-200 mesh) were purchased from Sigma-Aldrich for synthesizing peptides with amide and acid C-terminal respectively. All aldehyde and pyrrole building blocks are commercially available except the pyrrole for synthesizing **DP**₈ and **DP**₁₁ are synthesized according literature.^[1] Solvents and other reagent were purchased and used without further purification.



Fig. S7. Structure and abbreviate of unnatural amino acids.

Analytical HPLC: Analytical HPLC was performed on an Agilent 1100 series HPLC system (Agilent Technologies, Stockport, UK) equipped with a diode-array detection (DAD) detector and Agilent C18 column (250 mm x 4.6 mm) at the following gradients:

Gradient A:			
Time	A %	B %	Flow
(min)	(H ₂ O + 0.1 % TFA)	(MeCN + 0.1 % TFA)	(mL/min)
0	80	20	0.5
60	0	100	0.5
70	0	100	0.5
Gradient B:			Flow
(min)	$(H_2O + 0.1 \% 1FA)$	(MeCN + 0.1 % 1FA)	(mL/min)
0	80	20	0.5
40	20	80	0.5
41	0	100	0.5
55	0	100	0.5

Preparative HPLC: The purifications of products were carried out on Waters semi-preparative system with Waters 2707 Autosampler, Water 1525 Binary HPLC Pump, Waters 2998 Photodiode Array Detector and Waters Fraction Collector III and Atlantis® T3 Prep OBDTM column (C18, 5 μ m, 19×250 mm). The Gradient usually refer to the analytical HPLC but flow rate is 5 mL/min. The fractions were collected and verified by ESI-MS.

Mass spectrometry: High-resolution mass spectra, reported as m/z, were obtained from Bruker Autoflex MALDI-TOF mass spectrometer. Low-resolution mass spectra were conducted by SCIEX 3200Q ESI mass spectrometer was also used for monitoring reaction and determining correct fraction during purification of product.

Nuclear magnetic resonance: NMR spectra were recorded on a Bruker Ultrashield 400 Plus NMR spectrometer (¹H NMR on 400 MHz, ¹³C NMR on 101 MHz and ¹⁹F NMR on 376 mHz. The ¹H NMR chemical shifts were referenced to corresponding solvent peak (2.50 for DMSO-*d6* and 3.31 for methanol*d4*). The following abbreviations were used to explain the multiplicities: s = singlet, d = doublet, t = triplet, q = quartet, dd = doublet of doublets, m = multiplet, br = broad.

General procedure of solid phase peptide synthesis: Standard Fmoc-based SPPS procedure was carried out manually. The 5 mL SPE filtration tube with Frits were used. The Rink Amide resin and Wang resin were used for synthesizing peptides with amide and acid C-terminal respectively. To load first amino acid onto Rink Amide resin, Fmoc-deprotected resin was shaken with amino acid building block (3 eq.), PyBOP (3 eq.) and DIPEA (6 eq.) in DMF (4 mL/ 0.1 mmol) overnight. To load first amino acid onto Wang resin, resin was shaken with amino acid building block (3 eq.), PyBOP (3 eq.) and DMAP (1 eq.) in DCM/DMF, v/v, 8/2 (4 mL/ 0.1 mmol) overnight. After loading first amino acid, the resin was washed with DMF (4 mL ×3) and DCM (4 mL ×3). Then, the shaken with Ac₂O/Pyridine, v/v, 3/2 (4 mL/ 0.1 mmol) for 30 min to cap all remining reacting site on resin. During peptide elongation, coupling was carried out with amino acid building block (3 eq.) and DIPEA (6 eq.) in DMF (4 mL 20% piperidine in DMF (4 mL/ 0.1 mmol) for 2~12 h, and Fmoc deprotection was carried out with 4 mL 20% piperidine in DMF (4 mL/ 0.1 mmol) for 25 min. After all amino acid building blocks were coupled, the substitute value of resin bound peptide was calculated by the method from literature^[2]. Global cleavage was carried out with different cocktail (4 mL/ 0.1 mmol) and reaction time according different amino acid composition of each peptide. Cocktail A: TFA/TIPS/H₂O, v/v/v, 95/2.5/2.5; Cocktail B: TFA/EDT/p-Cresol/H₂O, v/v/v/v, 90/5/2.5/2.5.

H₂N-YFMVF-CONH₂ (Pep₁). Global cleavage condition: cocktail A, 2 h. Yield: 60 %. White powder. Analytic HPLC: Gradient A, retention time: 23.9 min, purity: 96.6 %. HRMS(MALDI-TOF): calc. for C₃₇H₄₉N₆O₆S⁺ [M+H]⁺ 705.3429, found 705.3489; calc. for C₃₇H₄₈N₆NaO₆S⁺ [M+Na]⁺ 727.3248, found 727.3251; calc. for C₃₇H₄₈KN₆O₆S⁺ [M+K]⁺ 743.2988, found 743.3027. ¹H NMR (400 MHz, Methanol-d₄) δ 7.26 – 7.14 (m, 10H), 7.11 – 7.04 (m, 2H), 6.81 – 6.72 (m, 2H), 4.89 (s, 1H), 4.70 (tt, J = 8.3, 5.9 Hz, 2H), 4.40 – 4.31 (m, 1H), 4.07 (dd, J = 8.6, 4.8 Hz, 1H), 3.20 – 3.05 (m, 3H), 2.98 – 2.79 (m, 3H), 2.56 – 2.38 (m, 2H), 2.01 (s, 6H), 0.90 (dd, J = 6.8, 5.1 Hz, 6H); ¹³C NMR (101 MHz, Methanol- d_4) δ 129.58, 128.28, 128.22, 127.43, 127.34, 125.74, 114.80, 53.39, 47.52, 47.31, 47.10, 46.89, 46.67, 46.46, 46.25, 37.23, 37.05, 35.71, 31.38, 30.27, 28.97, 17.65, 16.99, 13.27; ¹H NMR (400 MHz, DMSO-*d*₆) δ 9.38 (s, 1H), 8.77 (d, J = 8.1 Hz, 1H), 8.44 (d, J = 7.9 Hz, 1H), 8.02 (d, J = 8.2 Hz, 1H), 7.99 – 7.92 (m, 2H), 7.83 (d, J = 8.8 Hz, 1H), 7.38 (d, J = 2.2 Hz, 1H), 7.30 - 7.15 (m, 10H), 7.06 (s, 1H), 7.04 (d, J = 8.5 Hz, 2H),6.72 – 6.67 (m, 2H), 4.65 (td, J = 8.7, 4.2 Hz, 1H), 4.50 – 4.42 (m, 2H), 4.18 – 4.13 (m, 1H), 3.89 (s, 1H), 3.08 – 2.93 (m, 3H), 2.82 (ddd, J = 14.0, 9.3, 6.6 Hz, 3H), 2.42 (ddp, J = 13.1, 9.3, 6.9, 6.2 Hz, 2H), 2.03 $(s, 3H), 1.97 - 1.87 (m, 2H), 1.79 (dtd, J = 14.2, 9.4, 6.1 Hz, 1H), 0.79 (dd, J = 6.8, 2.2 Hz, 6H); {}^{13}C NMR$ (101 MHz, Methanol-d₄) δ 129.58, 128.28, 128.22, 127.43, 127.34, 125.74, 114.80, 53.39, 47.52, 47.31, 47.10, 46.89, 46.67, 46.46, 46.25, 37.23, 37.05, 35.71, 31.38, 30.27, 28.97, 17.65, 16.99, 13.27; ¹³C NMR (101 MHz, DMSO-*d*₆) δ 172.61, 170.66, 170.58, 170.40, 156.52, 137.70, 137.37, 130.53, 129.19, 129.00,

128.06, 127.91, 126.32, 126.14, 124.42, 115.25, 57.57, 53.96, 53.45, 53.23, 51.93, 37.57, 37.39, 36.08, 31.92, 30.59, 29.47, 19.08, 17.90, 14.58.

H₂N-C-Ahx-RrRKGGYFMVF-COOH (**Pep₂**). Global cleavage condition: cocktail B, 4 h. Yield: 54 %. White powder. Analytic HPLC: Gradient B, retention time: 16.8 min, purity: 98.4 %. HRMS(MALDI-TOF): calc. for $C_{71}H_{110}N_{19}O_{14}^+$ [M+H]⁺ 1452.8474, found 1452.8474; calc. for $C_{71}H_{109}N_{19}NaO_{14}^+$ [M+Na]⁺ 1474.8294, found 1474.8294.

H₂N-C-Ahx-YFMVFGGRrRK-COOH (Pep₃). Global cleavage condition: cocktail B, 4 h. Yield: 60 %. White powder. Analytic HPLC: Gradient B, retention time: 18.9 min, purity: 97.1 %. HRMS(MALDI-TOF): calc. for $C_{74}H_{118}N_{23}O_{15}S_2^+$ [M+H]⁺ 1632.8614, found 1632.8623; calc. for $C_{74}H_{117}N_{23}NaO_{15}S_2^+$ [M+Na]⁺ 1654.8433, found 1654.8431.

H₂N-C-Ahx-YFMVFGGRrRK-COOH (Pep4). Global cleavage condition: cocktail B, 4 h. Yield: 53 %. White powder. Analytic HPLC: Gradient B, retention time: 17.6 min, purity: 95.9 %. HRMS(MALDI-TOF): calc. for $C_{74}H_{118}N_{23}O_{15}S_2^+$ [M+H]⁺ 1632.8614, found 1632.8604; calc. for $C_{74}H_{117}N_{23}NaO_{15}S_2^+$ [M+Na]⁺ 1654.8433, found 1654.8440.

H₂N-NWYFIVF-COOH (**Pep₅**). Global cleavage condition: cocktail A, 2 h. Yield: 57 %. White powder. Analytic HPLC: Gradient A, retention time: 28.7 min, purity: 94.9 %. HRMS(MALDI-TOF): calc. for $C_{58}H_{73}N_{11}NaO_{12}^+$ [M+Na]⁺ 1138.5332, found 1138.5323.

H₂N-DEHYFIVF-COOH (Pep₆). Global cleavage condition: cocktail A, 2 h. Yield: 60 %. White powder. Analytic HPLC: Gradient A, retention time: 22.8 min, purity: 96.8 %. HRMS(MALDI-TOF): calc. for $C_{53}H_{69}N_{10}O_{14}^+$ [M+H]⁺ 1069.4989, found 1069.4988; calc. for $C_{53}H_{68}KN_{10}O_{14}^+$ [M+K]⁺ 1107.4548, found 1107.4424.

H₂N-Ahx-P-(pTyr)-LKTK-COOH (Pep₇). Global cleavage condition: cocktail B, 3 h. Yield: 59 %. White powder. Analytic HPLC: Gradient B, retention time: 8.4 min, purity: 93.7 %. HRMS(MALDI-TOF): calc. for $C_{42}H_{73}N_9O_{13}P^+$ [M+H]⁺ 942.5060, found 942.5063; calc. for $C_{42}H_{72}N_9NaO_{13}P^+$ [M+Na]⁺ 964.4879, found 964.4882; calc. for $C_{42}H_{72}KN_9O_{13}P^+$ [M+K]⁺ 980.4619, found 980.4627.

H₂N-Ahx-P-(pTyr)-LKTKRrRK-COOH (Pep₈). Global cleavage condition: cocktail B, 3 h. Yield: 62 %. White powder. Analytic HPLC: Gradient B, retention time: 33.5 min, purity: 98.4 %. HRMS(MALDI-TOF): calc. for $C_{66}H_{121}N_{23}O_{17}P^+$ [M+H]⁺ 1538.9043, found 1538.9043; calc. for $C_{66}H_{120}N_{23}NaO_{17}P^+$ [M+Na]⁺ 1560.8862, found 1560.8860.

H₂N-Nal-Cpa-Pal-SY-Cit-LRPA-CONH₂ (Pep₉). Global cleavage condition: cocktail A, 3 h. Yield: 64 %. White powder. Analytic HPLC: Gradient B, retention time: 16.3 min, purity: 99.0 %. HRMS(MALDI-TOF): calc. for $C_{68}ClH_{91}N_{17}O_{13}^+$ [M+H]⁺ 1388.6665, found 1388.6555; calc. for $C_{68}ClH_{90}N_{17}NaO_{13}^+$ [M+Na]⁺ 1410.6485, found 1410.6362.

H₂N-DRVYIHPF-CONH₂ (Pep₁₀). Global cleavage condition: cocktail A, 2 h. Yield: 58 %. White powder. Analytic HPLC: Gradient B, retention time: 13.3 min, purity: 96.2 %. HRMS(MALDI-TOF): calc. for $C_{50}H_{73}N_{14}O_{11}^+$ [M+H]⁺ 1045.5578, found 1045.5859; calc. for $C_{50}H_{72}N_{14}NaO_{11}^+$ [M+Na]⁺ 1067.5397, found 1067.5725.

H₂**N- GHK-CONH**₂ (**Pep**₁₁). Before global cleavage, Alloc deprotection was required. Soak resin in 4 mL DCM, the Pd(PPh₃)₄ (0.5 eq) and PhSiH₃ (10 eq.) was added. The SPE tube was sealed tightly, and shaken overnight. After reaction, little resin was taken for cleaving, and resulting solution was verified by ESI-MS to check if Alloc was deprotected completely. Global cleavage condition: cocktail A, 2 h. Yield: 70 %. White powder. Analytic HPLC: Gradient B, retention time: 6.0 min, purity: 92.8 %. HRMS(MALDI-TOF): calc. for $C_{14}H_{26}N_7O_3^+$ [M+H]⁺ 340.2092, found 340.2039; calc. for $C_{14}H_{25}N_7NaO_3^+$ [M+Na]⁺ 362.1911, found 362.1856. ¹H NMR (400 MHz, DMSO-*d*₆) δ 14.51 (s, 2H), 8.97

(t, J = 1.1 Hz, 1H), 8.68 (d, J = 8.0 Hz, 1H), 8.27 (d, J = 7.5 Hz, 1H), 8.07 (t, J = 6.0 Hz, 3H), 7.82 (s, 3H), 7.55 (s, 1H), 7.37 (s, 1H), 7.19 (s, 1H), 4.71 (q, J = 6.8 Hz, 1H), 4.14 (td, J = 8.3, 5.0 Hz, 1H), 3.59 (d, J = 5.6 Hz, 2H), 3.04 (qd, J = 15.3, 6.2 Hz, 2H), 2.75 (q, J = 6.5 Hz, 2H), 1.74 – 1.41 (m, 4H), 1.30 (q, J = 9.5, 8.1 Hz, 2H); ¹³C NMR (101 MHz, DMSO- d_6) δ 173.65, 169.17, 165.91, 133.76, 128.64, 117.10, 52.47, 51.48, 39.97 (read from HSQC), 38.53, 31.09, 27.44, 26.57, 22.30.

Synthetic procedure of symmetric dipyrrin peptide conjugates: Resin-bound peptide (0.1 mmol) from SPPS was placed in SPE tube, then the aldehyde building block was coupled as routine coupling procedure of SPPS. Upon completion, the liquid phase was removed, and the resin was washed with DMF (4 mL \times 3) and DCM (4 mL \times 3), little part of resin could be taken and be cleaved as a reference. The resin was soared in 4 mL DMF, then pyrrole building block (1.0 mmol) and BF₃.OEt₂ (0.1 mmol) was added into SPE tube directly by pipette. The SPE tube was shaken for 3-12 h (usually overnight) in dark. After that, the liquid phase was removed by filtration and resin was washed with DMF (4 mL \times 3) and DCM (4 mL \times 3). Resin was soared in DCM, and DDQ (0.5 mmol) solid was added directly and shaking for 1 h. The resin was washed thoroughly with DMF and DCM until liquid phase was colorless. Finally, 4 mL cleaving cocktail was use for global cleavage. The crude product was purified by preparative HPLC, dry crude product may used for boron complexation directly.

DP₁-HN-YFMVF-CONH₂ (**DP₁-Pep₁**). Global cleavage condition: cocktail A, 2 h. Yield: 51 %. Red powder. Analytic HPLC: Gradient A, retention time: 33.3 min, purity: 96.3 %. HRMS(MALDI-TOF): calc. for $C_{57}H_{67}N_8O_7S^+$ [M+H]⁺ 1007.4848, found 1007.4843.

DP₂-HN-YFMVF-CONH₂ (DP₂-Pep₁). Global cleavage condition: cocktail A, 2 h. Yield: 41 %. Orange powder. Analytic HPLC: Gradient A, retention time: 31.3 min, purity: 94.0 %. HRMS(MALDI-TOF): calc. for $C_{55}H_{63}N_8O_7S^+$ [M+H]⁺ 979.4535, found 979.4522; calc. for $C_{55}H_{62}N_8NaO_7S^+$ [M+Na]⁺ 1001.4354, found 1001.4316.

DP₃-HN-YFMVF-CONH₂ (**DP₃-Pep₁**). Global cleavage condition: cocktail A, 2 h. Yield: 53 %. Red powder. Analytic HPLC: Gradient A, retention time: 39.3 min, purity: 96.6 %. HRMS(MALDI-TOF): calc. for $C_{61}H_{75}N_8O_7S^+$ [M+H]⁺ 1063.5474, found 1063.5477; calc. for $C_{61}H_{74}N_8NaO_7S^+$ [M+Na]⁺ 1085.5293, found 1085.5297.

DP₄-HN-YFMVF-CONH₂ (DP₄-Pep₁). Global cleavage condition: cocktail A, 2 h. Yield: 10 %. Yellow powder. Analytic HPLC: Gradient A, retention time: 28.9 min, purity: 96.0 %. HRMS(MALDI-TOF): calc. for $C_{53}H_{59}N_8O_7S^+$ [M+H]⁺ 951.4222, found 951.4234; calc. for $C_{53}H_{58}N_8NaO_7S^+$ [M+Na]⁺ 973.4041, found 973.4025.

DP₅-HN-YFMVF-CONH₂ (**DP₅-Pep₁**). Global cleavage condition: cocktail A, 2 h. Yield: 51 %. Red powder. Analytic HPLC: Gradient A, retention time: 32.6 min, purity: 97.6 %. HRMS(MALDI-TOF): calc. for $C_{61}H_{63}N_8O_7S^+$ [M+H]⁺ 1051.4535, found 1051.4539; calc. for $C_{61}H_{62}N_8NaO_7S^+$ [M+Na]⁺ 1073.4354, found 1073.4337.

 DP_6 -HN-YFMVF-CONH₂ (DP_6 -Pep₁). Global cleavage condition: cocktail A, 2 h. Yield: 50 %. Red powder. Analytic HPLC: Gradient A, retention time: 33.2 min, purity: 94.8 %. HRMS(MALDI-TOF): calc. for $C_{63}H_{67}N_8O_9S^+$ [M+H]⁺ 1111.4746, found 1111.4750.

DP₉-HN-YFMVF-CONH₂ (**DP₉-Pep₁**). Global cleavage condition: cocktail A, 2 h. Yield: 35 %. Purple powder. Analytic HPLC: Gradient A, retention time: 40.2 min, purity: 95.2 %. HRMS(MALDI-TOF): calc. for $C_{65}H_{67}N_8O_7S^+$ [M+H]⁺ 1103.4848, found 1103.5282.

 DP_{10} -HN-YFMVF-CONH₂ (DP_{10} -Pep₁). Global cleavage condition: cocktail A, 2 h. Yield: 47 %. Red powder. Analytic HPLC: Gradient A, retention time: 32.4 min, purity: 95.2 %. HRMS(MALDI-TOF): calc. for $C_{57}H_{67}N_8O_7S^+$ [M+H]⁺ 1007.4848, found 1007.4864; calc. for $C_{57}H_{66}N_8NaO_7S^+$ [M+Na]⁺ 1029.4667, found 1029.4450.

 DP_{12} -HN-YFMVF-CONH₂ (DP_{12} -Pep₁). Global cleavage condition: cocktail A, 2 h. Yield: 40 %. Red powder. Analytic HPLC: Gradient A, retention time: 33.5 min, purity: 96.0 %. HRMS(MALDI-TOF): calc. for $C_{58}H_{69}N_8O_8S^+$ [M+H]⁺ 1037.4954, found 1037.4929.

 DP_{13} -HN-YFMVF-CONH₂ (DP_{13} -Pep₁). Global cleavage condition: cocktail A, 2 h. Yield: 40 %. Red powder. Analytic HPLC: Gradient A, retention time: 32.8 min, purity: 97.6 %. HRMS(MALDI-TOF): calc. for $C_{58}H_{69}N_8O_8S^+$ [M+H]⁺ 1037.4954, found 1037.4922; calc. for $C_{58}H_{68}N_8NaO_8S^+$ [M+Na]⁺ 1059.4773, found 1059.4777.

DP₁₄-**HN-YFMVF-CONH**₂ (**DP**₁₄-**Pep**₁). Global cleavage condition: cocktail A, 2 h. Yield: 34 %. Orange powder. Analytic HPLC: Gradient A, retention time: 33.1 min, purity: 96.4 %. HRMS(MALDI-TOF): calc. for $C_{57}H_{70}N_9O_7S^+$ [M+H]⁺ 1024.5113, found 1024.5127.

DP₁-HN-C-Ahx-RrRKGGYFMVF-COOH (**DP₁-Pep₂**). Global cleavage condition: cocktail B, 4 h. Yield: 44 %. Red powder. Analytic HPLC: Gradient B, retention time: 23.1 min, purity: 95.8 %. HRMS(MALDI-TOF): calc. for $C_{91}H_{128}N_{21}O_{15}^+$ [M+H]⁺ 1755.9927, found 1755.9933.

DP₁-HN-C-Ahx-YFMVFGGRrRK-COOH (**DP₁-Pep₃**). Global cleavage condition: cocktail B, 4 h. Yield: 49 %. Red powder. Analytic HPLC: Gradient B, retention time: 21.8 min, purity: 97.0 %. HRMS(MALDI-TOF): calc. for $C_{94}H_{136}N_{25}O_{16}S_2^+$ [M+H]⁺ 1936.0066, found 1936.0118.

DP₁-HN-C-Ahx-YFMVFGGRrRK-COOH (**DP₁-Pep₄**). Global cleavage condition: cocktail B, 4 h. Yield: 42 %. Red powder. Analytic HPLC: Gradient B, retention time: 22.2 min, purity: 96.6 %. HRMS(MALDI-TOF): calc. for $C_{94}H_{136}N_{25}O_{16}S_2^+$ [M+H]⁺ 1936.0066, found 1936.0017.

DP₁-HN-NWYFIVF-COOH (**DP₁-Pep₅**). Global cleavage condition: cocktail A, 2 h. Yield: 47 %. Red powder. Analytic HPLC: Gradient A, retention time: 34.2 min, purity: 99.0 %. HRMS(MALDI-TOF): calc. for $C_{78}H_{92}N_{13}O_{13}^+$ [M+H]⁺ 1418.6932, found 1418.6955.

DP₁-HN-Ahx-P-(pTyr)-LKTK-COOH (DP₁-Pep₇). Global cleavage condition: cocktail B, 3 h. Yield: 47 %. Red powder. Analytic HPLC: Gradient B, retention time: 17.6 min, purity: 98.2 %. HRMS(MALDI-TOF): calc. for $C_{62}H_{91}N_{11}O_{14}P^+$ [M+H]⁺ 1244.6479, found 1244.6422.

DP₁-HN-Ahx-P-(pTyr)-LKTKRrRK-COOH (DP₁-Pep₈). Global cleavage condition: cocktail B, 3 h. Yield: 48 %. Red powder. Analytic HPLC: Gradient B, retention time: 25.0 min, purity: 96.8 %. HRMS(MALDI-TOF): calc. for $C_{86}H_{139}N_{25}O_{18}P^+$ [M+H]⁺ 1842.0496, found 1842.0535.

DP₁-HN-DRVYIHPF-CONH₂ (**DP₁-Pep₁₀**). Global cleavage condition: cocktail A, 2 h. Yield: 53 %. Red powder. Analytic HPLC: Gradient B, retention time: 15.8 min, purity: 98.9 %. HRMS(MALDI-TOF): calc. for $C_{70}H_{91}N_{16}O_{12}^+$ [M+H]⁺ 1347.6997, found 1347.7072.

DP₁-HN-GHK-CONH₂ (DP₁-Pep₁₁). Before global cleavage, Alloc deprotection was required (the procedure described on **Pep₁₁**). Global cleavage condition: cocktail A, 2 h. Yield: 59 %. Red powder. Analytic HPLC: Gradient B, retention time: 12.1 min, purity: 95.9 %. HRMS(MALDI-TOF): calc. for $C_{34}H_{44}N_9O_4^+$ [M+H]⁺ 642.3511, found 642.3905; calc. for $C_{34}H_{43}N_9NaO_4^+$ [M+Na]⁺ 664.3330, found

664.3734. ¹H NMR (400 MHz, DMSO-*d*₆) δ 14.44 (s, 2H), 12.20 (s, 2H), 9.10 (t, J = 5.8 Hz, 1H), 9.00 (d, J = 1.5 Hz, 1H), 8.38 (d, J = 8.0 Hz, 1H), 8.13 (d, J = 7.5 Hz, 1H), 8.11 – 8.02 (m, 2H), 7.81 (s, 3H), 7.53 (d, J = 8.1 Hz, 2H), 7.50 (d, J = 2.0 Hz, 1H), 7.41 (d, J = 1.3 Hz, 1H), 7.22 – 7.15 (m, 1H), 6.53 (s, 2H), 4.65 (td, J = 7.8, 5.4 Hz, 1H), 4.16 (td, J = 8.5, 4.9 Hz, 1H), 3.94 (d, J = 5.7 Hz, 2H), 3.20 – 2.98 (m, 2H), 2.78 (h, J = 6.0 Hz, 2H), 2.43 (s, 6H), 1.83 – 1.38 (m, 10H), 1.33 (q, J = 9.2, 8.3 Hz, 2H); ¹³C NMR (101 MHz, DMSO-*d*₆) δ 173.67, 169.67, 168.94, 165.75, 152.41, 145.34, 142.32, 138.40, 136.91, 133.69, 129.09, 127.93, 120.48, 116.98, 52.48, 51.49, 42.70, 38.59, 31.07, 27.07, 26.60, 22.31, 13.79, 13.73.

DP₁-HN-GHK-CONH₂ (DP₁-Pep₁₁)*. Fmoc and Alloc dual-protected peptide on resin was used. Alloc deprotection was conducted as procedure described on **Pep₁₁**. Then, the dipyrrin was constructed as general procedure above. Fmoc was deprotected before global cleavage. Global cleavage condition: cocktail A, 2 h. Yield: 51 %. Red powder. Analytic HPLC: Gradient B, retention time: 13.1 min, purity: 98.9 %. HRMS(MALDI-TOF): calc. for $C_{34}H_{44}N_9O_4^+$ [M+H]⁺ 642.3511, found 642.3593; calc. for $C_{34}H_{43}N_9NaO_4^+$ [M+Na]⁺ 664.3330, found 664.3391. ¹H NMR (400 MHz, DMSO-*d*₆) δ 14.38 (s, 2H), 12.16 (s, 2H), 8.99 (s, 1H), 8.78 (t, *J* = 5.7 Hz, 1H), 8.68 (d, *J* = 8.0 Hz, 1H), 8.29 (d, *J* = 7.2 Hz, 1H), 8.04 (s, 3H), 8.02 (s, 2H), 7.58 (s, 1H), 7.50 (d, *J* = 8.0 Hz, 2H), 7.40 (s, 1H), 7.21 (s, 1H), 6.53 (s, 2H), 4.74 (q, *J* = 6.7 Hz, 1H), 4.19 - 4.15 (m, 1H), 3.63 (s, 2H), 3.27 (t, *J* = 6.8 Hz, 2H), 3.09 - 3.01 (m, 2H), 2.43 (s, 6H), 1.60 (ddp, *J* = 37.7, 15.0, 7.7, 6.9 Hz, 10H), 1.39 - 1.30 (m, 2H).

Synthetic procedure of asymmetric dipyrrin peptide conjugates: Resin-bound peptide was loaded in SPE tube, then the 5-formyl-2,4-dimethyl-3-pyrrolecarboxylic acid was coupled as general coupling procedure of SPPS. Upon completion, the liquid phase was removed by filtration, and the resin was washed with DMF (4 mL \times 3) and DCM (4 mL \times 3). The resin was soaked in DCM, and the pyrrole building block (0.5 mmol) and POCl₃ (0.5 mmol) was added by pipette into SPE tube directly. The mixture was shaken overnight in dark. Then, the resin was washed thoroughly with DMF and DCM until liquid phase was colorless, suitable cleavage cocktail was use for global cleavage. The crude product was purified by preparative HPLC.

DP₁₆-**HN-YFMVF-CONH**₂ (**DP**₁₆-**Pep**₁). Global cleavage condition: cocktail A, 2 h. Yield: 42 %. Red powder. Analytic HPLC: Gradient A, retention time: 31.4 min, purity: 95.1 %. HRMS(MALDI-TOF): calc. for C₅₄H₆₃N₈O₈S⁺ [M+H]⁺ 983.4484, found 983.5748; calc. for C₅₄H₆₂N₈NaO₈S⁺ [M+Na]⁺ 1005.4304, found 1005.5553. ¹H NMR (400 MHz, DMSO-*d*₆) δ 13.78 (s, 1H), 12.55 (s, 1H), 9.03 (s, 1H), 8.48 (s, 1H), 8.28 (d, *J* = 7.8 Hz, 2H), 8.21 (dd, *J* = 8.3, 3.3 Hz, 1H), 8.00 (d, *J* = 8.3 Hz, 1H), 7.87 (d, *J* = 2.4 Hz, 1H), 7.82 (d, *J* = 8.7 Hz, 1H), 7.54 (d, *J* = 8.8 Hz, 1H), 7.36 (d, *J* = 2.3 Hz, 1H), 7.25 – 7.18 (m, 10H), 7.08 (d, *J* = 8.4 Hz, 2H), 7.05 (s, 1H), 7.01 (dd, *J* = 8.8, 2.4 Hz, 1H), 6.66 (d, *J* = 8.4 Hz, 2H), 4.67 – 4.61 (m, 2H), 4.48 (m, 1H), 4.41 (m, 1H), 4.17 – 4.14 (m, 1H), 3.88 (s, 3H), 3.00 (td, *J* = 8.5, 7.9, 3.7 Hz, 3H), 2.81 (d, *J* = 9.1 Hz, 3H), 2.41 (td, *J* = 7.3, 6.7, 3.1 Hz, 2H), 2.35 (s, 3H), 2.30 (s, 3H), 2.02 (s, 3H), 1.94 – 1.88 (m, 2H), 1.80 – 1.76 (m, 1H), 0.79 (dd, *J* = 6.8, 4.0 Hz, 6H).

General procedure of boron complexation of dipyrrin conjugates: To a suspension of dipyrrin peptide conjugate (0.02 mmol) in acetonitrile (1.0 mL), DIPEA (170 uL) was added by pipette. The mixture was shaken or sonicated for 5 min. $BF_3.OEt_2$ (280 uL) was added by pipette in one portion. The mixture was

further shaken for 10 min. The crude product was concentrated under vacuum and was purified by preparative HPLC.

BODIPY₁-HN-YFMVF-CONH₂ (BODIPY₁-Pep₁). Yield: 73 %. Red powder. Analytic HPLC: Gradient A, retention time: 47.5 min, purity: 97.0 %. HRMS(MALDI-TOF): calc. for BC₅₇H₆₈N₈O₉S⁺ [M-2F+2OH+H]⁺ 1051.4987, found 1051.4934; calc. for BC₅₇F₂H₆₅KN₈O₇S⁺ [M+K]⁺ 1093.4460, found 1093.4703. ¹H NMR (400 MHz, DMSO- d_6) δ 9.20 (s, 1H), 8.74 (d, *J* = 8.2 Hz, 1H), 8.27 (dd, *J* = 28.2, 7.9 Hz, 2H), 8.05 (s, 1H), 8.02 (d, *J* = 8.4 Hz, 2H), 7.85 (d, *J* = 8.7 Hz, 1H), 7.55 (d, *J* = 8.1 Hz, 2H), 7.47 – 7.37 (m, 1H), 7.35 – 7.19 (m, 10H), 7.18 – 7.15 (m, 2H), 7.14 – 7.05 (m, 1H), 6.71 – 6.64 (m, 2H), 6.25 (s, 2H), 4.64 (dtd, *J* = 24.6, 8.6, 4.1 Hz, 2H), 4.54 (td, *J* = 8.6, 5.2 Hz, 1H), 4.47 (td, *J* = 8.3, 4.9 Hz, 1H), 4.20 (dd, *J* = 8.7, 6.7 Hz, 1H), 3.18 – 2.97 (m, 3H), 2.95 – 2.85 (m, 3H), 2.52 (s, 6H), 2.46 (tt, *J* = 6.6, 2.9 Hz, 2H), 2.07 (s, 3H), 2.01 – 1.92 (m, 2H), 1.84 (dt, *J* = 13.3, 4.7 Hz, 1H), 1.39 (s, 6H), 0.84 (dd, *J* = 6.8, 2.6 Hz, 6H); ¹³C NMR (101 MHz, DMSO- d_6) δ 172.65, 171.48, 170.88, 170.75, 170.45, 165.61, 155.68, 155.13, 142.63, 141.07, 137.76, 136.91, 134.52, 130.39, 130.06, 129.26, 129.06, 128.37, 127.98, 127.91, 126.20, 121.51, 114.83, 57.66, 55.29, 53.90, 53.49, 51.91, 37.61, 37.23, 35.98, 32.01, 30.60, 29.49, 29.01, 19.13, 17.99, 14.65, 14.22, 14.15; ¹⁹F NMR (376 MHz, DMSO- d_6) δ -145.48 (dd, *J* = 65.6, 30.6 Hz).

BODIPY₁-HN-YFMVF-CONH₂ (BODIPY₁-Pep₁). Yield: 73 % (from purified **DP₁-Pep₁**) or 45 % (from dry crude product of **DP₁-Pep₁** from SPPS) Red powder. Analytic HPLC: Gradient A, retention time: 47.5 min, purity: 97.0 %. HRMS(MALDI-TOF): calc. for $C_{57}H_{68}BN_8O_9S^+$ [M-2F+2OH+H]⁺ 1051.4987, found 1051.4934; calc. for $C_{57}H_{65}BF_2KN_8O_7S^+$ [M+K]⁺ 1093.4460, found 1093.4703.

BODIPY₂-HN-YFMVF-CONH₂ (BODIPY₂-Pep₁). Yield: 76 %. Orange powder. Analytic HPLC: Gradient A, retention time: 46.2 min, purity: 95.0 %. HRMS(MALDI-TOF): calc. for BC₅₅FH₆₁N₈O₇S⁺ [M-F]⁺ 1007.4525, found 1007.4451; calc. for C₅₅H₆₁BF₂N₈NaO₇S⁺ [M+Na]⁺ 1049.4407, found 1049.3821; calc. for C₅₅H₆₁BF₂KN₈O₇S⁺ [M+K]⁺ 1065.4147, found 1065.4182.

BODIPY₃-HN-YFMVF-CONH₂ (BODIPY₃-Pep₁). Yield: 70 %. Red powder. Analytic HPLC: Gradient A, retention time: 54.7 min, purity: 96.0 %. HRMS(MALDI-TOF): calc. for $C_{61}H_{75}N_8O_7S^+$ [M-BF2+2H]⁺ 1063.5474, found 1063.5389; calc. for $C_{61}H_{73}BF_2N_8NaO_7S^+$ [M+Na]⁺ 1133.5346, found 1133.5359; calc. for $C_{61}H_{73}BF_2KN_8O_7S^+$ [M+K]⁺ 1149.5086, found 1149.5101.

BODIPY₉-HN-YFMVF-CONH₂ (BODIPY₉-Pep₁). Yield: 55 %. Purple powder. Analytic HPLC: Gradient A, retention time: 53.0 min, purity: 94.6 %. HRMS(MALDI-TOF): calc. for $BC_{65}H_{68}N_8O_9S^+$ [M-2F+2OH+H]⁺ 1147.4987, found 1147.5021; calc. for $C_{65}H_{65}BF_2N_8NaO_7S^+$ [M+Na]⁺ 1173.4720, found 1173.4887; calc. for $C_{65}H_{65}BF_2KN_8O_7S^+$ [M+K]⁺ 1189.4460, found 1189.4789.

BODIPY₁₅-**HN-YFMVF-CONH**₂ (**BODIPY**₁₅-**Pep**₁). Yield: 71 %. Orange powder. Analytic HPLC: Gradient A, retention time: 42.8 min, purity: 94.1 %. HRMS(MALDI-TOF): calc. for BC₅₁FH₆₁N₈O₇S⁺ [M-F]⁺ 959.4525, found 959.5180; calc. for C₅₁H₆₁BF₂N₈NaO₇S⁺ [M+Na]⁺ 1001.4407, found 1001.5133; calc. for BC₅₁F₂H₆₁KN₈O₇S⁺ [M+K]⁺ 1017.4147, found 1017.5093.

BODIPY₁-HN-C-Ahx-YFMVFGGRrRK-COOH (BODIPY₁-Pep₄). Yield: 49 %. EDT was used as reductant during reaction to prevent the oxidation of Cys. Red powder. Analytic HPLC: Gradient B, retention time: 29.5 min, purity: 98.7 %. HRMS(MALDI-TOF): calc. for $C_{94}H_{135}BF_2N_{25}O_{16}S_2^+$ [M+H]⁺ 1984.0119, found 1983.9865.

BODIPY₁-HN-NWYFIVF-COOH (BODIPY₁-Pep₅). Yield: 63 %. Red powder. Analytic HPLC: Gradient A, retention time: 46.4 min, purity: 97.7 %. HRMS(MALDI-TOF): calc. for $C_{78}H_{90}BF_2N_{13}NaO_{13}^+$ [M+Na]⁺ 1488.6804, found 1488.6771; calc. for $C_{78}H_{90}BF_2KN_{13}O_{13}^+$ [M+K]⁺ 1504.6544, found 1504.6543.

BODIPY₁-HN-DEHYFIVF-COOH (BODIPY₁-Pep₆). Yield: 31 %. Red powder. Analytic HPLC: Gradient A, retention time: 35.8 min, purity: 95.2 %. HRMS(MALDI-TOF): calc. for $C_{73}H_{85}BF_2N_{12}NaO_{15}^+$ [M+Na]⁺ 1441.6281, found 1441.5949; calc. for $C_{73}H_{85}BF_2KN_{12}O_{15}^+$ [M+K]⁺ 1457.6020, found 1457.5786.

DP₁-HN-Ahx-P-(pTyr)-LKTK-COOH (BODIPY₁-Pep₇). Yield: 50 %. Red powder. Analytic HPLC: Gradient B, retention time: 19.3 min, purity: 95.9 %. HRMS(MALDI-TOF): calc. for $C_{62}H_{89}BFN_{11}O_{14}P^+$ [M-F]⁺ 1272.6470, found 1272.7580.

BODIPY₁-HN-DRVYIHPF-CONH₂ (BODIPY₁-Pep₁₀). Yield: 37 %. Red powder. Analytic HPLC: Gradient B, retention time: 19.3 min, purity: 95.9 %. HRMS(MALDI-TOF): calc. for $C_{70}H_{91}BF_2N_{16}O_{12}^+$ [M+H]⁺ 1396.7128, found 1396.6222.

Biological experiments

Cell Culture Conditions. Nasopharyngeal carcinoma (NPC) cell line C666 and Cervical carcinoma cell line HeLa were used in this study. C666 and HeLa were cultivated in Roswell Park Memorial Institute Medium (RPMI 1640) and Dulbecco's Modified Eagle Medium (DMEM) containing 10% v/v Fetal Bovine Serum (FBS) and 1% v/v Penicillin Streptomycin respectively. Both C666 and HeLa were maintained at 37 °C and 5% CO₂.

Dark Cytotoxicity Assay. The dark cytotoxicity and were assessed by MTT viability assay. Cells (6×10^3 per well) were seeded onto 96-well plates and then incubated at 37 °C with 5% CO₂ in dark for 24 h prior to the addition of samples. The cells were then incubated with samples for another 24 h. Medium were then removed, and the cell monolayers were washed with 1X PBS and then incubated with 100 mL medium with 5% v/v MTT solution (5 mg/mL) at 37 °C for 2.5 h. 80 mL of solution were removed and 100 mL Dimethyl sulfoxide (DMSO) were added to dissolve the formazan crystals. The absorbance of the formazan crystal was measured at 540 nm and 650 nm by dual-wavelength Azure microplate reader after 1 h of shaking.

Light Cytotoxicity Assay. The light cytotoxicity of samples was assessed with MTT viability assay. The procedures of the MTT viability assay were previously described. Cells were irradiated with optical dose of 5J/cm² after 24 h incubation with sample and the medium were replaced with fresh medium prior to irradiation.

In vitro imaging and co-staining. Cell were incubated with $BODIPY_1$ -Pep₄ (10mM) for 24h and then costained with Hoechst 33342 nuclear dye for 15 minutes. Imaging was performed by a Nikon Eclipse Ti2 confocal laser-scanning microscope.

Expression and purification of EBNA1 (a.a. 468-607). The gene construct for N-terminally hexahistidine tagged SMT3-EBNA1 DNA binding domain (residues 468-607) fusion protein was chemically synthesized and cloned into pET28a (+) vector (Genscript). The plasmid was transformed into Escherichia coli BL21 (DE3) competent cells and grown in 2YT media supplemented with 50 µg/ml kanamycin at 37 °C. When the OD_{600} of the cells reached 0.8, expression was induced with 0.5 mM isopropyl β -D-1thiogalactopyranoside (IPTG) and the cells were grown at 25 °C overnight. The cells were harvested by centrifugation at 5000 rpm (6,238 x g) for 10 mins at 4 °C. The following protein purification protocol was adapted from a previously published report^[3]. The cell pellet was resuspended in lysis buffer (20 mM Tris, pH 8.0, 500 mM NaCl, 10 mM imidazole, 5% (v/v) glycerol, 5 mM β-mercaptoethanol (BME), 17.4 µg/ml phenylmethylsulfonyl fluoride (PMSF) and 1 mM MgCl₂). The resuspended cells were lysed by sonication and the lysate was separated from the insoluble fractions by centrifugation at 24,000 rpm ($69,673 \times g$) for 30 min at 4 °C. The protein was purified by nickel affinity using a His-trap column (GE Healthcare) equilibrated with lysis buffer. The lysate was first loaded onto the His-trap column, then washed with 10 column volumes of wash buffer (20 mM Tris pH 8.0, 500 mM NaCl ,30 mM imidazole, 5% glycerol and 5 mM BME) and the protein was eluted with 3 - 4 column volumes of elution buffer (20 mM Tris pH 8.0, 500 mM NaCl, 300 mM imidazole, 5% glycerol and 5 mM BME). The eluted protein was treated with ULP1 to cleave the hexahistidine-SMT3 protein tag. Any residual uncleaved fusion protein and the histidine-tagged ULP1 protease were removed by nickel affinity while the tag-free EBNA1 (468-607) protein was recovered by flowing wash buffer through the His-trap column (GE Healthcare). The fractions were pooled, concentrated and further purified by size exclusion chromatography using a Superdex 200 Increase 10/300 column (GE Healthcare), equilibrated with a buffer containing 1 mM HEPES, pH 7.2, 500

mM NaCl and 10 mM dithiothreitol (DTT). The relevant protein fractions were analysed using SDS-PAGE, pooled, concentrated to 6 mg/ml and stored at -80 °C.

Fluorescent titration. The EBNA1 protein was prepared as the procedure above, while Bovine serum albumin (BSA) protein was purchased from Thermo Fisher Scientific. Both BSA and EBNA1 were further prepared as solution (120 μ M) in buffer (1 mM HEPES, pH 7.2, 500 mM NaCl and 10 mM dithiothreitol). The protein solution was gradually added into **BODIPY1-Pep4** (2000 μ L 1.2 μ M in same buffer) by pipette. Each time after addition of protein, the resulting solution was shaken slowly for around 2 min, then the fluorescent spectrum was recorded. The experiment was stopped when the influence on fluorescence was saturated. The increased of volume is less than 4% in total.

Reference:

- [1] M. Kondo, S. Furukawa, K. Hirai, S. Kitagawa, Angew. Chemie Int. Ed. 2010, 49, 5327–5330.
- [2] S. Eissler, M. Kley, D. Bächle, G. Loidl, T. Meier, D. Samson, J. Pept. Sci. 2017, 23, 757–762.
- [3] T. E. Messick, G. R. Smith, S. S. Soldan, M. E. McDonnell, J. S. Deakyne, K. A. Malecka, L. Tolvinski, P. A. J. van den Heuvel, B.-W. Gu, J. A. Cassel, D. H. Tran, B. R. Wassermann, Y. Zhang, V. Velvadapu, E. R. Zartler, P. Busson, A. B. Reitz, P. M. Lieberman, *Sci. Transl. Med.* 2019, *11*, eaau5612.

NMR spectra of products



3.4 3.3 3.2 3.1 3.0 2.9 2.8 2.7 2.6 2.5 2.4 2.3 2.2 2.1 2.0 1.9 1.8 1.7 1.6 1.5 1.4 1.3 1.2 1.1 1.0 0.9 0.8 0.7 0.6 0.5 0.4 0.3 0.2 0.1 f1 (ppm)

Fig. S8. Comparison and assignment of ¹H-NMR for **Pep1** (bottom), **DP1-Pep1** (middle) and **BODIPY1-Pep1** (top) in range 3.5~0.0 ppm. Signal of side chain sp³C–H and methyl groups on dipyrrin/BODIPY.



Fig. S9. Comparison and assignment of ¹H-NMR for **Pep**₁ (bottom), **DP**₁-**Pep**₁ (middle) and **BODIPY**₁-**Pep**₁ (top) in range 4.8~3.7 ppm. Signal of α -H on the backbone of peptide.



Fig. S10. Comparison and assignment of ¹H-NMR for **Pep**₁ (bottom), **DP**₁-**Pep**₁ (middle) and **BODIPY**₁-**Pep**₁ (top) in range 9.0~6.0 ppm. Signal of aryl proton from Phe, Tyr and dipyrrin/BODIPY, as well as amide proton from backbone of peptide.



Fig. S11. Comparison and assignment of ¹H-NMR for **Pep₁** (bottom), **DP₁-Pep₁** (middle) and **BODIPY₁-Pep₁** (top) in range 12.9~8.9 ppm. Signal of acidic proton from Tyr (phenol-H) and dipyrrin (NH).



¹H-NMR spectrum of **Pep**₁ in methanol-*d*₄.



¹³C-NMR spectrum of **Pep**₁ in methanol-*d*₄.



HSQC spectrum of **Pep**₁ in methanol-*d*₄.



HMBC spectrum of **Pep1** in methanol-*d4*.



¹H-NMR spectrum of **Pep**₁ in DMSO-*d*₆.







HSQC spectrum of **Pep1** in DMSO-*d*₆.



HMBC spectrum of **Pep1** in DMSO-*d*₆.



¹H-NMR spectrum of **DP₁-Pep₁** in DMSO- d_6 .















¹H-NMR spectrum of **BODIPY₁-Pep₁** in DMSO-*d*₆.



¹³C-NMR spectrum of **BODIPY₁-Pep₁** in DMSO-*d*₆.



HSQC spectrum of BODIPY1-Pep1 in DMSO-d6.



HMBC spectrum of **BODIPY1-Pep1** in DMSO-*d*₆.



¹⁹F-NMR spectrum of **BODIPY₁-Pep₁** in DMSO-*d*₆.



¹H-NMR spectrum of **DP₁₆-Pep₁** in DMSO-*d*₆.



HSQC spectrum of **DP₁₆-Pep₁** in DMSO-*d*₆.



¹H-NMR spectrum of **Pep**₁₁ in DMSO-*d*₆.



¹³C-NMR spectrum of **Pep**₁₁ in DMSO-*d*₆.







HMBC spectrum of **Pep**₁₁ in DMSO-*d*₆.



¹H-NMR spectrum of **DP₁-Pep₁₁** in DMSO-*d*₆.



¹³C-NMR spectrum of **DP₁-Pep₁₁** in DMSO-*d*₆.



HSQC spectrum of **DP₁-Pep₁₁** in DMSO-*d*₆.



HMBC spectrum of **DP₁-Pep₁₁** in DMSO-*d*₆.



¹H-NMR spectrum of **DP₁-Pep₁₁*** in DMSO-*d*₆.



HSQC spectrum of **DP1-Pep11*** in DMSO-*d*₆.

HPLC chromatographs and MALID-TOF HRMS spectra of products





Chemical Formula: C₃₇H₄₈N₆O₆S Exact Mass: 704.3356





Analytic HPLC of Pep1



HRMS(MAIDL-TOF) of Pep1



10 5 15 Analytic HPLC of Pep2



 NH_2



Pep2: H2N-Ahx-YFIVFGGKRPR-COOH







HRMS(MAIDL-TOF) of Pep3



HRMS(MAIDL-TOF) of Pep₄

C:\Users\Yue W...\Yue310-SM.mzML Injection 1 MS (+) profile MS + spectrum 0.00



_NH

 H_2N

⊌NH

 H_2N

Pep₄: H₂N-C-Ahx-YFMVF-GG-RrRK-COOH

Pep₅: H₂N-NWQYFIVF-COOH







S36






HRMS(MAIDL-TOF) of Pep₆

Pep7: H2N-Ahx-P-(pTyr)-LKTK-COOH



Chemical Formula: C₄₂H₇₂N₉O₁₃P Exact Mass: 941.4987







HRMS(MAIDL-TOF) of Pep7

Pep8: H2N-Ahx-P-(pTyr)-LKTKRrRK-COOH







HRMS(MAIDL-TOF) of Pep₈

HRMS(MAIDL-TOF) of Pep₉





C:\Users\Yue W...50-SM-prep.mzML Injection 1 MS1 (+) profile MS + spectrum 0.00





HRMS(MAIDL-TOF) of Pep10

500 600 700 800 900 1000 1100 1200 1300 1400 1500 1600 1700 1800 1900 2000 2100 2200 2300 2400 2500 2600 2700 2800 2900 3000 3100 3200 3300 340C m/z (Da)











DP₁-Pep₁: DP₁-NH-YFMVF-CONH₂



Analytic HPLC of DP1-Pep1



HRMS(MAIDL-TOF) of DP1-Pep1

DP₂-Pep₁: DP₂-NH-YFMVF-CONH₂



Analytic HPLC of DP2-Pep1





Analytic HPLC of **DP₃-Pep₁**



 $DP_{3}-Pep_{1}: DP_{3}-NH-YFMVF-CONH_{2}$

DP₄-Pep₁: DP₄-NH-YFMVF-CONH₂







HRMS(MAIDL-TOF) of DP4-Pep1





DP₅-Pep₁: DP₅-NH-YFMVF-CONH₂

н

DP₆-Pep₁: DP₆-NH-YFMVF-CONH₂



Analytic HPLC of **DP₆-Pep₁**



HRMS(MAIDL-TOF) of DP6-Pep1

DP₉-Pep₁: DP₉-NH-YFMVF-CONH₂



Chemical Formula: C65H66N8O7S Exact Mass: 1102.4775

C:\Users\Yue W...d\YUE434-PROD.D Injection 1 DAD B, Sig=280,8 Ref=off Chromatogram



Analytic HPLC of DP9-Pep1



HRMS(MAIDL-TOF) of DP9-Pep1

S50

HRMS(MAIDL-TOF) of DP10-Pep1





C:\Users\Yue W...d\YUE363-PREP.D Injection 1 DAD B, Sig=280,8 Ref=off Chromatogram

C:\Users\Yue W...ue363-prod.mzML Injection 1 MS (+) profile MS + spectrum 0.00



DP₁₂-Pep₁: DP₁₂-NH-YFMVF-CONH₂



Exact Mass: 1036.4881







HRMS(MAIDL-TOF) of DP12-Pep1

HRMS(MAIDL-TOF) of DP13-Pep1







C:\Users\Yue W...d\YUE453-PREP.D Injection 1 Function 1, mixed ion MS TIC



DP₁₃-Pep₁: DP₁₃-NH-YFMVF-CONH₂

DP₁₄-Pep₁: DP₁₄-NH-YFMVF-CONH₂



Analytic HPLC of **DP**₁₄-**Pep**₁



HRMS(MAIDL-TOF) of DP14-Pep1







C:\Users\Yue W...ue353-prep.mzML Injection 1 MS (+) profile MS + spectrum 0.00

HRMS(MAIDL-TOF) of DP15-Pep1



HRMS(MAIDL-TOF) of DP₁₆-Pep₁

C:\Users\Yue W...448-1-prod.mzML Injection 1 MS (+) profile MS + spectrum 0.00



DP₁₆-Pep₁: DP₁₆-NH-YFMVF-CONH₂

DP₁-Pep₂: DP₁-HN-Ahx-YFIVFGGKRPR-COOH







HRMS(MAIDL-TOF) of **DP₁-Pep₂**















600 700 800 900 1000 1100 1200 1300 1400 1500 1600 1700 1800 1900 200 2100 2200 2300 2400 2500 2600 2700 2800 2900 3000 3100 3200 3300 3400 350(m/z (Da)

HRMS(MAIDL-TOF) of DP1-Pep4







750 800 850 900 950 1000 1050 1100 1150 1200 1250 1300 1350 1400 1450 1500 1550 1600 1650 1700 1750 1800 1850 1900 1950 2000 2050 2100 2150 22 HRMS(MAIDL-TOF) of **DP₁-Pep**₅







HRMS(MAIDL-TOF) of **DP₁-Pep₆**







600 700 800 900 1000 1100 1200 1300 1400 1500 1600 1700 1800 1900 2000 2100 2200 2300 2400 2500 2600 2700 2800 2900 3000 3100 3200 3300 3400 350(m/z (Da)

HRMS(MAIDL-TOF) of DP1-Pep7

S62

HRMS(MAIDL-TOF) of DP1-Pep8

120000



D:\Onedirve\On...ue365-prod.mzML Injection 1 MS1 (+) profile MS + spectrum 0.00 160000 1842.0535 100.00% 140000



*⊾*NH

ŃН

 NH_2

H₂N

ŅH₂

DP1-Pep8: DP1-HN-Ahx-P-(pTyr)-LKTKRrRK-COOH

OPO₂H







500 600 700 800 900 1000 1100 1200 1300 1400 1500 1600 1700 1800 1900 2000 2100 2200 2300 2400 2500 2600 2700 2800 2900 3000 3100 3200 3300 3400 m/z (Da)

HRMS(MAIDL-TOF) of DP1-Pep9







HRMS(MAIDL-TOF) of DP1-Pep10







HRMS(MAIDL-TOF) of DP1-Pep11



C:\Users\Yue W...455-2-prep.mzML Injection 1 MS1 (+) profile MS + spectrum 0.00











BODIPY₁-Pep₁: BODIPY₁-NH-YFMVF-CONH₂

S68









BODIPY₂-Pep₁: BODIPY₂-NH-YFMVF-CONH₂

S69



HRMS(MAIDL-TOF) of BODIPY₃-Pep₁

Analytic HPLC of BODIPY₃-Pep₁





Chemical Formula: C₆₁H₇₃BF₂N₈O₇S

BODIPY₃-Pep₁: BODIPY₃-NH-YFMVF-CONH₂



1189.4789 100.00%

HRMS(MAIDL-TOF) of BODIPY9-Pep1

Analytic HPLC of BODIPY₉-Pep₁

50000

45000



Chemical Formula: C₆₅H₆₅BF₂N₈O₇S Exact Mass: 1150.4758

C:\Users\Yue W...446-2-prod.mzML Injection 1 MS (+) profile MS + spectrum 0.00



BODIPY9-Pep1: BODIPY9-NH-YFMVF-CONH2



HRMS(MAIDL-TOF) of BODIPY15-Pep1

C:\Users\Yue W...446-6-prod.mzML Injection 1 MS (+) profile MS + spectrum 0.00



BODIPY₁₅-Pep₁: BODIPY₁₅-NH-YFMVF-CONH₂





1985.0777

21.29%

1984.080 26.<u>64%</u>



14 12 Total Area % Start time End time RT Scan Туре Area 10-3.291 0.033 29.496 4424 BB BB 98.68 29.336 29.836 8.189 8.236 1235 0.98 8.489 8 2 0.449 67 BB 0.011 0.34 0.236 0.529 6 4 2 0 ų -2 10 15 5 20 25 30 Retention time (min) 35 40 45 50 Analytic HPLC of BODIPY₁-Pep₄

29.5

C:\Users\Yue W...d\YUE420-PREP.D Injection 1 DAD B, Sig=280,8 Ref=off Chromatogram

18

16

20000



BODIPY₁-Pep₄: BODIPY₁-HN-C-Ahx-YFMVF-GG-RrRK-COOH


50000

40000

30000



700 750 800 850 900 950 1000 1050 1100 1150 1200 1250 1300 1350 1400 1450 1500 1650 1600 1650 1700 1750 1800 1850 1900 1950 2000 2050 2100 2150 22 m/z (Da)

1488.6771 100.00%

1504.6543 72.42%

C:\Users\Yue W...446-7-prod.mzML Injection 1 MS (+) profile MS + spectrum 0.00







Analytic HPLC of **BODIPY₁-Pep₆**



HRMS(MAIDL-TOF) of BODIPY1-Pep6



500 600 700 800 900 1000 1100 1200 1300 1400 1500 1600 1700 1800 1900 2000 2100 2200 2300 2400 2500 2600 2700 2800 2900 3000 3100 3200 3300 3400 m/z (Da)







HRMS(MAIDL-TOF) of BODIPY1-Pep10



Analytic HPLC of BODIPY1-Pep10





