Supplementary Information (SI) for ChemComm.

ELECTRONIC SUPPORTING INFORMATION

Peptide Structure and Silver Ion Affinity: Influence on the Formation of α-Helices upon Metal Binding

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Table of contents

Experimental methods

Solid-Phase Peptide Synthesis

The majority of the peptides used in this study were obtained from Bachem SA (purities ≥ 95%). The remaining peptides (M1-B2, M15-B2, M16-B2, M17-B2, M18-B2, and M19-B2,) were synthesized using SPPS (Solid-Phase Peptide Synthesis) on a Rink-Amide resin (ChemMatrix, loading 0.42-0.47 mmol/g) with a Biotage Initiator+ Alstra automated peptide synthesizer, following a procedure reported in the literature.[1]

Electrospray ionization mass spectrometry

The ESI-MS (Brucker Esquire HCT) in positive ion mode was performed on the six undecapeptides synthesized in-house, immediately following the purification process. This procedure was conducted to verify the identity of the undecapeptide obtained (Fig. S11-S18).

Determination of peptide concentrations

Approximately 1 mg of each lyophilized peptide was dissolved in 700 µL of bidistillated H_2O, and the concentrations were determined by UV-Vis spectroscopy (Perkin Elmer Lambda 25) and the Beer-Lambert law: $A_\lambda = \varepsilon_\lambda cl$, where *A* is the absorbance, ε_λ is the molar extinction coefficient at wavelength λ, *c* is the concentration, and *l* is the length of the cuvette (1 cm in this research). The molar extinction coefficient at 205 nm (ε_{205}) of each peptide was determined by using the formula of Anthis *et al.*:[2]

$$\varepsilon_{205} = \sum(\varepsilon_i n_i) + \varepsilon_{bb}(r-1),$$

where for each amino acid *i*, ε_i is the molar extinction coefficient of the amino acid side chain (from Goldfarb *et al.*)[3], n_i is the number of occurrences of that amino acid in the peptide sequence, ε_{bb} is the molar extinction coefficient for a single backbone peptide bond, and *r* is the number of amino acid residues in the peptide sequence. In the case of HEWM probe, the exact concentration was determined from the molar extinction coefficient at 280 nm (ε_{205} = 5540 $M^{-1}\cdot cm^{-1}$).[4]

Determination of Ag^+/peptide secondary structure

As previously reported, the study of the secondary structure was investigated using a circular dichroism (CD) spectrometer (Applied Photophysics Chirascan V100).[1] CD spectra (Fig S20-S27) were recorded at 25°C by adding increasing amounts of $AgNO_3$ (silver nitrate, Fisher Chemical ≥99.9%) dissolved in bidistillated H_2O, ranging from 0 to 20 equivalents.

DichroWeb analysis server

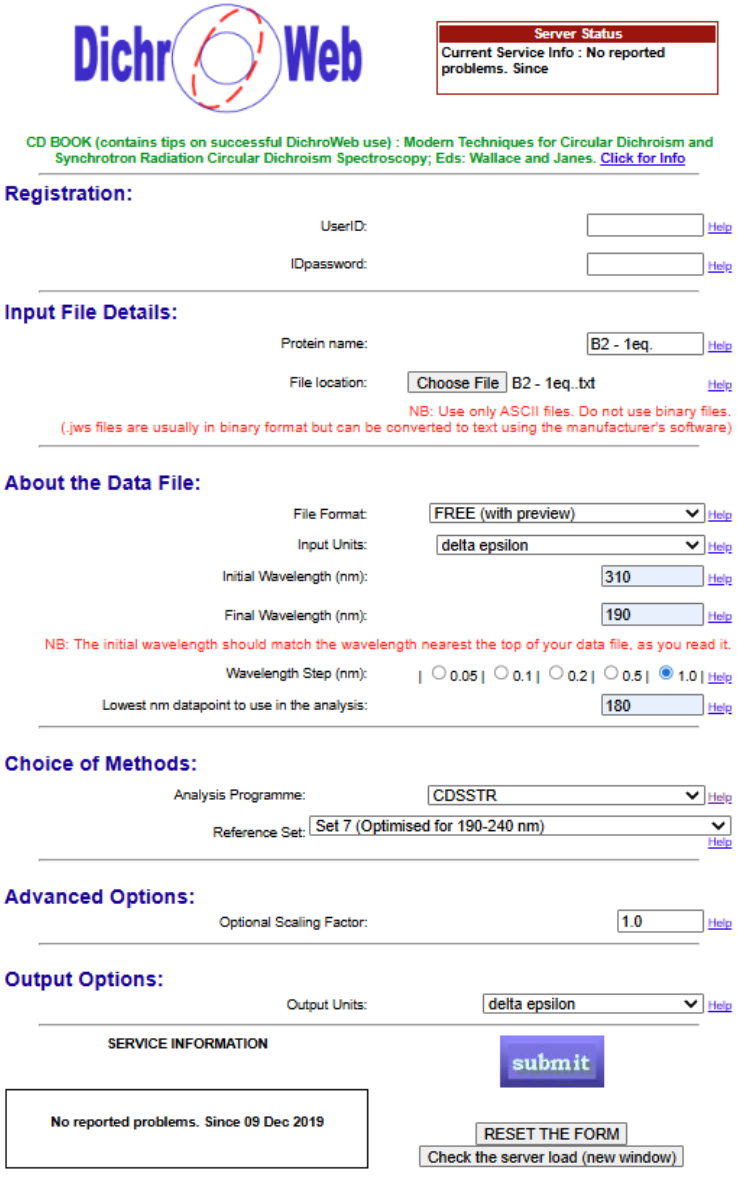

Fig. S1 Example of data input interface of the DichroWeb server,[5–7] used for the CD analysis of HQAMAEAHRRM (B2) titrated with 1 equivalent Ag^+. The ASCII-format CD data file (B2 – 1eq.txt), containing ellipticity values in Δε [$M^{-1}{\cdot}cm^{-1}$], is uploaded under the "Input File Details" section. The following key experimental parameters are provided: wavelength range (310-190 nm), and the step size (1.0 nm). The minimum wavelength employed for analysis is set to 180 nm. In the "Choice of Methods" section, the CDSSTR algorithm is selected with reference dataset Set 7, which has been optimized for the 190-240 nm range. The output units are maintained at a consistent level in order to ensure precise and reliable measurements. These settings enable precise estimation of the secondary structure composition from CD spectrum.

Determination of Ag^+/peptide binding constants

In accordance with previously reported methodologies, the silver binding constants (log($K_{b\text{-}1/b\text{-}2}$)) of each peptide were determined using a fluorescence spectrometer (Perkin Elmer LS 50 B).[1] Each peptide was subjected to three titrations at two different concentrations ($1 \cdot 10^{-5}$ M and $2 \cdot 10^{-5}$ M) employing a competition titration strategy with HEWM probe (1 equivalent). The experiments were conducted in MOPS (3-(N-morpholino)propansulfonic acid, Alfa Aesar ≥99%) buffer (20 equivalents, pH 7.4-7.5) by addition of $AgNO_3$ (silver nitrate, Fisher Chemical ≥99.9%) solution in bidistillated H_2O (0 to 5.5 equivalents) at 25°C (Fig S28-S71).

Dynafit coding

```
[task]
   task = fit
   data = equilibria
[mechanism] ; "M" = metal, "P" = peptide, "P*" = labelled peptide
   M + P*     <==> MP*    :     Kd1     dissoc
   M + P      <==> MP     :     Kd2      dissoc
   MP + M     <==> MMP    :     Kd3      dissoc
   MMP + M    <==> MMMP   :     Kd4      dissoc
   MMMP + M   <==> MMMMP  :     Kd5      dissoc
[constants]
   Kd1 = 3.79e-7
   Kd2 = 1.2e-07 ??
   Kd3 = 1.2e-07 ??
   Kd4 = 1.2e-07 ??
   Kd5 = 1.2e-07 ??
[responses]
 P* = 38681.00 ?, MP* = 1.98E+04 ?
[data]
   variable M, P, P*
   plot titration ;

   set 1

[output]
   directory ./data/output/fit
[settings]
{Output}
   XAxisLabel = [Metal], M
   YAxisLabel = Fluorescence, A.U.
;_____________________________________________________________________
[set:1]
M, M            P, M            P*, M           Fluorescence
0               0.019684583     0.023902309     924.5653
0.004016787     0.019668848     0.023883203     884.17
0.008027157     0.019653138     0.023864127     838.31
0.016028708     0.019621793     0.023826066     771.92
0.024004777     0.019590548     0.023788126     699.07
0.035921366     0.019543867     0.023731443     599.06
0.0477813       0.019497408     0.023675029     523.98
0.063507109     0.019435805     0.023600226     480.35
0.086910377     0.019344126     0.023488904     469.29
0.117773438     0.019223226     0.023342099     464.84
0.155813953     0.019074208     0.023161152     459.76
0.193269231     0.018927484     0.02298299      455.89
[end]
;_____________________________________________________________________
;_____________________________________________________________________
```

Fig. S2 Example of Dynafit code used to determine the binding constants for the competition titration between HQAMAEAHRRM (B2) and HEWM, both at $2 \cdot 10^{-5}$ M. *M* represents the metal ion (Ag^+), *P* represents the peptide (B2), *P** represents the probe (HEWM). The dissociation constant of the probe (K_{d1}) was previously determined by Chabert *et al.*[8–10]

Experimental data

HPLC: Retention times of undecapeptides

Table S1 Retention time [min] of the synthesized peptide using semi-preparative reverse phase HPLC with a linear gradient from 95% to 70% of A in B, at a flow rate of 5 mL/min for 25 min, where A is a solution of 0.1% TFA in H_2O, and B is a solution of 0.1% TFA in ACN.

Model	Retention time [min]	Model	Retention time [min]
HQAMAAAHRRM	12.68	MKKMAEAHQQH	9.80
MQAMAEAHRRM	14.93	HQQHAAAHQQH	2.87
HQAMAEAMRRM	17.98	MKKMAAAMKKM	15.53
MKKMAEAMKKM	18.98	MKKMAAAHQQH	2.43

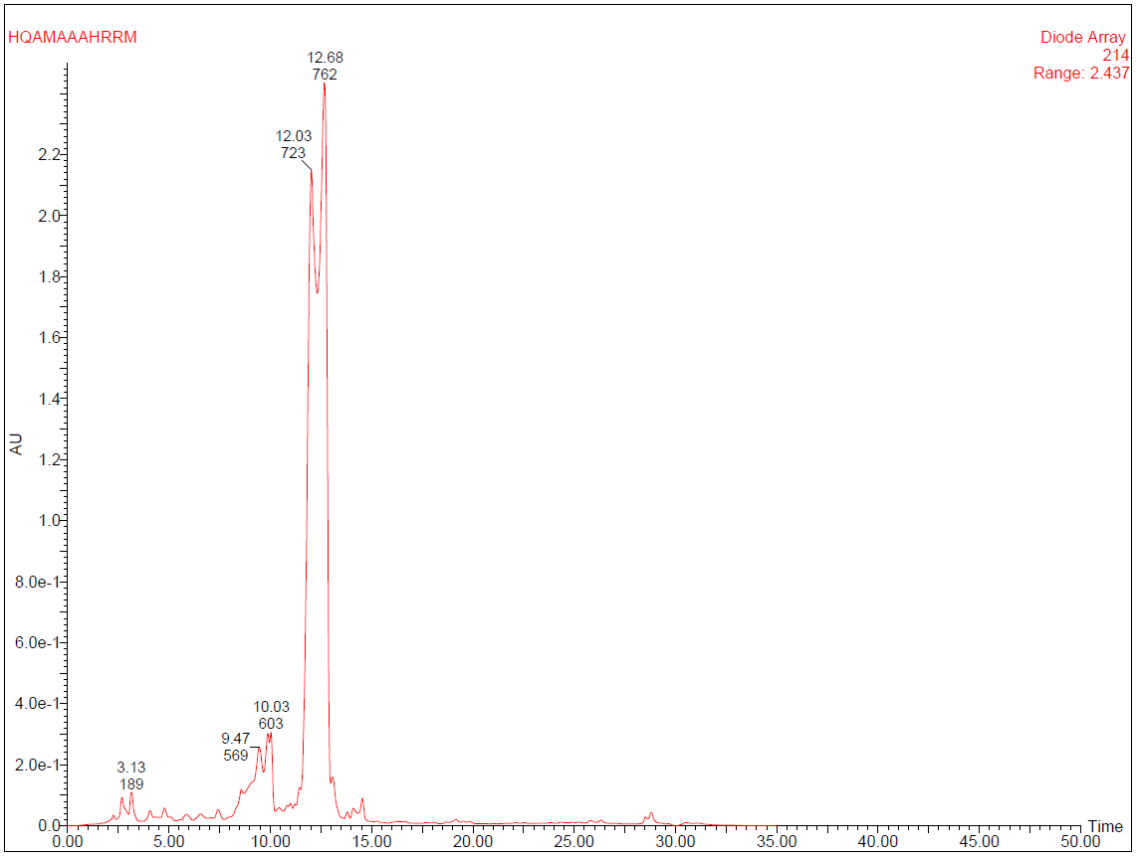

Fig. S3 HPLC chromatogram of HQAMAAAHRRM (M1-B2)

Fig. S4 HPLC chromatogram of MQAMAEAHRRM (M11-B2)

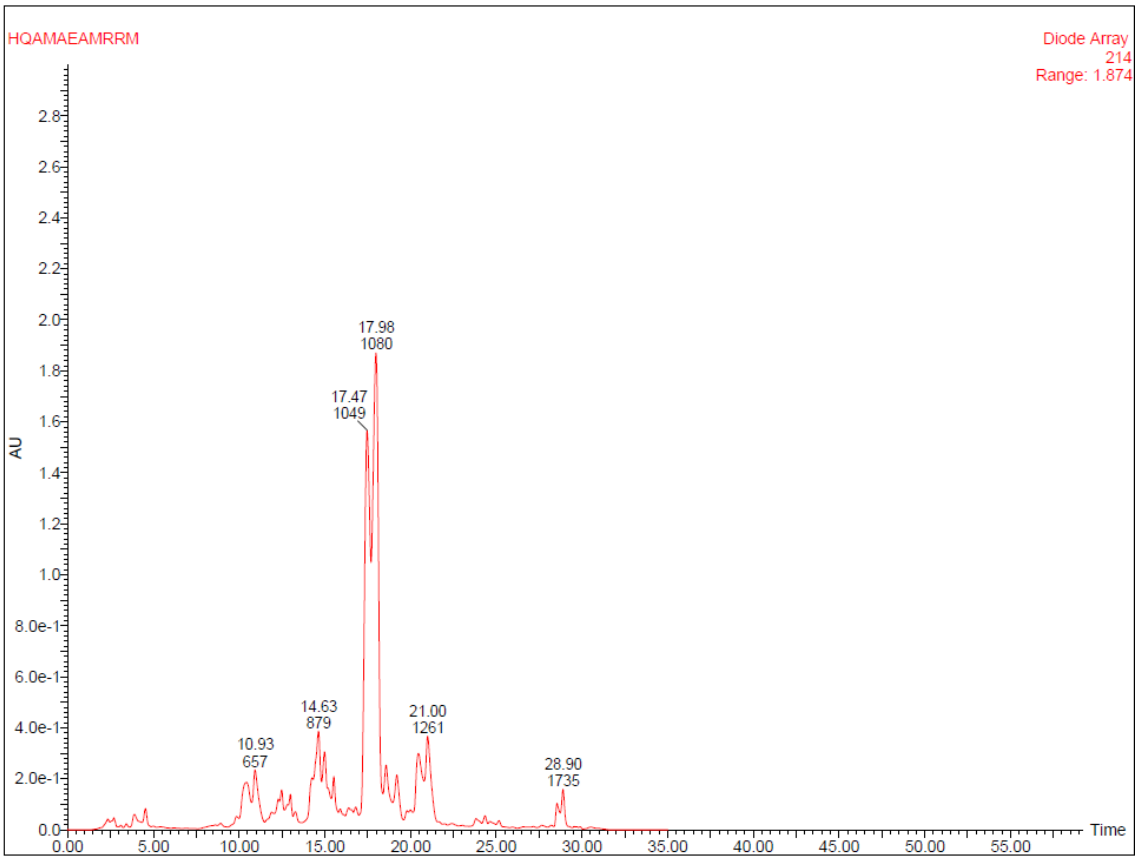

Fig. S5 HPLC chromatogram of HQAMAEAMRRM (M13-B2)

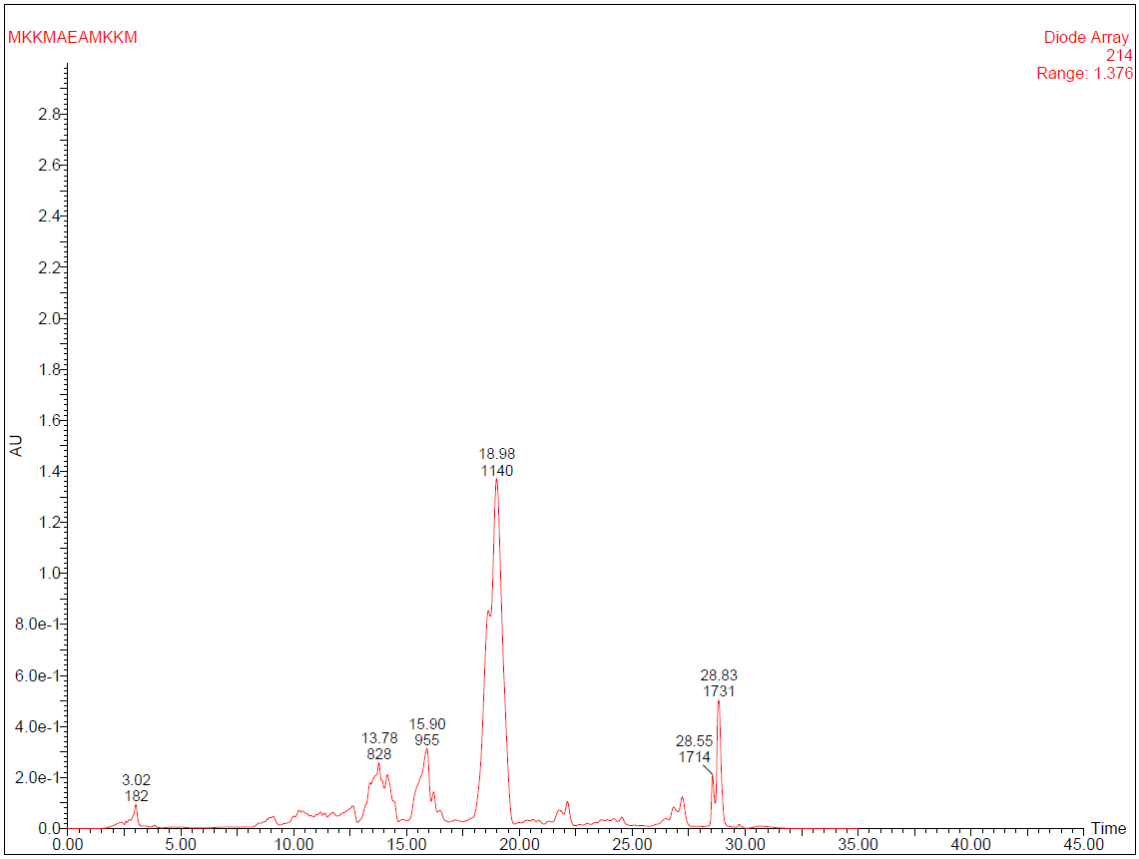

Fig. S6 HPLC chromatogram of MKKMAEAMKKM (M17-B2)

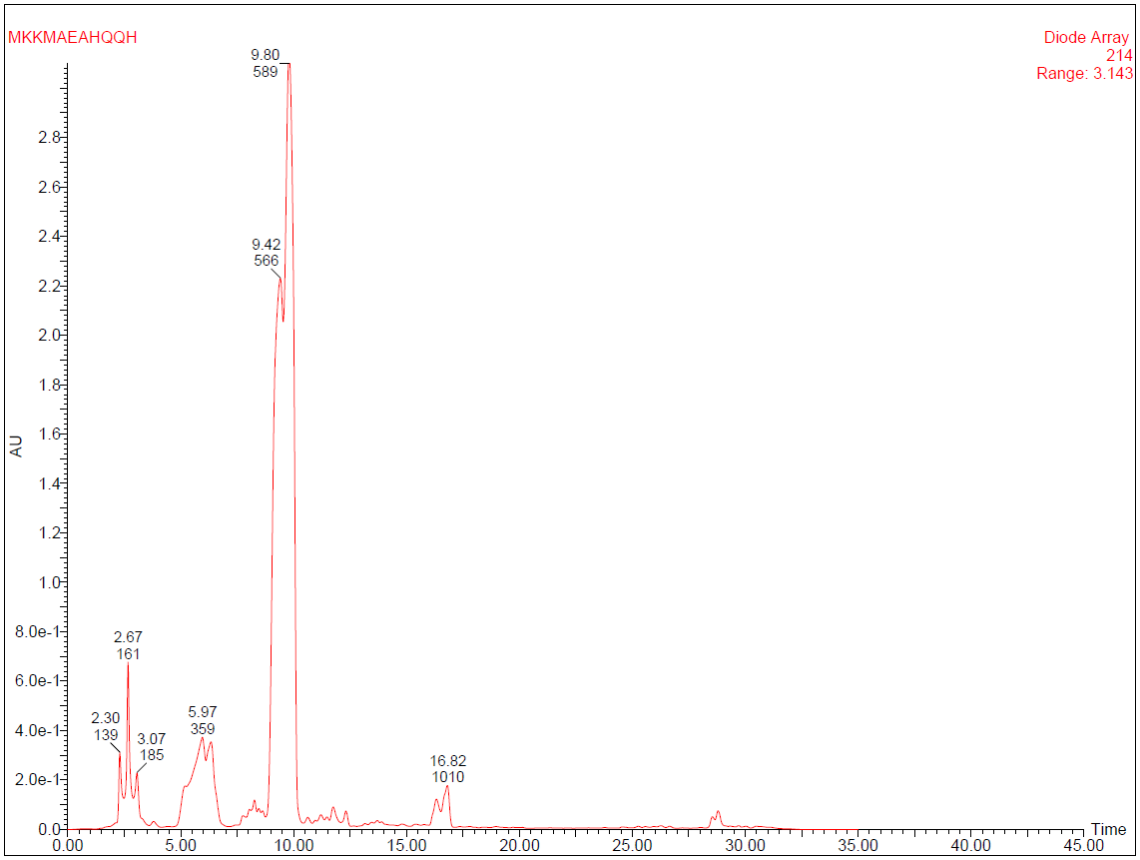

Fig. S7 HPLC chromatogram of MKKMAEAHQQH (M18-B2)

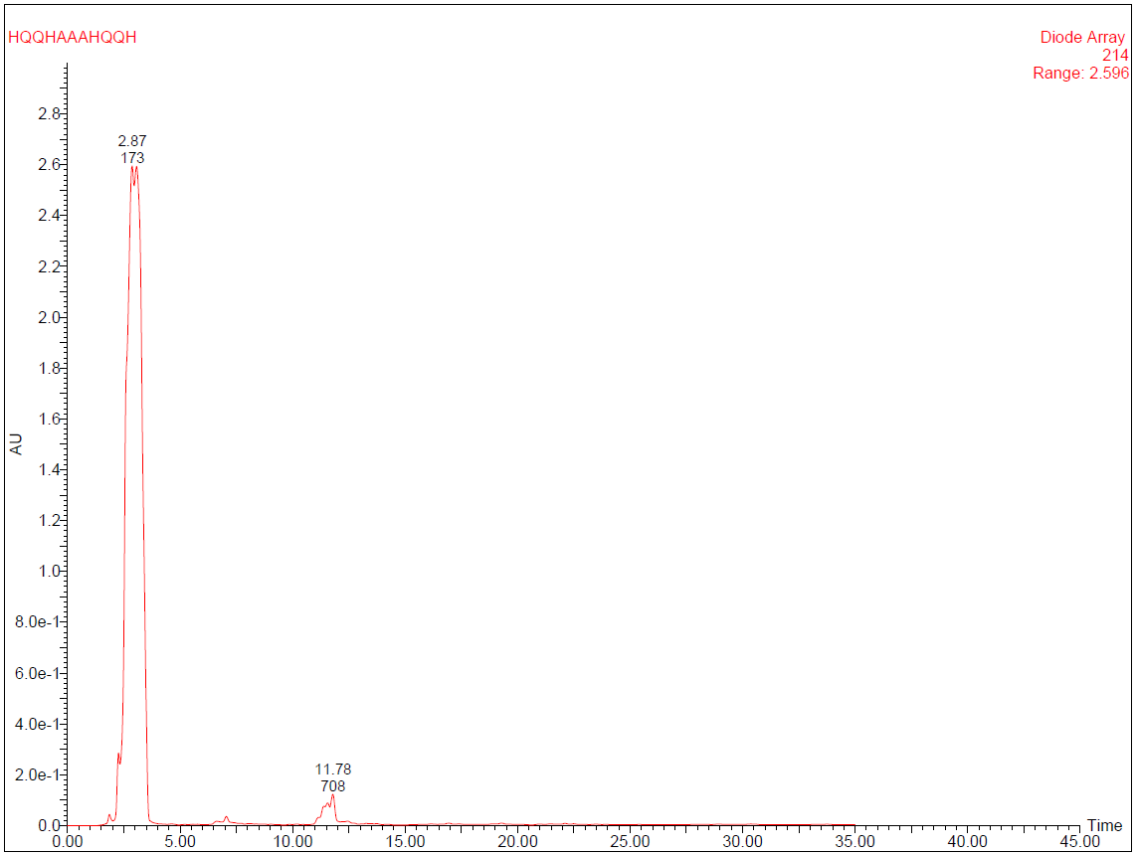

Fig. S8 HPLC chromatogram of HQQHAAAHQQH (M19-B2)

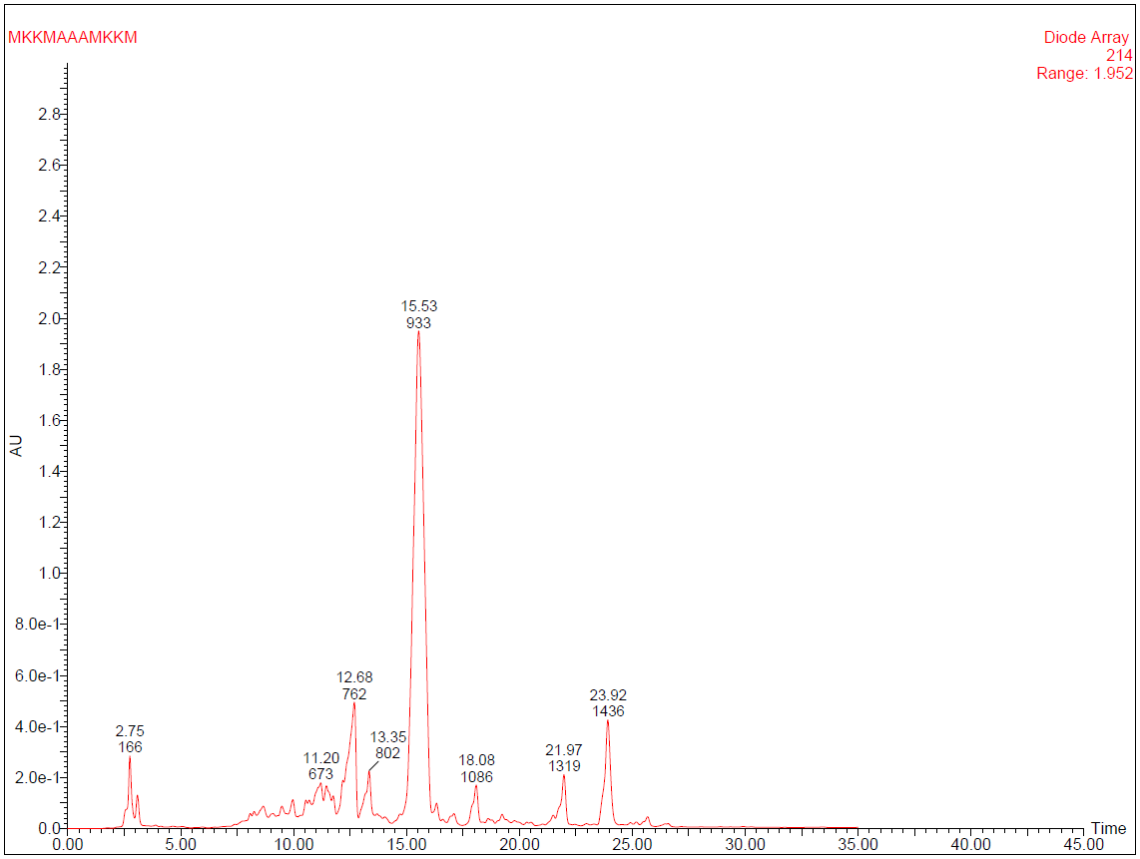

Fig. S9 HPLC chromatogram of MKKMAAAMKKM (M20-B2)

Fig. S10 HPLC chromatogram of MKKMAAAHQQH (M21-B2)

Electrospray ionization mass spectrometry

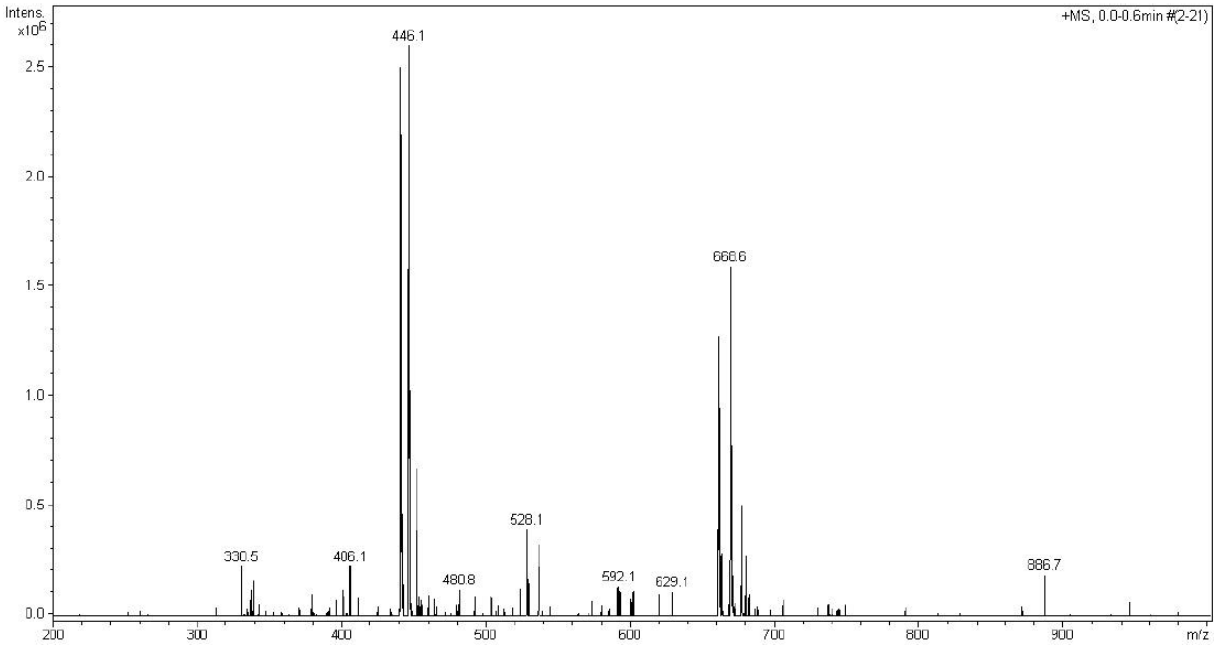

Fig. S11 ESI-MS spectrum of HQAMAAAHRRM (M1-B2). $[M+H]^{+}_{calc}$ (m/z) : 1320.6 ; $[M+2H]^{2+}_{exp}$ (m/z) : 660.6 ; $[M+3H]^{3+}_{exp}$ (m/z) : 440.8 ; $[M+2H]^{2+}_{exp}$ (m/z) : 330.5

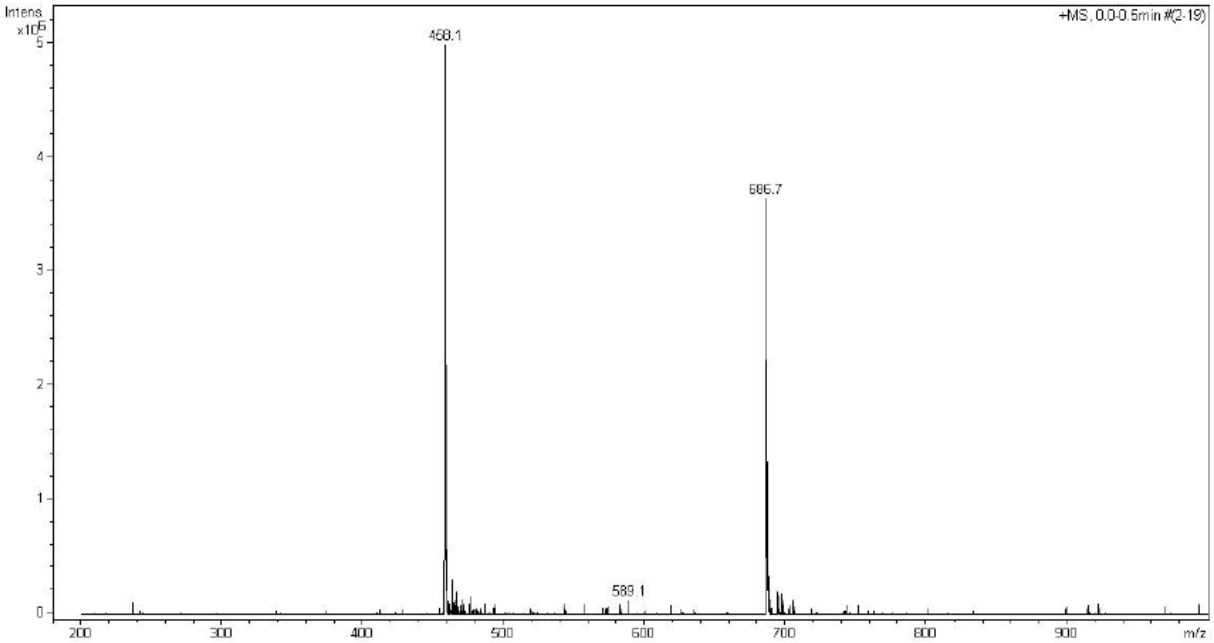

Fig. S12 ESI-MS spectrum of MQAMAEAHRRM (M11-B2). $[M+H]^{+}_{calc}$ (m/z) : 1372.6 ; $[M+2H]^{2+}_{exp}$ (m/z) : 686.7 ; $[M+3H]^{3+}_{exp}$ (m/z) : 458.1

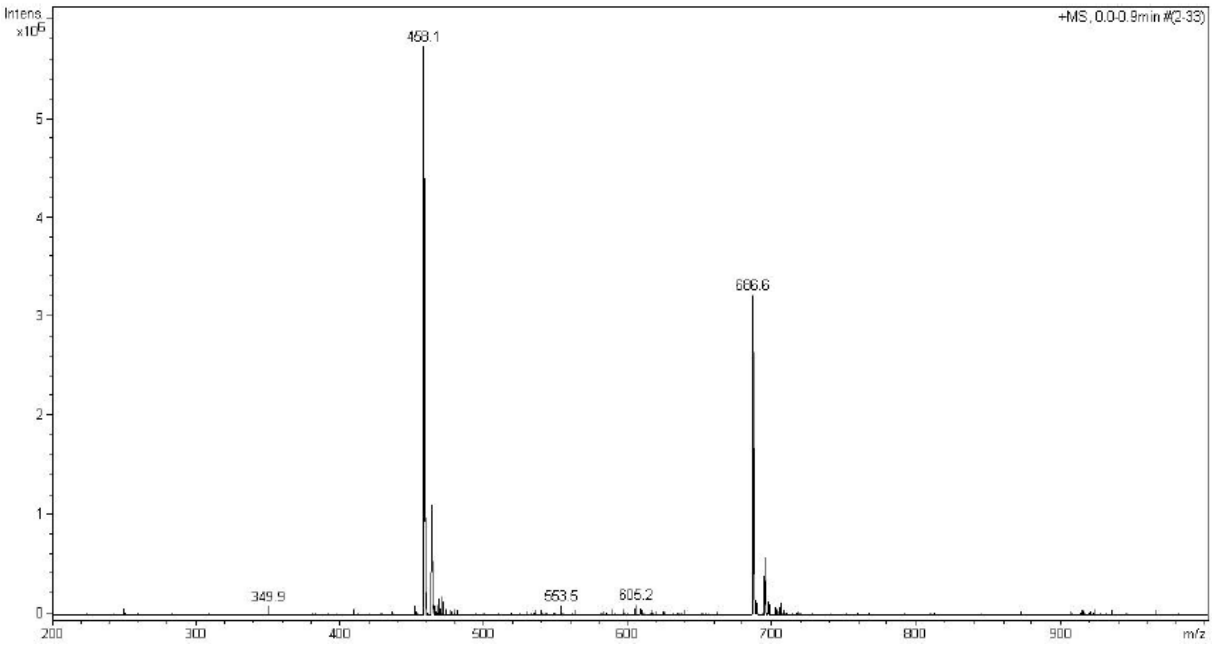

Fig. S13 ESI-MS spectrum of HQAMAEAMRRM (M13-B2). $[M+H]^{+}_{calc}$ (m/z) : 1372.6 ; $[M+2H]^{2+}_{exp}$ (m/z) : 686.6 ; $[M+3H]^{3+}_{exp}$ (m/z) : 458.1

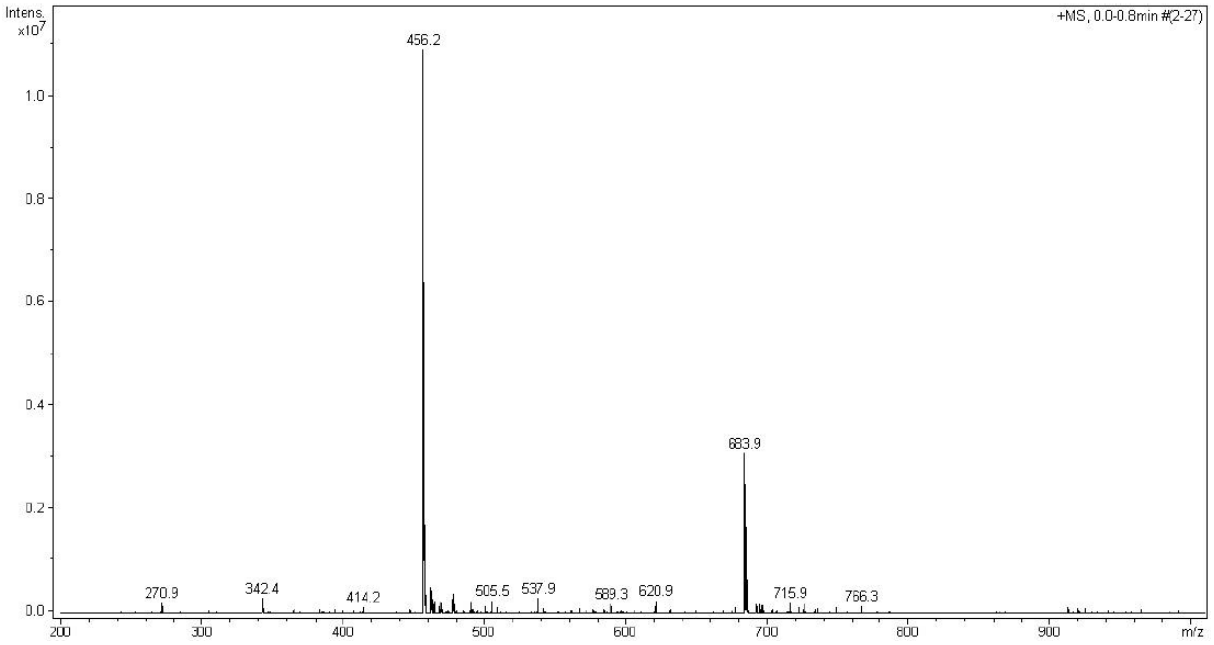

Fig. S14 ESI-MS spectrum of MKKMAEAMKKM (M17-B2). $[M+H]^{+}_{calc}$ (m/z) : 1367.7 ; $[M+2H]^{2+}_{exp}$ (m/z) : 683.9 ; $[M+3H]^{3+}_{exp}$ (m/z) : 456.2 ; $[M+4H]^{4+}_{exp}$ (m/z) : 342.4

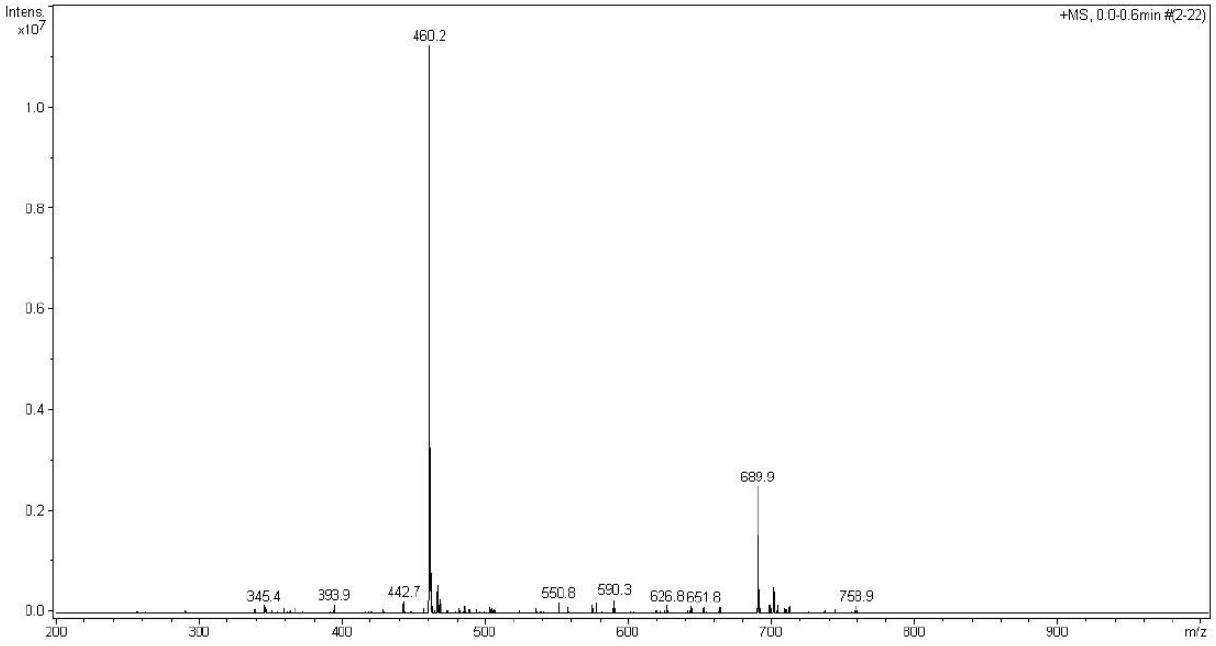

Fig. S15 ESI-MS spectrum of MKKMAEAHQQH (M18-B2). $[M+H]^{+}_{calc}$ (m/z) : 1379.7 ; $[M+2H]^{2+}_{exp}$ (m/z) : 689.9 ; $[M+3H]^{3+}_{exp}$ (m/z) : 460.2 ; $[M+4H]^{4+}_{exp}$ (m/z) : 345.4

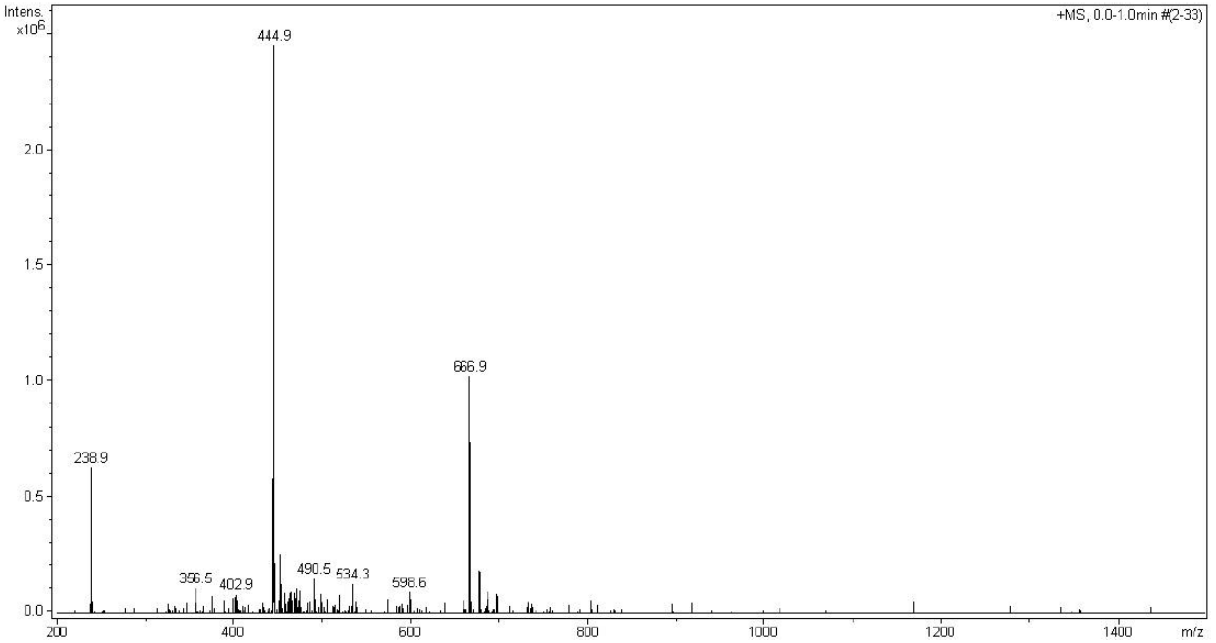

Fig. S16 ESI-MS spectrum of HQQHAAAHQQH (M19-B2). $[M+H]^{+}_{calc}$ (m/z) : 1332.6 ; $[M+2H]^{2+}_{exp}$ (m/z) : 666.9 ; $[M+3H]^{3+}_{exp}$ (m/z) : 444.9 ; $[M+4Na]^{4+}_{exp}$ (m/z) : 356.5

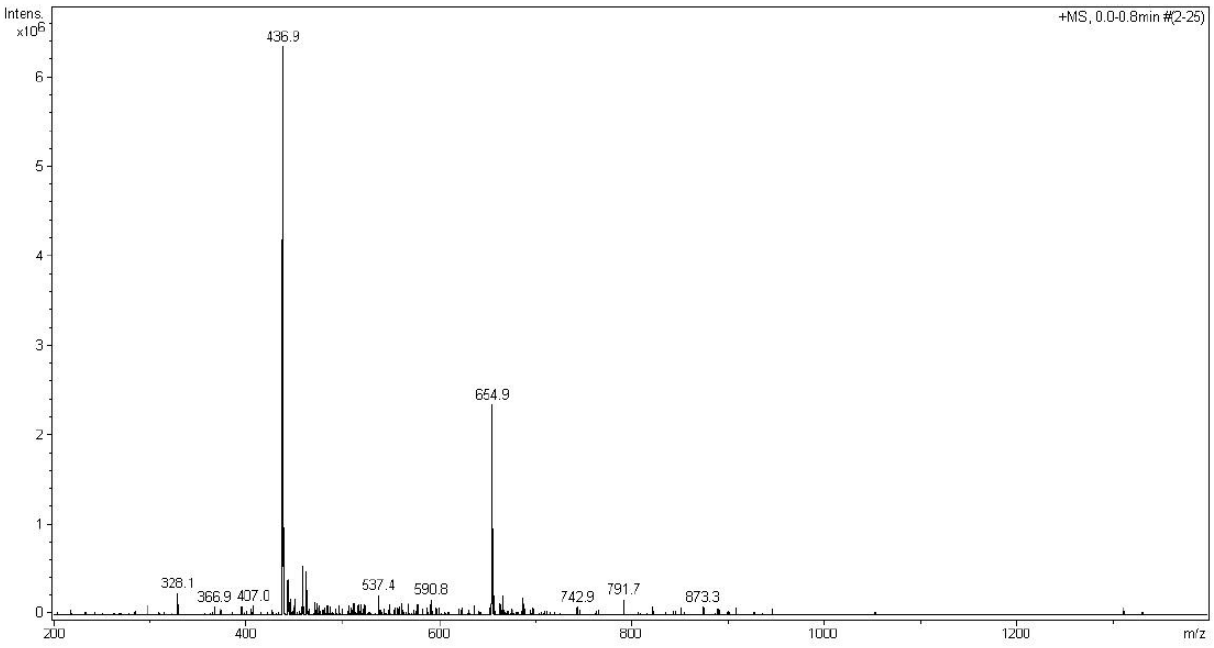

Fig. S17 ESI-MS spectrum of MKKMAAAMKKM (M20-B2). $[M+H]^{+}_{calc}$ (m/z) : 1308.7 ; $[M+2H]^{2+}_{exp}$ (m/z) : 654.9 ; $[M+3H]^{3+}_{exp}$ (m/z) : 436.9 ; $[M+4H]^{4+}_{exp}$ (m/z) : 328.1

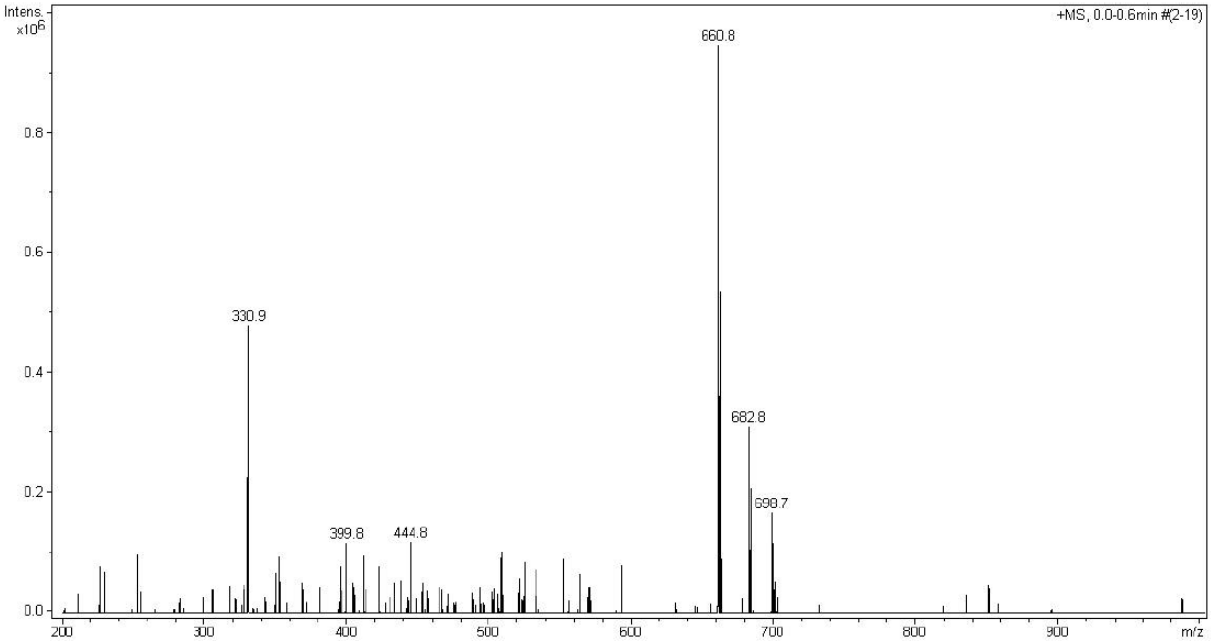

Fig. S18 ESI-MS spectrum of MKKMAAAHQQH (M21-B2). $[M+H]^{+}_{calc}$ (m/z) : 1320.7 ; $[M+2H]^{2+}_{exp}$ (m/z) : 660.8 ; $[M+H+Na]^{2+}_{exp}$ (m/z) : 682.8 ; $[M+4H]^{4+}_{exp}$ (m/z) : 330.9

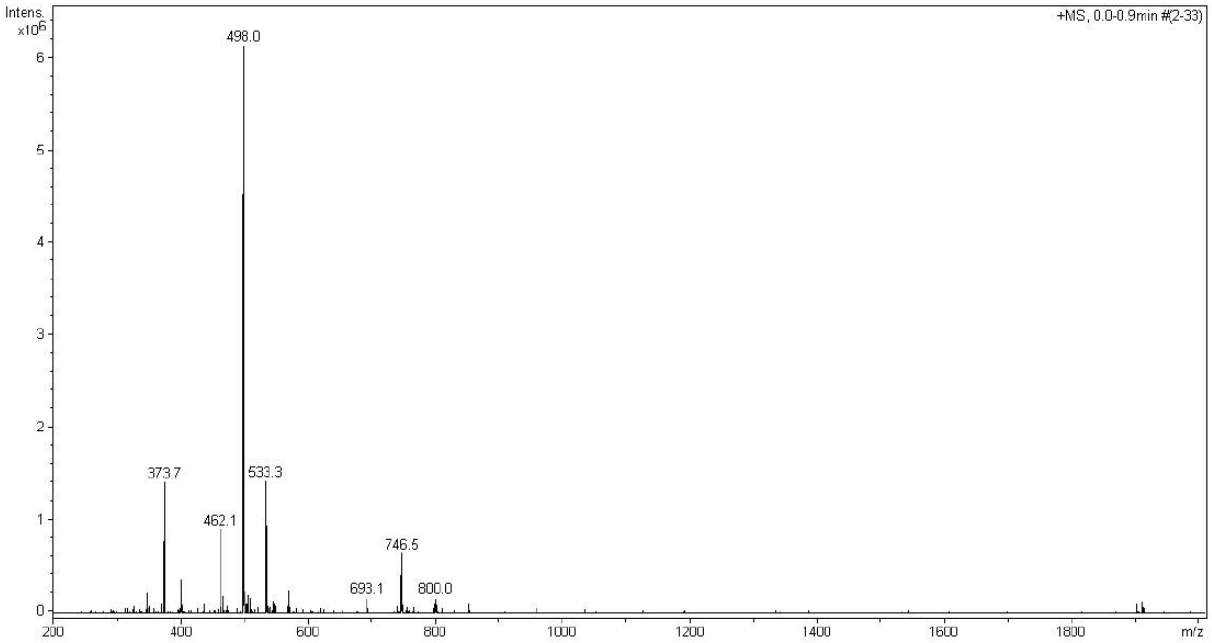

Fig. S19 ESI-MS spectrum of HQAHAEAHRRM (M10-B2) in the presence of excess Ag^+. $[M+H]^+_{calc}$ (m/z) : 1390.7 ; $[M+2Ag]^{2+}_{exp}$ (m/z) : 800.0 ; $[M+Ag+H]^{2+}_{exp}$ (m/z) : 746.5 ; $[M+2Ag+H]^{3+}_{exp}$ (m/z) : 533.3 ; $[M+Ag+2H]^{3+}_{exp}$ (m/z) : 498.0 ; $[M+Ag+3H]^{4+}_{exp}$ (m/z) : 373.7.

CD titrations

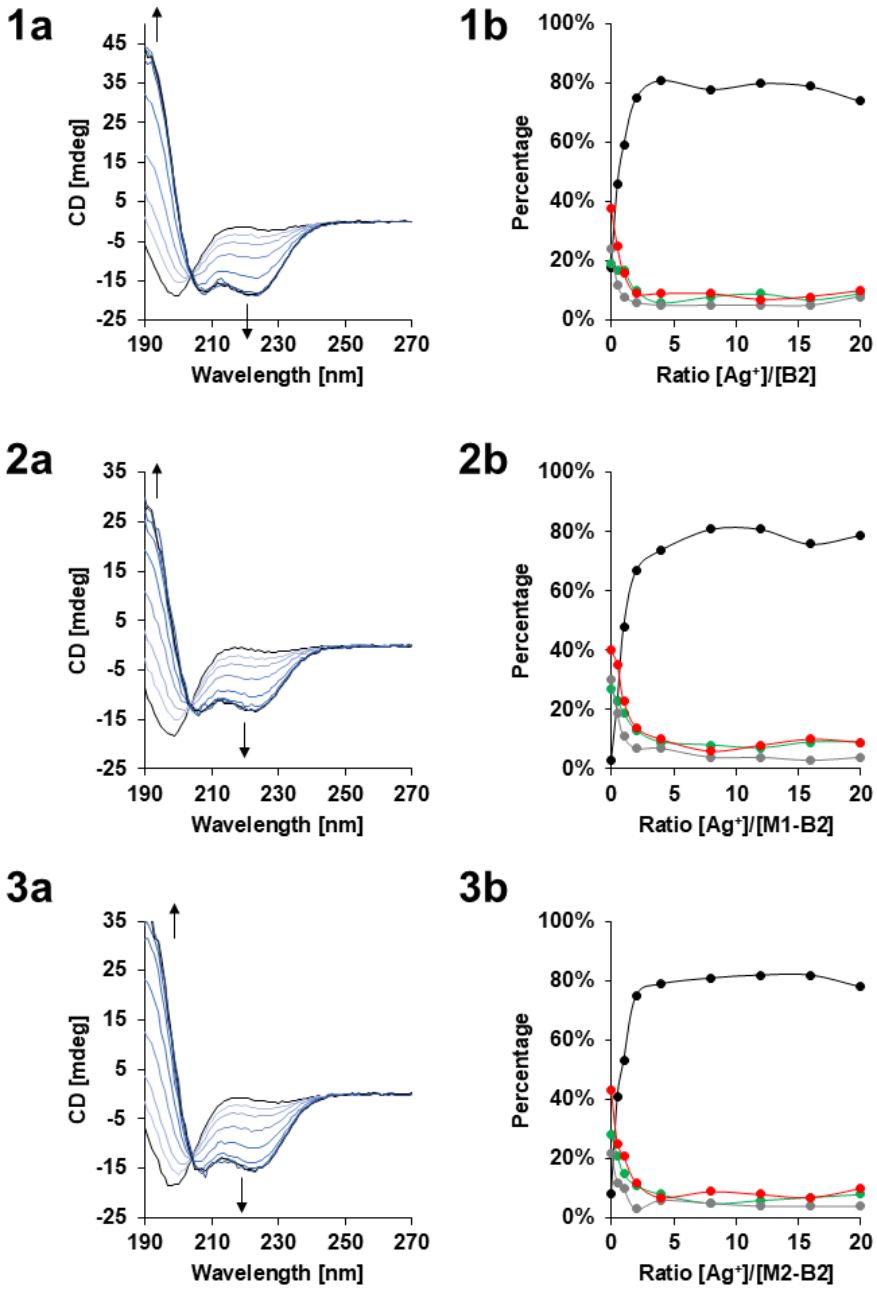

Fig. S20 (a) CD spectra of peptide at $1 \cdot 10^{-5}$ M (1: B2, 2: M1-B2, and 3: M2-B2) upon titration with Ag^+ (0 to 20 equivalents) at 25°C, showing the evolution of secondary structure upon Ag^+ binding. (b) Corresponding secondary structure compositions have been calculated using the DichroWeb server with the CDSSTR algorithm.[5–7] Structural elements are designated by specific colors: α-helix (black), β-strand (green), turn (gray, and unordered (red).

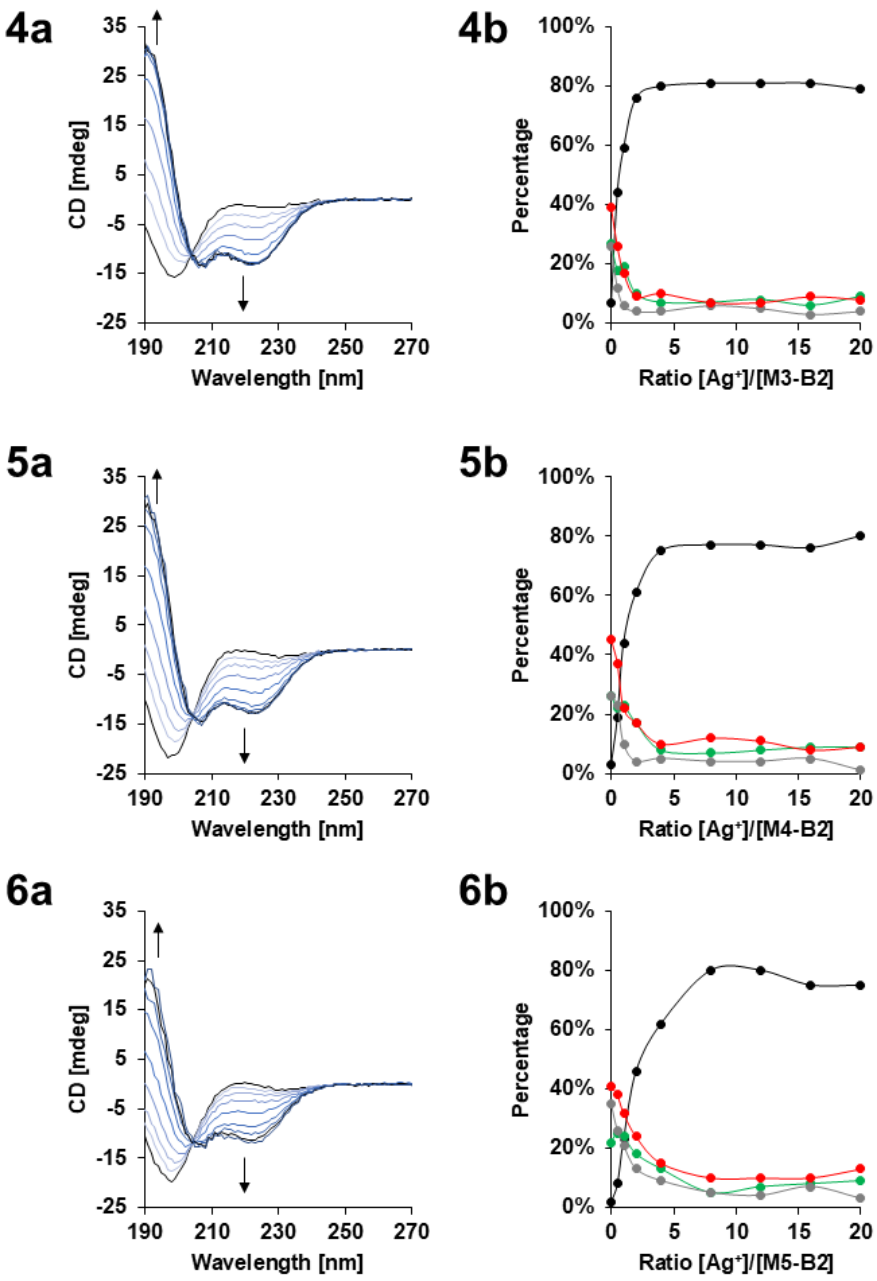

Fig. S21 (a) CD spectra of peptide at $1 \cdot 10^{-5}$ M (4: M3-B2, 5: M4-B2, and 6: M5-B2) upon titration with Ag^+ (0 to 20 equivalents) at 25°C, showing the evolution of secondary structure upon Ag^+ binding. (b) Corresponding secondary structure compositions have been calculated using the DichroWeb server with the CDSSTR algorithm.[5–7] Structural elements are designated by specific colors: α-helix (black), β-strand (green), turn (gray, and unordered (red).

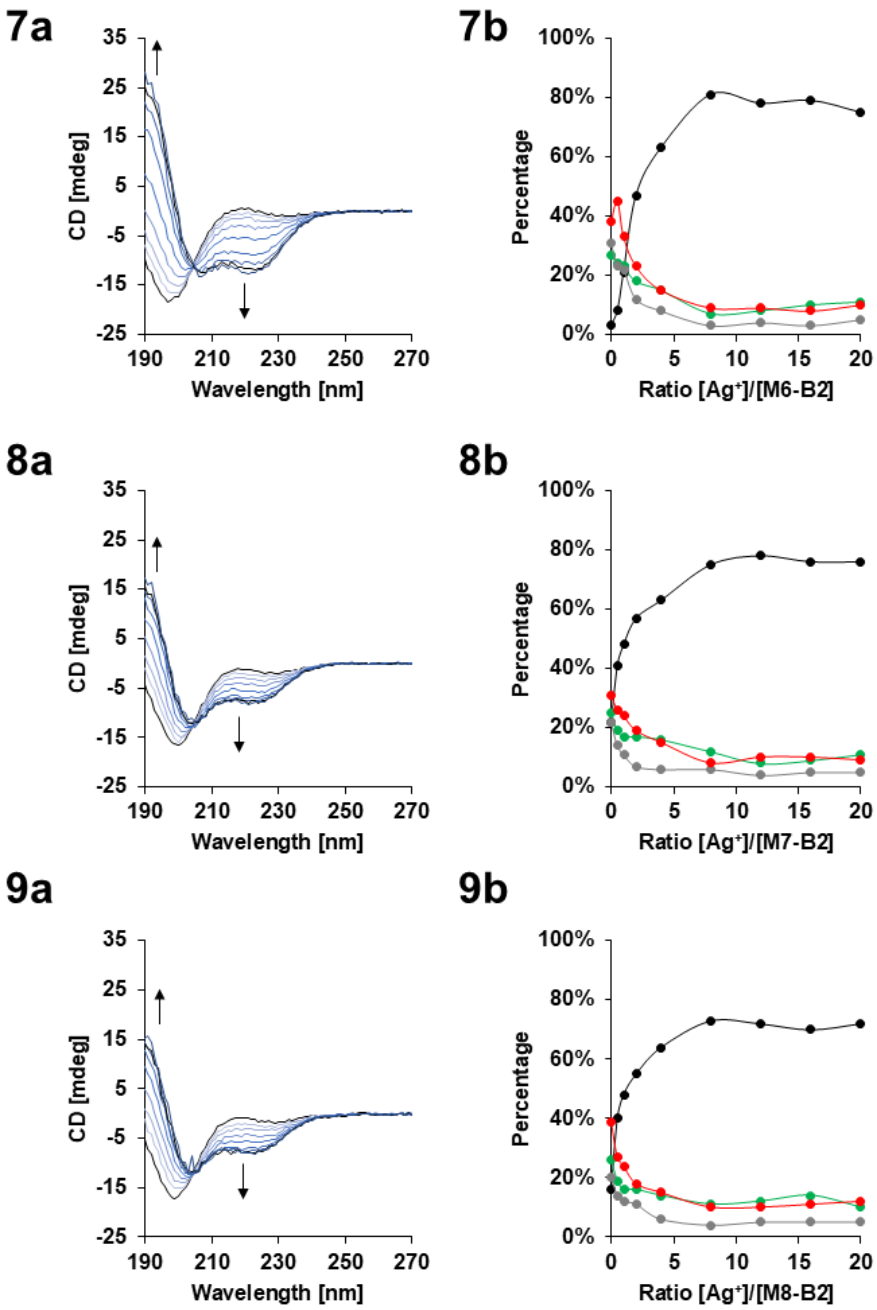

Fig. S22 (a) CD spectra of peptide at $1 \cdot 10^{-5}$ M (7: M6-B2, 8: M7-B2, and 9: M8-B2) upon titration with Ag^+ (0 to 20 equivalents) at 25°C, showing the evolution of secondary structure upon Ag^+ binding. (b) Corresponding secondary structure compositions have been calculated using the DichroWeb server with the CDSSTR algorithm.[5–7] Structural elements are designated by specific colors: α-helix (black), β-strand (green), turn (gray, and unordered (red).

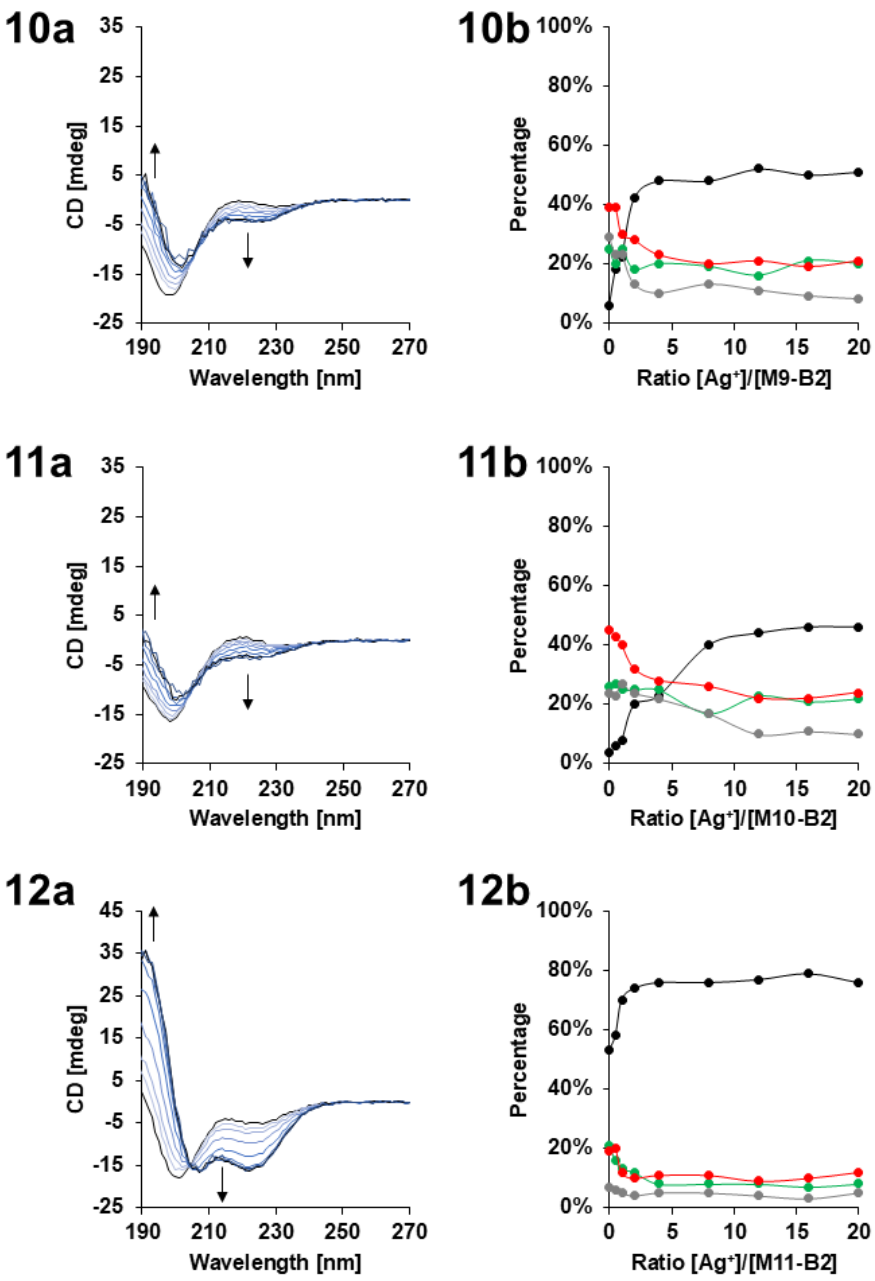

Fig. S23 (a) CD spectra of peptide at $1 \cdot 10^{-5}$ M (10: M9-B2, 11: M10-B2, and 12: M11-B2) upon titration with Ag^+ (0 to 20 equivalents) at 25°C, showing the evolution of secondary structure upon Ag^+ binding. (b) Corresponding secondary structure compositions have been calculated using the DichroWeb server with the CDSSTR algorithm.[5–7] Structural elements are designated by specific colors: α-helix (black), β-strand (green), turn (gray, and unordered (red).

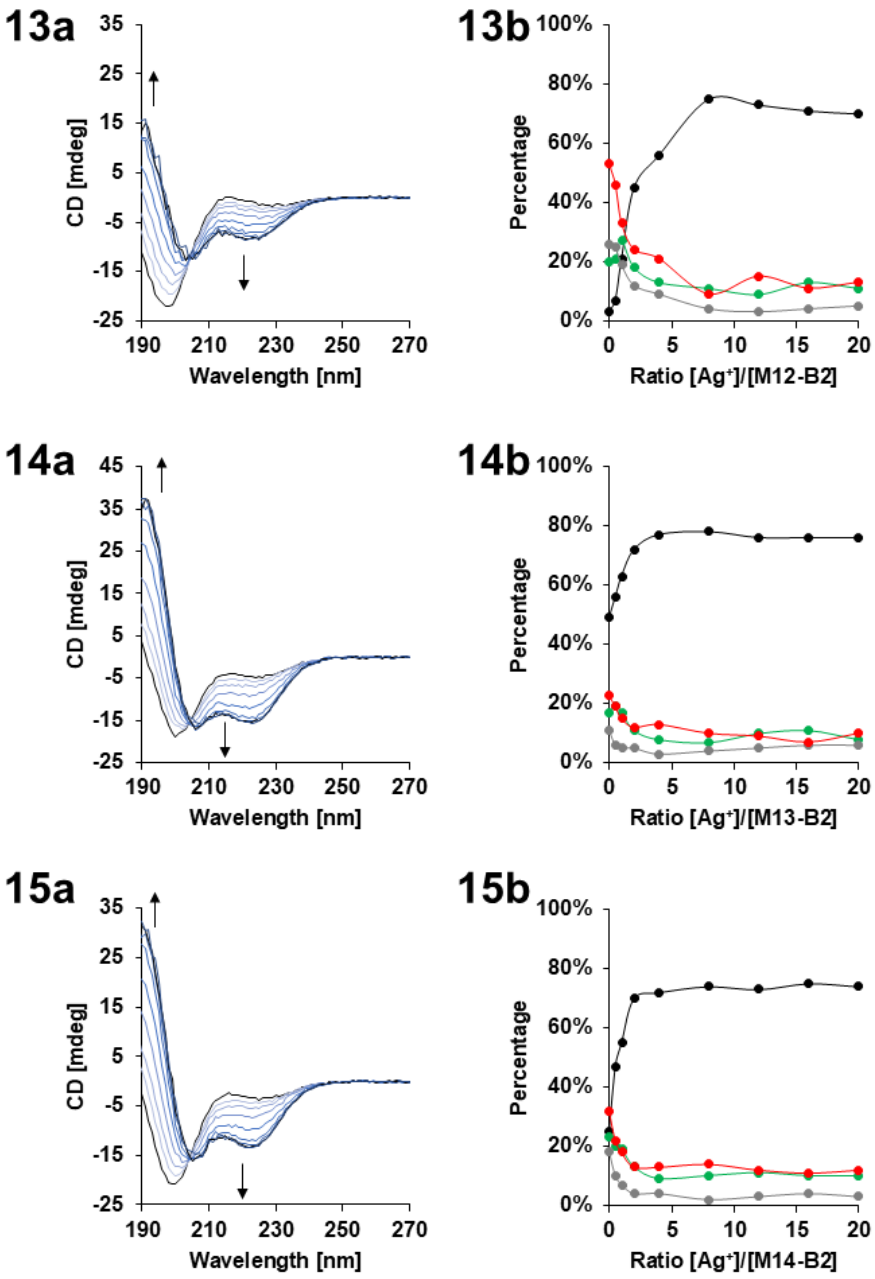

Fig. S24 (a) CD spectra of peptide at $1 \cdot 10^{-5}$ M (13: M12-B2, 14: M13-B2, and 15: M14-B2) upon titration with Ag^+ (0 to 20 equivalents) at 25°C, showing the evolution of secondary structure upon Ag^+ binding. (b) Corresponding secondary structure compositions have been calculated using the DichroWeb server with the CDSSTR algorithm.[5–7] Structural elements are designated by specific colors: α-helix (black), β-strand (green), turn (gray, and unordered (red).

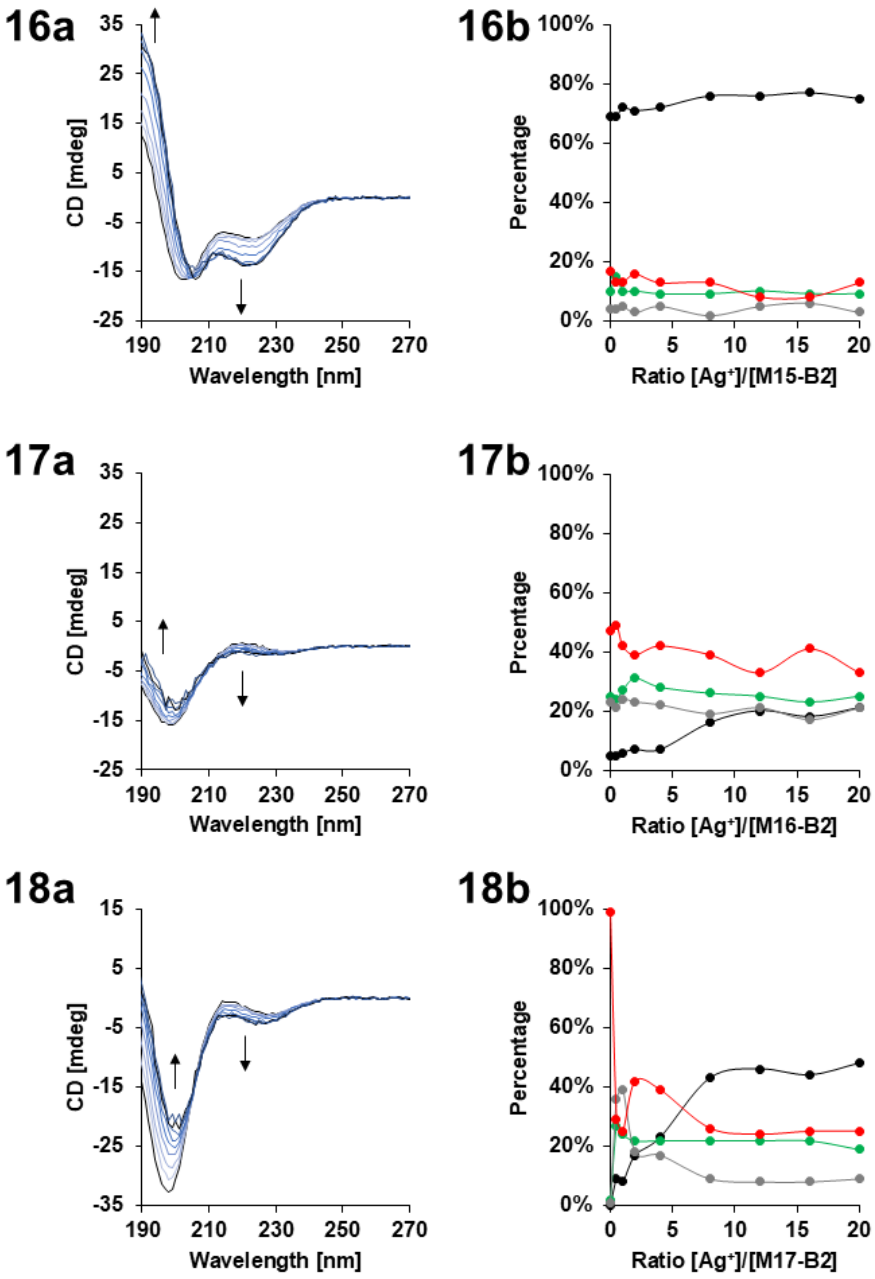

Fig. S25 (a) CD spectra of peptide at 1·10-5 M (16: M15-B2, 17: M16-B2, and 18: M17-B2) upon titration with Ag+ (0 to 20 equivalents) at 25°C, showing the evolution of secondary structure upon Ag+ binding. (b) Corresponding secondary structure compositions have been calculated using the DichroWeb server with the CDSSTR algorithm.5–7 Structural elements are designated by specific colors: α-helix (black), β-strand (green), turn (gray, and unordered (red).

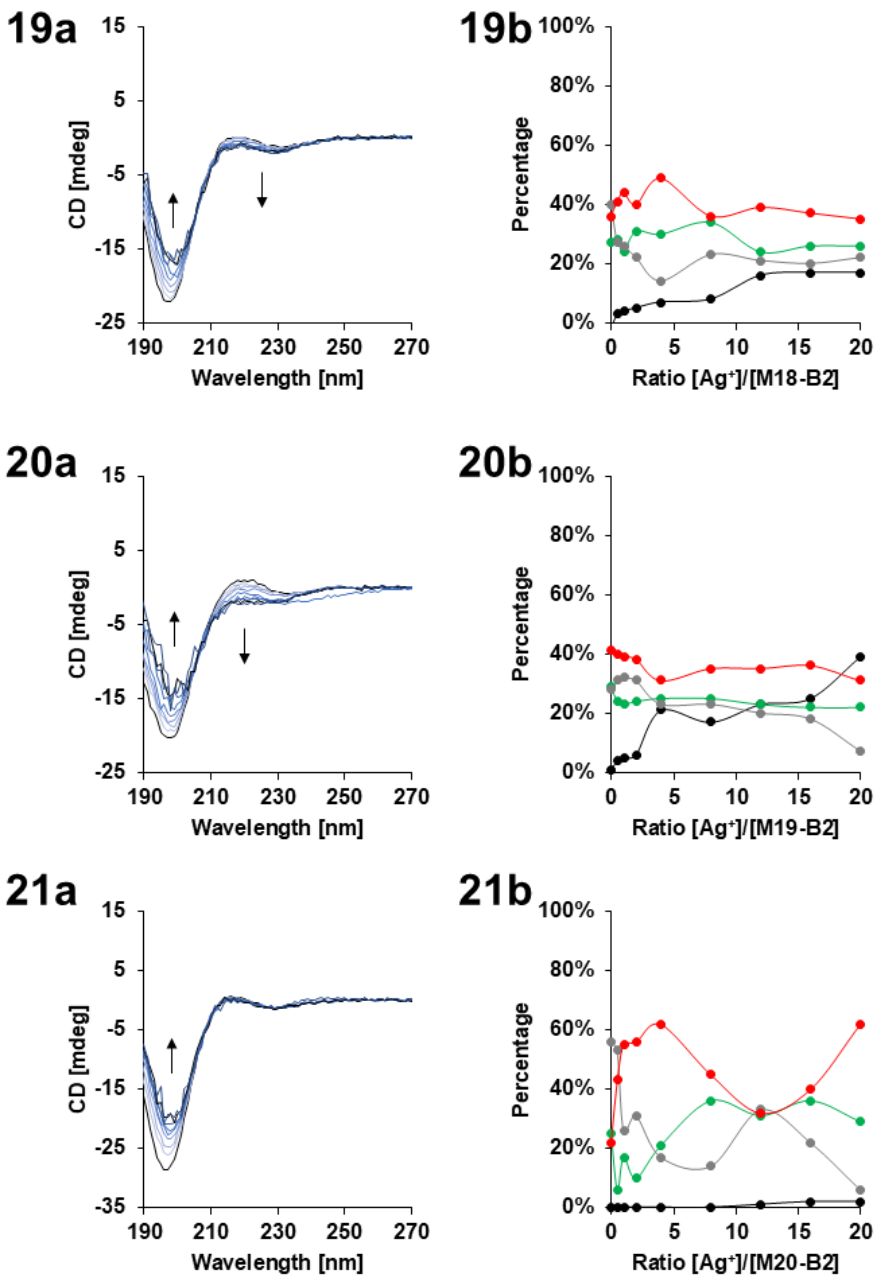

Fig. S26 (a) CD spectra of peptide at $1 \cdot 10^{-5}$ M (19: M18-B2, 20: M19-B2, and 21: M20-B2) upon titration with Ag^+ (0 to 20 equivalents) at 25°C, showing the evolution of secondary structure upon Ag^+ binding. (b) Corresponding secondary structure compositions have been calculated using the DichroWeb server with the CDSSTR algorithm.[5–7] Structural elements are designated by specific colors: α-helix (black), β-strand (green), turn (gray, and unordered (red).

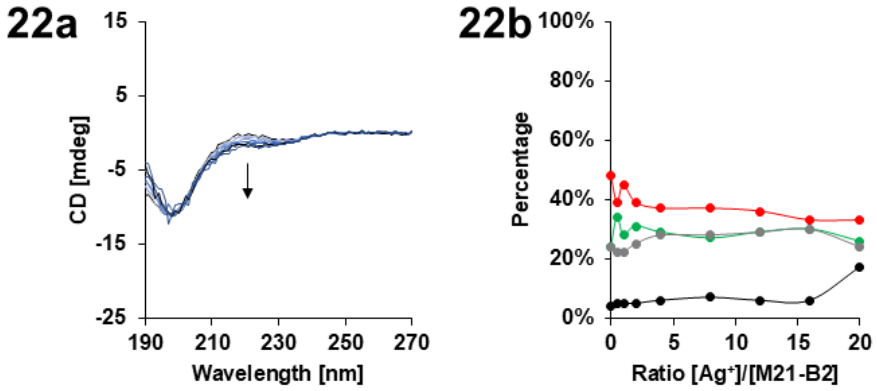

Fig. S27 (a) CD spectra of peptide at $1 \cdot 10^{-5}$ M (22: M21-B2) upon titration with Ag^+ (0 to 20 equivalents) at 25°C, showing the evolution of secondary structure upon Ag^+ binding. (b) Corresponding secondary structure compositions have been calculated using the DichroWeb server with the CDSSTR algorithm.[5–7] Structural elements are designated by specific colors: α-helix (black), β-strand (green), turn (gray, and unordered (red).

Fluorescence titrations

HQAMAEAHRRM (B2)

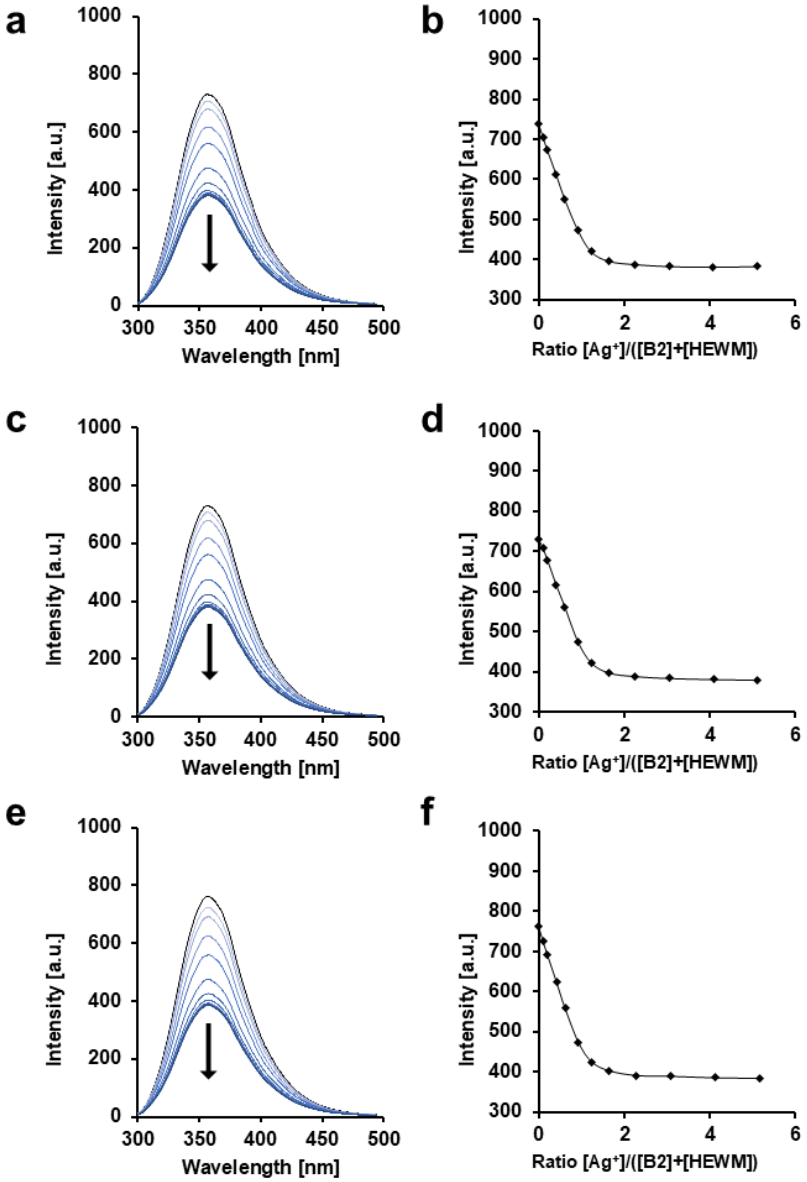

Fig. S28 HQAMAEAHRRM (B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

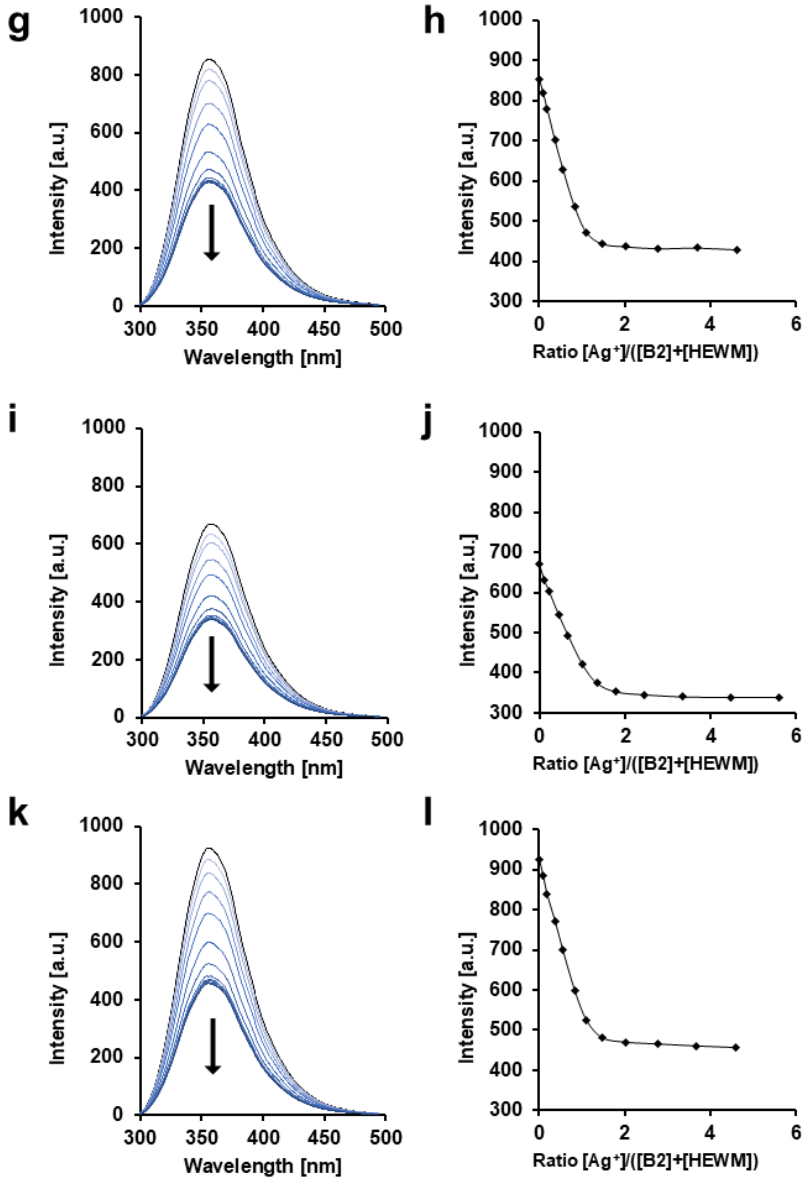

Fig. S29 HQAMAEAHRRM (B2) / HEWM competition titrations, both at $2 \cdot 10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of B2 ($2 \cdot 10^{-5}$ M) in competition with HEWM probe ($2 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S2 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of HQAMAEAHRRM peptide

Model	$1 \cdot 10^{-5}$ M[a]		$2 \cdot 10^{-5}$ M[a]	
HQAMAEAHRRM (B2)	$\log(K_{b\text{-}1}) = 6.51 \pm 0.02$	$\log(K_{b\text{-}2}) = 5.52 \pm 0.05$	$\log(K_{b\text{-}1}) = 6.40 \pm 0.02$	$\log(K_{b\text{-}2}) = 5.09 \pm 0.06$
	$\log(K_{b\text{-}1}) = 6.68 \pm 0.02$	$\log(K_{b\text{-}2}) = 5.48 \pm 0.06$	$\log(K_{b\text{-}1}) = 6.49 \pm 0.04$	$\log(K_{b\text{-}2}) = 5.75 \pm 0.06$
	$\log(K_{b\text{-}1}) = 6.52 \pm 0.02$	$\log(K_{b\text{-}2}) = 5.41 \pm 0.05$	$\log(K_{b\text{-}1}) = 6.47 \pm 0.04$	$\log(K_{b\text{-}2}) = 5.53 \pm 0.10$
Average	$\log(K_{b\text{-}1}) = 6.51 \pm 0.09$		$\log(K_{b\text{-}2}) = 5.46 \pm 0.22$	

[a] The values correspond to the peptide and probe concentrations.

HQAMAAAHRRM (M1-B2)

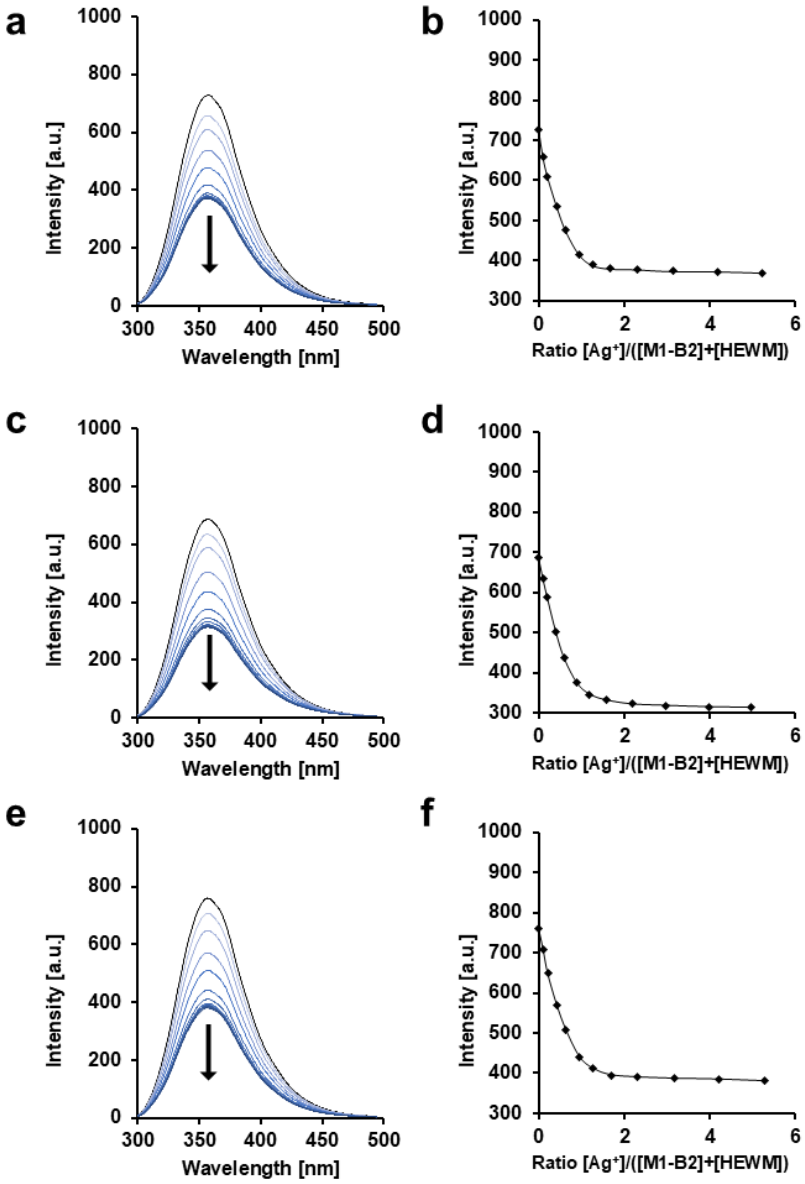

Fig. S30 HQAMAAAHRRM (M1-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M1-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

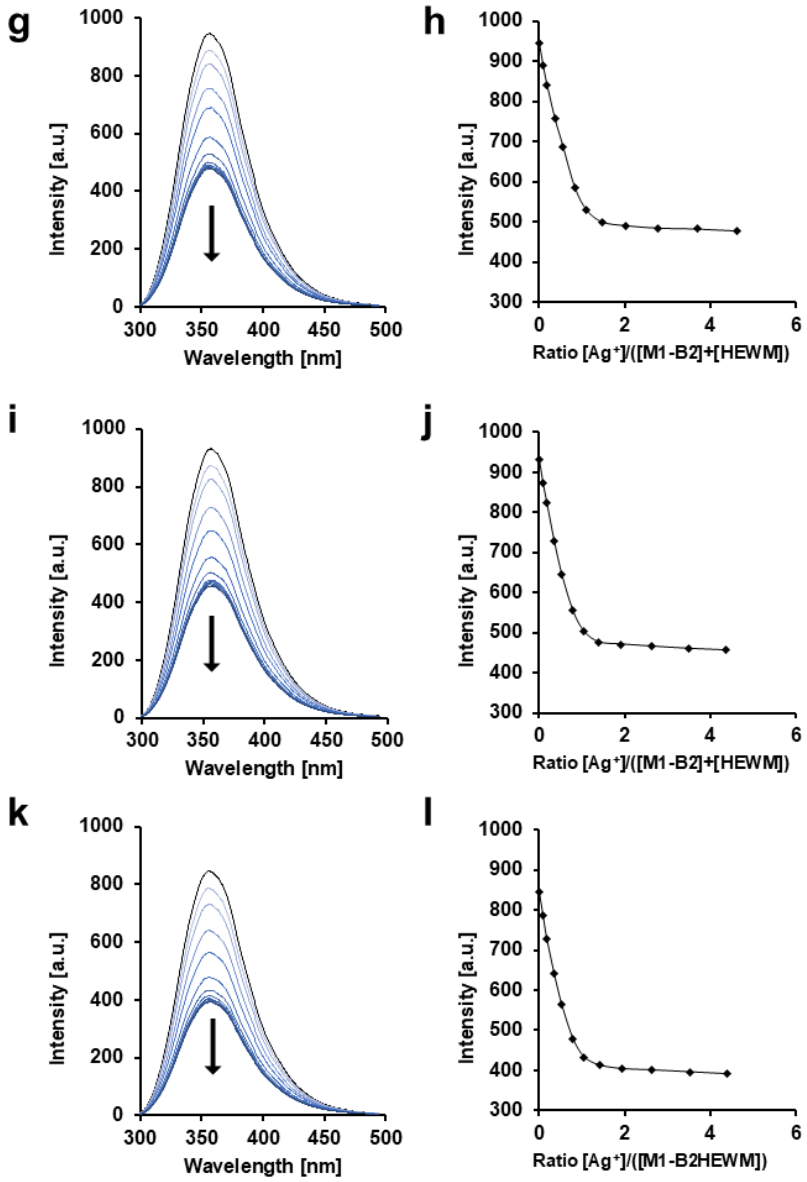

Fig. S31 HQAMAAAHRRM (M1-B2) / HEWM competition titrations, both at $2{\cdot}10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M1-B2 ($2{\cdot}10^{-5}$ M) in competition with HEWM probe ($2{\cdot}10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S3 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of HQAMAAAHRRM peptide

Model	$1{\cdot}10^{-5}$ M[a]		$2{\cdot}10^{-5}$ M[a]	
HQAMAAAHRRM (M1-B2)	$\log(K_{b\text{-}1}) = 5.87\pm0.10$	$\log(K_{b\text{-}2}) = 5.28\pm0.29$	$\log(K_{b\text{-}1}) = 6.21\pm0.05$	$\log(K_{b\text{-}2}) = 5.32\pm0.16$
	$\log(K_{b\text{-}1}) = 6.00\pm0.02$	$\log(K_{b\text{-}2}) = 5.04\pm0.09$	$\log(K_{b\text{-}1}) = 6.03\pm0.02$	$\log(K_{b\text{-}2}) = 4.95\pm0.08$
	$\log(K_{b\text{-}1}) = 5.98\pm0.06$	$\log(K_{b\text{-}2}) = 5.43\pm0.16$	$\log(K_{b\text{-}1}) = 5.89\pm0.04$	$\log(K_{b\text{-}2}) = 5.06\pm0.18$
Average	$\log(K_{b\text{-}1}) = 6.00 \pm 0.12$		$\log(K_{b\text{-}2}) = 5.18 \pm 0.19$	

[a] The values correspond to the peptide and probe concentrations.

HQQMAEAHRRM (M2-B2)

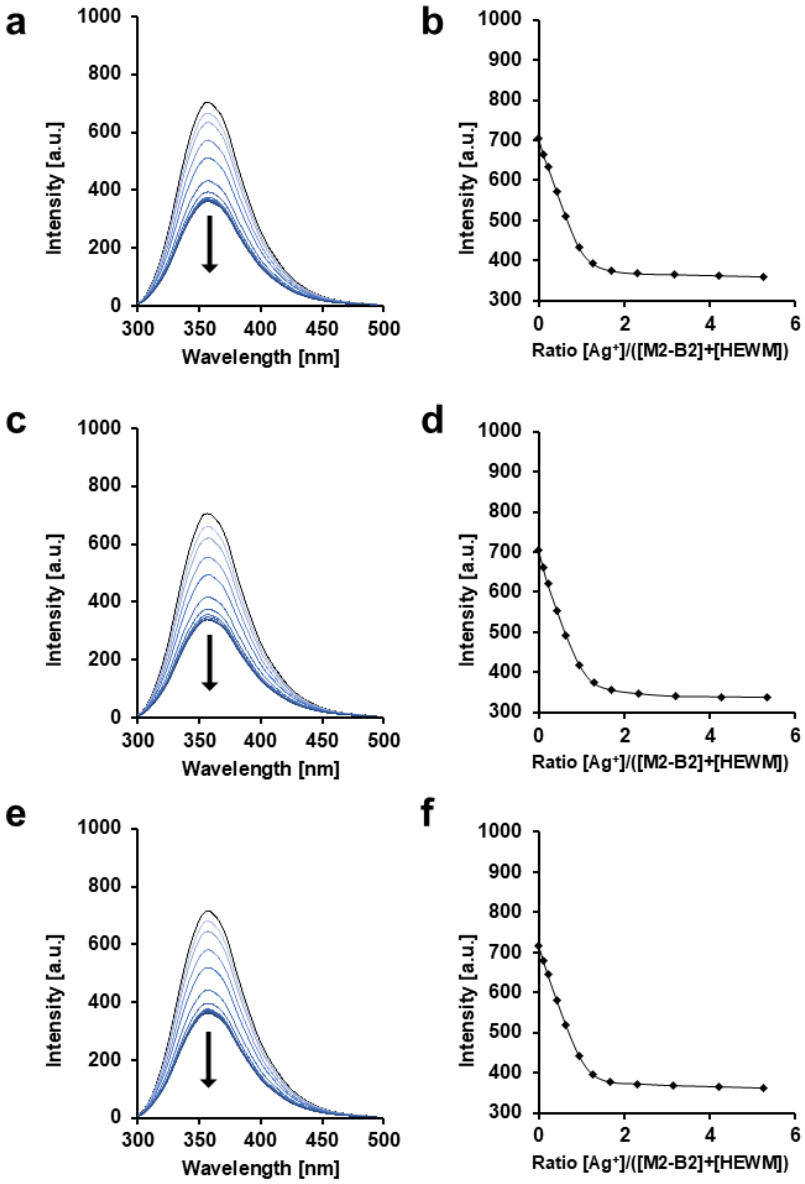

Fig. S32 HQQMAEAHRRM (M2-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M2-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

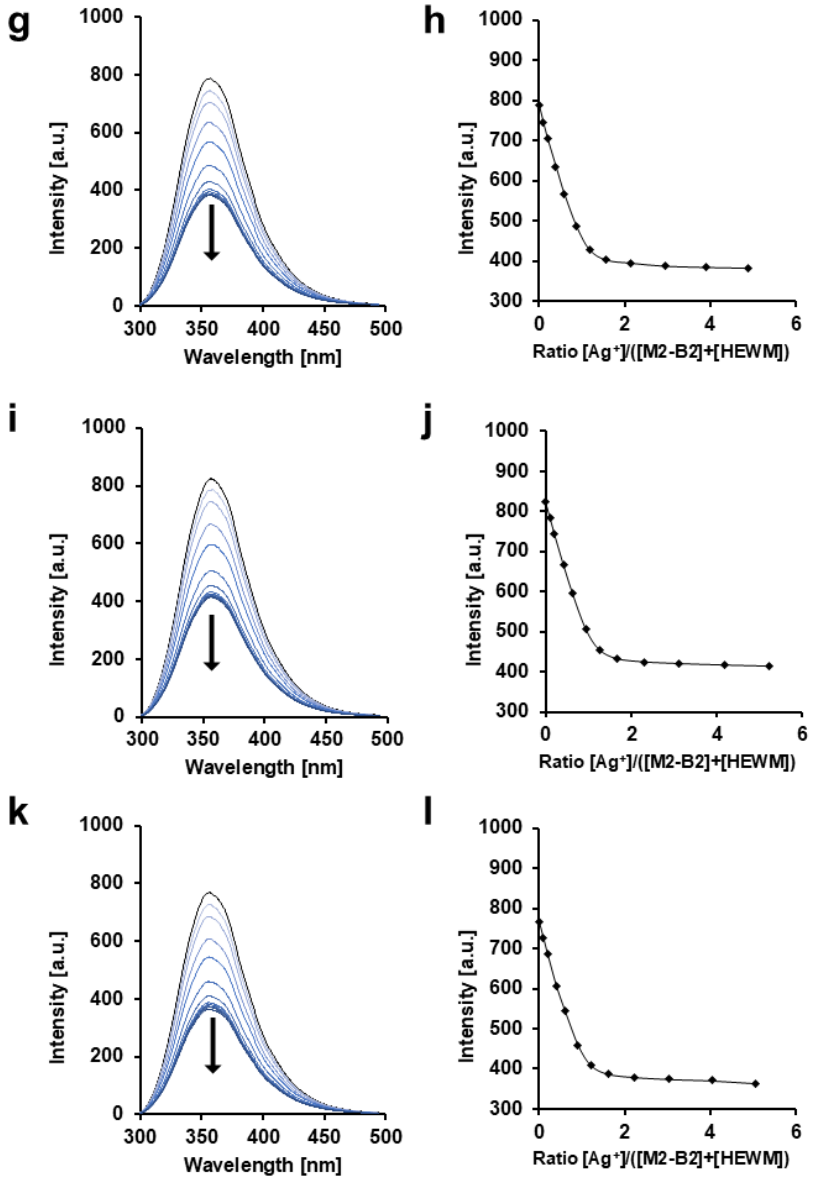

Fig. S33 HQQMAEAHRRM (M2-B2) / HEWM competition titrations, both at $2{\cdot}10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M2-B2 ($2{\cdot}10^{-5}$ M) in competition with HEWM probe ($2{\cdot}10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S4 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of HQQMAEAHRRM peptide

Model	$1{\cdot}10^{-5}$ M[a]		$2{\cdot}10^{-5}$ M[a]	
HQQMAEAHRRM (M2-B2)	$\log(K_{b\text{-}1})$ = 6.48±0.03	$\log(K_{b\text{-}2})$ = 5.31±0.09	$\log(K_{b\text{-}1})$ = 6.37±0.02	$\log(K_{b\text{-}2})$ = 5.45±0.05
	$\log(K_{b\text{-}1})$ = 6.33±0.04	$\log(K_{b\text{-}2})$ = 5.58±0.09	$\log(K_{b\text{-}1})$ = 6.44±0.01	$\log(K_{b\text{-}2})$ = 5.38±0.02
	$\log(K_{b\text{-}1})$ = 6.46±0.03	$\log(K_{b\text{-}2})$ = 5.48±0.08	$\log(K_{b\text{-}1})$ = 6.34±0.03	$\log(K_{b\text{-}2})$ = 5.42±0.08
Average	$\log(K_{b\text{-}1})$ = 6.40 ± 0.06		$\log(K_{b\text{-}2})$ = 5.44 ± 0.09	

[a] The values correspond to the peptide and probe concentrations.

HQAMAEAHKRM (M3-B2)

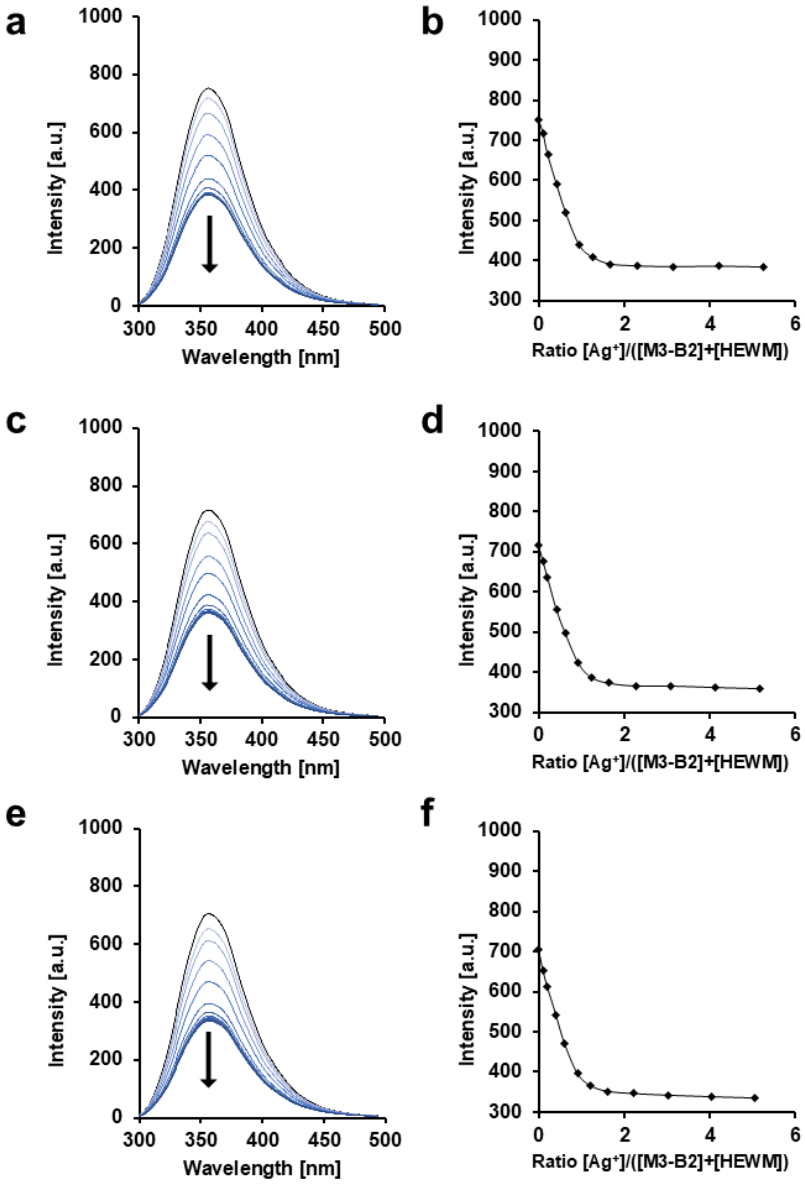

Fig. S34 HQAMAEAHKRM (M3-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M3-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

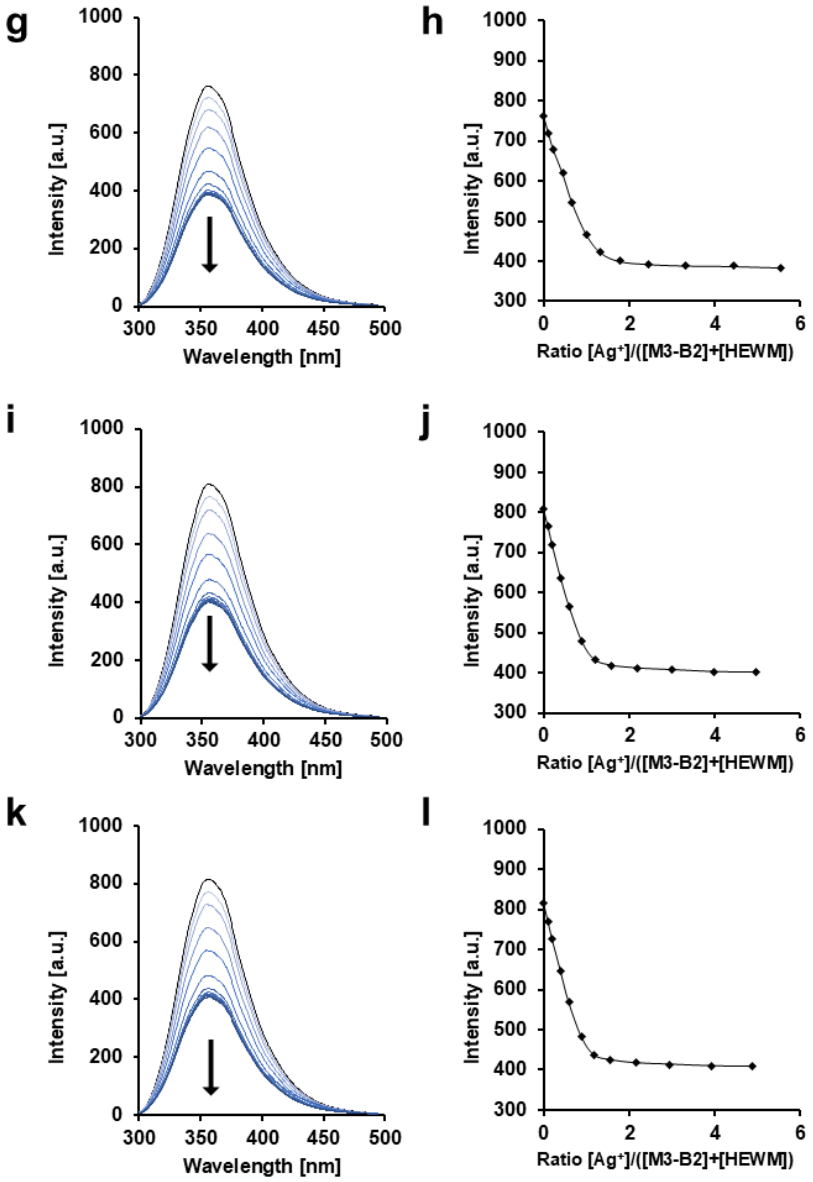

Fig. S35 HQAMAEAHKRM (M3-B2) / HEWM competition titrations, both at $2 \cdot 10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M3-B2 ($2 \cdot 10^{-5}$ M) in competition with HEWM probe ($2 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S5 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of HQAMAEAHKRM peptide

Model	$1 \cdot 10^{-5}$ M[a]		$2 \cdot 10^{-5}$ M[a]	
HQAMAEAHKRM (M3-B2)	$\log(K_{b\text{-}1}) = 6.29 \pm 0.04$	$\log(K_{b\text{-}2}) = 4.96 \pm 0.21$	$\log(K_{b\text{-}1}) = 6.48 \pm 0.05$	$\log(K_{b\text{-}2}) = 5.51 \pm 0.11$
	$\log(K_{b\text{-}1}) = 6.25 \pm 0.03$	$\log(K_{b\text{-}2}) = 5.15 \pm 0.10$	$\log(K_{b\text{-}1}) = 6.27 \pm 0.01$	$\log(K_{b\text{-}2}) = 5.04 \pm 0.04$
	$\log(K_{b\text{-}1}) = 6.21 \pm 0.04$	$\log(K_{b\text{-}2}) = 5.03 \pm 0.24$	$\log(K_{b\text{-}1}) = 6.26 \pm 0.02$	$\log(K_{b\text{-}2}) = 4.84 \pm 0.10$
Average	$\log(K_{b\text{-}1}) = 6.29 \pm 0.09$		$\log(K_{b\text{-}2}) = 5.09 \pm 0.23$	

[a] The values correspond to the peptide and probe concentrations.

HQQMAEAHKKM (M4-B2)

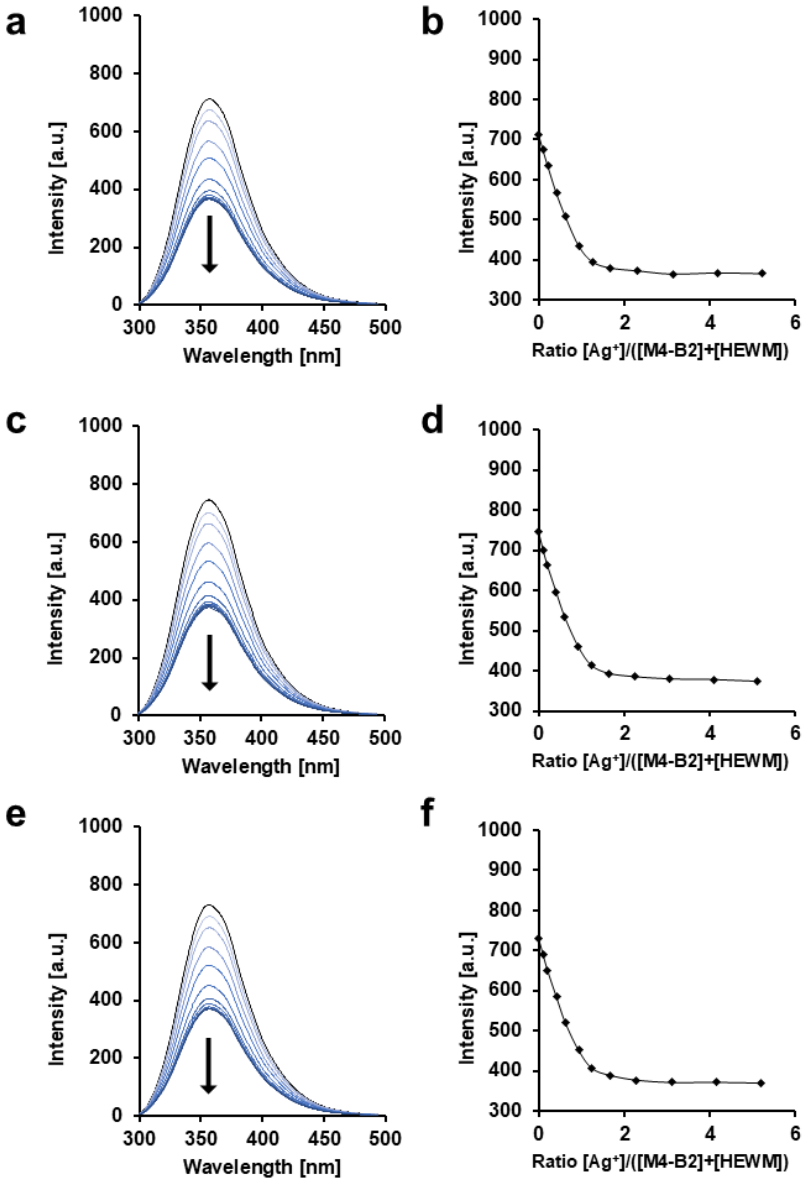

Fig. S36 HQQMAEAHKKM (M4-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M4-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

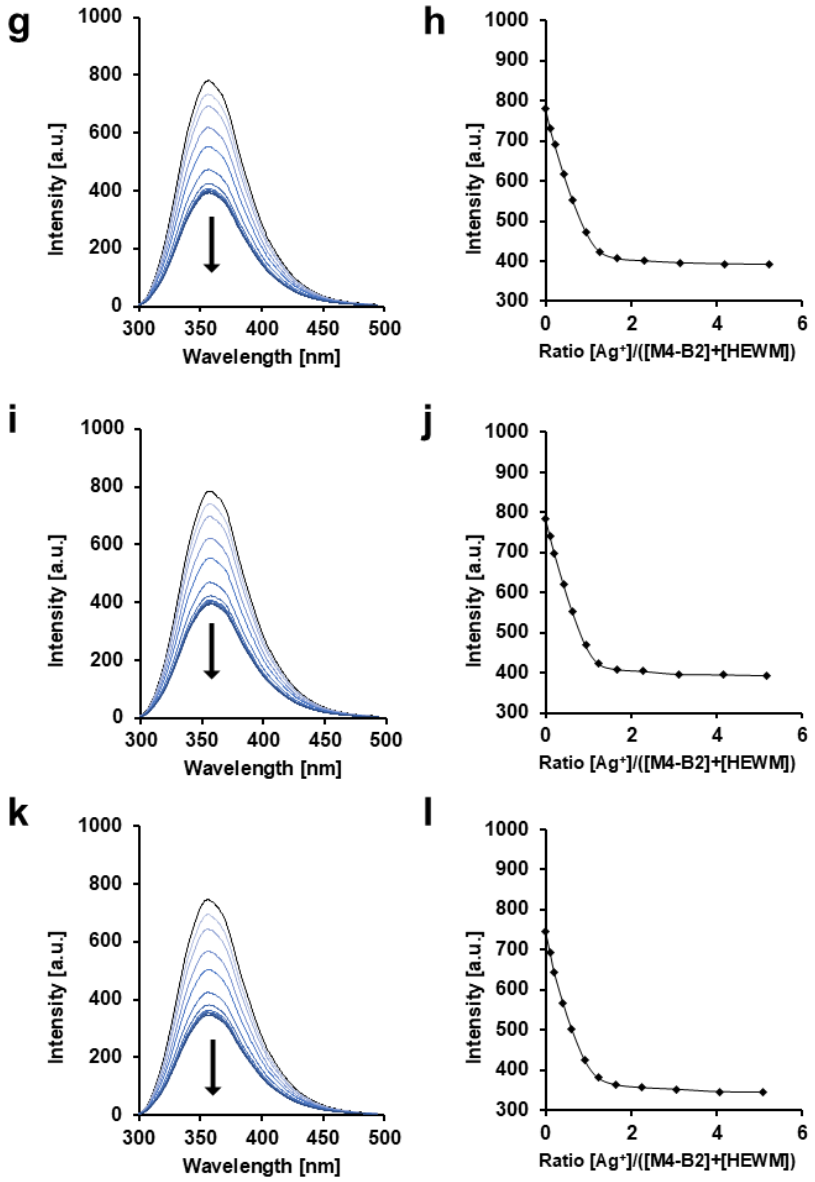

Fig. S37 HQQMAEAHKKM (M4-B2) / HEWM competition titrations, both at $2{\cdot}10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M4-B2 ($2{\cdot}10^{-5}$ M) in competition with HEWM probe ($2{\cdot}10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S6 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of HQQMAEAHKKM peptide

Model	$1{\cdot}10^{-5}$ M[a]		$2{\cdot}10^{-5}$ M[a]	
HQQMAEAHKKM (M4-B2)	$\log(K_{b\text{-}1})$ = 6.32±0.03	$\log(K_{b\text{-}2})$ = 5.38±0.07	$\log(K_{b\text{-}1})$ = 6.28±0.03	$\log(K_{b\text{-}2})$ = 5.43±0.08
	$\log(K_{b\text{-}1})$ = 6.30±0.04	$\log(K_{b\text{-}2})$ = 5.58±0.11	$\log(K_{b\text{-}1})$ = 6.33±0.02	$\log(K_{b\text{-}2})$ = 5.23±0.06
	$\log(K_{b\text{-}1})$ = 6.34±0.06	$\log(K_{b\text{-}2})$ = 5.51±0.06	$\log(K_{b\text{-}1})$ = 6.16±0.04	$\log(K_{b\text{-}2})$ = 5.41±0.11
Average	$\log(K_{b\text{-}1})$ = 6.29 ± 0.07		$\log(K_{b\text{-}2})$ = 5.42 ± 0.12	

[a] The values correspond to the peptide and probe concentrations.

HQAHAEAHRRM (M5-B2)

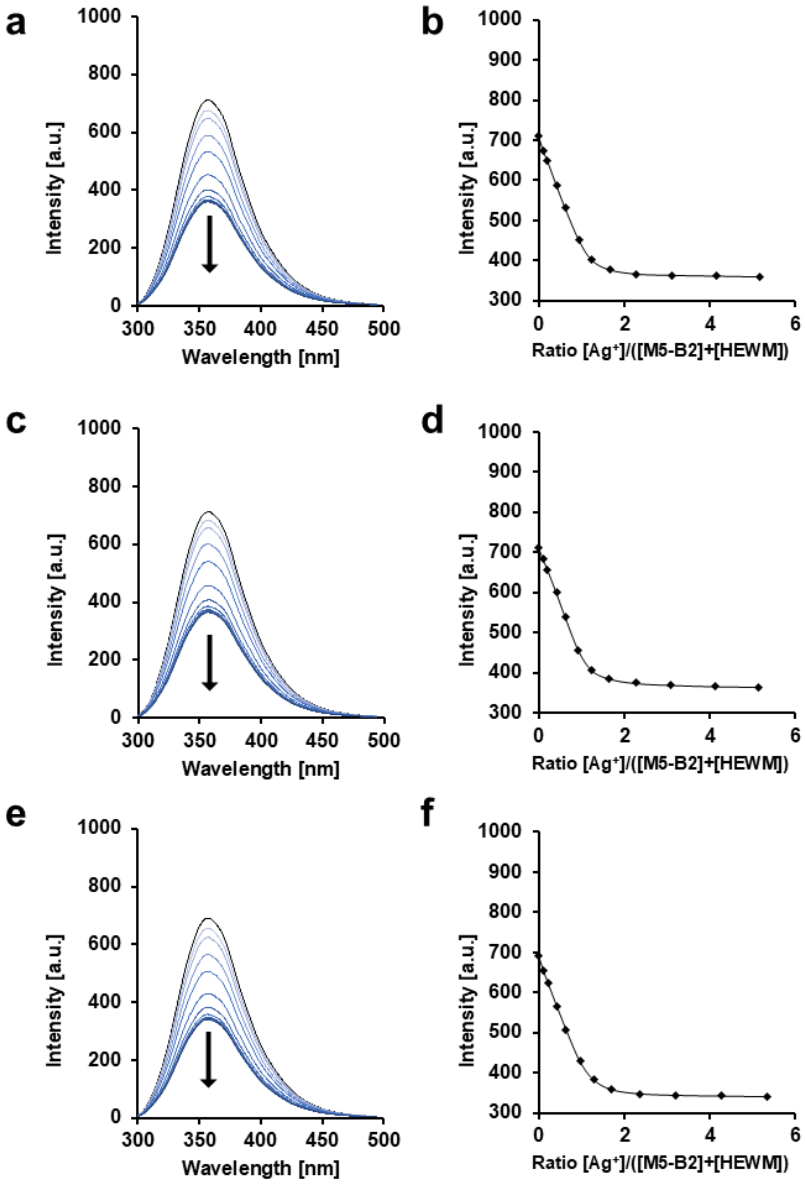

Fig. S38 HQAHAEAHRRM (M5-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M5-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

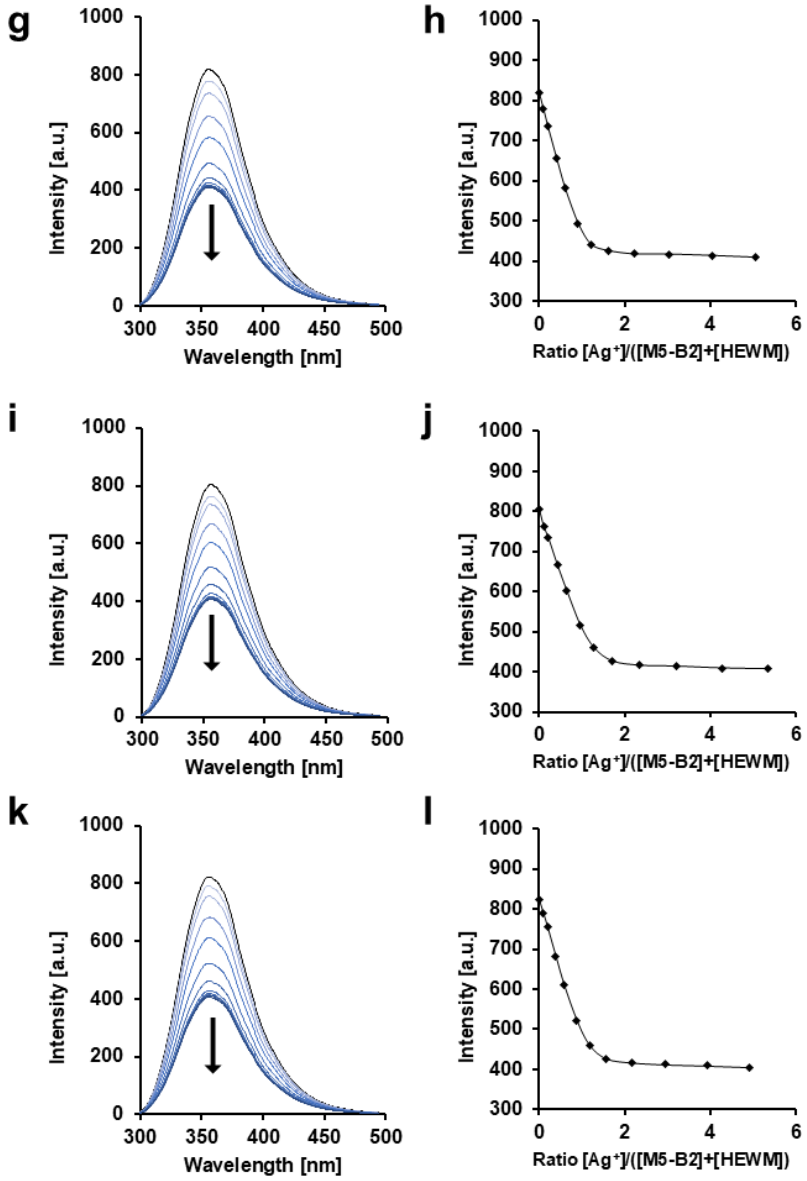

Fig. S39 HQAHAEAHRRM (M5-B2) / HEWM competition titrations, both at $2{\cdot}10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M5-B2 ($2{\cdot}10^{-5}$ M) in competition with HEWM probe ($2{\cdot}10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S7 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of HQAHAEAHRRM peptide

Model	$1{\cdot}10^{-5}$ M[a]		$2{\cdot}10^{-5}$ M[a]	
HQAHAEAHRRM (M5-B2)	$\log(K_{b\text{-}1}) = 6.52\pm0.10$	$\log(K_{b\text{-}2}) = 5.64\pm0.07$	$\log(K_{b\text{-}1}) = 6.37\pm0.02$	$\log(K_{b\text{-}2}) = 5.12\pm0.05$
	$\log(K_{b\text{-}1}) = 6.66\pm0.02$	$\log(K_{b\text{-}2}) = 5.46\pm0.04$	$\log(K_{b\text{-}1}) = 6.57\pm0.04$	$\log(K_{b\text{-}2}) = 5.69\pm0.07$
	$\log(K_{b\text{-}1}) = 6.54\pm0.02$	$\log(K_{b\text{-}2}) = 5.60\pm0.05$	$\log(K_{b\text{-}1}) = 6.52\pm0.02$	$\log(K_{b\text{-}2}) = 5.42\pm0.04$
Average	$\log(K_{b\text{-}1}) = 6.53 \pm 0.10$		$\log(K_{b\text{-}2}) = 5.49 \pm 0.21$	

[a] The values correspond to the peptide and probe concentrations.

HQQHAEAHRRM (M6-B2)

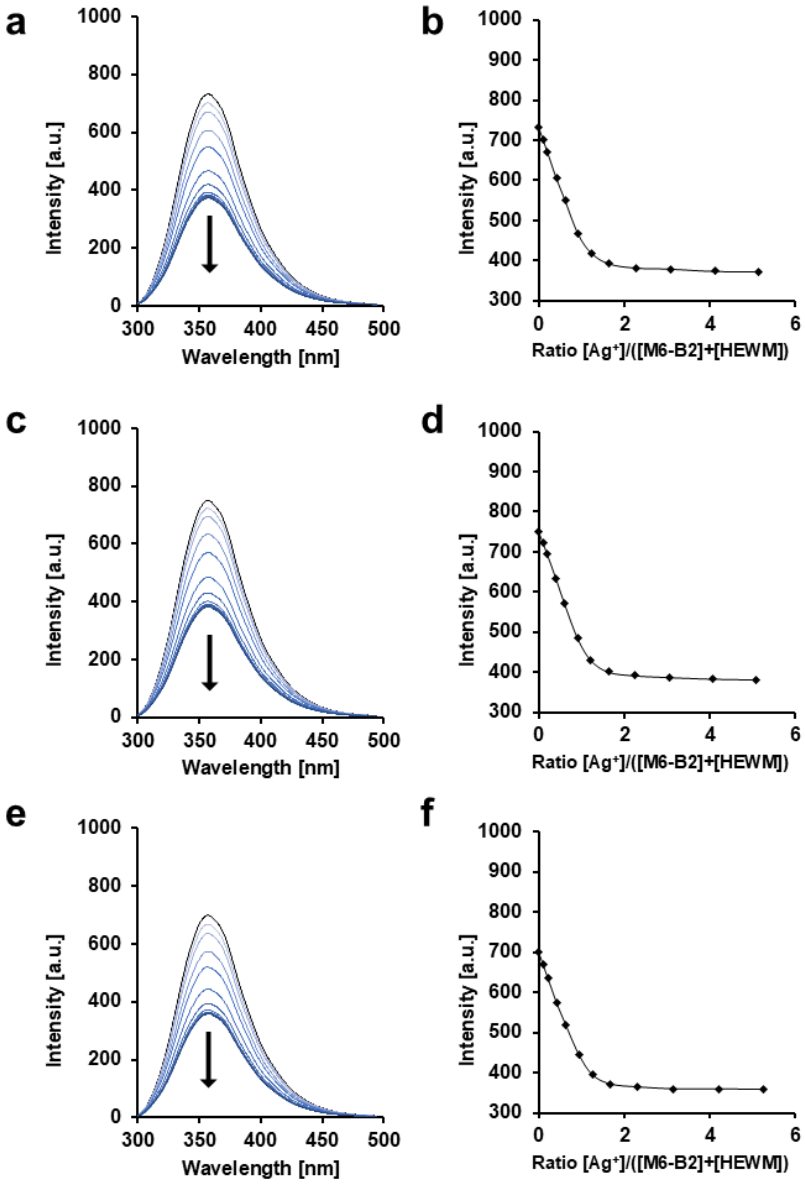

Fig. S40 HQQHAEAHRRM (M6-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M6-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

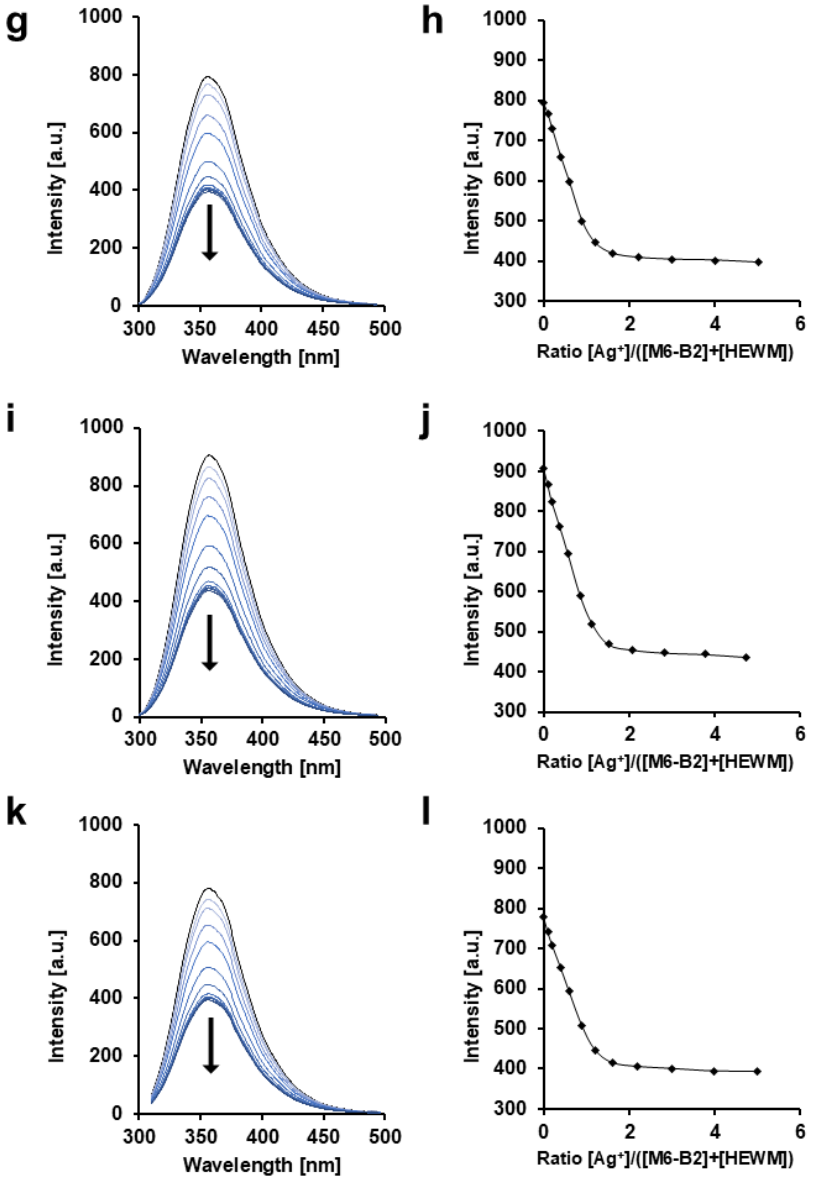

Fig. S41 HQQHAEAHRRM (M6-B2) / HEWM competition titrations, both at $2 \cdot 10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M6-B2 ($2 \cdot 10^{-5}$ M) in competition with HEWM probe ($2 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S8 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of HQQHAEAHRRM peptide

Model	$1 \cdot 10^{-5}$ M[a]		$2 \cdot 10^{-5}$ M[a]	
HQQHAEAHRRM (M6-B2)	$\log(K_{b\text{-}1}) = 6.57 \pm 0.03$	$\log(K_{b\text{-}2}) = 5.50 \pm 0.07$	$\log(K_{b\text{-}1}) = 6.59 \pm 0.04$	$\log(K_{b\text{-}2}) = 5.32 \pm 0.10$
	$\log(K_{b\text{-}1}) = 6.66 \pm 0.02$	$\log(K_{b\text{-}2}) = 5.48 \pm 0.04$	$\log(K_{b\text{-}1}) = 6.54 \pm 0.06$	$\log(K_{b\text{-}2}) = 5.74 \pm 0.12$
	$\log(K_{b\text{-}1}) = 6.50 \pm 0.02$	$\log(K_{b\text{-}2}) = 5.59 \pm 0.03$	$\log(K_{b\text{-}1}) = 6.52 \pm 0.05$	$\log(K_{b\text{-}2}) = 5.59 \pm 0.10$
Average	$\log(K_{b\text{-}1}) = 6.56 \pm 0.06$		$\log(K_{b\text{-}2}) = 5.55 \pm 0.15$	

[a] The values correspond to the peptide and probe concentrations.

HQAMAEAHRRH (M7-B2)

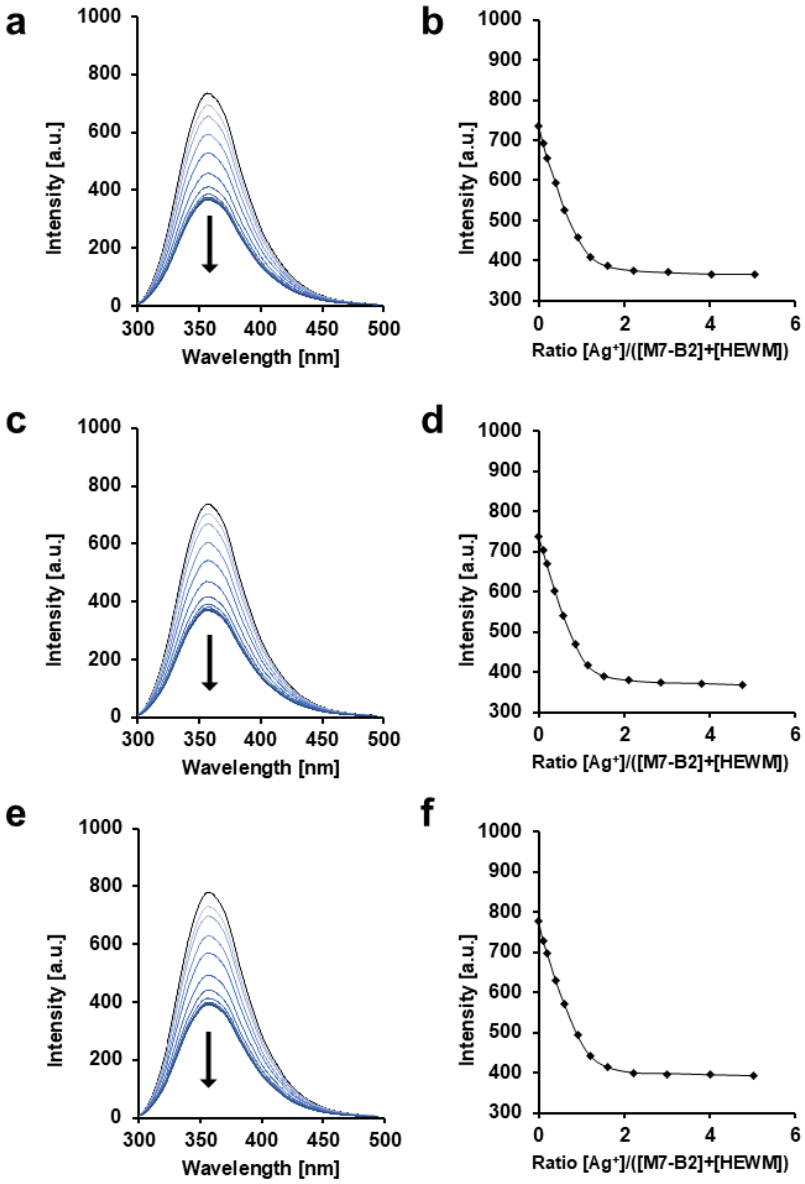

Fig. S42 HQAMAEAHRRH (M7-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M7-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

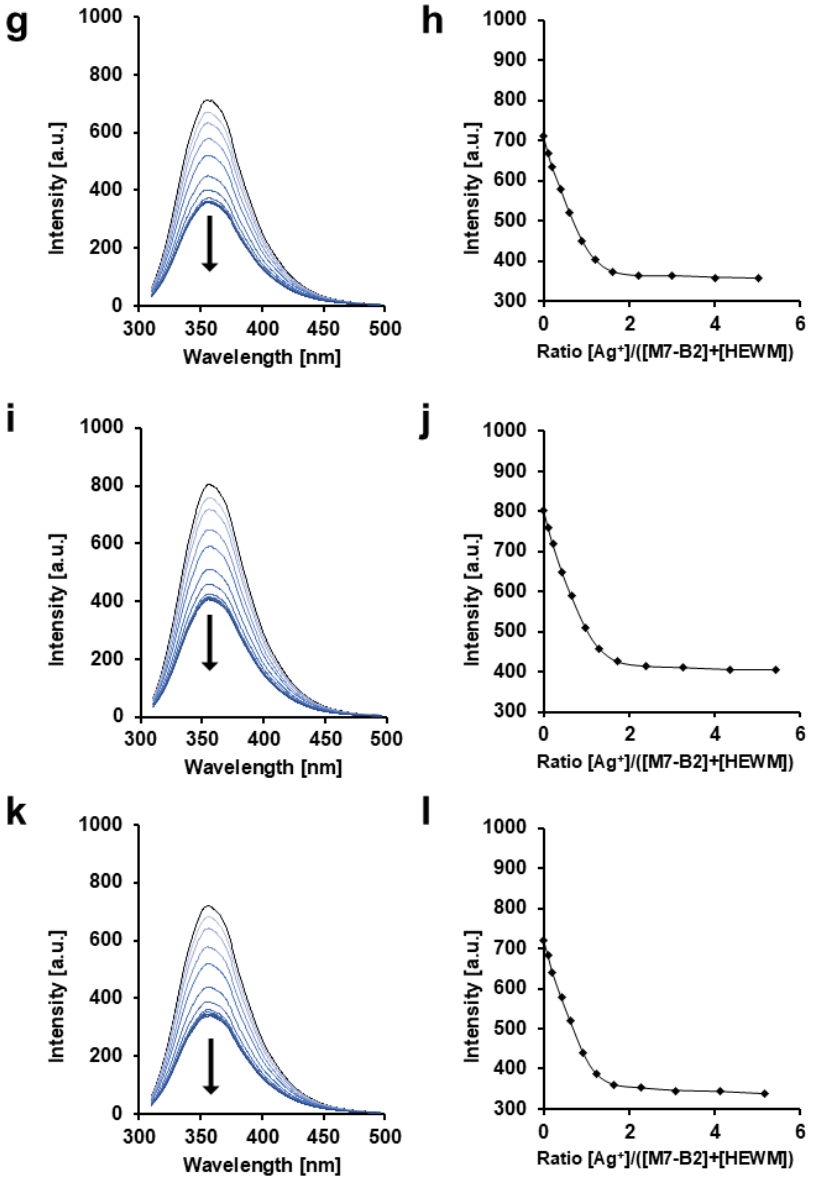

Fig. S43 HQAMAEAHRRH (M7-B2) / HEWM competition titrations, both at $2 \cdot 10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M7-B2 ($2 \cdot 10^{-5}$ M) in competition with HEWM probe ($2 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S9 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of HQAMAEAHRRH peptide

Model	$1 \cdot 10^{-5}$ M[a]		$2 \cdot 10^{-5}$ M[a]	
HQAMAEAHRRH (M7-B2)	$\log(K_{b\text{-}1}) = 6.33 \pm 0.03$	$\log(K_{b\text{-}2}) = 5.57 \pm 0.08$	$\log(K_{b\text{-}1}) = 6.31 \pm 0.06$	$\log(K_{b\text{-}2}) = 5.67 \pm 0.13$
	$\log(K_{b\text{-}1}) = 6.38 \pm 0.02$	$\log(K_{b\text{-}2}) = 5.48 \pm 0.05$	$\log(K_{b\text{-}1}) = 6.37 \pm 0.03$	$\log(K_{b\text{-}2}) = 5.84 \pm 0.05$
	$\log(K_{b\text{-}1}) = 6.31 \pm 0.05$	$\log(K_{b\text{-}2}) = 5.71 \pm 0.11$	$\log(K_{b\text{-}1}) = 6.41 \pm 0.04$	$\log(K_{b\text{-}2}) = 5.68 \pm 0.08$
Average	$\log(K_{b\text{-}1}) = 6.35 \pm 0.04$		$\log(K_{b\text{-}2}) = 5.66 \pm 0.13$	

[a] The values correspond to the peptide and probe concentrations.

HQAMAEAHKRH (M8-B2)

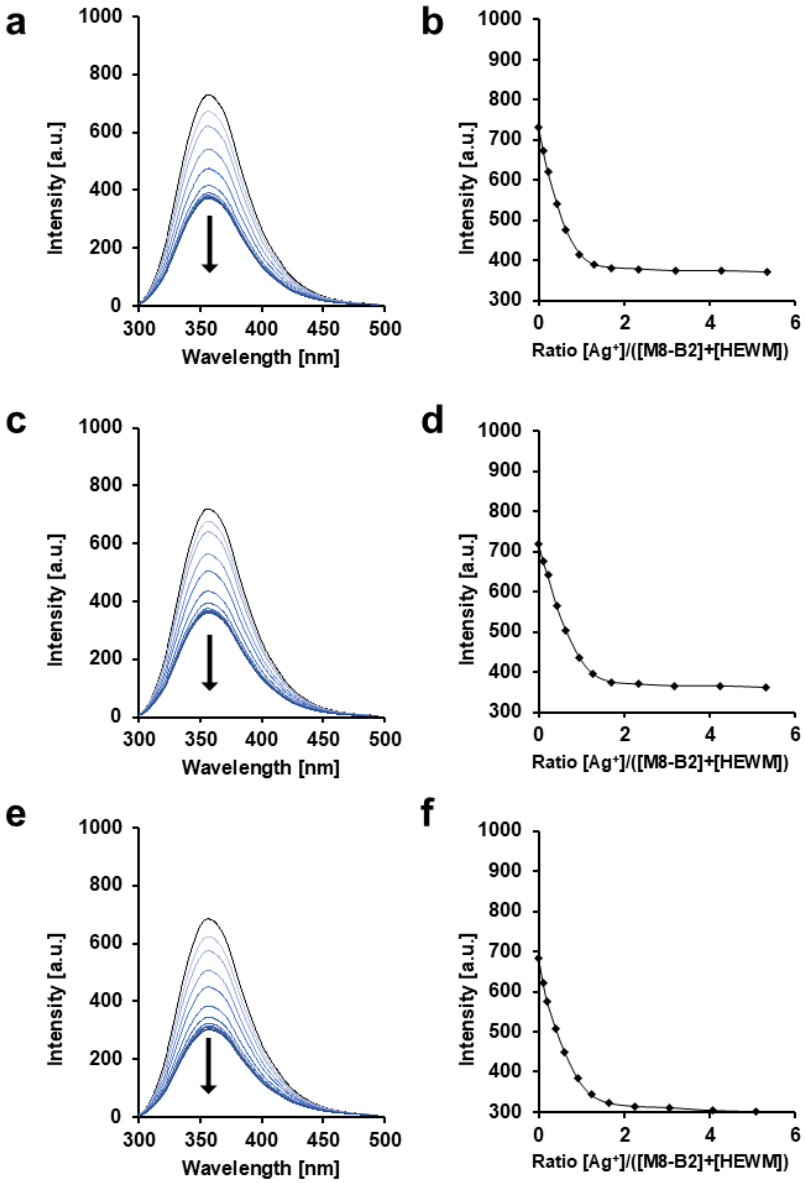

Fig. S44 HQAMAEAHKRH (M8-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M8-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

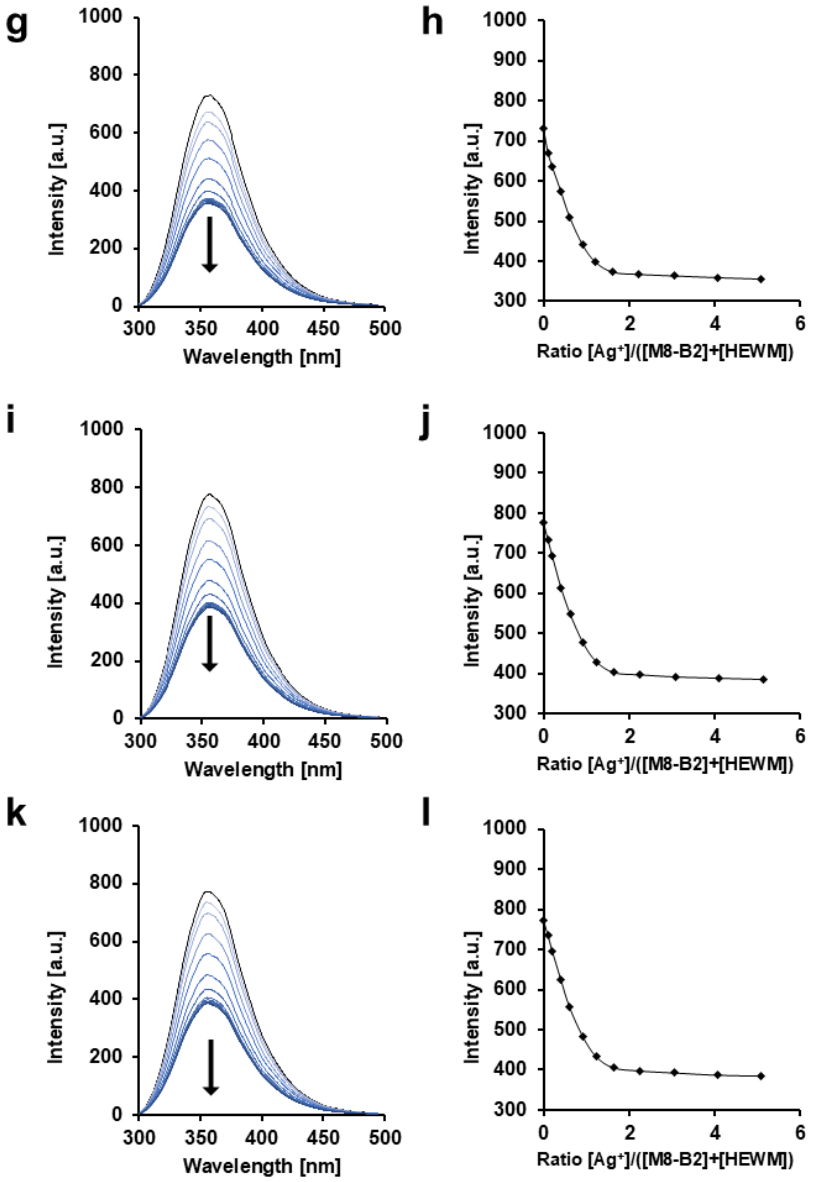

Fig. S45 HQAMAEAHKRH (M8-B2) / HEWM competition titrations, both at $2 \cdot 10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M8-B2 ($2 \cdot 10^{-5}$ M) in competition with HEWM probe ($2 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S10 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of HQAMAEAHKRH peptide

Model	$1 \cdot 10^{-5}$ M[a]		$2 \cdot 10^{-5}$ M[a]	
HQAMAEAHKRH (M8-B2)	$\log(K_{b\text{-}1}) = 5.95 \pm 0.03$	$\log(K_{b\text{-}2}) = 5.16 \pm 0.13$	$\log(K_{b\text{-}1}) = 6.21 \pm 0.08$	$\log(K_{b\text{-}2}) = 5.57 \pm 0.19$
	$\log(K_{b\text{-}1}) = 6.28 \pm 0.03$	$\log(K_{b\text{-}2}) = 5.47 \pm 0.07$	$\log(K_{b\text{-}1}) = 6.27 \pm 0.02$	$\log(K_{b\text{-}2}) = 5.48 \pm 0.04$
	$\log(K_{b\text{-}1}) = 6.00 \pm 0.10$	$\log(K_{b\text{-}2}) = 5.74 \pm 0.21$	$\log(K_{b\text{-}1}) = 6.37 \pm 0.03$	$\log(K_{b\text{-}2}) = 5.47 \pm 0.08$
Average	$\log(K_{b\text{-}1}) = 6.18 \pm 0.17$		$\log(K_{b\text{-}2}) = 5.48 \pm 0.19$	

[a] The values correspond to the peptide and probe concentrations.

HQAMAEAHQQH (M9-B2)

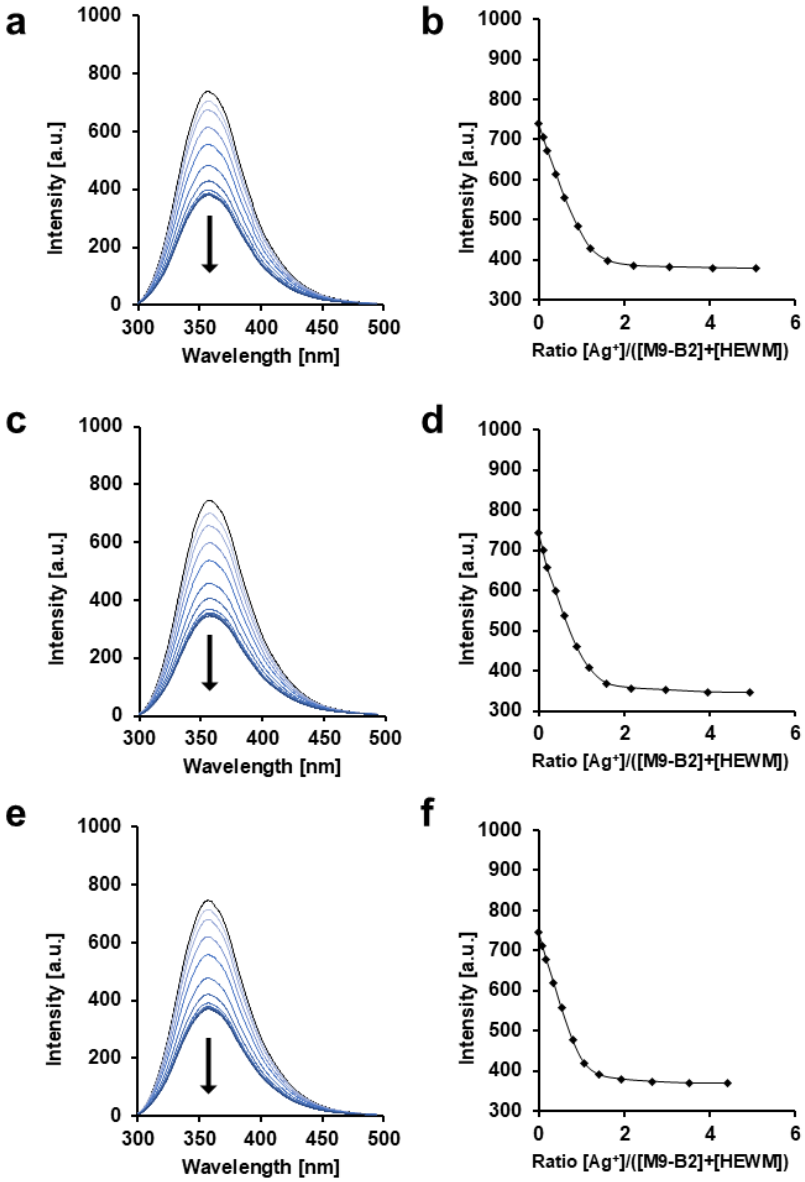

Fig. S46 HQAMAEAHQQH (M9-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M9-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

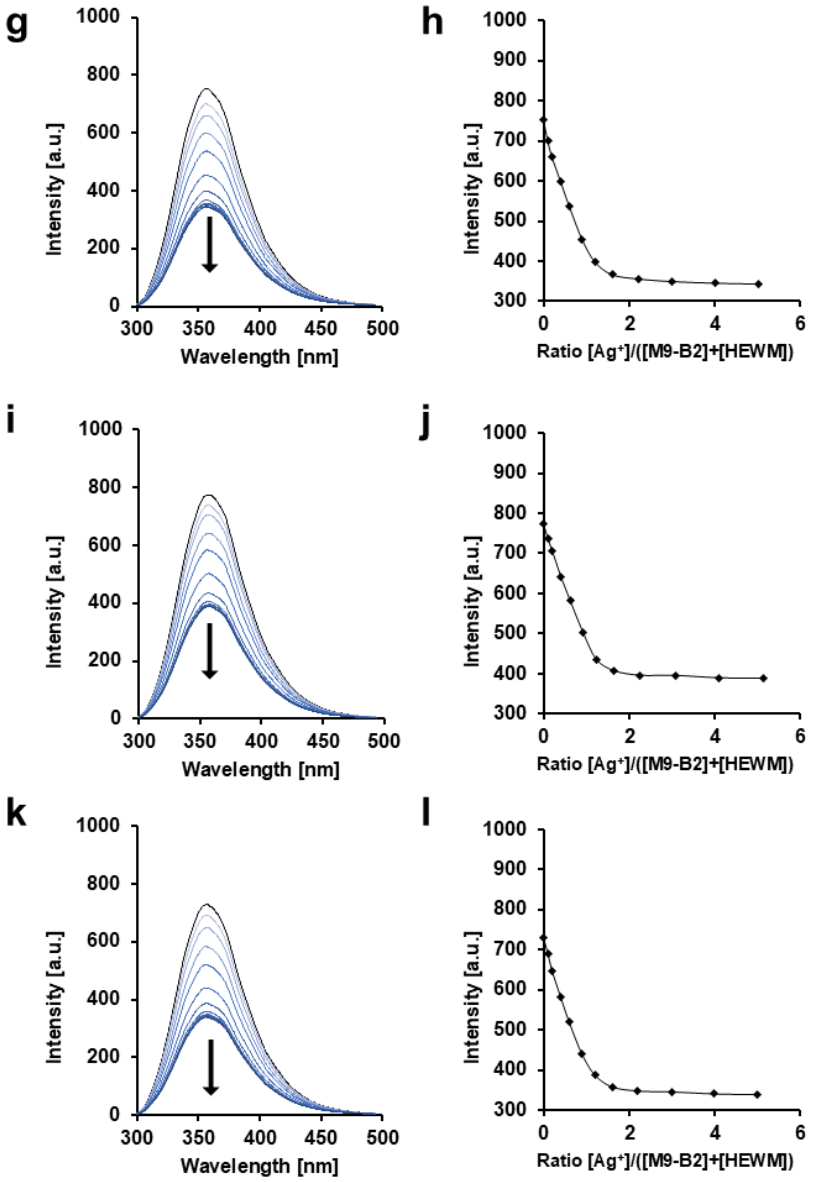

Fig. S47 HQAMAEAHQQH (M9-B2) / HEWM competition titrations, both at $2 \cdot 10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M9-B2 ($2 \cdot 10^{-5}$ M) in competition with HEWM probe ($2 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S11 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of HQAMAEAHQQH peptide

Model	$1 \cdot 10^{-5}$ M[a]		$2 \cdot 10^{-5}$ M[a]	
HQAMAEAHQQH (M9-B2)	$\log(K_{b\text{-}1}) = 6.49 \pm 0.02$	$\log(K_{b\text{-}2}) = 5.67 \pm 0.03$	$\log(K_{b\text{-}1}) = 6.34 \pm 0.08$	$\log(K_{b\text{-}2}) = 5.72 \pm 0.16$
	$\log(K_{b\text{-}1}) = 6.33 \pm 0.06$	$\log(K_{b\text{-}2}) = 5.80 \pm 0.12$	$\log(K_{b\text{-}1}) = 6.55 \pm 0.04$	$\log(K_{b\text{-}2}) = 5.69 \pm 0.07$
	$\log(K_{b\text{-}1}) = 6.43 \pm 0.01$	$\log(K_{b\text{-}2}) = 5.15 \pm 0.05$	$\log(K_{b\text{-}1}) = 6.37 \pm 0.03$	$\log(K_{b\text{-}2}) = 5.55 \pm 0.06$
Average	$\log(K_{b\text{-}1}) = 6.42 \pm 0.09$		$\log(K_{b\text{-}2}) = 5.60 \pm 0.23$	

[a] The values correspond to the peptide and probe concentrations.

HQAHAEAHRRH (M10-B2)

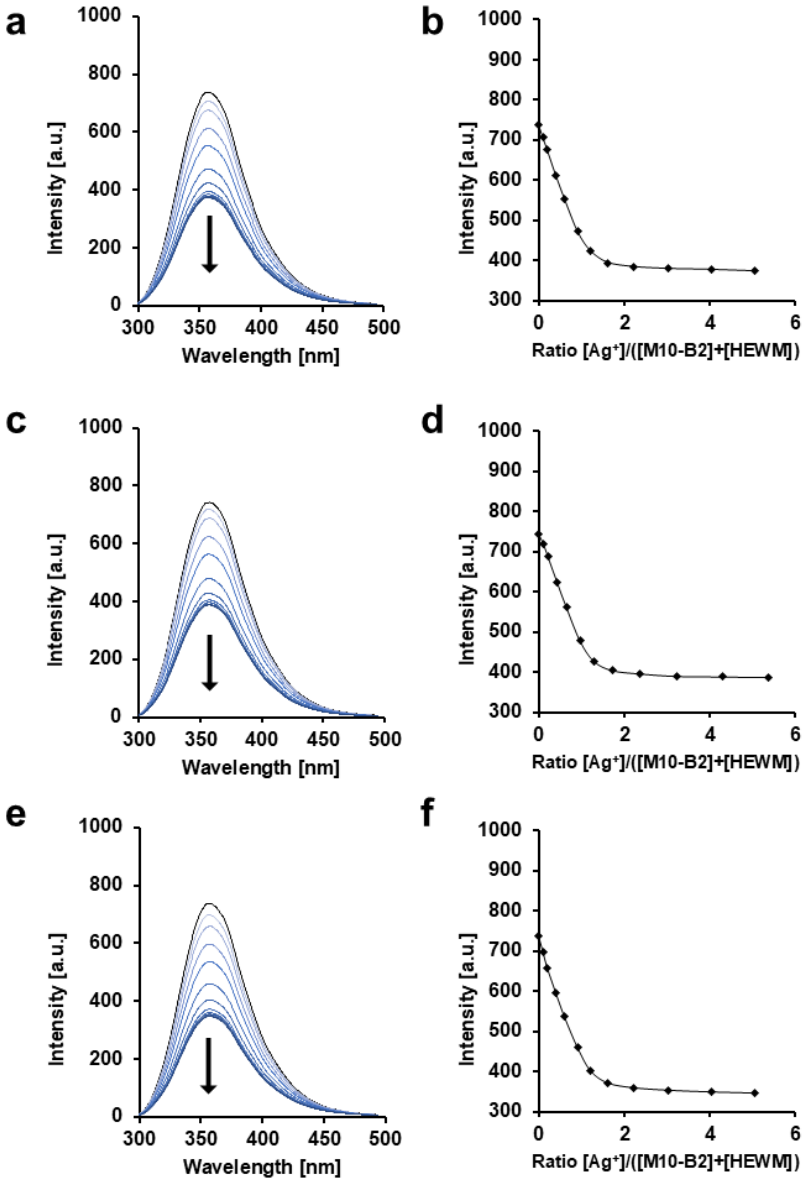

Fig. S48 HQAHAEAHRRH (M10-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M10-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

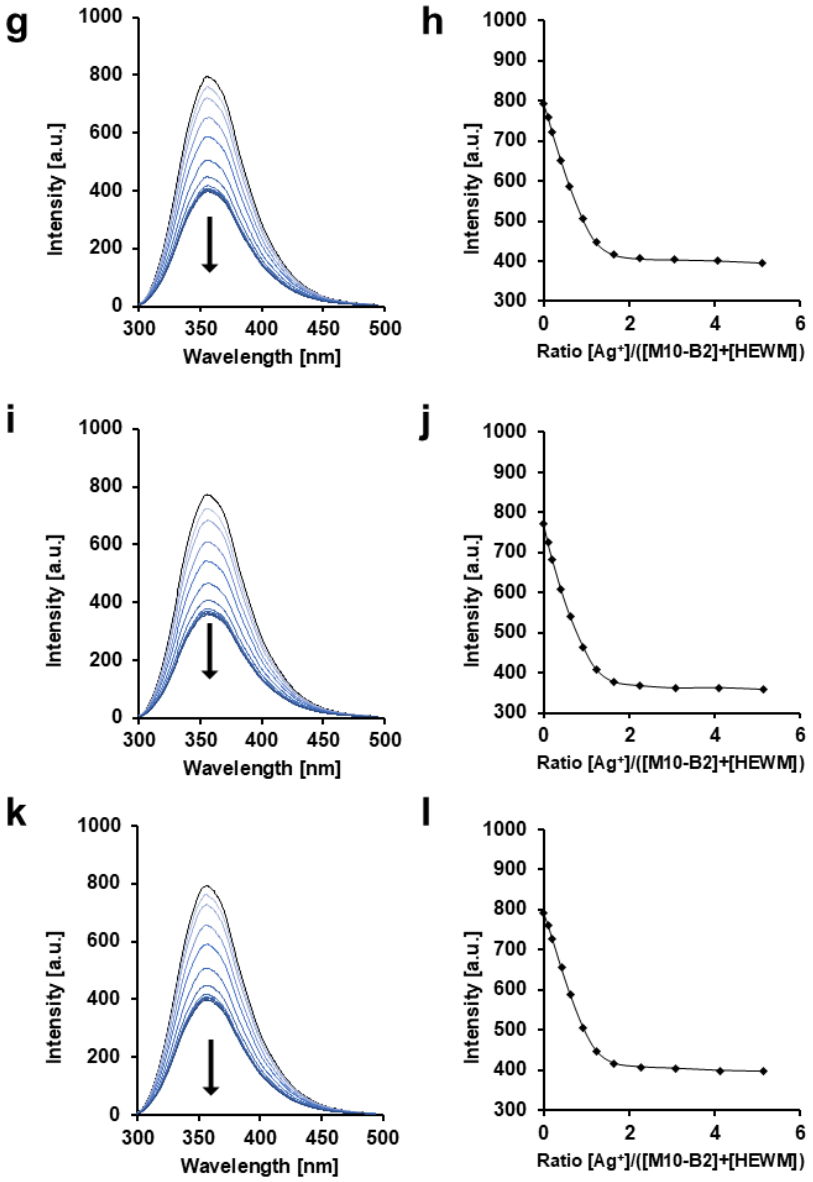

Fig. S49 HQAHAEAHRRH (M10-B2) / HEWM competition titrations, both at $2{\cdot}10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M10-B2 ($2{\cdot}10^{-5}$ M) in competition with HEWM probe ($2{\cdot}10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S12 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of HQAHAEAHRRH peptide

Model	$1{\cdot}10^{-5}$ M[a]		$2{\cdot}10^{-5}$ M[a]	
HQAHAEAHRRH (M10-B2)	$\log(K_{b\text{-}1})$ = 6.53±0.05	$\log(K_{b\text{-}2})$ = 5.50±0.03	$\log(K_{b\text{-}1})$ = 6.47±0.02	$\log(K_{b\text{-}2})$ = 5.55±0.04
	$\log(K_{b\text{-}1})$ = 6.67±0.03	$\log(K_{b\text{-}2})$ = 5.58±0.06	$\log(K_{b\text{-}1})$ = 6.28±0.02	$\log(K_{b\text{-}2})$ = 5.76±0.04
	$\log(K_{b\text{-}1})$ = 6.41±0.03	$\log(K_{b\text{-}2})$ = 5.76±0.06	$\log(K_{b\text{-}1})$ = 6.55±0.02	$\log(K_{b\text{-}2})$ = 5.54±0.05
Average	$\log(K_{b\text{-}1})$ = 6.49 ± 0.13		$\log(K_{b\text{-}2})$ = 5.62 ± 0.11	

[a] The values correspond to the peptide and probe concentrations.

MQAMAEAHRRM (M11-B2)

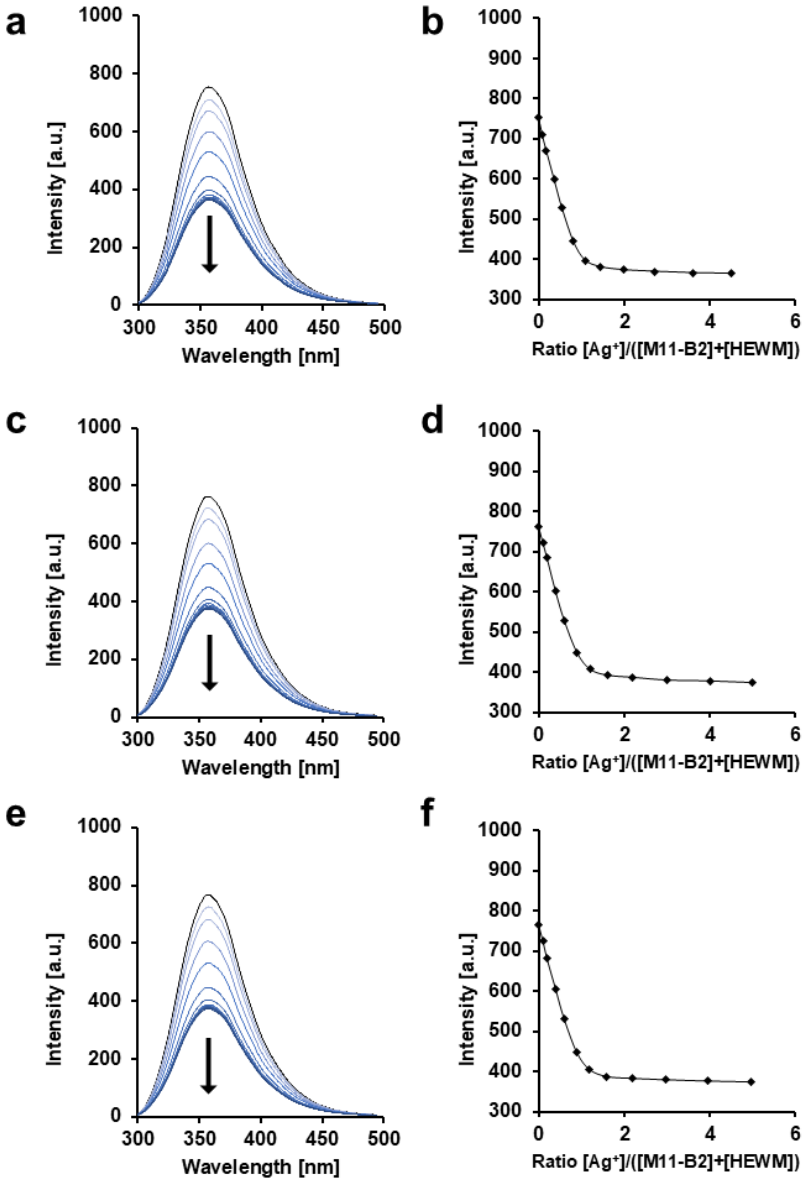

Fig. S50 MQAMAEAHRRM (M11-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M11-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

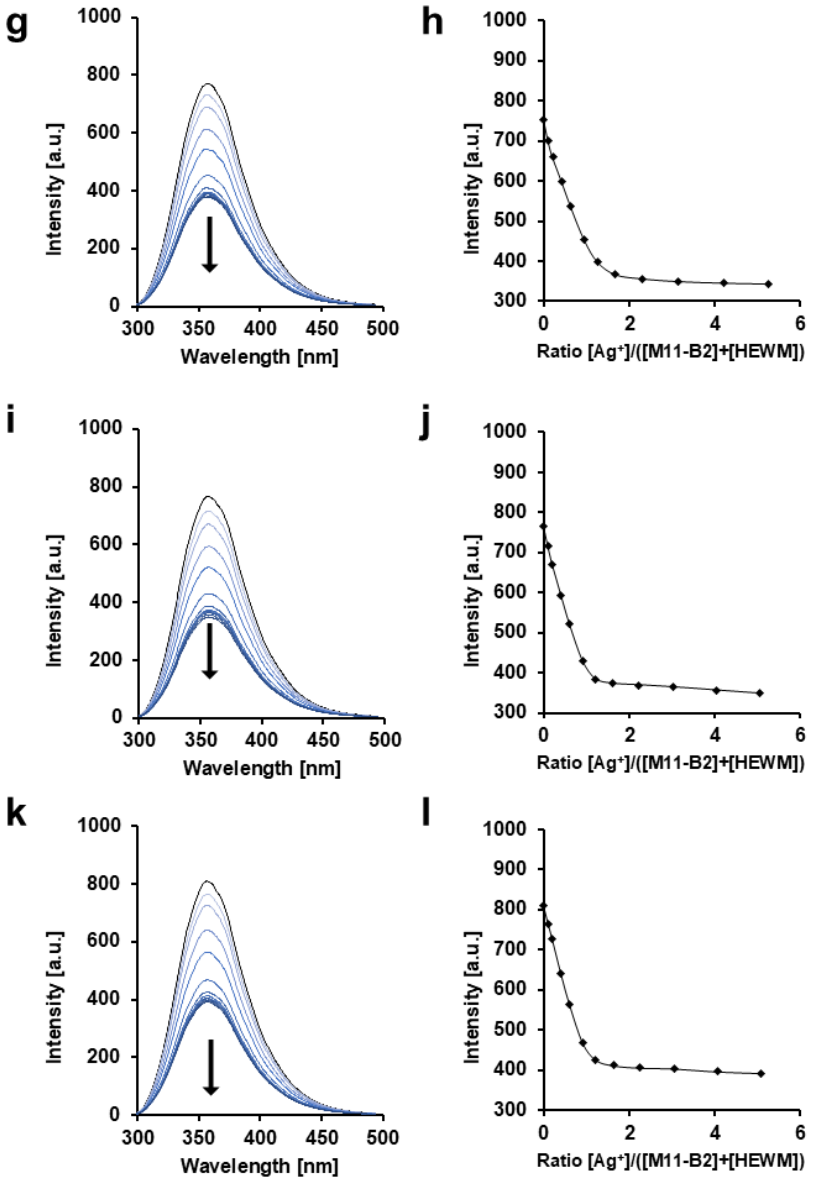

Fig. S51 MQAMAEAHRRM (M11-B2) / HEWM competition titrations, both at $2{\cdot}10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M11-B2 ($2{\cdot}10^{-5}$ M) in competition with HEWM probe ($2{\cdot}10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S13 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of MQAMAEAHRRM peptide

Model	$1{\cdot}10^{-5}$ M[a]		$2{\cdot}10^{-5}$ M[a]	
MQAMAEAHRRM (M11-B2)	$\log(K_{b\text{-}1})$ = 6.24±0.02	$\log(K_{b\text{-}2})$ = 4.69±0.16	$\log(K_{b\text{-}1})$ = 6.40±0.02	$\log(K_{b\text{-}2})$ = 5.16±0.06
	$\log(K_{b\text{-}1})$ = 6.32±0.04	$\log(K_{b\text{-}2})$ = 5.09±0.20	$\log(K_{b\text{-}1})$ = 6.31±0.04	$\log(K_{b\text{-}2})$ = 5.09±0.21
	$\log(K_{b\text{-}1})$ = 6.31±0.02	$\log(K_{b\text{-}2})$ = 5.02±0.10	$\log(K_{b\text{-}1})$ = 6.37±0.02	$\log(K_{b\text{-}2})$ = 4.88±0.12
Average	$\log(K_{b\text{-}1})$ = 6.32 ± 0.05		$\log(K_{b\text{-}2})$ = 4.99 ± 0.18	

[a] The values correspond to the peptide and probe concentrations.

MKKMAEAHRRRM (M12-B2)

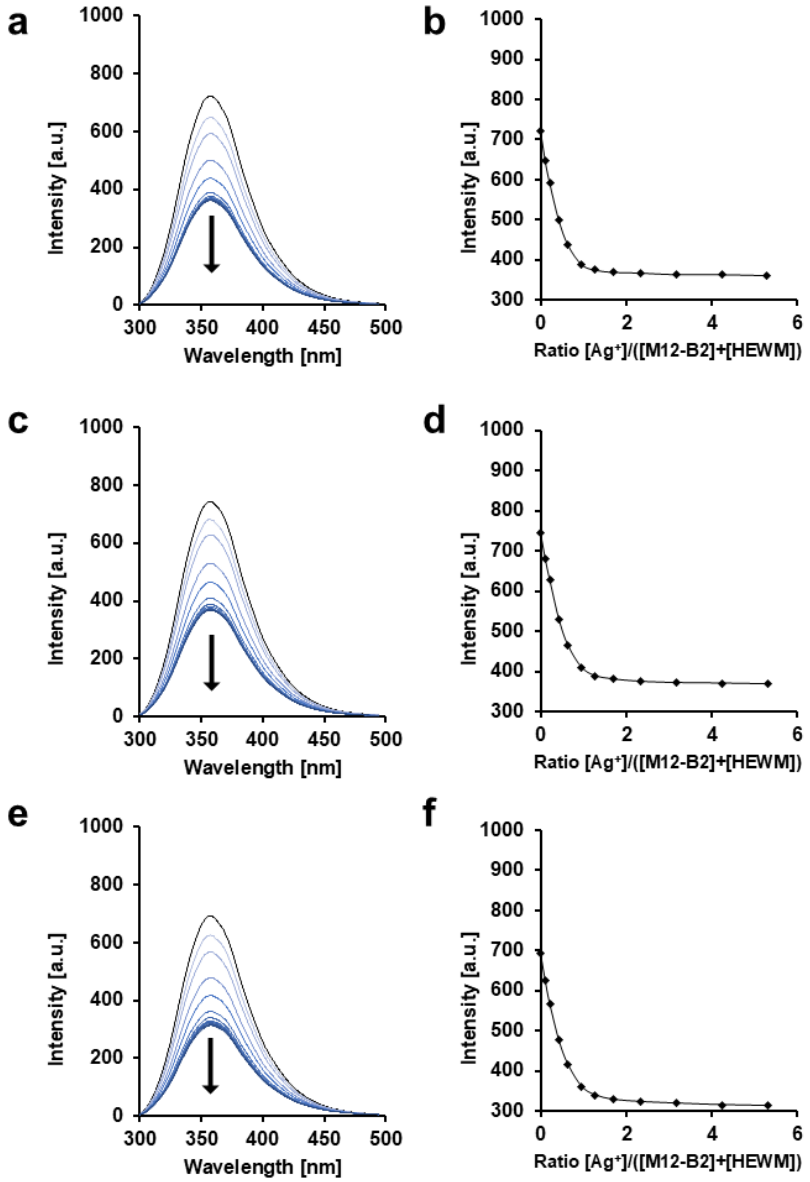

Fig. S52 MKKMAEAHRRRM (M12-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M12-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

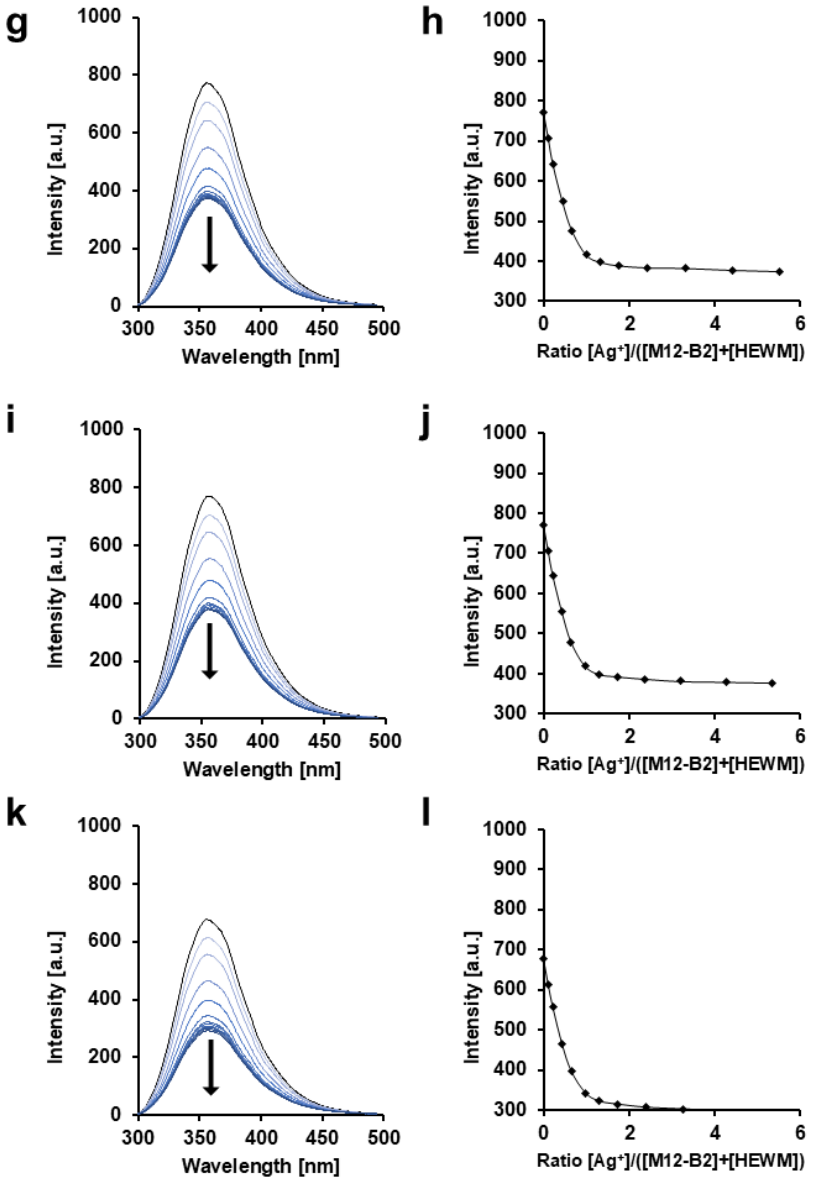

Fig. S53 MKKMAEAHRRM (M12-B2) / HEWM competition titrations, both at $2{\cdot}10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M12-B2 ($2{\cdot}10^{-5}$ M) in competition with HEWM probe ($2{\cdot}10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S14 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of MKKMAEAHRRM peptide

Model	$1{\cdot}10^{-5}$ M[a]		$2{\cdot}10^{-5}$ M[a]	
MKKMAEAHRRM (M12-B2)	$\log(K_{b\text{-}1})$ = 5.62±0.06	$\log(K_{b\text{-}2})$ = 4.92±0.32	$\log(K_{b\text{-}1})$ = 5.83±0.04	$\log(K_{b\text{-}2})$ = 5.03±0.19
	$\log(K_{b\text{-}1})$ = 5.82±0.02	$\log(K_{b\text{-}2})$ = 5.01±0.08	$\log(K_{b\text{-}1})$ = 5.84±0.03	$\log(K_{b\text{-}2})$ = 4.89±0.19
	$\log(K_{b\text{-}1})$ = 5.74±0.05	$\log(K_{b\text{-}2})$ = 5.37±0.15	$\log(K_{b\text{-}1})$ = 5.85±0.04	$\log(K_{b\text{-}2})$ = 5.12±0.19
Average	$\log(K_{b\text{-}1})$ = 5.78 ± 0.09		$\log(K_{b\text{-}2})$ = 5.06 ± 0.17	

[a] The values correspond to the peptide and probe concentrations.

HQAMAEAMRRM (M13-B2)

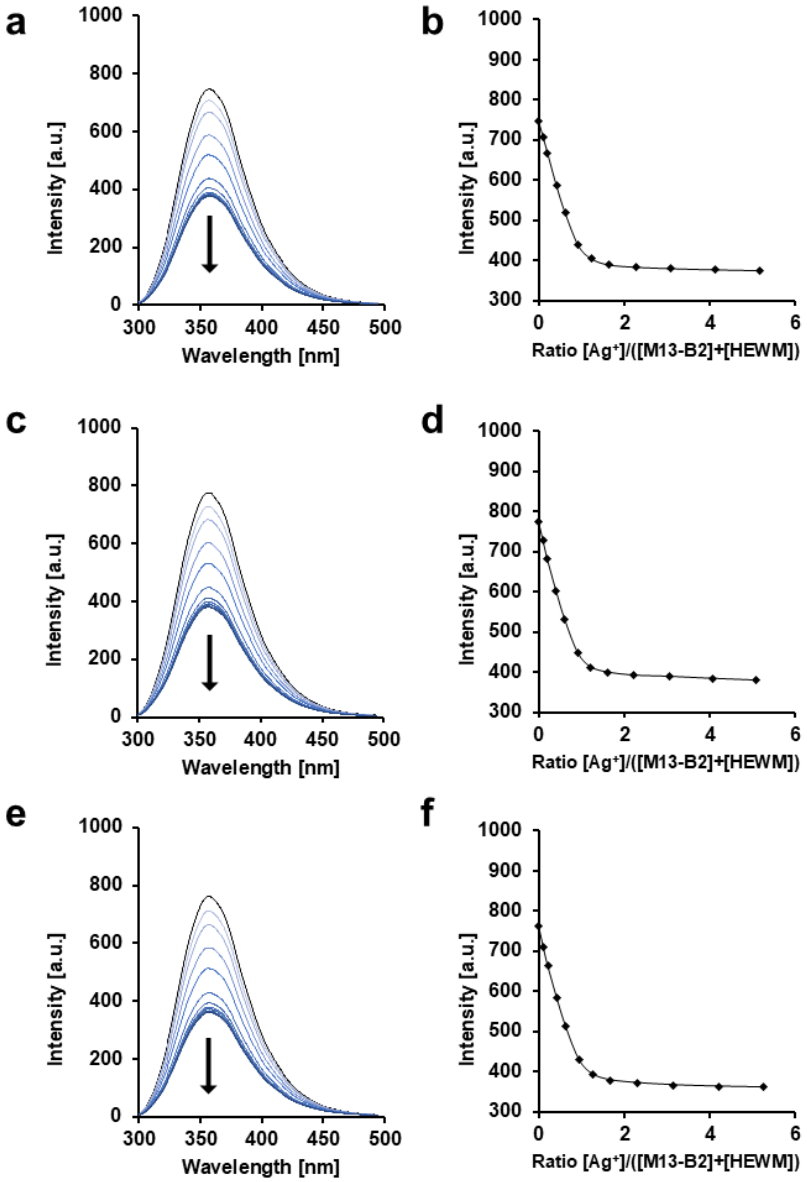

Fig. S54 HQAMAEAMRRM (M13-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M13-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

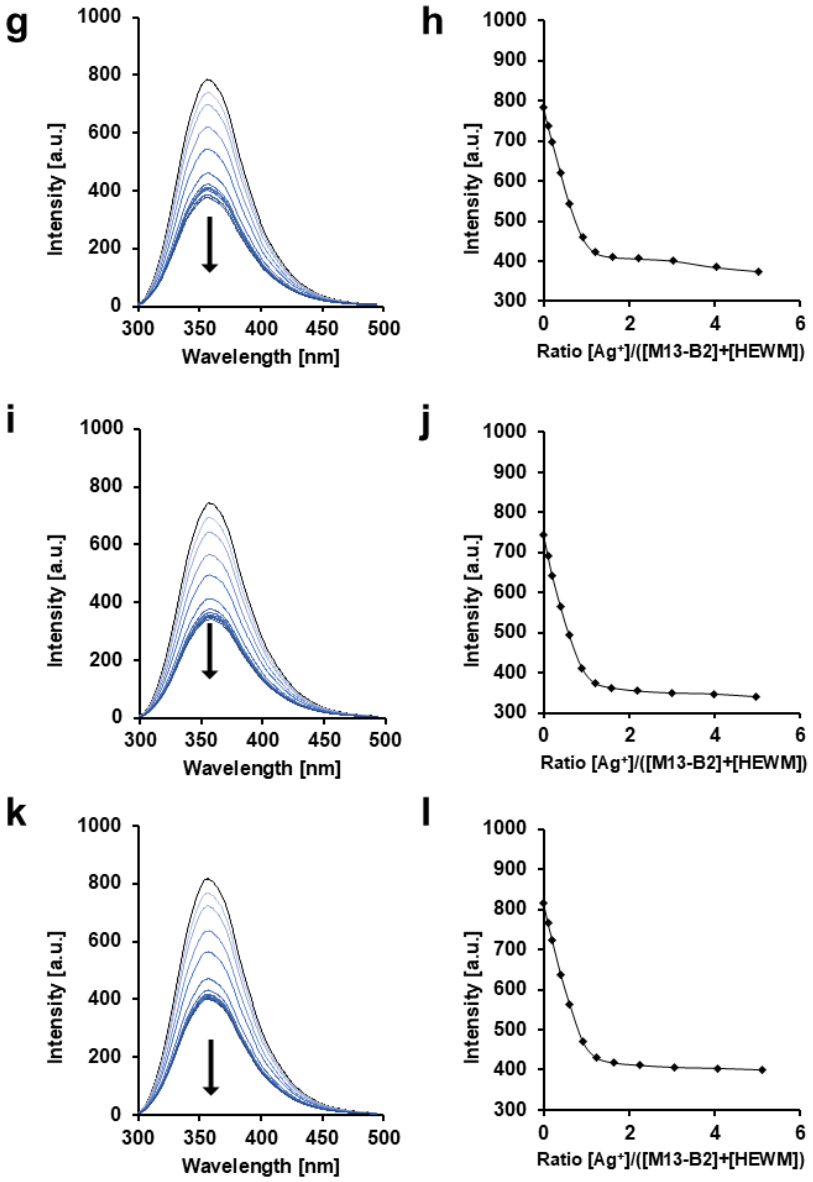

Fig. S55 HQAMAEAMRRM (M13-B2) / HEWM competition titrations, both at $2{\cdot}10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M13-B2 ($2{\cdot}10^{-5}$ M) in competition with HEWM probe ($2{\cdot}10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S15 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of HQAMAEAMRRM peptide

Model	$1{\cdot}10^{-5}$ M[a]		$2{\cdot}10^{-5}$ M[a]	
HQAMAEAMRRM (M13-B2)	$\log(K_{b\text{-}1})$ = 6.32±0.02	$\log(K_{b\text{-}2})$ = 4.89±0.13	$\log(K_{b\text{-}1})$ = 6.33±0.05	$\log(K_{b\text{-}2})$ = 5.04±0.38
	$\log(K_{b\text{-}1})$ = 6.24±0.05	$\log(K_{b\text{-}2})$ = 5.10±0.25	$\log(K_{b\text{-}1})$ = 6.16±0.05	$\log(K_{b\text{-}2})$ = 5.12±0.24
	$\log(K_{b\text{-}1})$ = 6.25±0.03	$\log(K_{b\text{-}2})$ = 5.24±0.13	$\log(K_{b\text{-}1})$ = 6.28±0.01	$\log(K_{b\text{-}2})$ = 4.94±0.07
Average	$\log(K_{b\text{-}1})$ = 5.26 ± 0.06		$\log(K_{b\text{-}2})$ = 5.06 ± 0.13	

[a] The values correspond to the peptide and probe concentrations.

HQAMAEAMKKM (M14-B2)

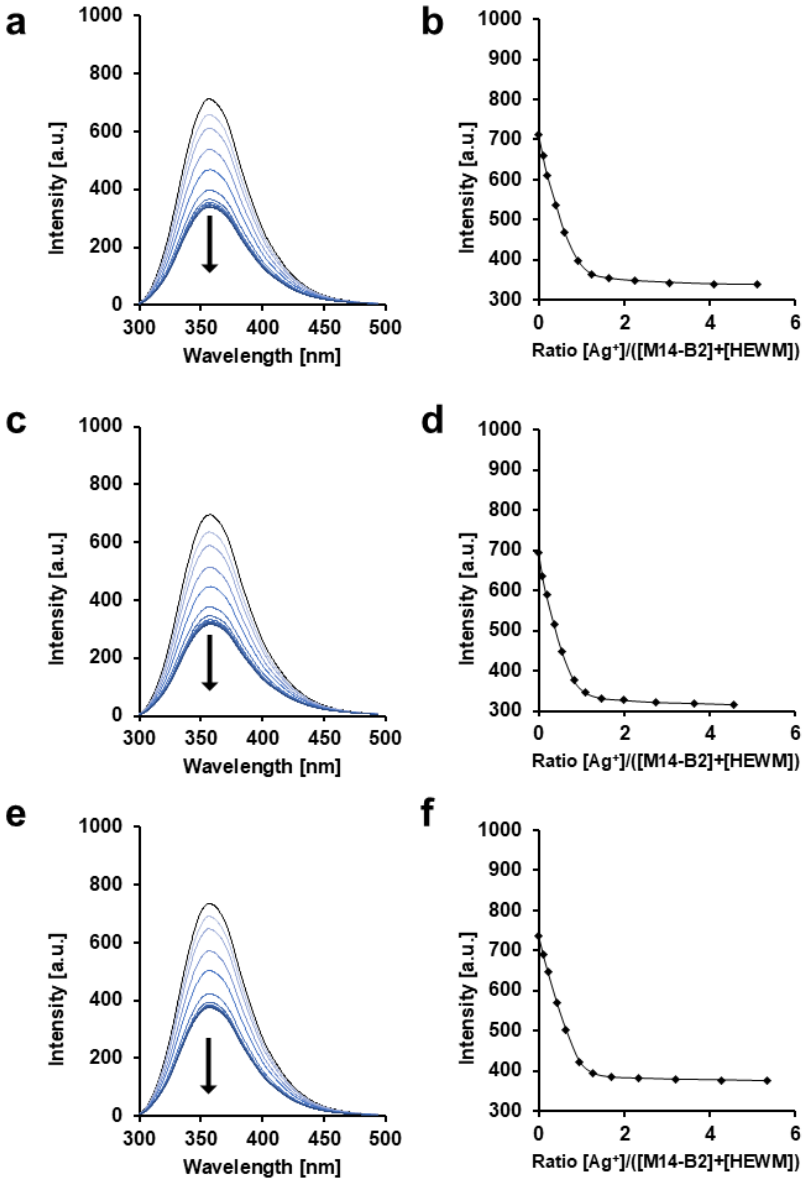

Fig. S56 HQAMAEAMKKM (M14-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M14-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

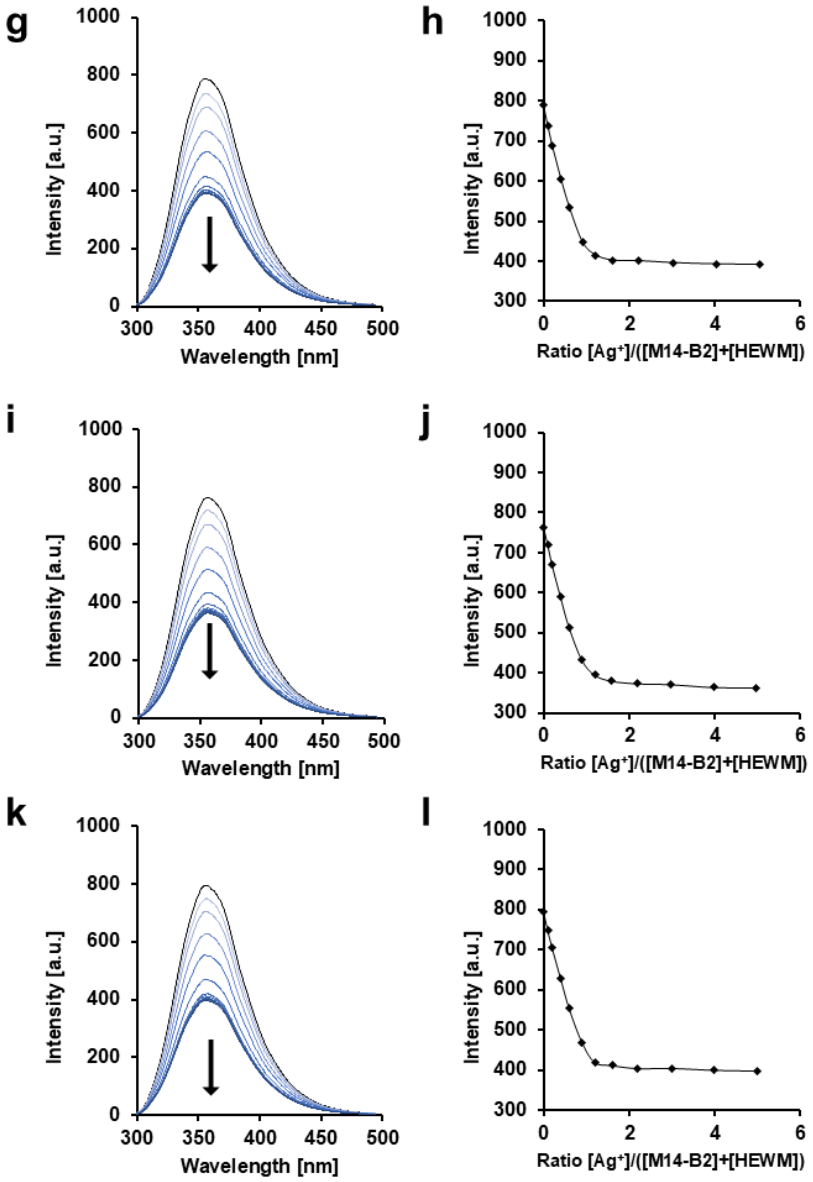

Fig. S57 HQAMAEAMKKM (M14-B2) / HEWM competition titrations, both at $2{\cdot}10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M14-B2 ($2{\cdot}10^{-5}$ M) in competition with HEWM probe ($2{\cdot}10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S16 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of HQAMAEAMKKM peptide

Model	$1{\cdot}10^{-5}$ M[a]		$2{\cdot}10^{-5}$ M[a]	
HQAMAEAMKKM (M14-B2)	$\log(K_{b\text{-}1}) = 6.07\pm0.05$	$\log(K_{b\text{-}2}) = 5.23\pm0.20$	$\log(K_{b\text{-}1}) = 6.17\pm0.02$	$\log(K_{b\text{-}2}) = 4.74\pm0.09$
	$\log(K_{b\text{-}1}) = 5.93\pm0.05$	$\log(K_{b\text{-}2}) = 4.94\pm0.32$	$\log(K_{b\text{-}1}) = 6.21\pm0.02$	$\log(K_{b\text{-}2}) = 4.88\pm0.10$
	$\log(K_{b\text{-}1}) = 6.28\pm0.01$	$\log(K_{b\text{-}2}) = 4.93\pm0.06$	$\log(K_{b\text{-}1}) = 6.28\pm0.02$	$\log(K_{b\text{-}2}) = 4.90\pm0.10$
Average	$\log(K_{b\text{-}1}) = 6.15 \pm 0.13$		$\log(K_{b\text{-}2}) = 4.94 \pm 0.16$	

[a] The values correspond to the peptide and probe concentrations.

MQAMAEAMRRM (M15-B2)

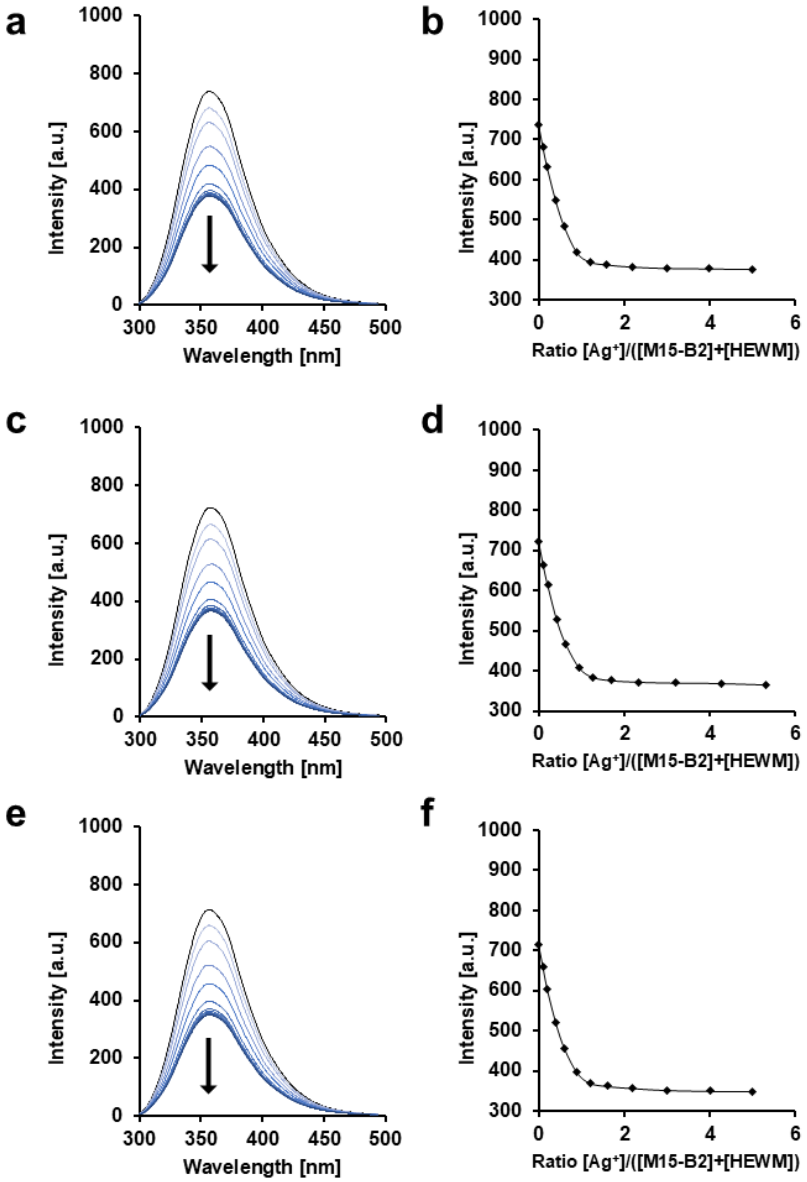

Fig. S58 MQAMAEAMRRM (M15-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M15-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

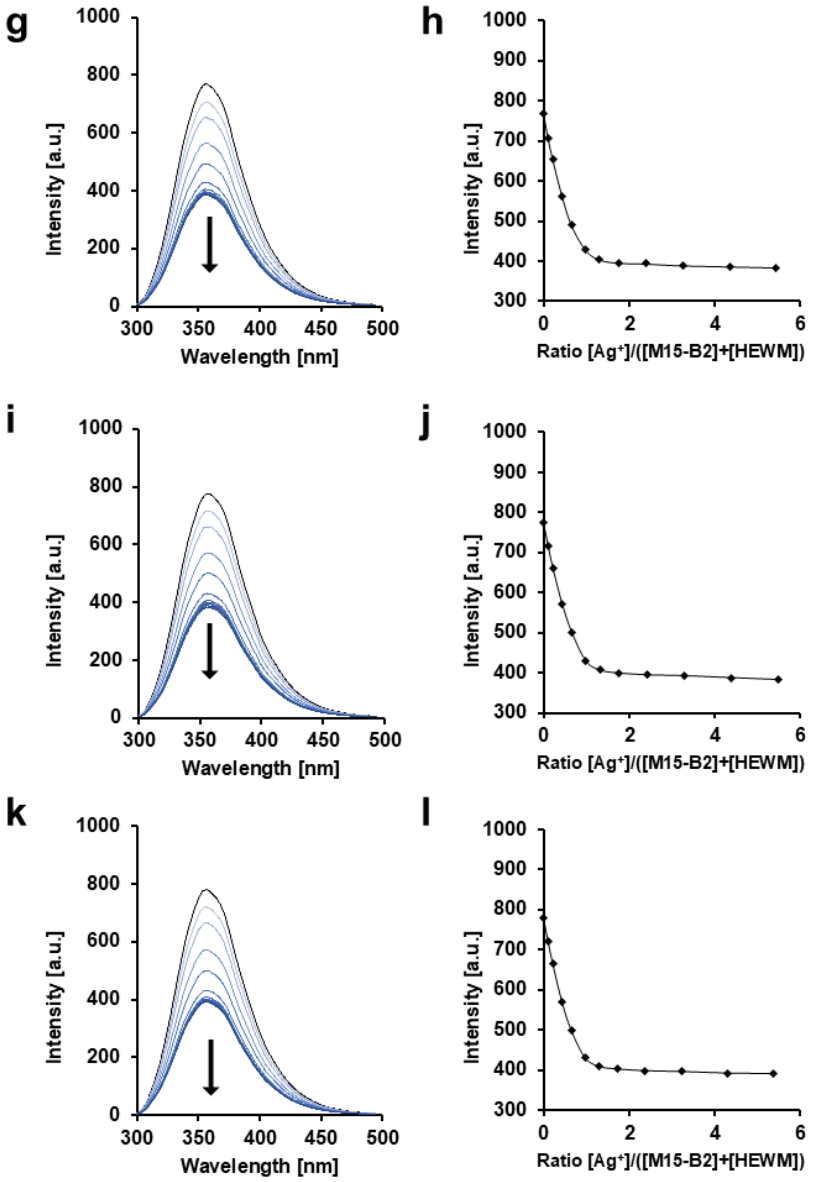

Fig. S59 MQAMAEAMRRM (M15-B2) / HEWM competition titrations, both at $2 \cdot 10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M15-B2 ($2 \cdot 10^{-5}$ M) in competition with HEWM probe ($2 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S17 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of MQAMAEAMRRM peptide

Model	$1 \cdot 10^{-5}$ M[a]		$2 \cdot 10^{-5}$ M[a]	
MQAMAEAMRRM (M15-B2)	$\log(K_{b\text{-}1}) = 5.91 \pm 0.02$	$\log(K_{b\text{-}2}) = 4.80 \pm 0.14$	$\log(K_{b\text{-}1}) = 5.92 \pm 0.02$	$\log(K_{b\text{-}2}) = 5.02 \pm 0.10$
	$\log(K_{b\text{-}1}) = 5.90 \pm 0.02$	$\log(K_{b\text{-}2}) = 5.09 \pm 0.08$	$\log(K_{b\text{-}1}) = 6.02 \pm 0.03$	$\log(K_{b\text{-}2}) = 5.00 \pm 0.17$
	$\log(K_{b\text{-}1}) = 5.83 \pm 0.03$	$\log(K_{b\text{-}2}) = 5.09 \pm 0.14$	$\log(K_{b\text{-}1}) = 5.94 \pm 0.01$	$\log(K_{b\text{-}2}) = 4.78 \pm 0.06$
Average	$\log(K_{b\text{-}1}) = 5.92 \pm 0.06$		$\log(K_{b\text{-}2}) = 4.96 \pm 0.14$	

[a] The values correspond to the peptide and probe concentrations.

HQQHAEAHQQH (M16-B2)

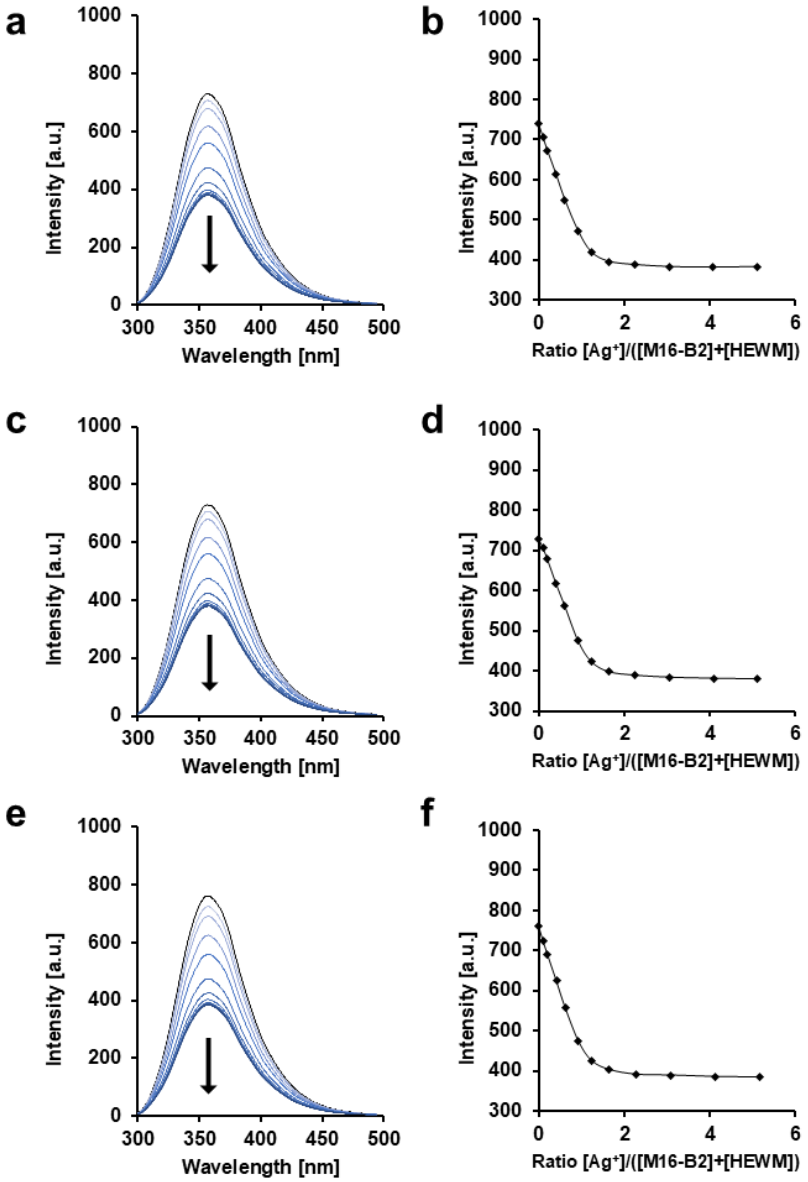

Fig. S60 HQQHAEAHQQH (M16-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M16-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

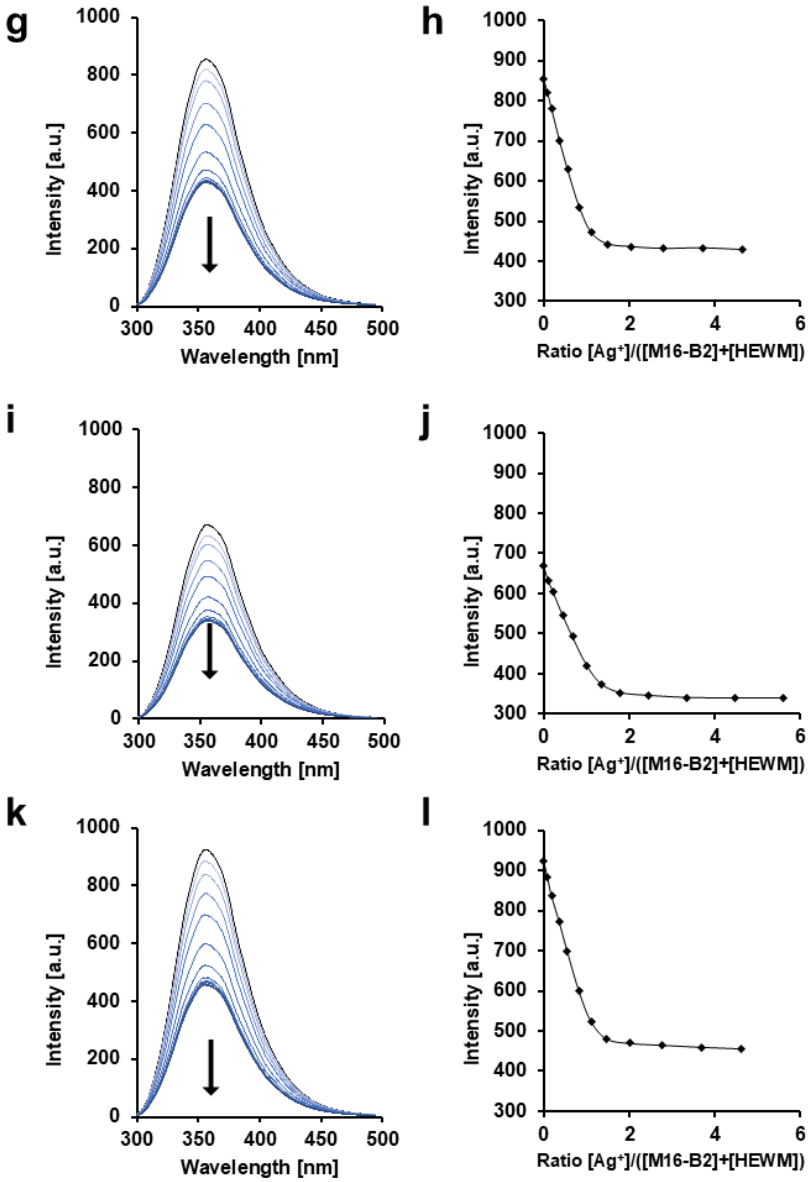

Fig. S61 HQQHAEAHQQH (M16-B2) / HEWM competition titrations, both at $2{\cdot}10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M16-B2 ($2{\cdot}10^{-5}$ M) in competition with HEWM probe ($2{\cdot}10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S18 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of HQQHAEAHQQH peptide

Model	$1{\cdot}10^{-5}$ M[a]		$2{\cdot}10^{-5}$ M[a]	
HQQHAEAHQQH (M16-B2)	$\log(K_{b\text{-}1})$ = 6.79±0.03	$\log(K_{b\text{-}2})$ = 5.94±0.04	$\log(K_{b\text{-}1})$ = 6.77±0.02	$\log(K_{b\text{-}2})$ = 6.00±0.02
	$\log(K_{b\text{-}1})$ = 6.53±0.04	$\log(K_{b\text{-}2})$ = 5.92±0.06	$\log(K_{b\text{-}1})$ = 6.74±0.03	$\log(K_{b\text{-}2})$ = 6.05±0.04
	$\log(K_{b\text{-}1})$ = 6.84±0.03	$\log(K_{b\text{-}2})$ = 5.89±0.03	$\log(K_{b\text{-}1})$ = 6.83±0.02	$\log(K_{b\text{-}2})$ = 6.10±0.03
Average	$\log(K_{b\text{-}1})$ = 6.75 ± 0.11		$\log(K_{b\text{-}2})$ = 5.98 ± 0.08	

[a] The values correspond to the peptide and probe concentrations.

MKKMAEAMKKM (M17-B2)

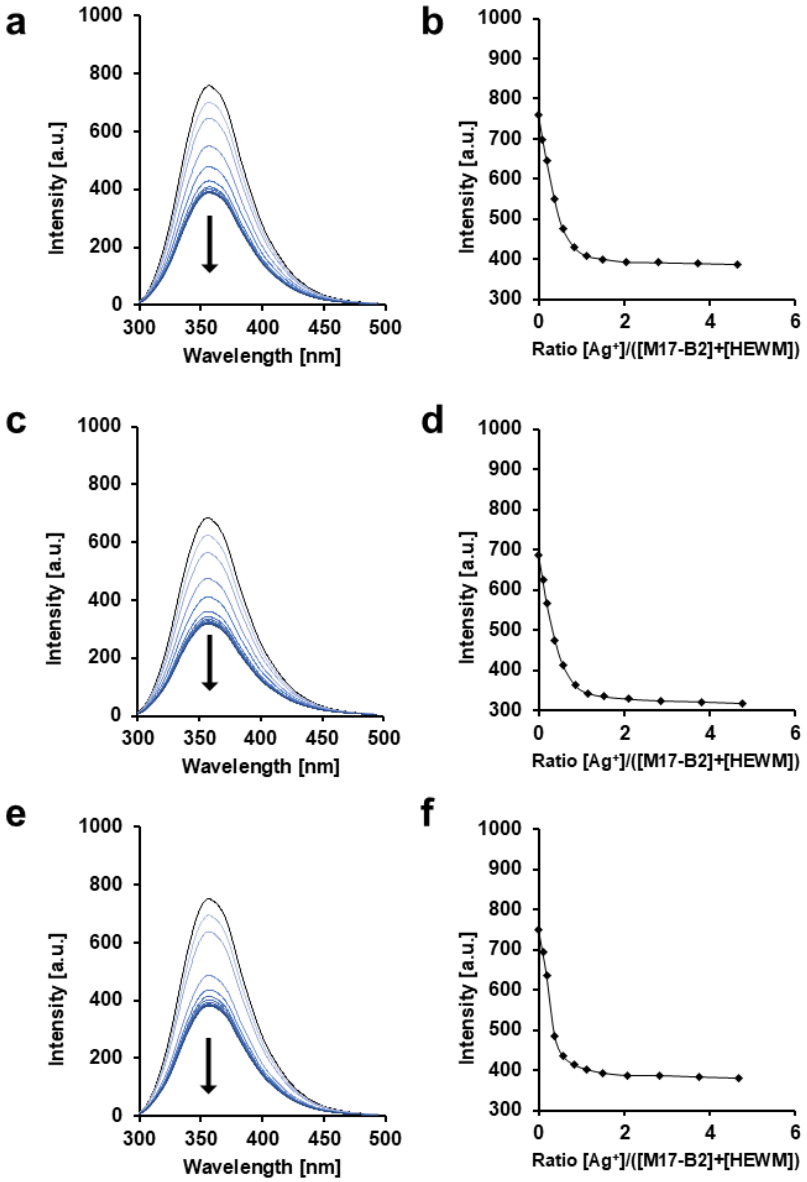

Fig. S62 MKKMAEAMKKM (M17-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M17-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

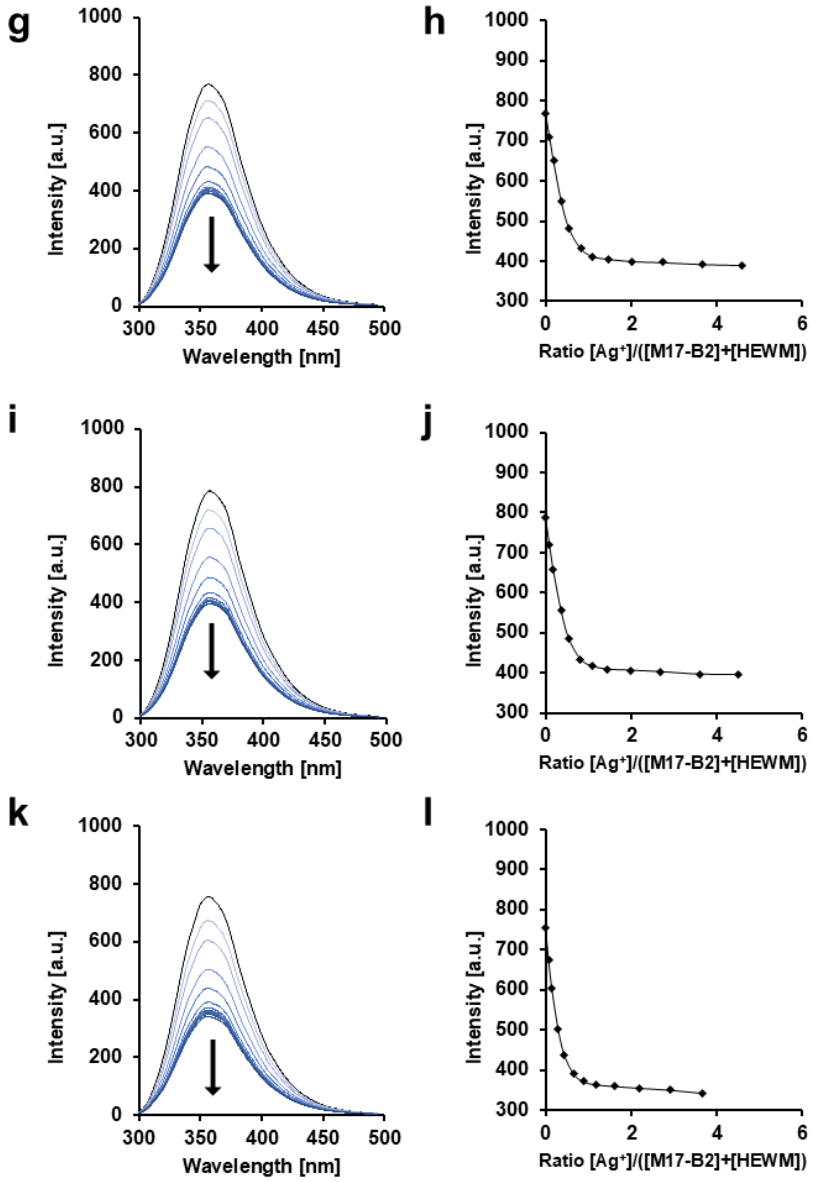

Fig. S63 MKKMAEAMKKM (M17-B2) / HEWM competition titrations, both at $2{\cdot}10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M17-B2 ($2{\cdot}10^{-5}$ M) in competition with HEWM probe ($2{\cdot}10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S19 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of MKKMAEAMKKM peptide

Model	$1{\cdot}10^{-5}$ M[a]		$2{\cdot}10^{-5}$ M[a]	
MKKMAEAMKKM (M17-B2)	$\log(K_{b\text{-}1})$ = 5.68±0.02	$\log(K_{b\text{-}2})$ = 4.35±0.37	$\log(K_{b\text{-}1})$ = 5.59±0.02	$\log(K_{b\text{-}2})$ = 4.28±0.33
	$\log(K_{b\text{-}1})$ = 5.70±0.03	$\log(K_{b\text{-}2})$ = 4.94±0.23	$\log(K_{b\text{-}1})$ = 5.49±0.02	$\log(K_{b\text{-}2})$ = 4.46±0.21
	$\log(K_{b\text{-}1})$ = 5.62±0.06	$\log(K_{b\text{-}2})$ = 4.62±0.38	$\log(K_{b\text{-}1})$ = 5.21±0.09	$\log(K_{b\text{-}2})$ = 4.77±0.40
Average	$\log(K_{b\text{-}1})$ = 5.55 ± 0.18		$\log(K_{b\text{-}2})$ = 4.57 ± 0.24	

[a] The values correspond to the peptide and probe concentrations.

MKKMAEAHQQH (M18-B2)

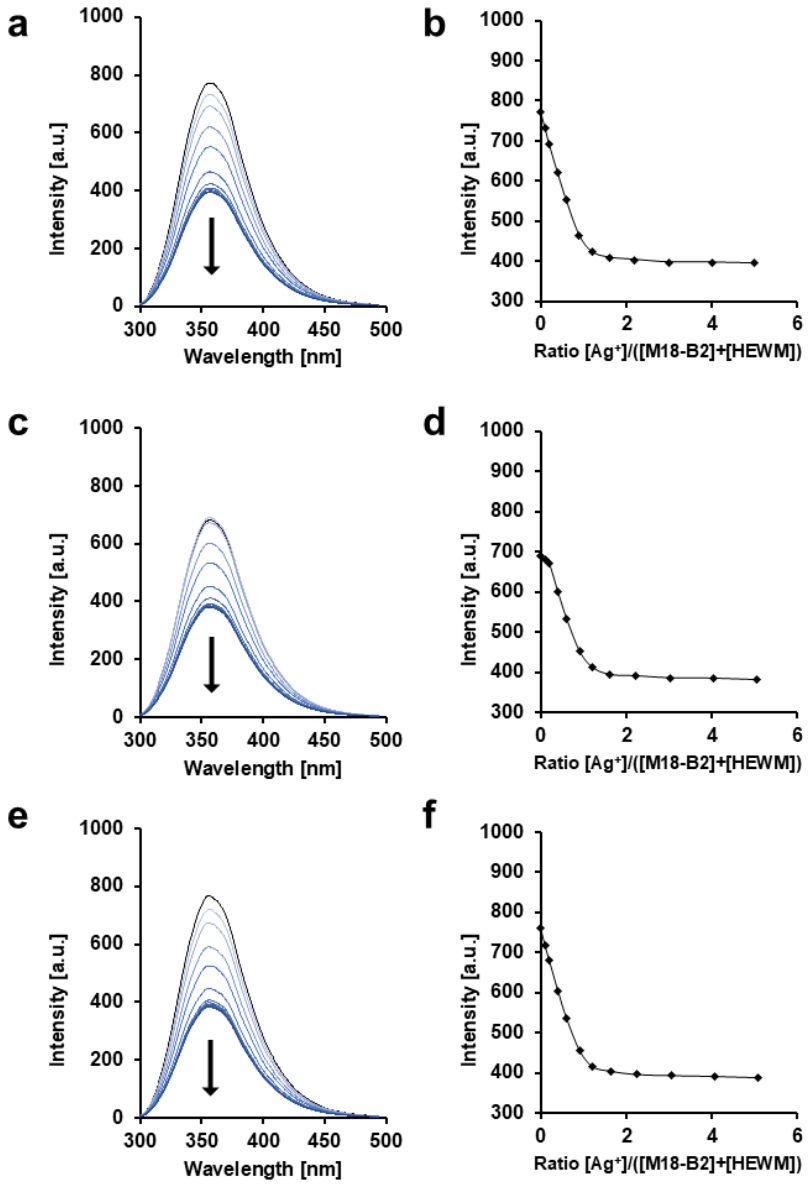

Fig. S64 MKKMAEAHQQH (M18-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M18-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

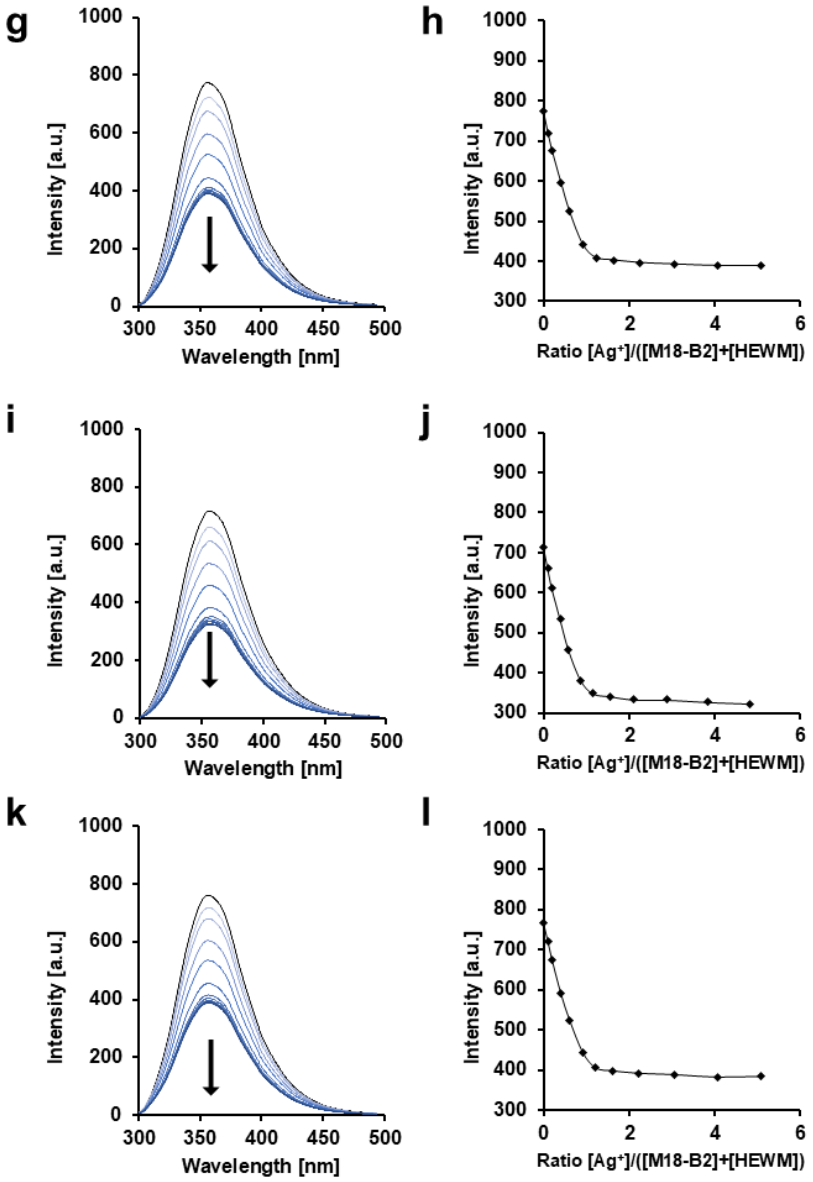

Fig. S65 MKKMAEAHQQH (M18-B2) / HEWM competition titrations, both at $2 \cdot 10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M18-B2 ($2 \cdot 10^{-5}$ M) in competition with HEWM probe ($2 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S20 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of MKKMAEAHQQH peptide

Model	$1 \cdot 10^{-5}$ M[a]		$2 \cdot 10^{-5}$ M[a]	
MKKMAEAHQQH (M18-B2)	$\log(K_{b\text{-}1}) = 6.35 \pm 0.01$	$\log(K_{b\text{-}2}) = 5.08 \pm 0.06$	$\log(K_{b\text{-}1}) = 6.17 \pm 0.02$	$\log(K_{b\text{-}2}) = 4.76 \pm 0.15$
	$\log(K_{b\text{-}1}) = 6.75 \pm 0.05$	$\log(K_{b\text{-}2}) = 4.94 \pm 0.24$	$\log(K_{b\text{-}1}) = 6.05 \pm 0.04$	$\log(K_{b\text{-}2}) = 4.62 \pm 0.31$
	$\log(K_{b\text{-}1}) = 6.31 \pm 0.01$	$\log(K_{b\text{-}2}) = 5.06 \pm 0.06$	$\log(K_{b\text{-}1}) = 6.18 \pm 0.02$	$\log(K_{b\text{-}2}) = 4.93 \pm 0.10$
Average	$\log(K_{b\text{-}1}) = 6.30 \pm 0.24$		$\log(K_{b\text{-}2}) = 4.90 \pm 0.18$	

[a] The values correspond to the peptide and probe concentrations.

HQQHAAAHQQH (M19-B2)

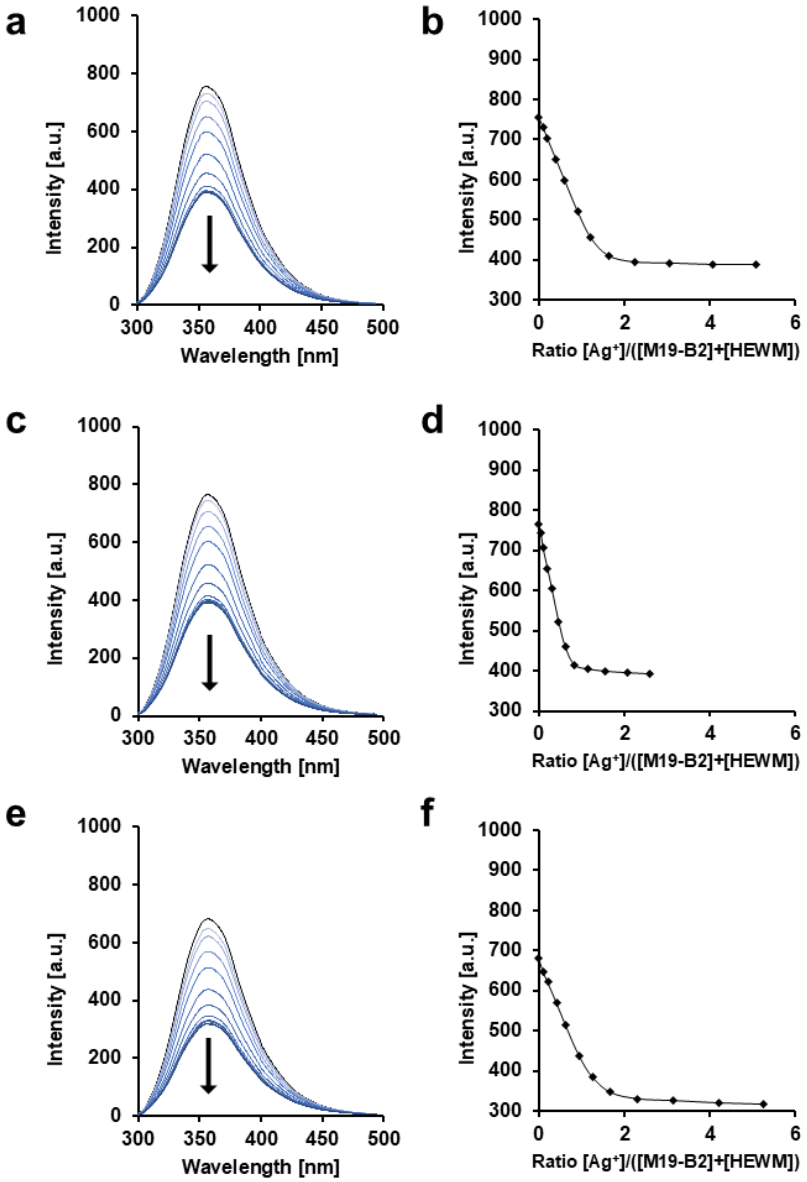

Fig. S66 HQQHAAAHQQH (M19-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M19-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

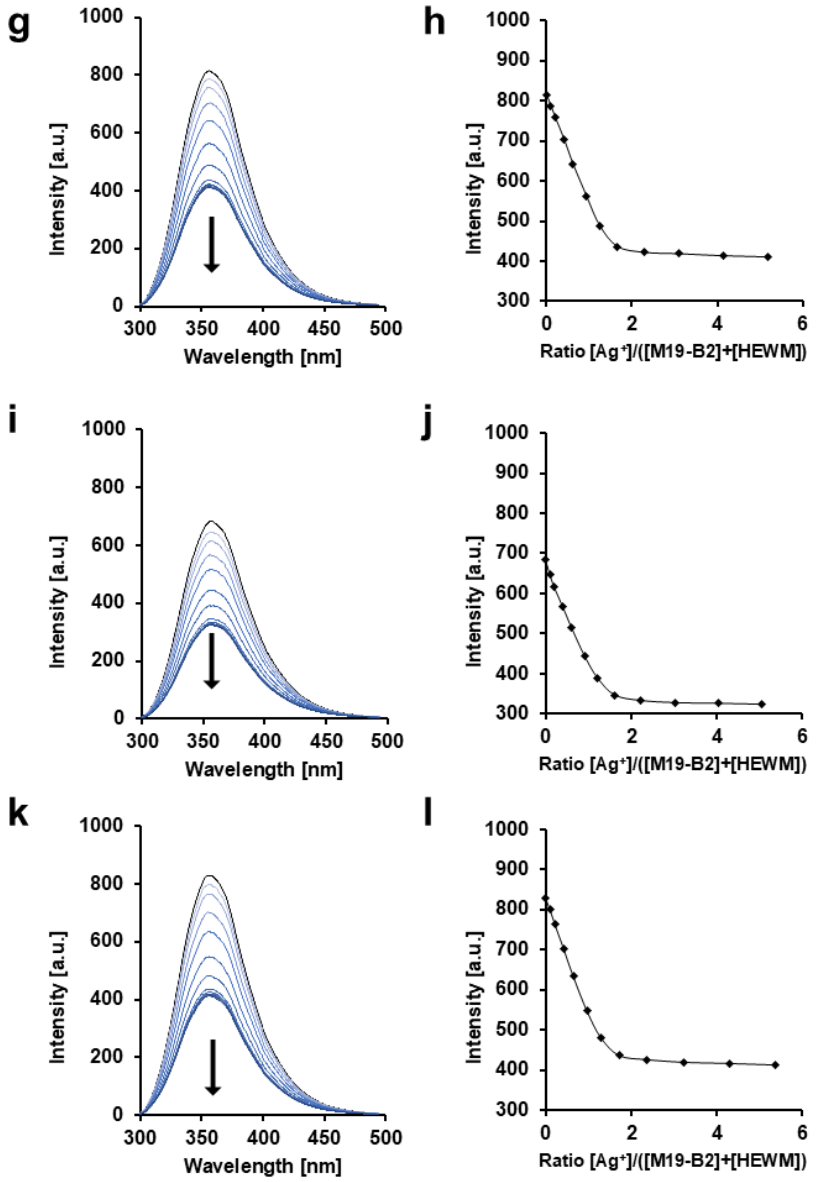

Fig. S67 HQQHAAAHQQH (M19-B2) / HEWM competition titrations, both at $2{\cdot}10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M19-B2 ($2{\cdot}10^{-5}$ M) in competition with HEWM probe ($2{\cdot}10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S21 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of HQQHAAAHQQH peptide

Model	$1{\cdot}10^{-5}$ M[a]		$2{\cdot}10^{-5}$ M[a]	
HQQHAAAHQQH (M19-B2)	$\log(K_{b\text{-}1})$ = 6.72±0.02	$\log(K_{b\text{-}2})$ = 5.88±0.03	$\log(K_{b\text{-}1})$ = 6.71±0.02	$\log(K_{b\text{-}2})$ = 6.01±0.03
	$\log(K_{b\text{-}1})$ = 6.66±0.06	$\log(K_{b\text{-}2})$ = 5.97±0.08	$\log(K_{b\text{-}1})$ = 6.45±0.05	$\log(K_{b\text{-}2})$ = 5.99±0.08
	$\log(K_{b\text{-}1})$ = 6.60±0.06	$\log(K_{b\text{-}2})$ = 5.95±0.11	$\log(K_{b\text{-}1})$ = 6.67±0.02	$\log(K_{b\text{-}2})$ = 5.85±0.03
Average	$\log(K_{b\text{-}1})$ = 6.63 ± 0.10		$\log(K_{b\text{-}2})$ = 5.94 ± 0.06	

[a] The values correspond to the peptide and probe concentrations.

MKKMAAAMKKM (M20-B2)

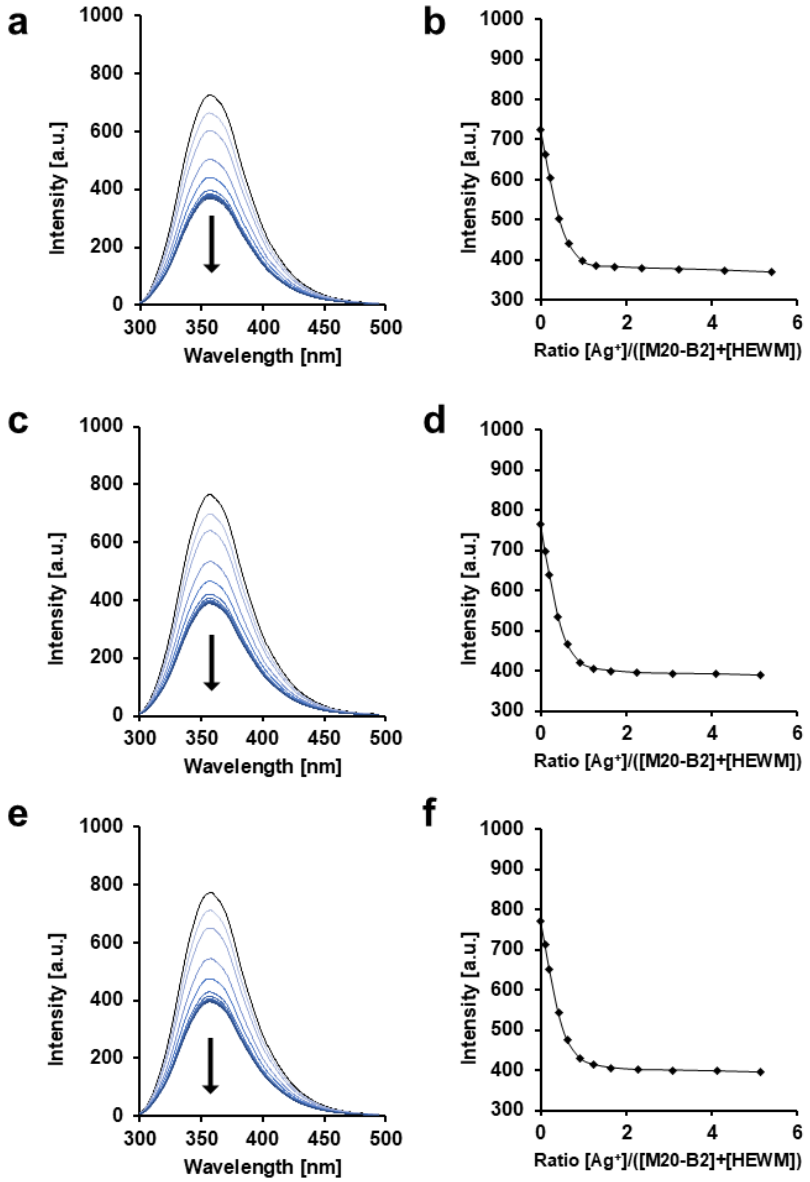

Fig. S68 MKKMAAAMKKM (M20-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M20-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

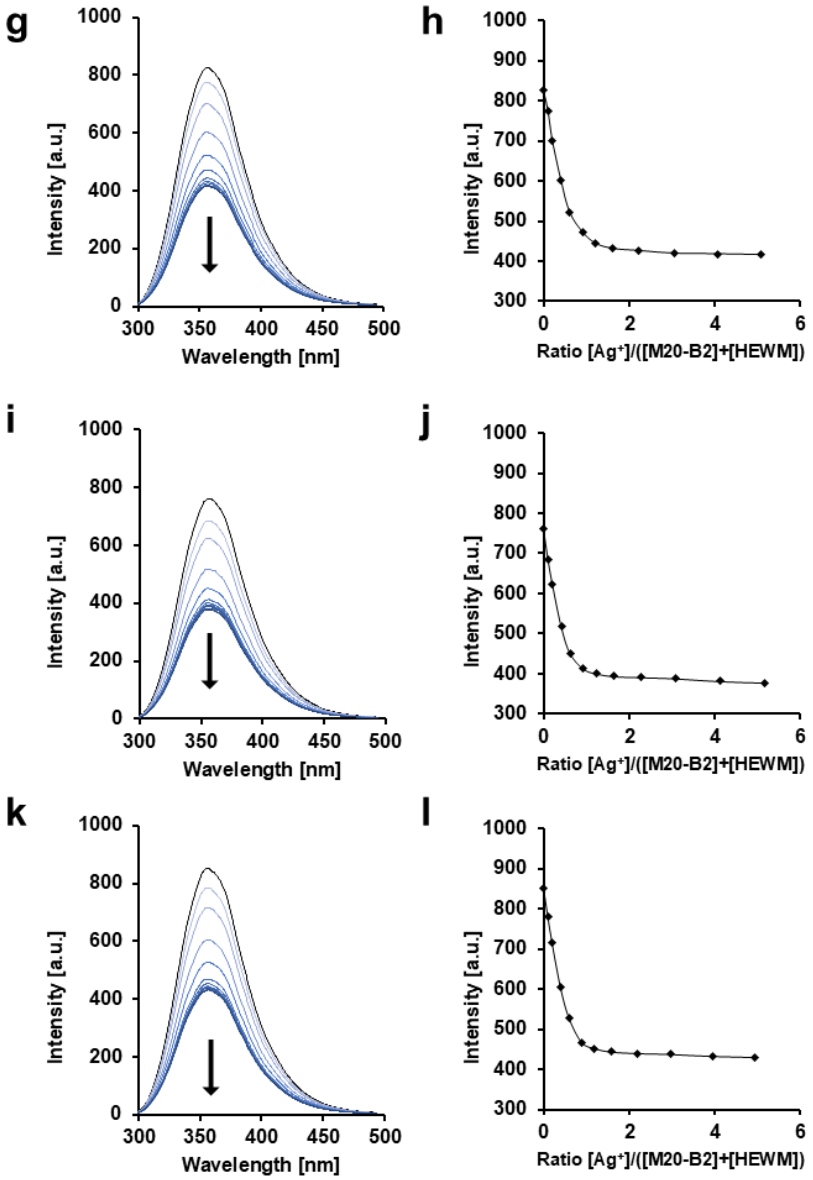

Fig. S69 MKKMAAAMKKM (M20-B2) / HEWM competition titrations, both at $2 \cdot 10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M20-B2 ($2 \cdot 10^{-5}$ M) in competition with HEWM probe ($2 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S22 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of MKKMAAAMKKM peptide

Model	$1 \cdot 10^{-5}$ M[a]		$2 \cdot 10^{-5}$ M[a]	
MKKMAAAMKKM (M20-B2)	$\log(K_{b\text{-}1}) = 5.61 \pm 0.04$	$\log(K_{b\text{-}2}) = 4.68 \pm 0.31$	$\log(K_{b\text{-}1}) = 5.74 \pm 0.07$	$\log(K_{b\text{-}2}) = 4.95 \pm 0.38$
	$\log(K_{b\text{-}1}) = 5.56 \pm 0.03$	$\log(K_{b\text{-}2}) = 4.71 \pm 0.19$	$\log(K_{b\text{-}1}) = 5.40 \pm 0.06$	$\log(K_{b\text{-}2}) = 4.85 \pm 0.34$
	$\log(K_{b\text{-}1}) = 5.63 \pm 0.03$	$\log(K_{b\text{-}2}) = 4.46 \pm 0.36$	$\log(K_{b\text{-}1}) = 5.56 \pm 0.02$	$\log(K_{b\text{-}2}) = 4.49 \pm 0.15$
Average	$\log(K_{b\text{-}1}) = 5.58 \pm 0.11$		$\log(K_{b\text{-}2}) = 4.69 \pm 0.19$	

[a] The values correspond to the peptide and probe concentrations.

MKKMAAAHQQH (M21-B2)

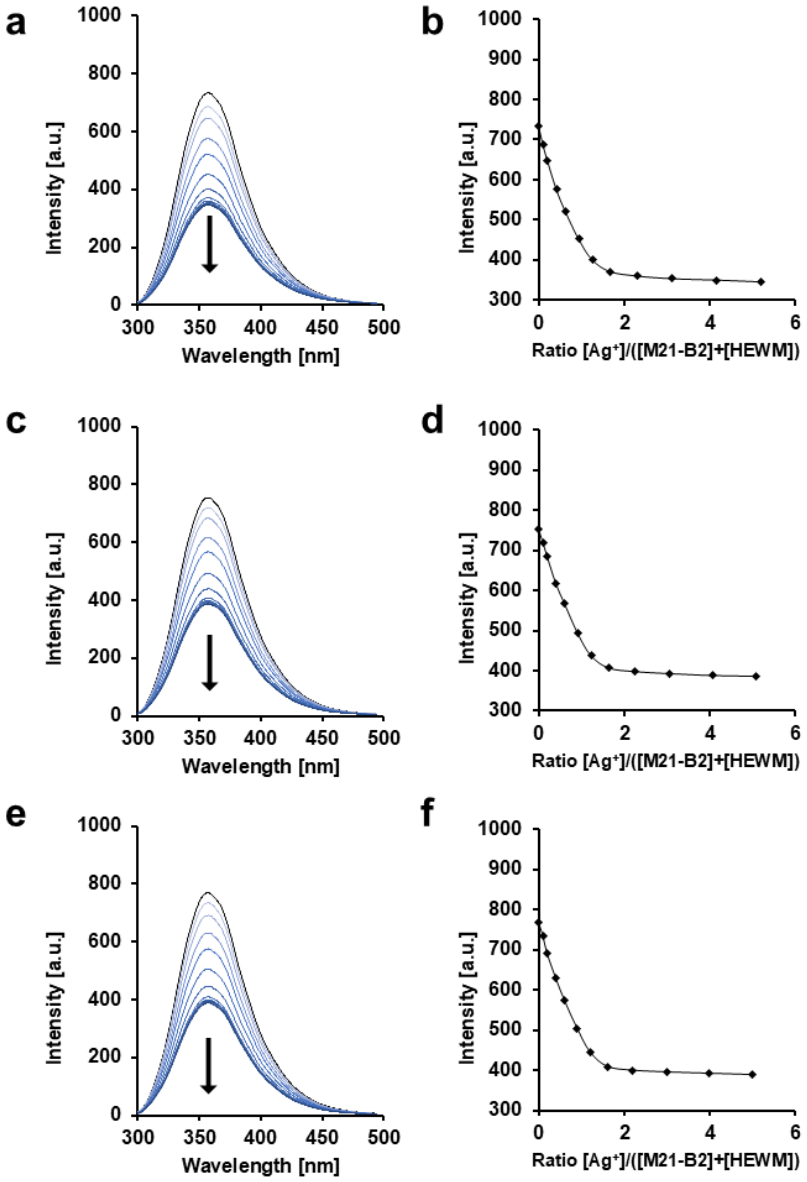

Fig. S70 MKKMAAAHQQH (M21-B2) / HEWM competition titrations, both at $1 \cdot 10^{-5}$ M. (a, c & e) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M21-B2 ($1 \cdot 10^{-5}$ M) in competition with HEWM probe ($1 \cdot 10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (b, d & f) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

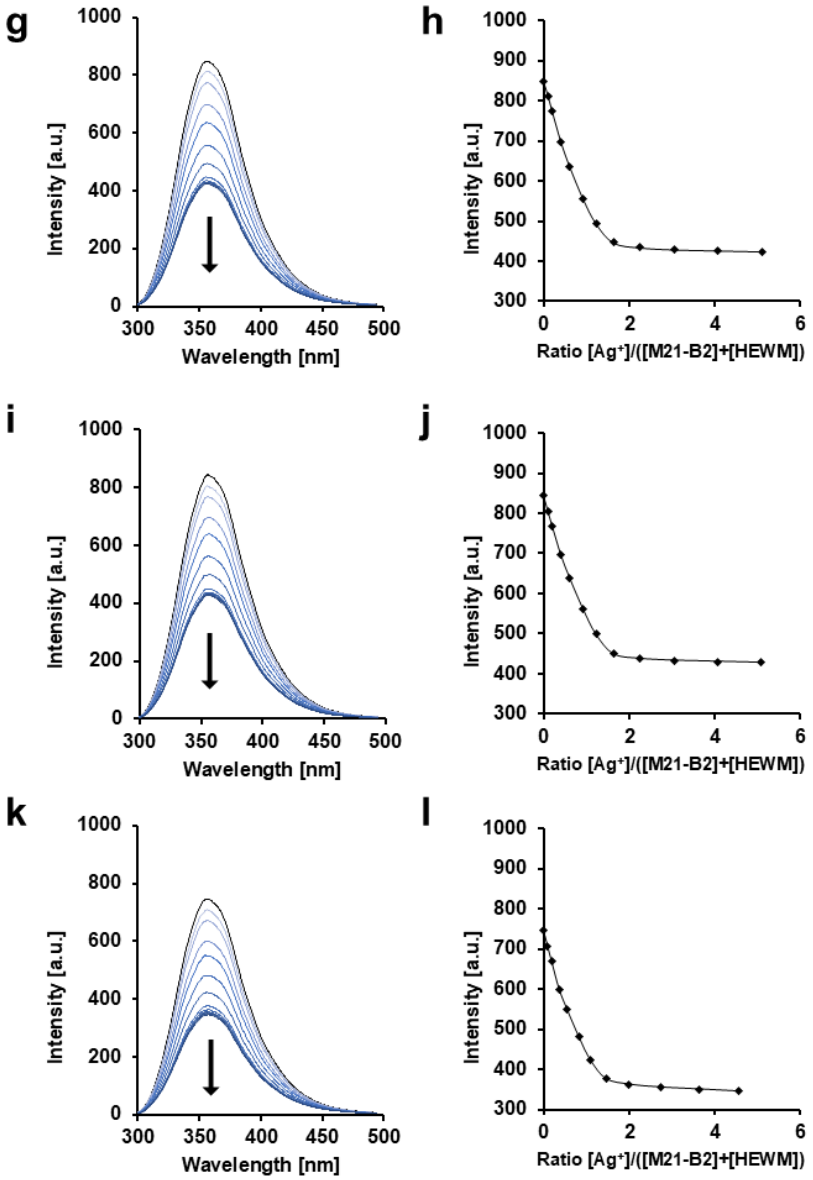

Fig. S71 MKKMAAAHQQH (M21-B2) / HEWM competition titrations, both at $2{\cdot}10^{-5}$ M. (g, i & k) Tryptophan fluorescence (λ_{ex}:280 nm) quench by addition of $AgNO_3$ (0 to 5.5 equivalents) to a solution of M21-B2 ($2{\cdot}10^{-5}$ M) in competition with HEWM probe ($2{\cdot}10^{-5}$ M), in MOPS buffer (20 equivalents, pH 7.4-7.5) at 25°C. (h, j & l) Plot of the maxima of fluorescence intensities. The solid line corresponds to the fit obtained using Dynafit software.[9,10]

Table S23 Determination of the binding constants ($\log(K_{b\text{-}1/b\text{-}2})$) of MKKMAAAHQQH peptide

Model	$1{\cdot}10^{-5}$ M[a]		$2{\cdot}10^{-5}$ M[a]	
MKKMAAAHQQH (M21-B2)	$\log(K_{b\text{-}1})$ = 6.24±0.04	$\log(K_{b\text{-}2})$ = 5.90±0.06	$\log(K_{b\text{-}1})$ = 6.44±0.03	$\log(K_{b\text{-}2})$ = 5.80±0.05
	$\log(K_{b\text{-}1})$ = 6.42±0.04	$\log(K_{b\text{-}2})$ = 5.80±0.08	$\log(K_{b\text{-}1})$ = 6.41±0.02	$\log(K_{b\text{-}2})$ = 5.89±0.03
	$\log(K_{b\text{-}1})$ = 6.38±0.05	$\log(K_{b\text{-}2})$ = 5.85±0.09	$\log(K_{b\text{-}1})$ = 6.29±0.04	$\log(K_{b\text{-}2})$ = 5.77±0.07
Average	$\log(K_{b\text{-}1})$ = 6.36 ± 0.08		$\log(K_{b\text{-}2})$ = 5.83 ± 0.05	

[a] The values correspond to the peptide and probe concentrations.

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