

Structural Optimization of Reversible Dibromomaleimide Peptide Stapling

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SUPPORTING INFORMATION

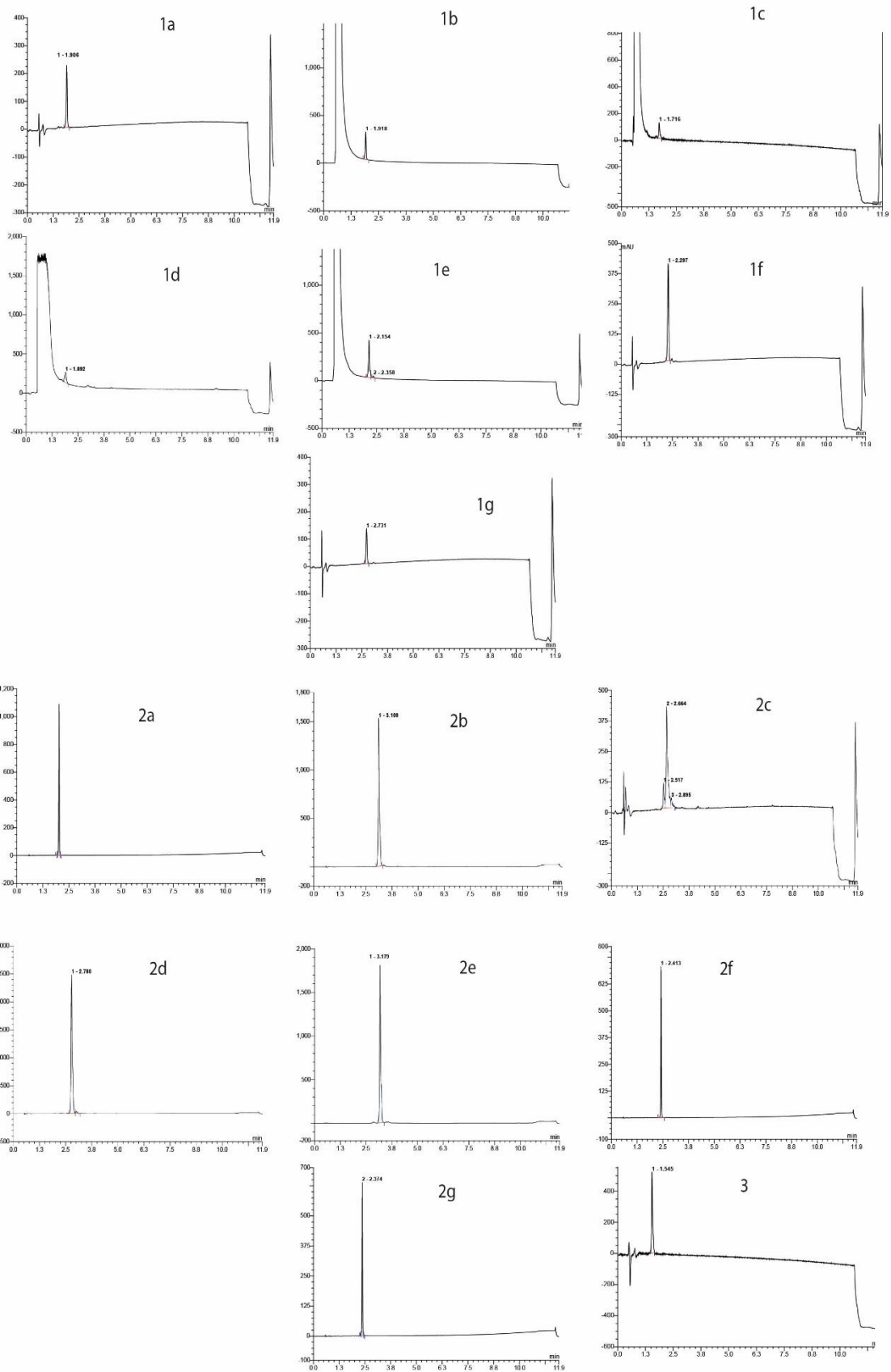
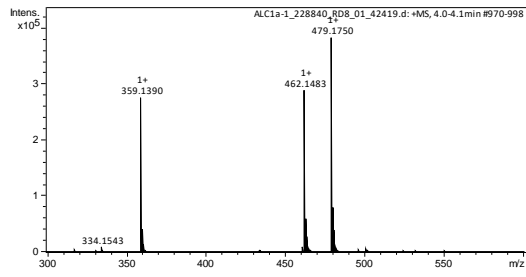


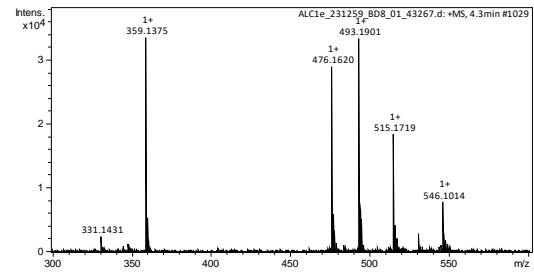
Figure S1. HPLC traces for synthetic peptides

1b

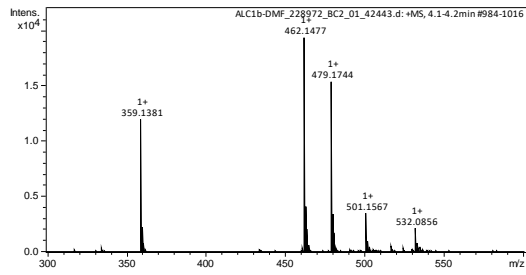
1a



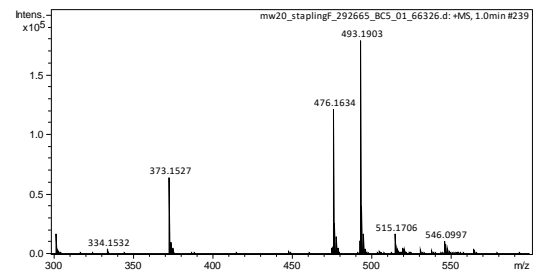
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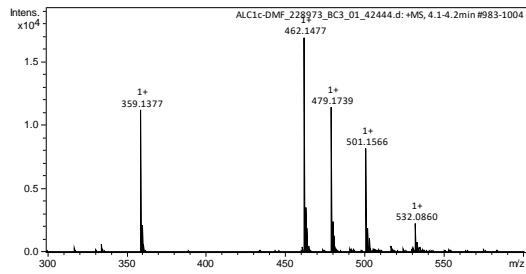
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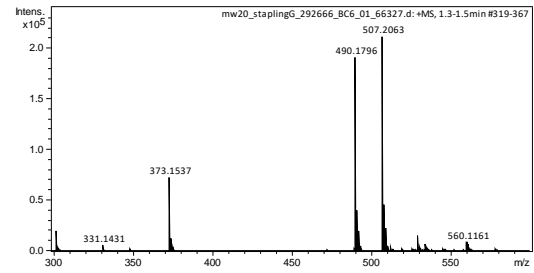
1f



1c



1g



1d

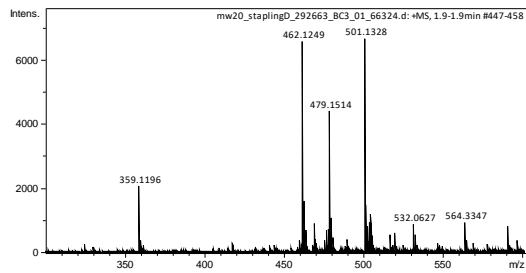
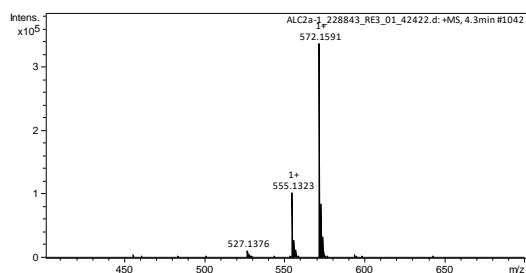


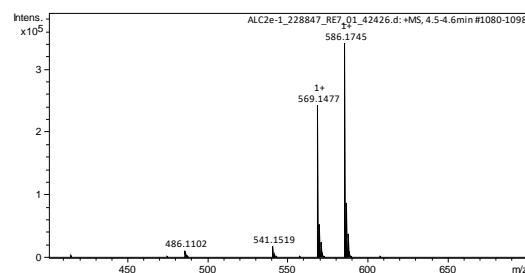
Figure S2. MS spectra for linear synthetic peptides

Except for $M+H^+$ in most of the MS spectra additional peaks corresponding to $M+Na^+$ and $[M-NH_2]^+$ can be observed

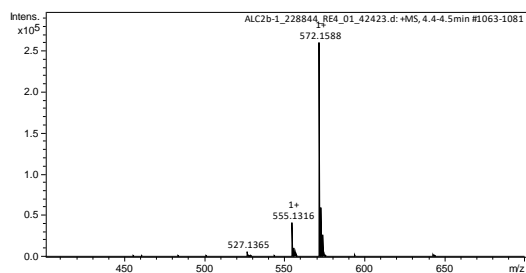
2a



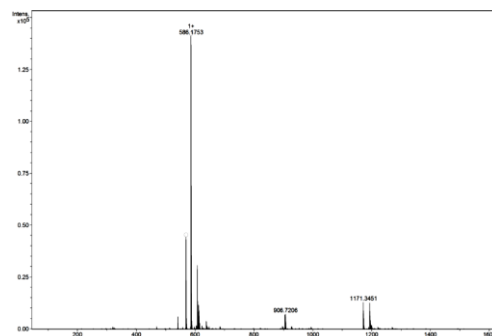
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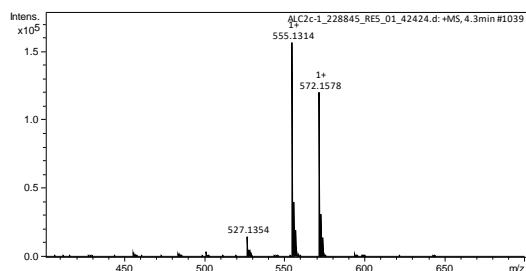
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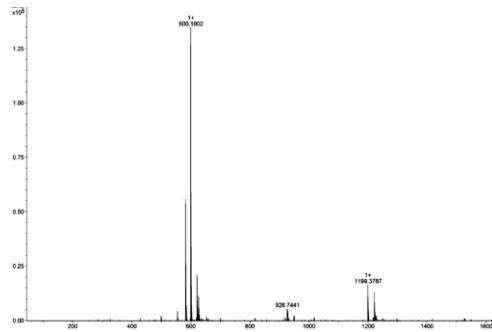
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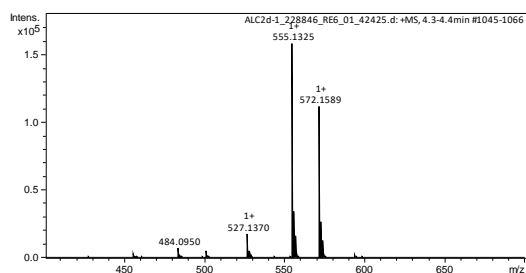
2c



2g



2d



3

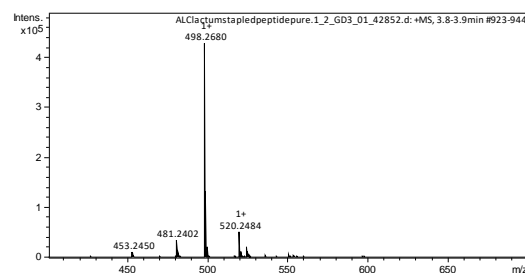


Figure S3. MS spectra for cyclic synthetic peptides.

Except for $M+H^+$ in most of the MS spectra additional peaks corresponding to $[M-NH_2]^+$ can be observed

Empirical formula	C ₂₁ H ₃₃ N ₇ O ₁₀ S ₂
Formula weight	607.66
Temperature/K	120(2)
Crystal system	triclinic
Space group	P1
a/Å	4.9248(3)
b/Å	12.6348(9)
c/Å	12.6584(7)
α/°	115.628(6)
β/°	96.817(5)
γ/°	95.044(6)
Volume/Å ³	696.56(8)
Z	1
ρ _{calc} /cm ³	1.449
μ/mm ⁻¹	2.311
F(000)	320.0
Crystal size/mm ³	0.14 × 0.04 × 0.02
Radiation	CuKα (λ = 1.54184)
2θ range for data collection/°	7.856 to 147.64
Index ranges	-6 ≤ h ≤ 6, -15 ≤ k ≤ 15, -14 ≤ l ≤ 15
Reflections collected	7059
Independent reflections	4047 [R _{int} = 0.0447, R _{sigma} = 0.0602]
Data/restraints/parameters	4047/3/413
Goodness-of-fit on F ²	1.073
Final R indexes [I ≥ 2σ (I)]	R ₁ = 0.0402, wR ₂ = 0.0945
Final R indexes [all data]	R ₁ = 0.0448, wR ₂ = 0.0973
Largest diff. peak/hole / e Å ⁻³	0.34/-0.27
Flack parameter	0.03(2)

Table S1 Experimental data for the crystal structure determination of **2a**. CCDC-1976850 contains additional information in cif format and can be obtained from the CCDC via www.ccdc.cam.ac.uk/structures/.