

Design and pharmacological characterization of $\alpha_4\beta_1$ integrin cyclopeptide agonists: Computational investigation of ligand's determinants for agonism versus antagonism

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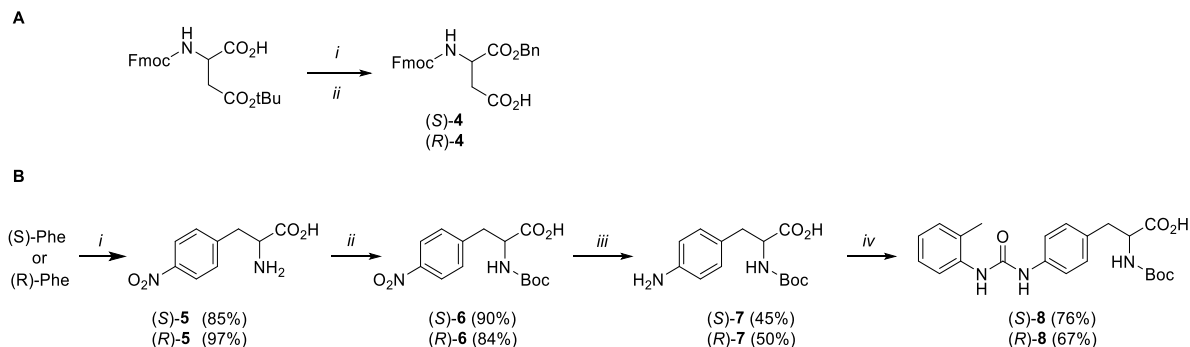
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Chemistry

(*S*)-, (*R*)-*Fmoc-Asp-OBn*, (*S*)-**4**, (*R*)-**4**. A mixture of either (*S*) or (*R*)-*Fmoc-Asp*(*Ot*Bu)-OH (1.0 mmol), tetra-butylammonium bromide (1.0 mmol), and anhydrous K_2CO_3 (1.1 mmol) in acetonitrile (5 mL) was stirred at RT for 20 min. A solution of benzyl bromide (1.1 mmol) in acetonitrile (4 mL) was then added dropwise under vigorous stirring. The mixture was stirred for 12 h at RT, then the precipitate was filtered off, and the filtrate was evaporated to dryness. The resulting crude material was dissolved in EtOAc, and the organic layer was washed three times with sat. $NaHCO_3$, H_2O and brine, dried over Na_2SO_4 , and finally the solvent was evaporated at reduced pressure to afford the product as a white solid, used without further isolation. (*S*)-*Fmoc-Asp*(*Ot*Bu)-*OBn* (98%, 85% pure as determined by RP HPLC, General Methods). ESI MS m/z calcd. for $[C_{30}H_{31}NO_6Na]^+$ 524.2, found 524.2 $[M+Na]^+$. (*R*)-*Fmoc-Asp*(*Ot*Bu)-*OBn* (94%, 90% pure), ESI MS m/z calcd. for $[C_{30}H_{31}NO_6Na]^+$ 524.2, found 524.2 $[M+Na]^+$.

Either (*S*)- or (*R*)-*Asp*(*Ot*Bu)-*OBn* were treated with 25% TFA in DCM (4 mL) at 0°C under stirring for 3 h. The solvent was distilled at reduced pressure, then ice-cold water was added to the residue and the suspension was allowed to stir overnight. The resulting precipitate was collected by filtration, dried under high *vacuum* and used without further purifications. (*S*)-**4** (98%, 89% pure as determined by RP HPLC, General Methods), ESI MS m/z calcd. for $[C_{26}H_{24}NO_6]^+$ 446.2, found 446.2 $[M+H]^+$. (*R*)-**4** (95%, 92% pure), ESI MS m/z calcd. for $[C_{26}H_{24}NO_6]^+$ 446.2, found 446.3 $[M+H]^+$.



Scheme S1. (A) Preparation of (*S*)- or (*R*)-*Fmoc-Asp-OBn*, (*S*)-**4** or (*R*)-**4**. *Reagents and conditions*: i) benzyl-Br, Bu_4NBr , K_2CO_3 ; ii) TFA, DCM, RT. (B) Preparation of (*S*)- or (*R*)-*Boc-Phu-OH* (*S*)-**8** or (*R*)-**8**. *Reagents and conditions*: i) H_2SO_4 , HNO_3 , 0 °C, 1 h; ii) Boc_2O , Na_2CO_3 , H_2O /dioxane, RT, 12 h; iii) H_2 , Pd/C, MeOH, RT, 3 h; iv) *o*-tolyl isocyanate, DMF, RT, 3 h.

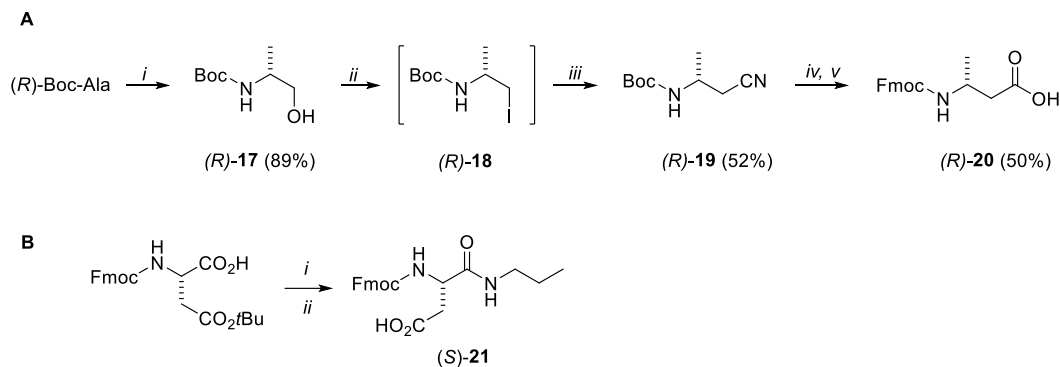
(*S*)-, (*R*)-*4-NO₂-Phe*, (*S*)-**5**, (*R*)-**5**. Phenylalanine (1.0 mmol) was added in small portion to conc. H_2SO_4 (6.0 mmol) until complete dissolution. The mixture was then cooled to 0°C, and conc. HNO_3 (0.65 mmol) was added dropwise. The reaction was stirred for 1 h at 0°C. Then, ice-cold H_2O (20 mL) was slowly added to the reaction mixture and stirred for additional 15 min. The mixture was heated to 100°C for 1 min and cooled to RT, then pH was corrected to 5-6 with 28% NH_4OH . The mixture was concentrated at reduced pressure and kept overnight for crystallization. The crystals were filtered, washed with water (5 mL) and dried under high *vacuum* to give (*S*)- or (*R*)-**5** as white solids. (*S*)-**5** (85%, 95% pure as determined by RP HPLC), ESI-MS m/z calcd. for $[C_9H_{11}N_2O_4]^+$ 211.1, found 211.2 $[M+H]^+$. (*R*)-**6** (97%, 94% pure), ESI-MS m/z calcd. for $[C_9H_{11}N_2O_4]^+$ 211.1, found 211.1 $[M+H]^+$.

(*S*)-, (*R*)-*Boc-4-NO₂-Phe*, (*S*)- **6**, (*R*)-**6**. Boc_2O (1.2 mmol) was added to a suspension of (*S*)- or (*R*)-**5** (1.0 mmol) and Na_2CO_3 (2.0 mmol) in 1:1 H_2O /Dioxane (10 mL) at 0°C, and the mixture was stirred overnight at RT. Dioxane was distilled under reduced pressure, the alkaline aqueous layer was adjusted to pH 3-4 with 0.5 M HCl, then the mixture was extracted three times with EtOAc (10 mL). The combined organic phases were dried over Na_2SO_4 , and the solvent was removed at reduced pressure, to afford (*S*)- or (*R*)-**6**, which were used without further purifications. (*S*)-**6** (90%, 90% pure as determined by RP HPLC, General

Methods), ESI-MS m/z calcd. for $[C_{14}H_{18}N_2O_6Na]^+$ 333.1, found 333.2 $[M+Na]^+$. (*R*)-**6** (84%, 90% pure), ESI-MS m/z calcd. for $[C_{14}H_{18}N_2O_6Na]^+$ 333.1, found 333.1 $[M+Na]^+$.

(*S*)-, (*R*)-*Boc-4-NH₂-Phe*, (*S*)-**7**, (*R*)-**7**. The nitro group of (*S*)- or (*R*)-**6** (1.0 mmol) was reduced by hydrogenation in MeOH in the presence of 10% *w/w* Pd/C while stirring for 3 h at RT. The mixture was filtered over a Celite® pad and the solvent was removed under reduced pressure. Then, Et₂O was added to the residue and the suspension was allowed to stir overnight. The resulting precipitate was collected by filtration, dried under high *vacuum* and used without further purifications: (*S*)-**7** (45%, 95% pure as determined by RP HPLC, General Methods), ESI MS m/z calcd. for $[C_{14}H_{21}N_2O_4]^+$ 281.1, found 281.1 $[M+H]^+$, 181.2 $[M-Boc+H]^+$. (*R*)-**7** (50%, 95% pure), ESI MS m/z calcd. for $[C_{14}H_{21}N_2O_4]^+$ 281.1, found 281.1 $[M+H]^+$.

(*S*)-, (*R*)-*Boc-Phu-OH*, (*S*)-**8**, (*R*)-**8**. *o*-Tolyl isocyanate (1.1 mmol) was added dropwise to a solution of either (*S*)-**7** or (*R*)-**7** (1.0 mmol) in DMF (3 mL) at RT under N₂ atmosphere. The mixture was stirred for 3 h, then ice-cold Et₂O (20 mL) was added and the precipitate (*S*)-**8** or (*R*)-**8** was collected as a brownish solid by filtration. (*S*)-**8** (76%, 95% pure as determined by RP HPLC, General Methods), ESI MS m/z calcd. for $[C_{22}H_{27}N_3O_5Na]^+$ 436.1, found 436.2 $[M+Na]^+$, 314.2 $[M-Boc+H]^+$. (*R*)-**8** (67%, 95% pure), ESI MS m/z calcd. for $[C_{22}H_{27}N_3O_5Na]^+$ 436.1, found 436.2 $[M+Na]^+$, 314.1 $[M-Boc+H]^+$. ¹H NMR (400 MHz, DMSO-*d*₆) δ 7.63 (d, 1H), 7.43 (d, 1H), 6.85-7.25 (m, 6H), 4.23 (m, 1H), 3.15 (dd, 1H), 2.9 (dd, 1H), 2.3 (s, 3H), 1.4 (s, 9H).



Scheme S2. (A) Preparation of (*R*)-*N*-Boc- β^3 -homoAla **20**. *Reagents and conditions:* i) NMM, ethyl chloroformate, THF, 0°C - RT, 15 min, then NaBH₄, 0°C - RT, 10 min; ii) PPh₃, I₂, imidazole, DCM, reflux, 3 h; iii) KCN, DMSO, 60 °C, 4 h; iv) HCl 3M, reflux, 12 h; v) Fmoc-Cl, Na₂CO₃, in 1:1 H₂O/dioxane at RT. (B) Synthesis of Fmoc-(*R*)-Asp-propylamide. *Reagents and conditions:* i) *n*-propylamine, EDC·HCl, HOBt, TEA, DM1F/DCM, RT, 3 h; ii) TFA, DCM, RT, 1 h.

(*R*)-*tBu*-(1-hydroxypropan-2-yl)carbamate, **17**. To a stirred solution of NMM (1.1 mmol) and Boc-(*R*)-Ala-OH (1.0 mmol) in dry THF (5 mL), ethyl chloroformate (1.1 mmol) was added dropwise at 0 °C under inert atmosphere. After 15min, the solution was filtered and the precipitated was washed with THF (5 mL). The filtrates were collected, and a solution of NaBH₄ (1.25 mmol) in H₂O (5 mL) was then added dropwise at 0°C under stirring. The mixture was risen to RT, and after 10 min the solvent was distilled under reduced pressure. The residue was re-dissolved in EtOAc (30 mL) and the suspension was washed with H₂O and brine (5 mL each), then dried Na₂SO₄. The solvent was distilled under reduced pressure, giving **17** (89%) as a yellow oil, which was used without further purifications. ¹H-NMR (400 MHz, CDCl₃) δ 4.67 (br s, 1H, NH), 3.78-3.60 (m, 1H, CH α), 3.50 (dd, *J* = 13.8, 7.0 Hz, 1H, CH β), 3.26 (dd, *J* = 12.4, 7.0 Hz, 1H, CH β), 1.43 (s, 9H, *t*Bu), 1.27 (d, *J* = 6.8 Hz, 3H, CH₃). ESI-MS m/z calcd. for $[C_8H_{18}NO_3]^+$ 176.1, found 176.2 $[M+H]^+$.

(*R*)-*tBu*-(1-cyanopropan-2-yl)carbamate, **19**. To a stirred solution of triphenylphosphine (1.25 mmol) in dry DCM (10 mL), I₂ (1.3 mmol) was added at RT under inert atmosphere. After 15 min, imidazole (2.5 mmol) was added and the mixture was stirred for additional 15 min. A solution of the crude **17** (1.0 mmol) in

dry DCM (5 mL), was added and the mixture was heated to reflux for 3 h. Then the mixture was cooled and diluted with DCM (40 mL), and washed with 10% aq Na₂S₂O₅ (20 mL) and brine (20 mL). The organic layer was dried over Na₂SO₄ and the solvent was evaporated at reduced pressure. The crude iodide **18** so obtained was then dissolved in dry DMSO (30 mL) and KCN (2.0 mmol) was added in one portion. The mixture was stirred under inert atmosphere at 60 °C for 4 h. The solution was then poured into water (10 mL), and the mixture was extracted twice with EtOAc (40 mL). The organic layer was washed with brine (20 mL) and dried over Na₂SO₄ and then evaporated at reduced pressure. The crude residue was purified by flash chromatography over silica gel (eluent cyclohexane/EtOAc 80:20) to give **19** (52 % over two steps).

Fmoc-(R)-β³-homoAla **20**. The nitrile **19** (1.0 mmol) was dissolved in 6M HCl (10 mL) and heated to reflux for 12 h. The reaction mixture was then cooled at 0 °C and neutralized with 2M NaOH solution. The mixture was concentrated under reduced pressure to afford β³-homoAla as HCl salt. The resulting salt was suspended in a mixture of 1:1 H₂O/dioxane (5 mL) and Na₂CO₃ (2.0 mol) and finally Fmoc-Cl (1.0 mmol) was added at 0 °C. The reaction was stirred at RT overnight, then the mixture was concentrated under reduced pressure, and the basic aqueous layer was adjusted to pH 3-4 with 0.5 M HCl, and the mixture was extracted three times with EtOAc (20 mL). The combined organic phases were dried over Na₂SO₄, and concentrated under reduced pressure. The residue was purified by flash chromatography over silica gel (eluent cyclohexane/EtOAc/AcOH 60:40:1) to afford **20** (55%). ESI-MS *m/z* calcd. for [C₁₉H₂₀NO₄]⁺ 326.1, found 326.2 [M+H]⁺.

Fmoc-(R)-Asp-N-propylamide **21**. A mixture of Fmoc-(R)-Asp(OtBu)-OH (1.2 mmol), EDC·HCl (1.5 eq), HOBt (1.5 eq) and TEA (3.0 eq) in 3:1 DMF/DCM (5 mL) was stirred at RT for 10 min, then *n*-propylamine (1.5 mmol) was added, and the mixture was stirred under N₂ at RT for 3 h. Then the solvent was distilled at reduced pressure, and the residue was purified by flash chromatography over silica gel (eluent cyclohexane/EtOAc 70:30) to afford Fmoc-(R)-Asp(OtBu)-N-propylamide (69%). ¹H-NMR (400 MHz, CDCl₃) δ 7.78 (d, *J* = 7.5 Hz, 2H, ArH), 7.60 (d, *J* = 7.5 Hz, 2H, ArH), 7.42 (t, *J* = 7.5 Hz, 2H, ArH), 7.33 (t, *J* = 7.4 Hz, 2H, ArH), 6.47 (br.t, 1H, propylNH), 5.97 (d, *J* = 8.0 Hz, 1H, AspNH), 4.45 (d, *J* = 6.8 Hz, 2H, FmocCH₂), 4.23 (m, 1H, AspH_α), 3.22 (q, *J* = 5.9 Hz, 2H, propylCH₂), 2.93 (dd, *J* = 17.0, 3.8 Hz, 1H, AspH_β), 2.60 (dd, *J* = 17.2, 6.8 Hz, 1H, AspH_β), 1.57-1.48 (m, 2H, propylCH₂), 1.46 (s, 9H, *t*-Bu), 0.91 (t, *J* = 7.4 Hz, 3H, propylCH₃). ESI-MS *m/z* calcd. for [C₂₆H₃₃N₂O₅]⁺ 453.2, found 453.0 [M+H]⁺. Removal of *t*Bu-protecting group was performed with 25% TFA in DCM (4 mL) at 0°C under stirring for 3 h. Thereafter the solvent was distilled at reduced pressure and the residue was triturated in Et₂O (10 mL), giving **21** in quantitative yield, directly used in the next step without further purifications. ESI-MS *m/z* calcd. for [C₂₂H₂₅N₂O₅]⁺ 397.2, found 397.0 [M+H]⁺.

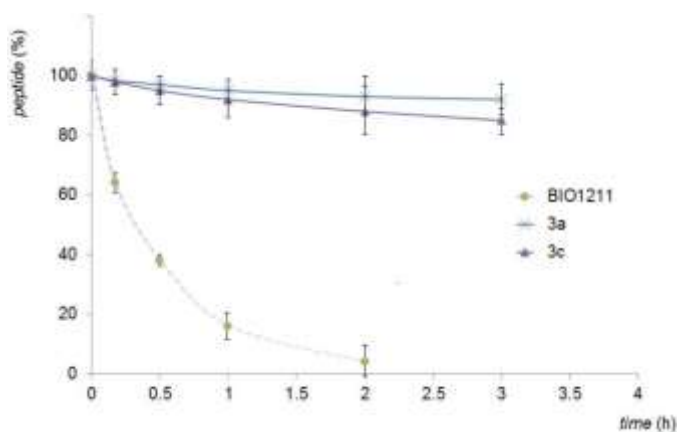


Figure S1

Degradation of BIO1211, **3a**, **3c** in mouse serum. Samples were collected from the incubation solution at the indicated times. Peptide stability was determined using an RP-HPLC ESI-MS analysis (described in the Methods). Values are presented as mean ± SD (n = 3).

Table S1. RP HPLC and ESI MS analyses of the linear precursors **9** and of the cyclopeptides **10**, and reaction yields.

9	Linear peptide sequence ^a	Yield (%) ^b	Purity (%) ^c	ESI MS [M+1] ⁺ found/calcd. ^d	10	Yield (%) ^e	Purity (%) ^f	ESI-MS [M+1] ⁺ found/calcd. ^d	CPP ^g
-	H-isoAsp(OBn)-Phu-Leu-Asp(OBn)-Val-OH	30	76	936.2/936.4 ^h	a	traces	nd	nd	3a
-	H-Asp(OBn)-Val-isoAsp(OBn)-Phu-Leu-OH	32	78	936.2/936.4 ^h	a	traces	nd	nd	3a
a	H-(<i>S</i>)-Phu-Leu-Asp(OBn)-Val-(<i>S</i>)-Asp-OBn	22	80	936.2/936.4 ^h	a	28	98	918.2/918.4 ⁱ	3a
b	H-(<i>S</i>)-Phu-Leu-Asp(OBn)-Val-(<i>R</i>)-Asp-OBn	24	81	936.2/936.4 ^h	b	19	97	918.2/918.4 ⁱ	3b
c	H-(<i>R</i>)-Phu-Leu-Asp(OBn)-Val-(<i>S</i>)-Asp-OBn	34	79	936.2/936.4 ^h	c	29	97	918.2/918.4 ⁱ	3c
d	H-(<i>R</i>)-Phu-Leu-Asp(OBn)-Val-(<i>R</i>)-Asp-OBn	44	85	936.6/936.4 ^h	d	34	99	918.6/918.4 ⁱ	3d
e	H-(<i>S</i>)-Phu-Leu-Asp(OBn)-Val-(<i>R</i>)-β ³ homoAla-OH	27	75	816.6/816.4 ^j	e	50	95	798.2/798.4 ^k	11a
f	H-(<i>S</i>)-Phu-Leu-Ala-Val-(<i>S</i>)-Asp-OBn	46	83	802.6/802.4 ^l	f	37	96	784.4/784.4 ^m	12a
g	H-(<i>S</i>)-Phu-Leu-Asp(OBn)-Val-(<i>S</i>)-Asp-nPr ^a	45	82	887.4/887.4 ⁿ	g	27	95	869.2/869.4 ^o	13
h	H-(<i>R</i>)-Phu-Leu-Asp(OBn)-Val-(<i>R</i>)-β ³ homoAla-OH	47	78	816.6/816.4 ^j	h	33	98	798.2/798.4 ^k	11c
i	H-(<i>R</i>)-Phu-Leu-Ala-Val-(<i>S</i>)-Asp-OBn	40	79	802.6/802.4 ^l	i	15	97	784.2/784.4 ^m	12c
j	H-(<i>S</i>)-Phu-Phe-Asp(OBn)-Val-(<i>S</i>)-Asp-OBn	48	73	970.2/970.4 ^p	j	25	97	952.2/952.4 ^q	14
k	H-(<i>S</i>)-Phu-Phe-Ala-Val-(<i>S</i>)-Asp-OBn	36	85	836.2/836.4 ^r	k	48	98	818.2/818.4 ^s	15
l	H-(<i>R</i>)-Phu-Leu-Asp(OBn)-Phg-(<i>S</i>)-Asp-OBn	37	74	970.2/970.4 ^p	l	43	96	952.2/952.4 ^q	16

^a isoAsp(OBn) corresponds to Asp-OBn; isoAsp(nPr) corresponds to Asp-nPr. ^b based on the estimated loading of the resin. ^c Determined by analytical RP HPLC (General methods) on a C18 RP column (100×3 mm, 3 μm, 110 Å), mobile phase from 9:1 H₂O/CH₃CN/0.1% HCOOH to 2:8 H₂O/CH₃CN/0.1% HCOOH in 20 min, flow rate of 1.0 mL min⁻¹. ^d MS single quadrupole HP 1100MSD detector. ^e Determined after semi-preparative RP HPLC (General methods) on a C18 RP column (21.2×150 mm, 7 μm 80 Å), mobile phase from 8:2 H₂O/CH₃CN to 100% CH₃CN in 10 min, flow rate 12 mL min⁻¹ for CPPs **10a-i**, or on a C18 RP column (19×150 mm, 5 μm 130 Å), isocratic mobile phase 1:1 H₂O/CH₃CN/0.1% TFA in 8 min, followed by 100% CH₃CN in 5 min, flow rate 10 mL min⁻¹ for CPPs **10j-l**. ^f Same stationary phase as for ^c, mobile phase from 9:1 H₂O/CH₃CN to 2:8 H₂O/CH₃CN in 20 min, flow rate 1.0 mL min⁻¹. ^g Ester deprotection proceeded in nearly quantitative yield; purities are reported in Table 1 and 2. ^h Calcd for [C₅₀H₆₂N₇O₁₁]⁺. ⁱ Calcd for [C₅₀H₆₀N₇O₁₀]⁺. ^j Calcd for [C₄₃H₅₈N₇O₉]⁺. ^k Calcd for [C₄₃H₅₆N₇O₈]⁺. ^l Calcd for [C₄₂H₅₆N₇O₉]⁺. ^m Calcd for [C₄₂H₅₄N₇O₈]⁺. ⁿ Calcd for [C₄₆H₆₃N₈O₁₀]⁺. ^o Calcd for [C₄₆H₆₁N₈O₉]⁺. ^p Calcd for [C₅₃H₆₀N₇O₁₁]⁺. ^q Calcd for [C₅₃H₅₈N₇O₁₀]⁺. ^r Calcd for [C₄₅H₅₄N₇O₉]⁺. ^s Calcd for [C₄₅H₅₂N₇O₈]⁺. nd: not determined.

Cell culture. Jurkat E6.1 (expressing $\alpha_4\beta_1$ and $\alpha_L\beta_2$ integrin), K562 (expressing $\alpha_5\beta_1$ integrin) and HL60 (expressing $\alpha_M\beta_2$ integrin) cell lines were purchased from ATCC (Rockville, MD, USA); these cells were routinely cultured in RPMI-1640 (Life Technologies) supplemented with glutamine and 10% FBS. RPMI8866 cells were a kind gift from Prof. A. Santoni (Mayo Foundation for Medical Education and Research, Rochester, MN, USA); RPMI8866 cells were routinely grown in RPMI-1640 enriched with 10% FBS, 5 mM Hepes and 0.5 mM sodium pyruvate and usually kept in 50 mL of culture medium and allowed to form large clumps. Cells were grown at 37 °C under 5% CO₂ humidified atmosphere. 40 h before the adhesion assays, K562 and HL60 cells were treated with 25 nM or 40 nM phorbol 12-myristate 13-acetate (PMA; Sigma-Aldrich), respectively, to induced cell differentiation and to increased $\alpha_5\beta_1$ or $\alpha_M\beta_2$ integrin expression on cell surface (Baiula et al., 2016).

Cell adhesion assays. Concentration-response curves, obtained from cell adhesion assays performed in presence of increasing concentrations of LDV-CPPs, are shown in the following figures.

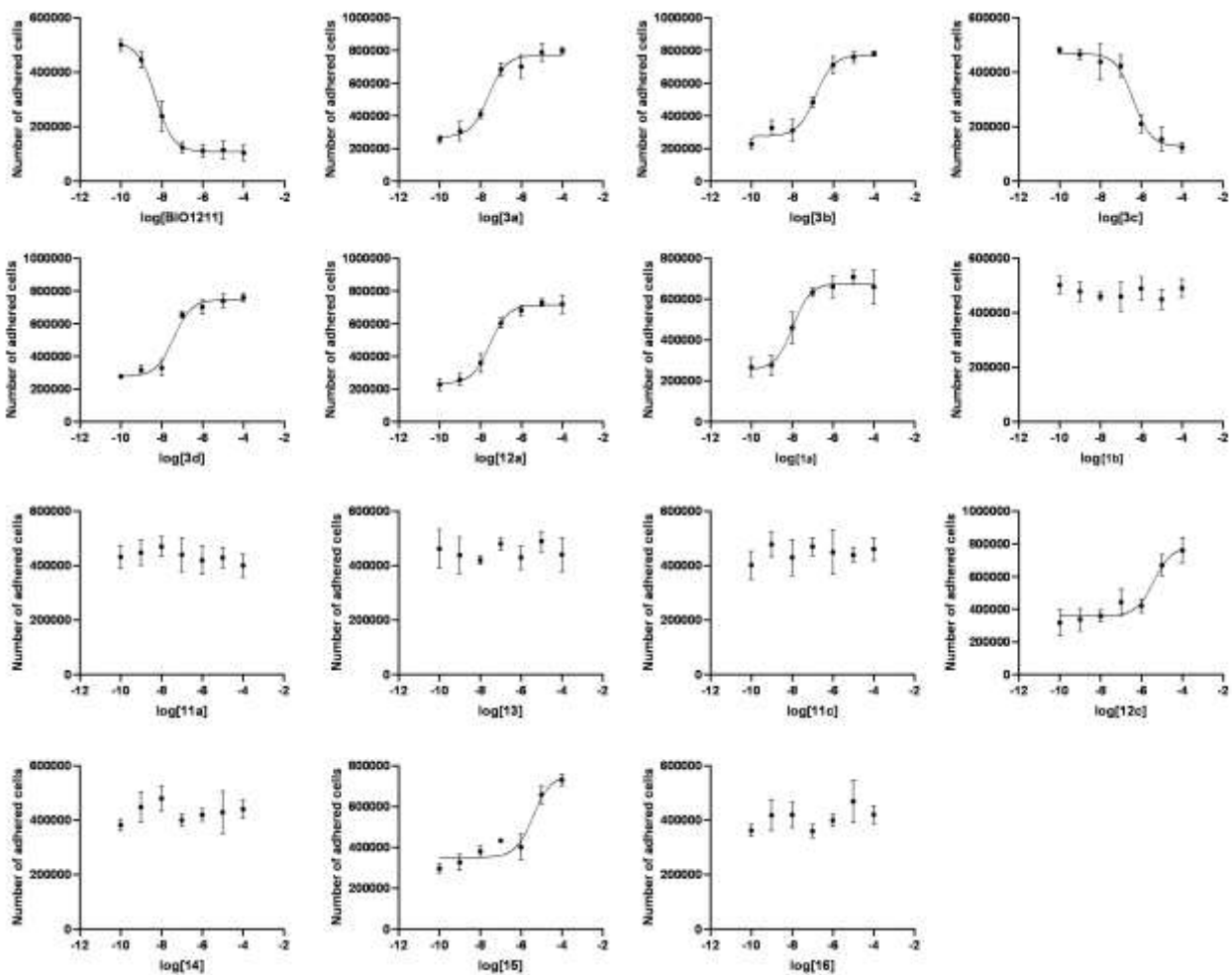


Figure S2 Concentration-response curves obtained from cell adhesion assays: evaluation of CPPs effects on $\alpha_4\beta_1$ -mediated Jurkat cell adhesion to FN. Values represent the mean \pm SD of three independent experiments carried out in quadruplicate.

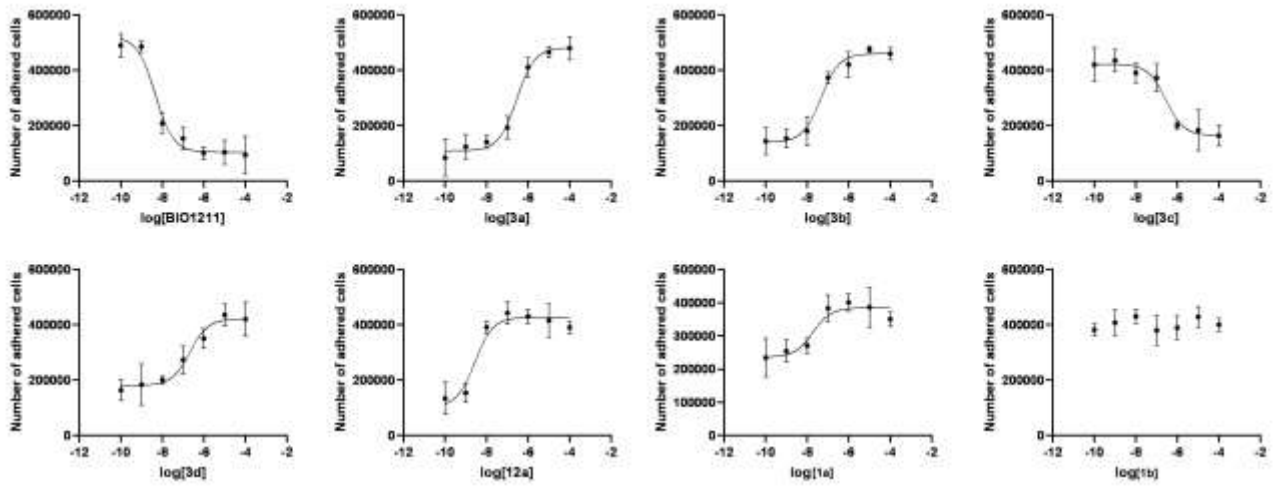


Figure S3 Concentration-response curves obtained from cell adhesion assays: evaluation of CPPs effects on $\alpha_4\beta_1$ -mediated Jurkat cell adhesion to VCAM-1. Values represent the mean \pm SD of three independent experiments carried out in quadruplicate.

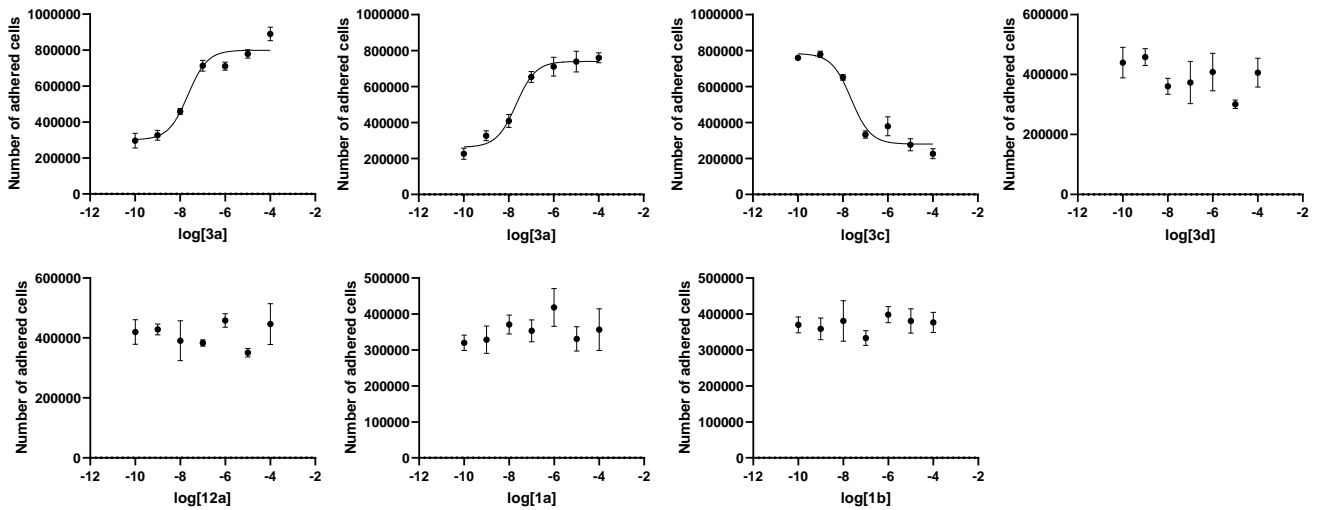


Figure S4 Concentration-response curves obtained from cell adhesion assays: evaluation of CPPs effects on $\alpha_4\beta_7$ -mediated RPMI8866 cell adhesion to MAdCam-1. Values represent the mean \pm SD of three independent experiments carried out in quadruplicate.

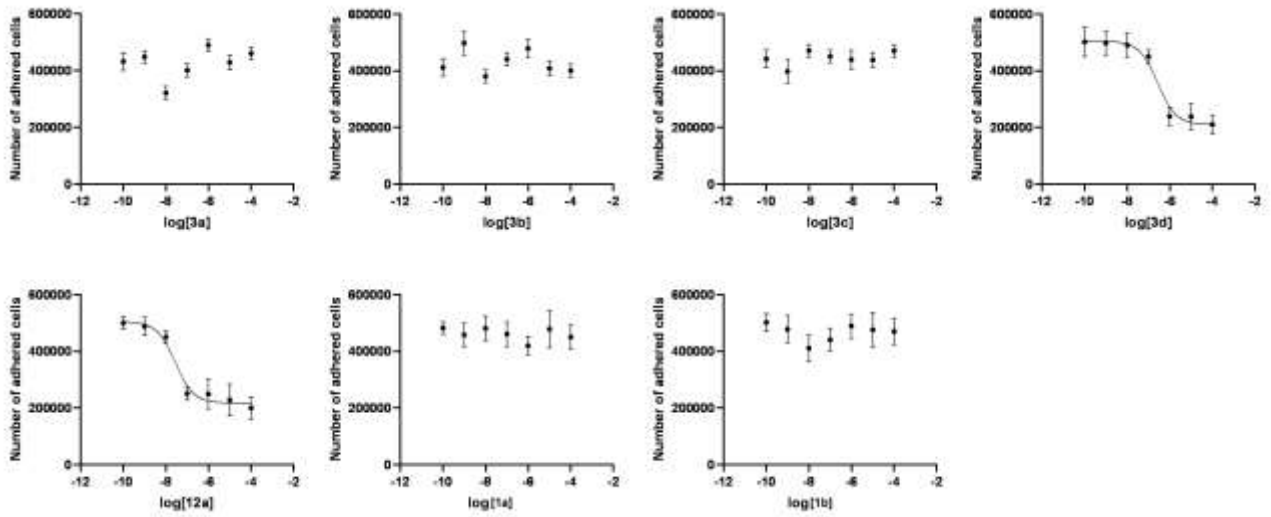


Figure S5 Concentration-response curves obtained from cell adhesion assays: evaluation of CPPs effects on $\alpha_M\beta_2$ -mediated HL60 cell adhesion to FN. Values represent the mean \pm SD of three independent experiments carried out in quadruplicate.

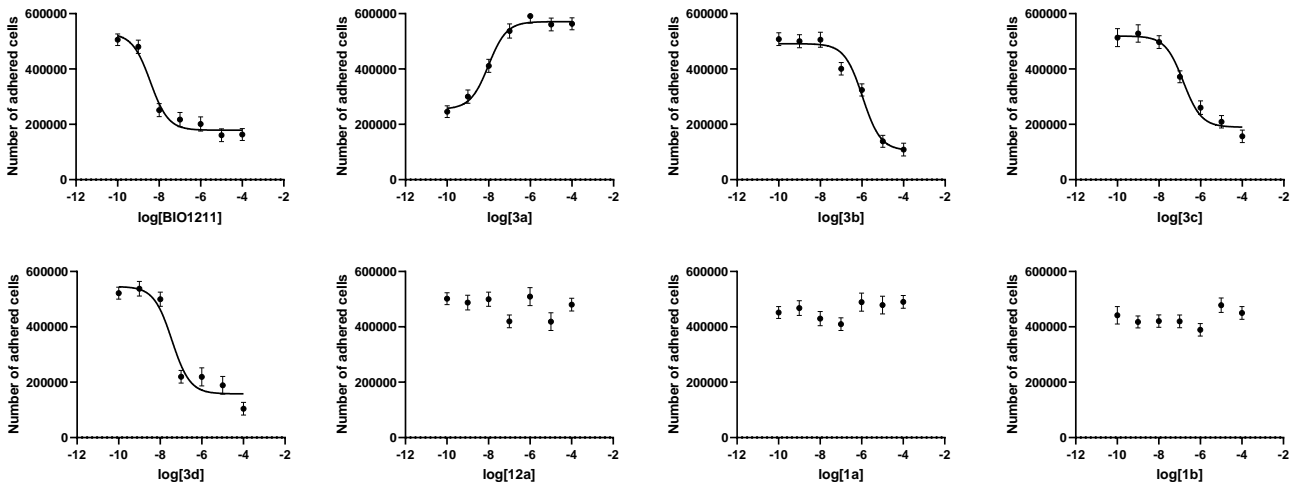


Figure S6 Concentration-response curves obtained from cell adhesion assays: evaluation of CPPs effects on $\alpha_L\beta_2$ -mediated Jurkat cell adhesion to ICAM-1. Values represent the mean \pm SD of three independent experiments carried out in quadruplicate.

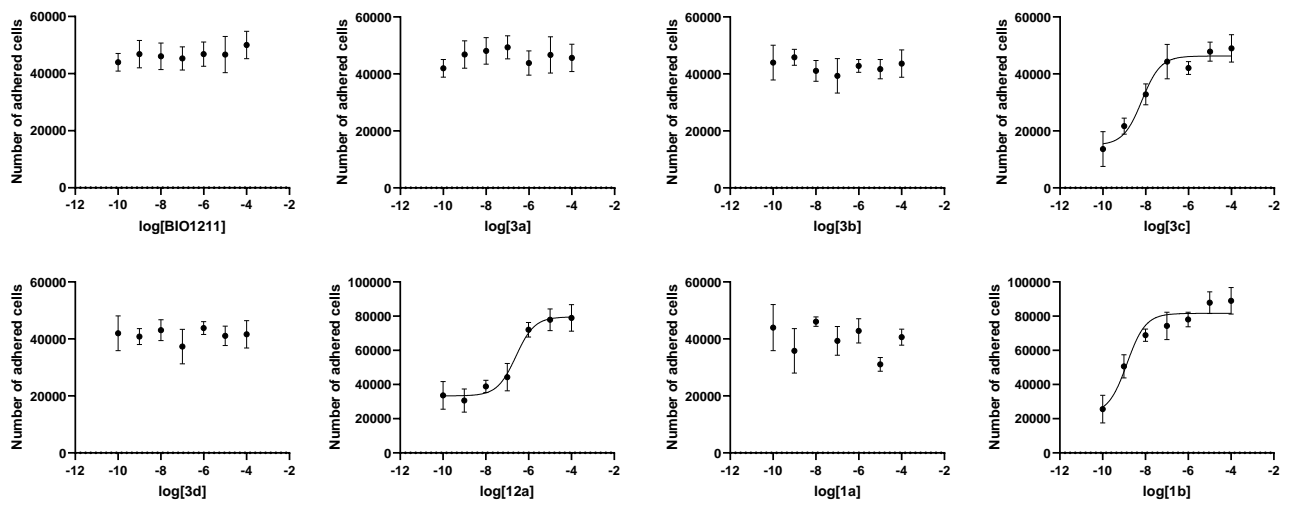


Figure S7 Concentration-response curves obtained from cell adhesion assays: evaluation of CPPs effects on $\alpha_5\beta_1$ -mediated K562 cell adhesion to FN. Values represent the mean \pm SD of three independent experiments carried out in quadruplicate.

Solid-Phase Binding Assays. Binding curves deriving from solid-phase binding assays are shown in the following figures.

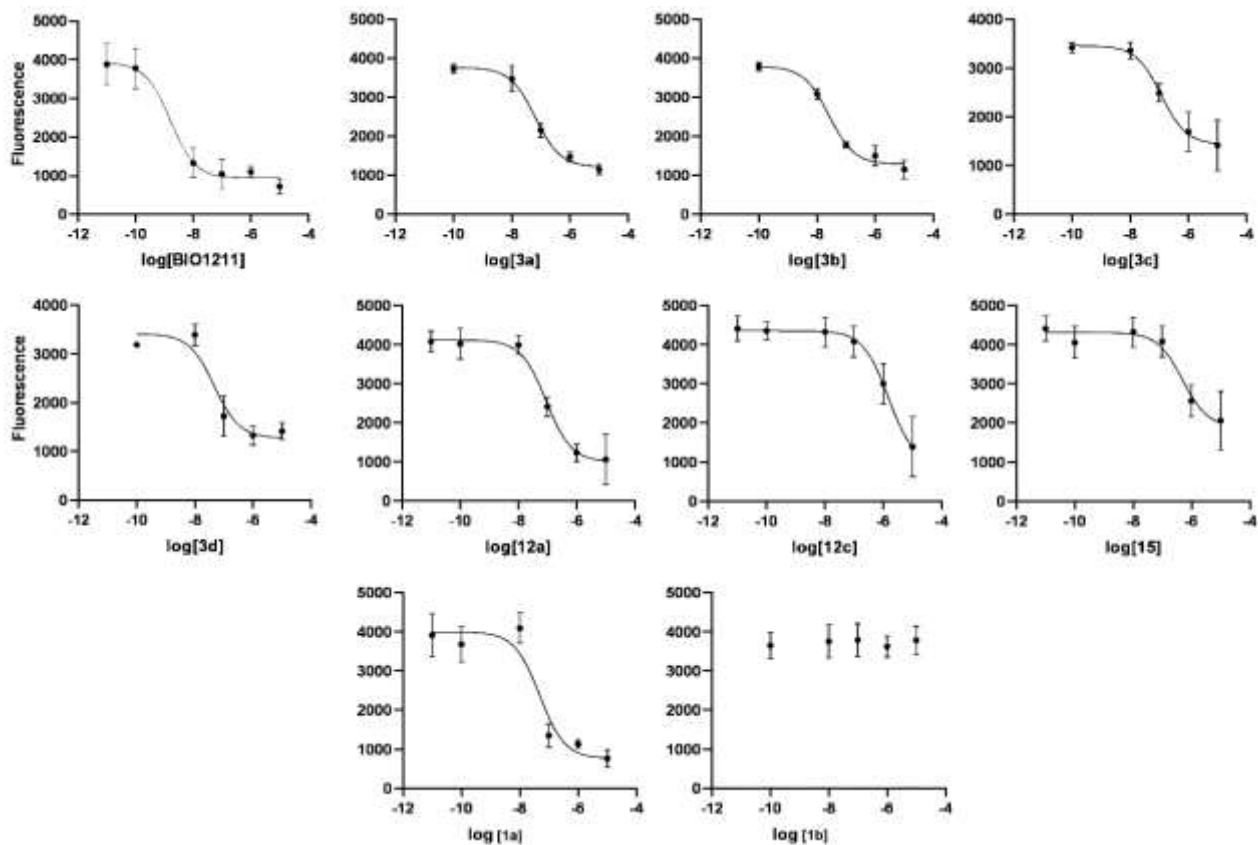


Figure S8 Binding assay curves for $\alpha_4\beta_1$ /FN in presence of increasing concentrations of LDV CPPs. Values represent the mean \pm SD of three independent experiments carried out in triplicate.

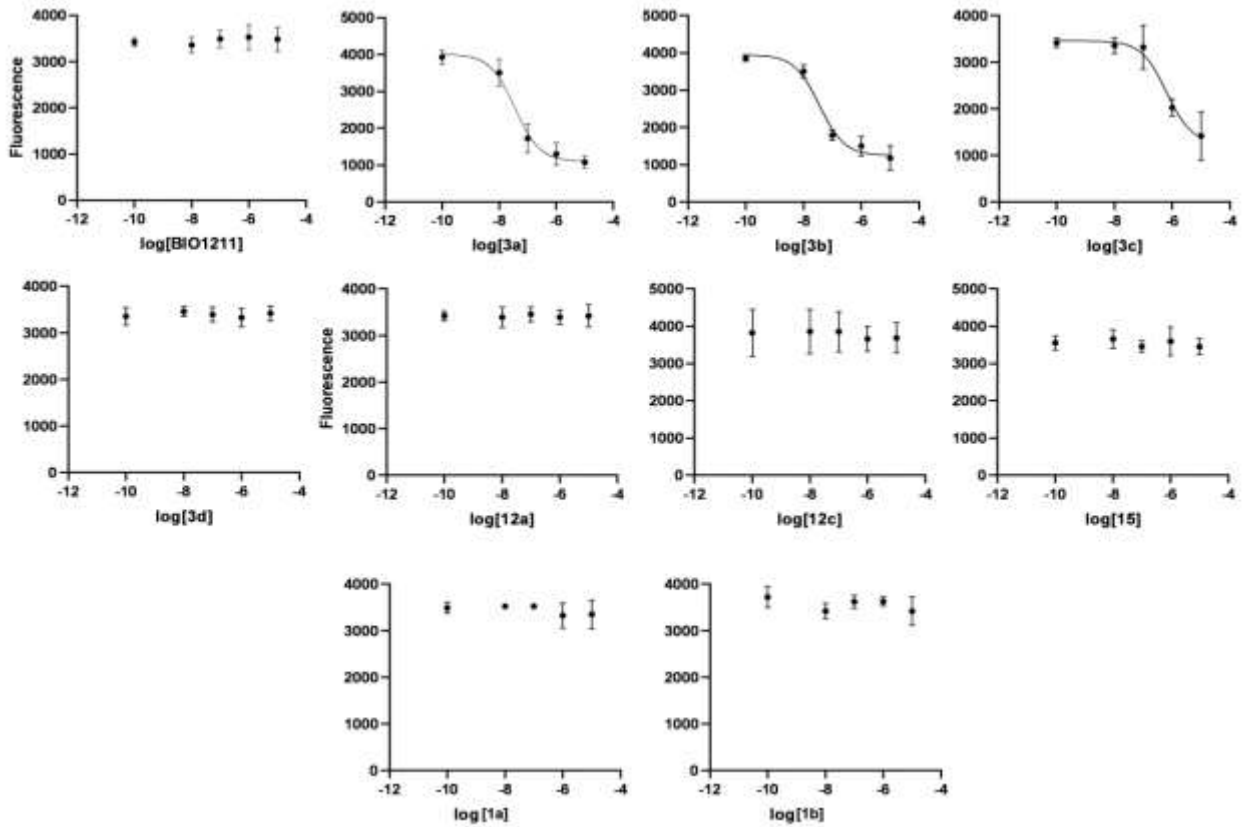


Figure S9 Binding assay curves for $\alpha_4\beta_7$ /MAdCAM-1 in presence of increasing concentrations of LDV CPPs. Values represent the mean \pm SD of three independent experiments carried out in triplicate.

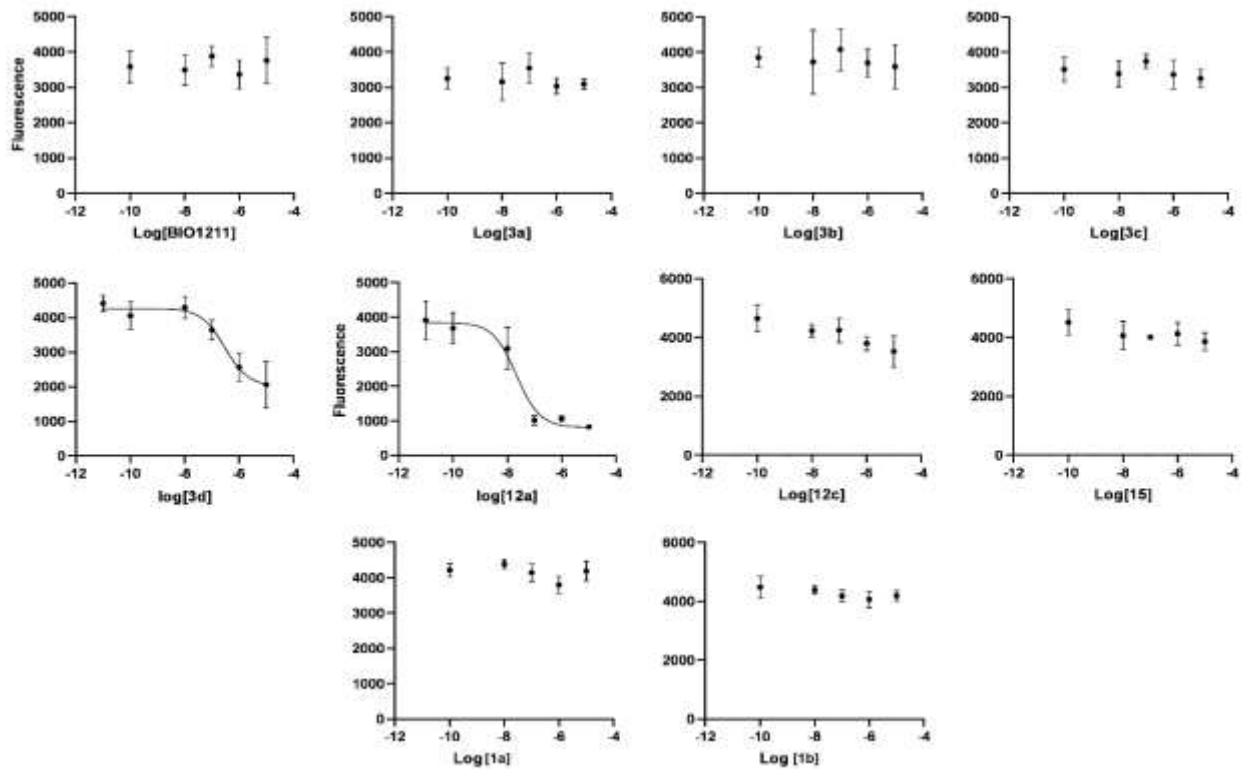


Figure S10 Binding assay curves for $\alpha_M\beta_2$ /fibrinogen in presence of increasing concentrations of LDV CPPs. Values represent the mean \pm SD of three independent experiments carried out in triplicate.

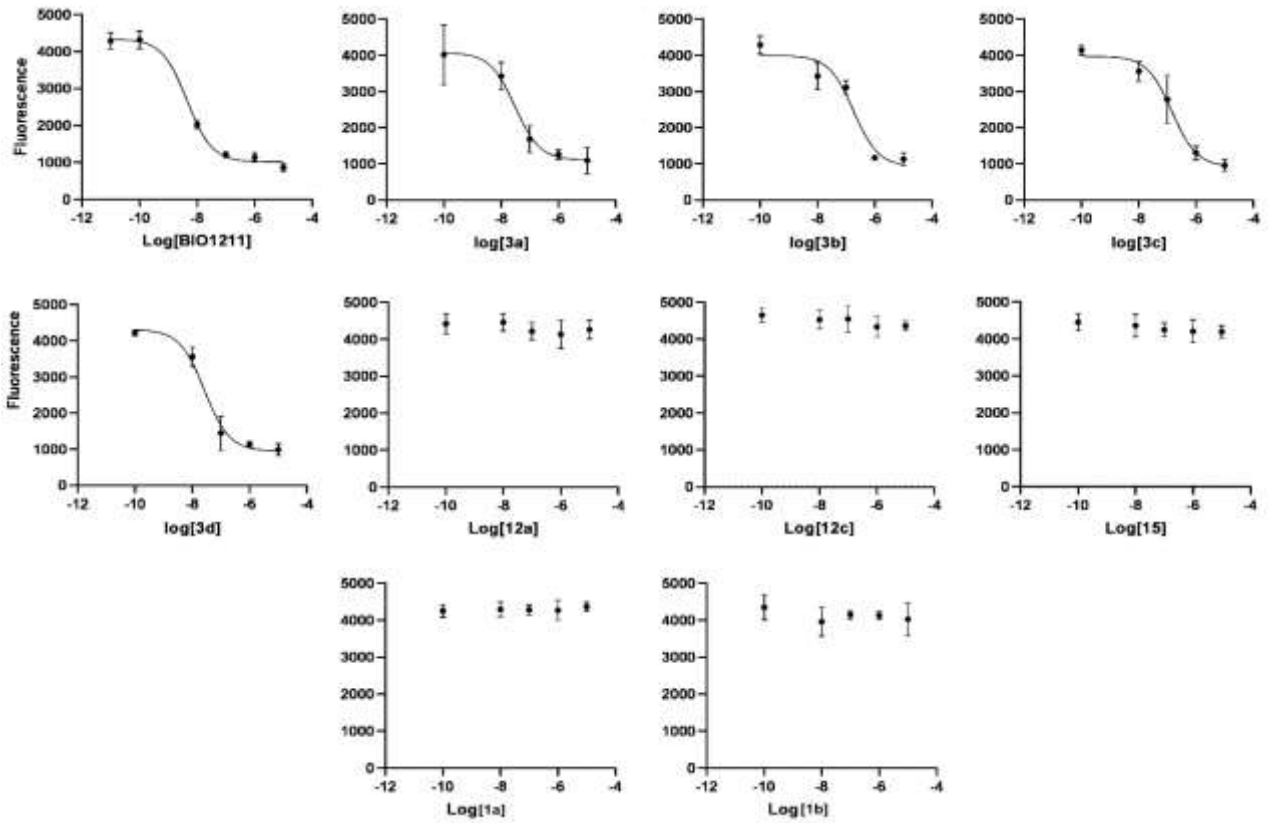


Figure S11 Binding assay curves for $\alpha_L\beta_2$ /ICAM-1 in presence of increasing concentrations of LDV CPPs. Values represent the mean \pm SD of three independent experiments carried out in triplicate.

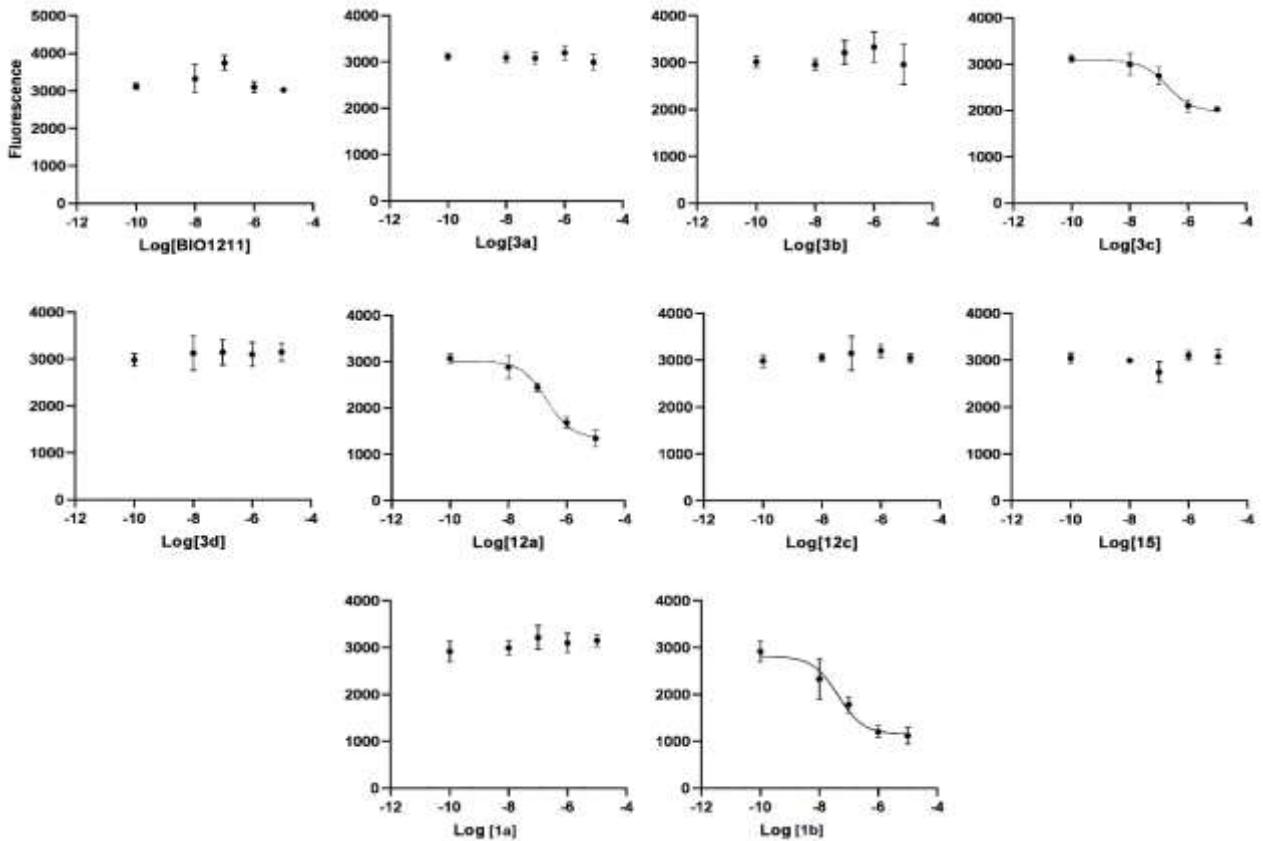


Figure S12 Binding assay curves for $\alpha_5\beta_1$ /FN in presence of increasing concentrations of LDV CPPs. Values represent the mean \pm SD of three independent experiments carried out in triplicate.

Correlation between adhesion assay-determined potency and ligand binding affinity of LDV CPPs.

The correlation was calculated on the basis of experimental data obtained for the LDV CPPs whose ligand binding affinities and potencies were obtained by solid-phase binding assays and cell adhesion assays, respectively. This evaluation was performed only for $\alpha_4\beta_1$ /FN, $\alpha_4\beta_1$ /VCAM-1 and $\alpha_L\beta_2$ /ICAM-1 having sufficient active compounds to conduct a proper analysis.

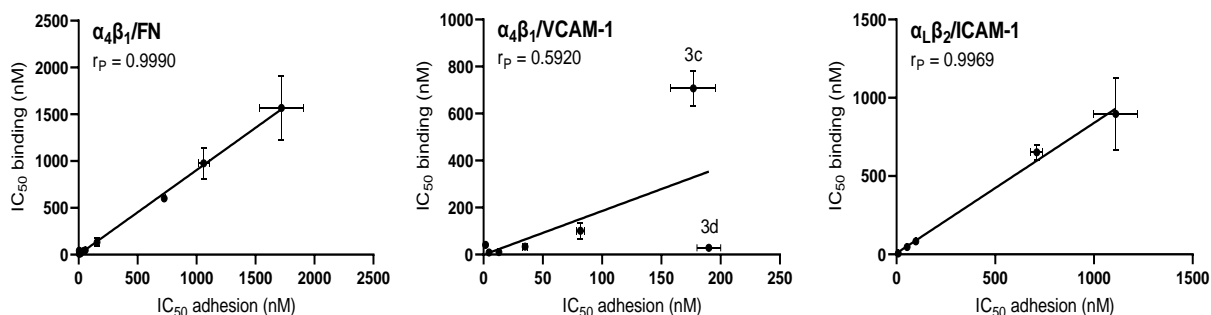


Figure S13 Relation between experimentally determined potencies (IC_{50}/EC_{50} deriving from cell adhesion assays) and ligand binding affinities (IC_{50} deriving from solid-phase binding assays) of the LDV CPPs. The IC_{50}/EC_{50} values \pm S.E. are obtained by Tables 1-3. Correlation was measured using Pearson (r_P) correlation coefficient.

Variable temperature (VT) analysis of the CPPs. 1H -NMR experiments in DMSO- d_6 /H $_2$ O (8:2) were recorded at diverse temperatures to determine if the amide protons were involved in intramolecular hydrogen bonding or were solvent exposed (Table S2). Generally, hydrogen bonded amide NH signals display comparatively lower $\Delta\delta/\Delta T$ values, $|\Delta\delta/\Delta T| < 2.0$ ppb K^{-1} , as compared to solvent-exposed amide. Since the viscosity of the cryo-mixture is temperature-dependent, the conformational equilibrium could change at diverse temperatures, altering the resonance pattern. However, as showed by 1H -NMR spectra, the CH resonances were perfectly maintained over the range of temperatures suggesting that the global conformations were not significantly altered. As reported in the Table, **3a** showed much lower $|\Delta\delta/\Delta T|$ values for Val 4 NH and isoAsp 5 NH, suggesting that these amide protons could be involved in strong hydrogen bonds ($|\Delta\delta/\Delta T| < 1$ ppb K^{-1}). The analysis of **3b** (Table 2) supported the presence of weak hydrogen bonds on Val 4 NH ($\Delta\delta/\Delta T = -1.9$ ppb K^{-1}) and isoAsp 5 NH ($\Delta\delta/\Delta T = -2.2$ ppb K^{-1}). For **3c** (Table S2), the very scarce dependence of chemical shifts from temperature supported a strong hydrogen bond on Asp 3 NH ($\Delta\delta/\Delta T = -0.3$ ppb K^{-1}). Finally, the VT NMR parameters of **3d** led to predict a very strong hydrogen bond on Asp 3 NH ($\Delta\delta/\Delta T = +0.4$ ppb K^{-1}), and possibly a weaker hydrogen bonds for Phu 1 NH and Leu 2 NH ($\Delta\delta/\Delta T = -2.1$ and -2.9 ppb K^{-1} , respectively).

The analysis of remaining CPPs showed the same trends of $\Delta\delta/\Delta T$ parameters as the parent peptides, suggesting that the hydrogen-bonding patterns and secondary structure elements were maintained. The CPPs **11a**, **12a** and **13**, showed comparatively lower $|\Delta\delta/\Delta T|$ values for Val 4 NH and for the amide proton of the β -amino acid at position 5, which is quite similar to the parent peptide **3a**. And the VT NMR parameters suggested the formation of extra hydrogen bonds involving Asp 3 NH ($\Delta\delta/\Delta T = -2.2$ ppb K^{-1}), Ala 3 NH ($\Delta\delta/\Delta T = +1.6$ ppb K^{-1}) and Phu 1 NH ($\Delta\delta/\Delta T = -1.7$ ppb K^{-1}) in CPPs **11a**, **12a** and **13** respectively. The VT-NMR analyses of **11c** and **12c** confirmed the hydrogen bonding network as for the parent **3c**, albeit with slightly different $\Delta\delta/\Delta T$ values (for **11c** Asp 3 NH $\Delta\delta/\Delta T = -0.7$ ppb K^{-1} , for **12c** Ala 3 NH $\Delta\delta/\Delta T = -2.2$ ppb K^{-1}). The VT-NMR analyses of CPPs **14** and **15** were consistent with parent peptide **3a**, supported again the presence of strong hydrogen bonds on Val 4 NH and isoAsp 5 NH. For peptide **16**, the VT-NMR results indicated the similar hydrogen bonding network on Asp 3 NH as for the parent **3c**, albeit with a much weaker hydrogen bond ($\Delta\delta/\Delta T = -2.6$ ppb K^{-1}).

Table S2. $\Delta\delta/\Delta t$ values (ppb K⁻¹) of amide protons for LDV CPPs (CPPs) **3a-d**, and of the correlated **11a, 11c, 12a, 12c, 13-16** by VT NMR spectroscopy, determined at 400 MHz (**3a-d, 11a, 11c, 12a, 12c, 13**) or at 600 MHz (**14-16**) in DMSO-*d*₆/H₂O (8:2) over the range 298-318 K.

CPP	Sequence	Phu ¹ NH	AA ² NH	AA ³ NH	AA ⁴ NH	isoAsp ⁵ NH
3a	<i>c</i> [(<i>S</i>)-Phu-LDV-(<i>S</i>)-isoAsp]	-5.0	-7.0	-4.0	-0.8	-0.5
3b	<i>c</i> [(<i>S</i>)-Phu-LDV-(<i>R</i>)-isoAsp]	-4.9	-3.5	-3.7	-1.9	-2.2
3c	<i>c</i> [(<i>R</i>)-Phu-LDV-(<i>S</i>)-isoAsp]	-5.5	-5.3	-0.3	-7.9	-5.5
3d	<i>c</i> [(<i>R</i>)-Phu-LDV-(<i>R</i>)-isoAsp]	-2.1	-2.9	+0.4	-3.0	-3.5
11a	<i>c</i> [(<i>S</i>)-Phu-LDV-(<i>R</i>)-βAla ⁵]	-4.5	-4.1	-2.2	-0.6	-1.1
12a	<i>c</i> [(<i>S</i>)-Phu-LAV-(<i>S</i>)-isoAsp ⁵]	-5.4	+1.6	-4.4	-0.5	0.0
13	<i>c</i> [(<i>S</i>)-Phu-LDV-(<i>S</i>)-isoAsp(NHPr)]	-1.7	-4.8	-4.9	-0.9	-0.2
11c	<i>c</i> [(<i>R</i>)-Phu-LDV-(<i>R</i>)-βAla]	-6.0	-3.9	-0.7	-6.4	-2.5
12c	<i>c</i> [(<i>R</i>)-Phu-LAV-(<i>S</i>)-isoAsp]	-3.7	-4.2	-2.2	-6.0	-6.0
14	<i>c</i> [(<i>S</i>)-Phu-FDV-(<i>S</i>)-isoAsp]	-3.5	-4.8	-3.7	-0.8	0.0
15	<i>c</i> [(<i>S</i>)-Phu-FAV-(<i>S</i>)-isoAsp]	-4.2	-5.8	-3.8	-0.6	+0.6
16	<i>c</i> [(<i>R</i>)-Phu-LD-Phg-(<i>S</i>)-isoAsp]	-5.7	-3.9	-2.6	-4.6	-4.6

Table S3. ROESY cross peaks for **3a** in 8:2 DMSO₆/H₂O; vs = very strong, s = strong, m = medium, w = weak.

Crosspeak	Intensity	Crosspeak	Intensity
PhuNHb-PhuMe	w	PhuArH2',6'-LeuHy	w
PhuNHb-LeuHα	w	PhuArH2',6'-PhuMe	w
LeuNH-LeuMe	m	PhuArH2',6'-isoAspHβ _{2.6}	w
LeuNH-LeuHy	m	PhuArH2',6'-PhuHβ _{2.7}	w
LeuNH-LeuHβ _{1.5}	w	PhuArH2',6'-PhuHβ _{2.9}	w
LeuNH-LeuHβ _{1.7}	m	PhuArH2',6'-PhuHα	w
LeuNH-PhuHβ _{2.9}	m	PhuArH3',5'-3,5-LeuMe	m
LeuNH-LeuHα	vs	PhuArH3',5'-3,5-LeuHy	w
LeuNH-PhuHα	s	PhuArH3',5'-3,5-LeuHβ	w
LeuNH-PhuArH3',5'	m	PhuArH3',5'-3,5-PhuMe	w
LeuNH-AspNH	s	PhuArH3',5'-3,5-PhuHα	vs
AspNH-LeuMe	w	PhuArH3',5'-3,5-isoAspHβ _{2.6}	w
AspNH-LeuHy	w	isoAspNH-ValMe	m
AspNH-LeuHβ _{1.5}	s	isoAspNH-PhuMe	w
AspNH-LeuHβ _{1.7}	s	isoAspNH-ValHβ	w
AspNH-AspHβ _{2.9}	w	isoAspNH-isoAspHβ _{2.6}	m
AspNH-AspHβ _{3.0}	w	isoAspNH-isoAspHβ _{2.7}	w
AspNH-LeuHα	s	isoAspNH-ValHα	s
AspNH-ValHα	w	isoAspNH-AspHα	w

AspNH-AspH α	vs	isoAspNH-isoAspH α	s
AspNH-ValNH	s	isoAspH α -ValMe	w
PhuNH-isoAspH $\beta_{2.6}$	s	isoAspH α -isoAspH $\beta_{2.6}$	m
PhuNH-isoAspH $\beta_{2.7}$	s	isoAspH α -isoAspH $\beta_{2.7}$	w
PhuNH-PhuH $\beta_{2.7}$	vs	PhuH α -PhuH $\beta_{2.7}$	m
PhuNH-PhuH $\beta_{2.9}$	m	PhuH α -PhuH $\beta_{2.9}$	s
PhuNH-PhuH α	m	AspH α -AspH $\beta_{2.9}$	m
PhuNH-isoAspH α	m	AspH α -AspH $\beta_{3.0}$	m
PhuNH-isoAspNH	m	ValH α -ValMe	vs
PhuNH-PhuArH3',5'	s	ValH α -ValH β	s
PhuNH α -LeuMe	w	ValH α -AspH $\beta_{2.9}$	w
PhuNH α -LeuH $\beta_{1.7}$	w	LeuH α -LeuMe	vs
PhuNH α -LeuH α	w	LeuH α -LeuH γ	m
PhuNH α -PhuH α	w	LeuH α -LeuH $\beta_{1.5}$	s
PhuNH α -PhuMe	vs	LeuH α -LeuH $\beta_{1.7}$	m
PhuNH α -PhuNHb	vs	PhuH $\beta_{3.0}$ -LeuH γ	m
ValNH-ValMe	vs	PhuH $\beta_{3.0}$ -LeuH $\beta_{1.5}$	w
ValNH-LeuH $\beta_{1.7}$	w	AspH $\beta_{2.8}$ -LeuH $\beta_{1.5}$	w
ValNH-ValH β	m	AspH $\beta_{2.9}$ -LeuMe	m
ValNH-AspH $\beta_{2.9}$	m	PhuH $\beta_{2.7}$ -LeuH γ	w
ValNH-ValH α	s	PhuMe-LeuMe	m
ValNH-AspH α	m	PhuMe-LeuH γ	w
ValNH-isoAspH α	w	PhuMe-LeuH $\beta_{1.5}$	w
ValNH-isoAspNH	s	PhuMe-LeuH $\beta_{1.7}$	w
PhuArH2',6'-LeuMe	m		

Table S4. ROESY cross peaks for **3b** in 8:2 DMSO₆/H₂O; vs = very strong, s = strong, m = medium, w = weak.

Crosspeak	Intensity	Crosspeak	Intensity
NHb-LeuMe	w	isoAspNH-isoAspH α	m/s
NHb-PhuH α	w	PhuNH α -ValMe	w
NHb-PhuMe	w	PhuNH α -PhuMe	s/vs
AspNH-Val/LeuMe	w	PhuArH6-LeuMe	w
AspNH-LeuH γ /LeuH $\beta_{1.5}$	s	PhuArH2',6'-LeuMe	w/m
AspNH-LeuH $\beta_{1.7}$	m	PhuArH2',6'-LeuH γ /LeuH $\beta_{1.7}$	w
AspNH-AspH $\beta_{2.9}$	m	PhuArH2',6'-LeuH $\beta_{1.5}$	vw
AspNH-LeuH α	w	PhuArH2',6'-PhuH $\beta_{2.7}$	w
AspNH-AspH α	vs	PhuArH2',6'-Phu $\beta_{3.0}$	vw
AspNH-ValNH	w	PhuArH2',6'-Phu α	vw
AspNH-LeuNH	w	PhuArH3',5',3,5-LeuMe	m/w
LeuNH-LeuMe	m	PhuArH3',5',3,5-LeuH γ /LeuH $\beta_{1.7}$	w
LeuNH-LeuH γ /LeuH $\beta_{1.5}$	m/s	PhuArH3',5',3,5-LeuH $\beta_{1.5}$	w

LeuNH-LeuH β _{1.7}	m	PhuArH3',5',3,5-PhuH β _{2.7}	s
LeuNH-PhuH β _{2.7}	w	PhuArH3'5',3,5-PhuH β _{3.0}	s
LeuNH-PhuH β _{3.0}	w/m	PhuArH3'5',3,5-PhuH α	s
LeuNH-LeuH α	s	AspH α -LeuH γ /LeuH β _{1.7}	w
LeuNH-PhuH α	m	AspH α -AspH β x2	vs
PhuNH-isoAspH β _{2.2}	vw	AspH α -ValH α	w
PhuNH-PhuH β _{2.7}	s/vs	PhuH α -PhuH β _{2.7}	m
PhuNH-isoAspH β _{2.8}	s/vs	PhuH α -PhuH β _{3.0}	vs
PhuNH-PhuH β _{3.0}	w	isoAspH α -isoAspH β _{2.4}	vs
PhuNH-PhuH α	m	isoAspH α -isoAspH β _{2.8}	w
PhuNH-PhuAr3',5'	m/s	isoAspH α -ValH α	w
ValNH-ValMe	s	LeuH α -LeuMe	vs
ValNH-LeuH γ /LeuH β	w,w	LeuH α -LeuH β _{1.7} /H γ	s/vs
ValNH-ValH β	m	LeuH α -LeuH β _{1.5}	w/m
ValNH-AspH β	m	ValH α -LeuMe	vs
ValNH-ValH α	m	ValH α -ValH β	vs
ValNH-AspH α	m/w	PhuH β _{3.0} -LeuH β _{1.7} /H γ	w
isoAspNH-ValMe	w	PhuH β _{3.0} -LeuMe	w
isoAspNH-ValH β	m/s	PhuH β _{2.7} -LeuMe	w
isoAspNH-isoAspH β _{2.8}	m/s	AspH β x2-LeuH β _{1.7} /H γ	w
isoAspNH-ValH α	w/m	AspH β x2-LeuH β _{1.5}	w

Table S5. ROESY cross peaks for **3c** in 8:2 DMSO₆/H₂O; vs = very strong, s = strong, m = medium, w = weak.

Crosspeak	Intensity	Crosspeak	Intensity
PhuNHb-LeuMe _{0.6}	w	PhuNH α -LeuMe _{0.7}	w
PhuNHb-LeuMe _{0.7}	m	PhuNH α -Phu(2-Me)	vs
PhuNHb-ValMe _{0.8}	w	PhuNH α -ValH α	w
PhuNHb-Phu(2-Me)	w	PhuArH6-LeuMe _{0.6}	w
PhuNHb-LeuNH	w	PhuArH6-LeuMe _{0.7}	w
PhuNHb-PhuNH	w	PhuArH6-Phu(2-Me)	w
PhuNHb-ValNH	w	AspNH-LeuH β	m
PhuNH-ValMe _{0.8}	w	AspNH-AspH β _{2.6}	m
PhuNH-isoAspH β	vs	AspNH-AspH β _{2.8}	m
PhuNH-PhuH β	vs	AspNH-LeuH α	s
PhuNH-PhuH α	s	AspNH-PhuH α	w
PhuNH-isoAspH α	w	AspNH-AspH α	s
PhuNH-PhuArH3',5'	m	PhuArH2',6'-LeuMe _{0.6}	m
PhuNH-AspNH	w	PhuArH2',6'-LeuMe _{0.7}	w
PhuNH-ValNH	w	PhuArH2',6'-ValMe _{0.8}	w
isoAspNH-ValMe _{0.8}	w	PhuArH2',6'-LeuH γ	m
isoAspNH-ValH β	m	PhuArH2',6'-PhuH α	w

isoAspNH-isoAspH β	w	PhuArH3',5'-LeuMe _{0.6}	m
isoAspNH-ValH α	s	PhuArH3',5'-LeuMe _{0.7}	w
isoAspNH-isoAspH α	m	PhuArH3',5'-ValMe _{0.8}	w
isoAspNH-AspH α	w	PhuArH3',5'-LeuH γ	m
isoAspNH-LeuH α	w	PhuArH3',5'-LeuH β	w
LeuNH-LeuMe _{0.6}	w	PhuArH3',5'-ValH β	w
LeuNH-LeuMe _{0.7}	w	PhuArH3',5'-isoAspH β	w
LeuNH-LeuH γ	s	PhuArH3',5'-LeuH α	w
LeuNH-LeuH β	vs	PhuArH3',5'-isoAspH α	w
LeuNH-AspH β _{2.6}	m	PhuArH3',5'-PhuH α	s
LeuNH-PhuH β	m	AspH α -ValMe _{0.7}	w
LeuNH-ValH α	w	AspH α -AspH β _{2.6}	s
LeuNH-LeuH α	s	AspH α -AspH β _{2.8}	s
LeuNH-isoAspH α	w	AspH α -ValH α	w
LeuNH-PhuH α	vs	AspH α -LeuH α	w
LeuNH-PhuArH3',5'	w	PhuH α -PhuH β	vs
LeuNH-AspNH	s	isoAspH α -isoAspH β	m
ValNH-ValMe _{0.8}	m	LeuH α -LeuMe _{0.6}	vs
ValNH-ValMe _{0.9}	w	LeuH α -LeuMe _{0.7}	m
ValNH-ValH β	m	LeuH α -LeuH γ	m
ValNH-AspH β _{2.6}	w	LeuH α -LeuH β	vs
ValNH-AspH β _{2.8}	m	ValH α -ValMe _{0.7}	s
ValNH-ValH α	vs	ValH α -ValMe _{0.8}	s
ValNH-AspH α	s	ValH α -ValH β	m
ValNH-AspNH	w	PhuH β -LeuH γ	w

Table S6. ROESY cross peaks for **3d** in 8:2 DMSO₆/H₂O; vs = very strong, s = strong, m = medium, w = weak.

Crosspeak	Intensity	Crosspeak	Intensity
PhuNHb-LeuMe _{0.6}	w	PhuNH α -PhuMe	vs
PhuNHb-LeuMe _{0.7}	w	PhuNH α -PhuArH6	vs
ValNH-ValMe	s	AspNH-LeuMe _{0.6}	m
ValNH-ValH β	w	AspNH-LeuMe _{0.7}	m
ValNH-AspH β _{2.8}	w	AspNH-LeuH γ	m
ValNH-ValH α	s	AspNH-AspH β _{2.5}	w
ValNH-AspH α	s	AspNH-AspH β _{2.8}	w
ValNH-AspNH	w	AspNH-LeuH α	w
ValNH-isoAspNH	w	AspNH-AspH α	m
PhuNH-LeuH γ	w	PhuArH2',6'-PhuH α	w
PhuNH-isoAspH β _{2.7}	s	PhuArH3',5'-LeuMe _{0.6}	w
PhuNH-PhuH β _{2.8}	s	PhuArH3',5'-LeuH γ	w
PhuNH-PhuH α	m	PhuArH3',5'-LeuH α	w

PhuNH-PhuArH3',5'	w	PhuArH3',5'-PhuH α	s
PhuNH-PhuNH α	w	AspH α -LeuHy	w
PhuNH-LeuNH	m	AspH α -AspH β _{2.5}	s
PhuNH-isoAspNH	m/s	AspH α -AspH β _{2.8}	m
isoAspNH-ValH β	w	AspH α -LeuH α	w
isoAspNH-isoAspH β _{2.6}	m	isoAspH α -isoAspH β _{2.6}	m
isoAspNH-ValH α	w	isoAspH α -isoAspH β _{2.7}	m
isoAspNH-isoAspH α	m	PhuH α -PhuArH3',5'	m
isoAspNH-ValMe	w	PhuH α -LeuNH	vs
isoAspNH-AspNH	w	LeuH α -LeuMe _{0.6}	s
isoAspNH-LeuNH	w	LeuH α -LeuMe _{0.7}	w
LeuNH-LeuMe _{0.6}	w	LeuH α -LeuHy	w
LeuNH-LeuMe _{0.7}	w	LeuH α -LeuH β _{1.4}	m
LeuNH-LeuHy	m	LeuH α -ValH α	w
LeuNH-LeuH β _{1.3}	m	ValH α -ValMe	vs
LeuNH-LeuH α	m	LeuH β _{1.4} -LeuMe _{0.6}	w
LeuNH-PhuH α	vs	LeuH β _{1.4} -LeuMe _{0.7}	w
LeuNH-AspNH	s	LeuH β _{1.3} -LeuMe _{0.6}	w
PhuNH α -PhuNH β	vs		

Table S7. ROESY cross peaks for **12a** in 8:2 DMSO_d₆/H₂O; vs = very strong, s = strong, m = medium, w = weak.

Crosspeak	Intensity	Crosspeak	Intensity
LeuNH-LeuMe _{0.5}	m	PhuArH3',5'-LeuH β _{1.8}	w
LeuNH-LeuH α	s	PhuArH3',5'-PhuH β _{2.6}	vs
LeuNH-PheH α	vs	PhuArH3',5'-PhuH β _{2.8}	s
PhuNH β -LeuMe _{0.7}	w	PhuArH3',5'-PhuH α	vs
PhuNH-ValMe _{1.1}	w	isoAspNH-isoAspH α	s
PhuNH-isoAspH β _{2.6}	m	isoAspNH-ValH α	m
PhuNH-PheH β _{2.8}	s	ValH α -ValMe _{0.9}	s
PhuNH-isoAspH β _{2.9}	s	ValH α -ValMe _{1.1}	m
PhuNH-PhuH α	m	ValH α -ValH β	vs
AlaNH-LeuH β _{1.2}	s	isoAspH α -isoAspH β _{2.6}	m
AlaNH-AlaMe	s	isoAspH α -isoAspH β _{2.9}	vs
AlaNH-LeuH β _{1.8}	s	PheH α -PheH β _{2.6}	m
AlaNH-AlaH α	m	PheH α -PheH β _{2.8}	s
AnaNH-ValNH	m	LeuH α -LeuMe _{0.5}	vs
PhuNH α -Phu(2-Me)	vs	LeuH α -LeuMe _{0.7}	m
ValNH-ValMe _{0.9}	m	LeuH α -LeuH β _{1.2}	vs
ValNH-ValMe _{1.1}	s	PhuH β _{2.8} -LeuH β _{1.2}	w
ValNH-AlaH α	m	LeuH β _{1.8} -LeuMe _{0.5}	s
ValNH-ValH α	m	LeuH β _{1.8} -LeuMe _{0.7}	s

ValNH-isoAspNH	vs	LeuH β _{1.8} -LeuH γ	w
PhuArH2',6'-LeuMe _{0.5}	m	AlaMe-LeuMe _{0.5}	w
PhuArH2',6'-LeuMe _{0.7}	s	AlaMe-LeuMe _{0.7}	w
PhuArH3',5'-LeuMe _{0.5}	m	LeuH β _{1.2} -LeuMe _{0.5}	m
PhuArH3',5'-LeuMe _{0.7}	w	LeuH β _{1.2} -LeuMe _{0.7}	s
PhuArH3',5'-LeuH β _{1.2}	w	LeuH β _{1.2} -LeuH γ	m

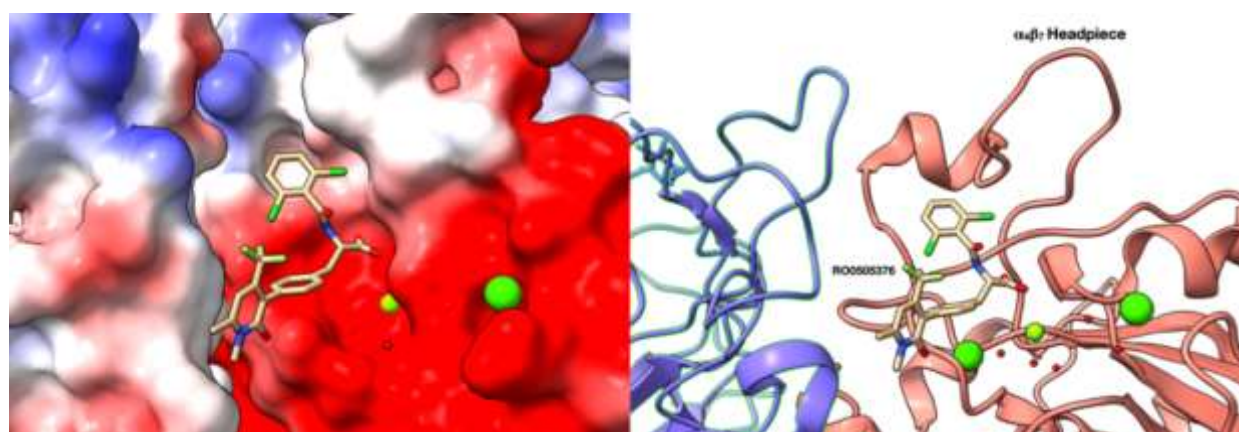


Figure S14. PDB 3V4V, crystal structure of $\alpha_4\beta_7$ headpiece complexed with RO0505376; left, the integrin is represented as molecular solvent-excluded surfaces (SES) and colored using Coulombic electrostatic potential (ESP). RO0505376 is rendered in sticks, while metal ions were rendered as green spheres.

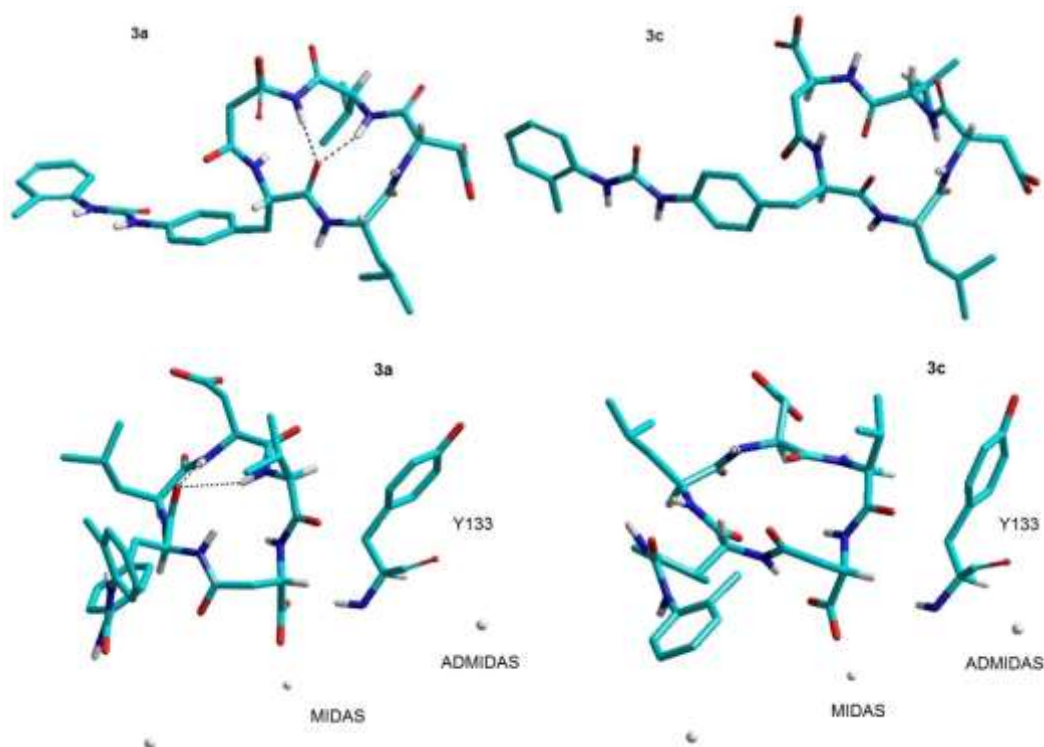


Figure S15. In-solution (top) and receptor-bound (bottom) structures of **3a**, **3c** showing hydrogen-bonded secondary structure elements (dotted lines). The structures differ only by the inversion of stereochemistry at Phu^1 . $\beta_1:\text{Tyr}^{133}$ and cations of the adhesion sites are shown for better comparison.

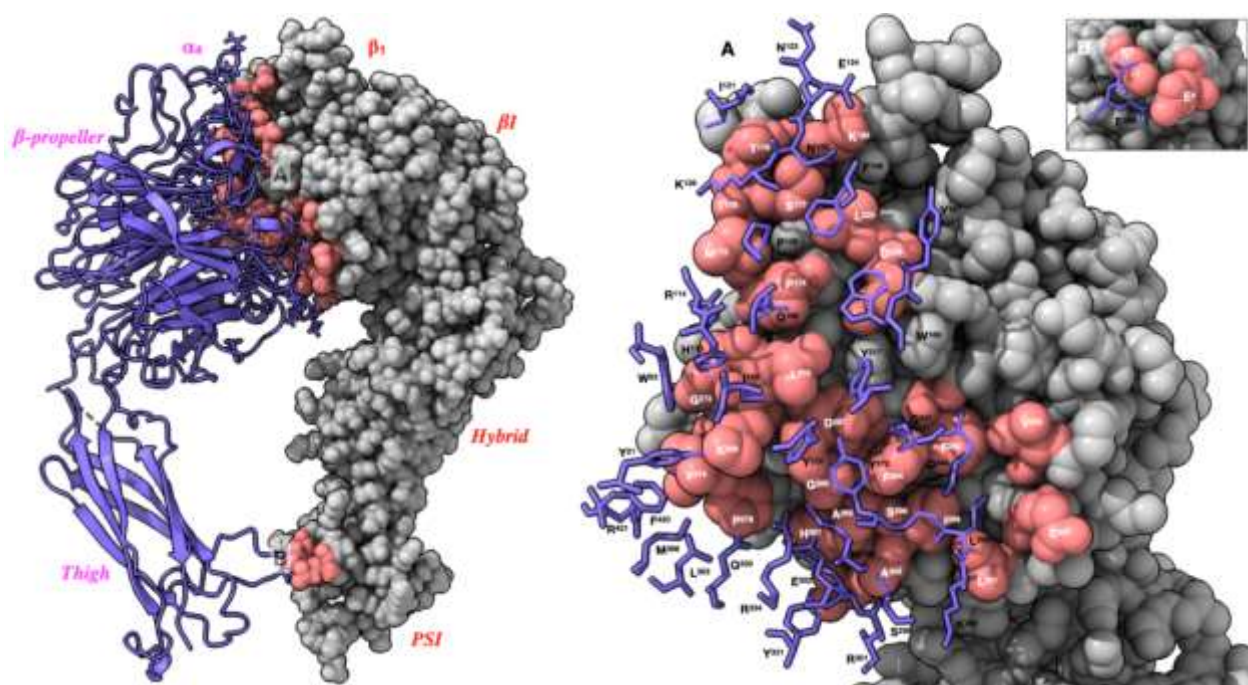


Figure S16. Left. Rendering of $\alpha_4\beta_1$ integrin model used in this work, with evidenced the β -propeller (α_4), Thigh (α_4), βI (β_1), Hybrid (β_1) and PSI (plexin–semaphorin–integrin, β_1) domains. The α_4 subunit is colored in blue and represented as solid ribbon, with key residues at the α_4/β_1 interface in stick. The β_1 subunit is represented as gray CPK, with key residues at the α_4/β_1 interface in pink. (A) Close look of the interface between the β -propeller (α_4) and βI (β_1) domains. The α_4 residues are shown in stick representation and colored in blue (black labels), while the β_1 residues are represented in CPK, with key residues colored in pink (white labels). (B) Particular of the interface between Thigh (α_4)

and PSI (β_1) domains. Again, the α_4 residues are represented as blue sticks (black labels), while the β_1 residues are represented in CPK, with key residues colored in pink (white labels). Molecular graphics and analyses performed with UCSF ChimeraX.

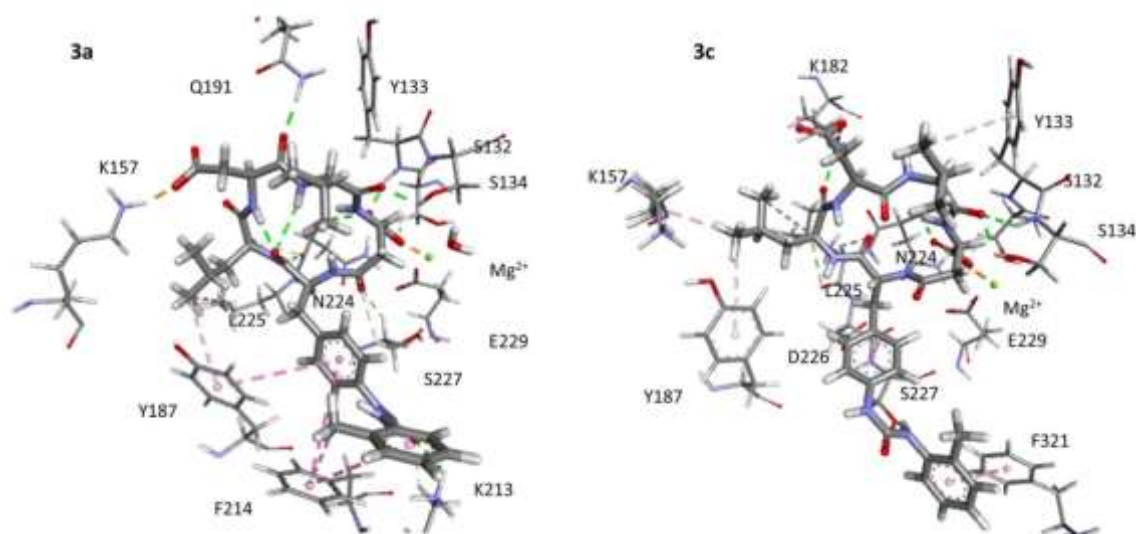


Figure S17. The agonist **3a**, *c*[(*S*)-Phu-LDV-(*S*)-isoAsp], makes many interactions with α_4 subunit. Phu¹MePh group interacts with α_4 :F²¹⁴ (π - π stacking), Phu¹Ph interacts with α_4 :F²¹⁴ (π - π T-shaped interaction), and with α_4 :Y¹⁸⁷ (π - π stacking). UreaC=O makes a hydrogen bond with α_4 :K²¹³ (2.31 Å). Phu¹C=O establishes intramolecular hydrogen bonds with Asp³NH (1.72 Å) and Val⁴NH (2.30 Å). The hydrophobic side chain of Leu² is included within a cavity delimited by α_4 :K¹⁵⁷, β_1 :L²²⁵, and α_4 :Y¹⁸⁷, while Leu²NH group makes a hydrogen bond with β_1 :N²²⁴O (1.84 Å). Asp³COO⁻ makes a salt bridge with α_4 :K¹⁵⁷N ζ^+ (1.63 Å), while Asp³C=O gives rise to an hydrogen bond with β_1 :Q¹⁹¹CONH₂ (1.78 Å). Val⁴C=O is hydrogen bonded to β_1 :S¹³⁴OH (1.97 Å). The isopropyl of Val⁴ is pseudo axial, therefore it does not get in touch with any residues of β_1 subunit. Finally, isoAsp⁵COO⁻ is coordinated to Mg²⁺ in MIDAS, with Mg²⁺ that exhibits a slightly distorted coordination geometry (RMSD 0.12). Two hydrogen bonds are formed with water (W) W1 (2.86 Å) and W3 (2.67 Å), an hydrogen bond with β_1 :Y¹³³NH (1.97 Å) and an hydrogen bond with β_1 :N²²⁴NH (2.75 Å).

The antagonist **3c**, *c*[(*R*)-Phu-LDV-(*S*)-isoAsp], differs from the all-*S* configured **3a** for the inverted stereochemistry at Phu¹. The most noticeable effect is represented by a greater interaction with β_1 subunit. Phu¹MePh makes a π - π stacking interaction with β_1 :F³²¹. UreaNH makes a hydrogen bond with β_1 :S²²⁷OG (2.11 Å), and Phu¹Ph interacts with the peptide bond between β_1 :D²²⁶ and β_1 :S²²⁷ (amide- π stacking). The side chain of Leu² is included within the cavity formed by α_4 :K¹⁵⁷, α_4 :Y¹⁸⁷, β_1 :L²²⁵. Leu²C=O makes an hydrogen bond with β_1 :K¹⁸²NH ζ^+ (1.77 Å), which in turn interacts with Asp³COO⁻ by a salt bridge (1.62 Å). Val⁴C=O makes two hydrogen bonds with β_1 :S¹³⁴OH (1.97 Å) and β_1 :S¹³⁴NH (1.52 Å). In contrast to **3a**, the isopropyl of Val⁴ is in contact with β_1 :Tyr¹³³ (π -alkyl, 4.76 Å). Finally, isoAsp⁵COO⁻ is coordinated with Mg²⁺. In this complex, the cation shows a distorted octahedral coordination geometry (RMSD 0.17); isoAsp⁵COO⁻ makes also other interactions: with β_1 :S¹³² (O-HC, 2.46 Å), two hydrogen bonds with W¹ (2.60 Å) and W³ (2.66 Å), hydrogen bond with β_1 :N²²⁴NH (1.92 Å).

Molecular graphics and detailed analysis of the interactions between ligands and integrin $\alpha_4\beta_1$ receptor model. The following figures show the best binding conformation of the ligands within $\alpha_4\beta_1$ integrin binding site, represented as molecular solvent-excluded surfaces (partially transparent), colored using Coulombic electrostatic potential (ESP), with default coloring ranging from red for negative potential through white to blue for positive potential. Ligands are rendered in sticks, while metal ions belonging to MIDAS and ADMIDAS are rendered as green colored spheres. Key receptor residues in thick sticks. Molecular graphics and analyses were performed with Biovia Discovery Studio visualizer.

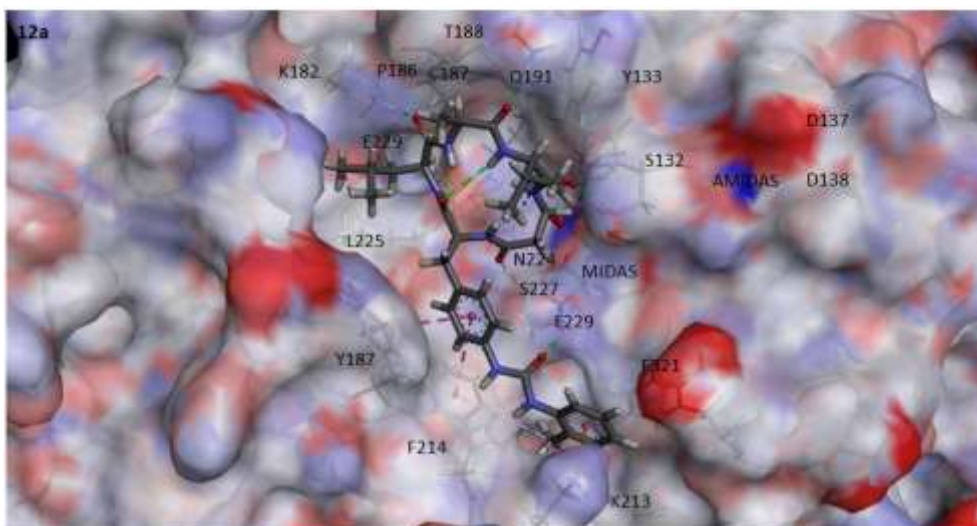


Figure S18. The CPPs **12a**, *c*[(*S*)-Phu-LAV-(*S*)-isoAsp], maintains the same stereochemistry as **3a**, but Asp³ is replaced by Ala³. Phu¹MePh group is in contact with β_1 :F³²¹ through a π - π stacking interaction and α_4 :K²¹³NH ζ^+ through a π -cation interaction (2.12 Å). UreaC=O makes a conventional hydrogen bond with β_1 :S²²⁷OH (2.21 Å). Phu¹Ph interacts with α_4 :F²¹⁴ through π - π T-shaped interaction and with α_4 :Y¹⁸⁷ through a stacked π - π interaction. Phu¹C=O makes two intramolecular hydrogen bonds with Ala³NH (1.78 Å) and Val⁴NH (2.91 Å). Leu²NH give rise to a hydrogen bond with β_1 :N²²⁴O (1.76 Å), while Leu²C=O makes a hydrogen with β_1 :K¹⁸²NH ζ^+ (2.01 Å). In addition to the intramolecular bond with Phu¹C=O, Ala³ shows an additional hydrogen bond between Ala³C=O and β_1 :N¹⁹¹H ϵ (1.89 Å). The methyl of Val³ nicely packs against methyl of β_1 :T¹⁸⁸. Val⁴C=O makes two hydrogen bonds, with β_1 :S¹³⁴NH (2.95 Å) and β_1 :S¹³⁴OH (1.69 Å). isoAsp⁵ residue coordinates Mg²⁺ (RMSD 0.11). Furthermore, isoAsp⁵COO⁻ is involved in a hydrogen bonds network with W¹ (2.83 Å), W³ (2.72 Å), β_1 :Y¹³³NH (2.45 Å), β_1 :N²²⁴NH (2.08 Å) and β_1 :N²²⁴NH δ 21 (2.55 Å).

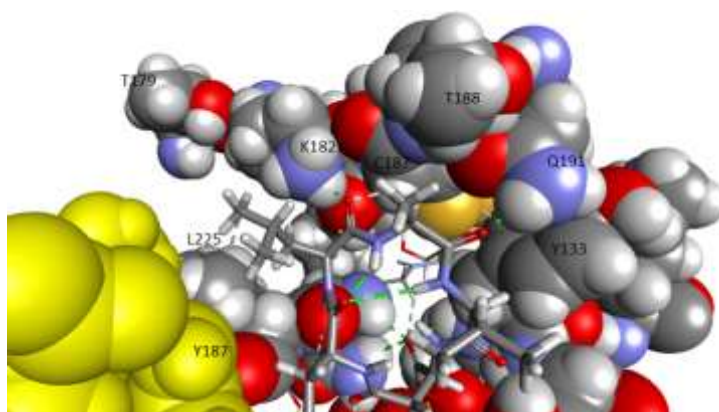


Figure S19. Detail of the upper region of the binding site of $\alpha_4\beta_1$ integrin hosting **12a**, *c*[(*S*)-Phu-LAV-(*S*)-isoAsp]. Receptor residues in contact with the cyclopeptide are rendered as CPK models; residues of α_1 subunit are highlighted in yellow. The sequence A¹⁸¹-K-L-R-N-P-C-T¹⁸⁸ of the β_1 subunit is replaced by S¹⁹¹-K-L-R-H-P-C-P¹⁹⁸ in β_7 subunit. In the $\alpha_4\beta_1$ -**12a** complex, the side chain of Thr¹⁸⁸ of β_1 subunit invades the space of Val³, so that the methyl of the latter nicely packs against the methyl of Thr¹⁸⁸. In the β_7 subunits, this residue is mutated for Pro¹⁹⁸.

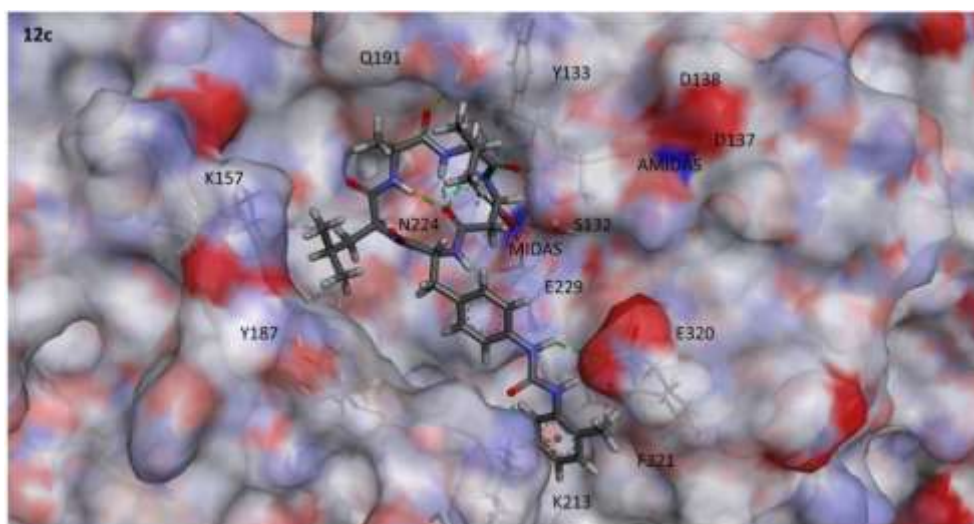


Figure S20. The CPPs **12c**, *c*[(*R*)-Phu-LAV-(*S*)-isoAsp], is an analogue of **3c**, sharing the same stereochemistry array, in which Asp³ is replaced by Ala³. This cyclopeptide shows interactions with both α_4 and β_1 subunits. MePh group of Phu¹ is in contact with α_4 :K²¹³ (π -cation interaction with NH ζ^+ , 3.76 Å, plus π -alkyl, 3.76 Å) and with β_1 :F³²¹ (π -alkyl, 4.37 Å). UreaC=O is hydrogen bonded to α_4 :K²¹³NH ζ^+ (1.84 Å), while both ureaNHs are hydrogen bonded to β_1 :Glu³²⁰COO⁻ (1.94 Å, 2.90 Å). The side chain of Leu² is inserted within the cavity delimited by β_1 :L²²⁵, α_4 :K¹⁵⁷, α_4 :Y¹⁸⁷, making hydrophobic interactions. Ala³NH is involved in an intramolecular hydrogen bond with isoAspC=O (2.03 Å), Ala³C=O makes a hydrogen bond with β_1 :N¹⁹¹CONH₂ (2.19 Å), while Ala³methyl is close to β_1 :T¹⁸⁸methyl (alkyl interaction). Val⁴NH is involved in an intramolecular hydrogen bond with isoAspC=O (1.81 Å), Val⁴C=O is hydrogen bonded to β_1 :S¹³⁴NH (2.79 Å), but Val⁴isopropyl is directed perpendicularly above the molecular plane, therefore making very little contacts with any residues of β_1 subunit. Finally, isoAsp⁵COO⁻ is coordinated to Mg²⁺ in MIDAS.

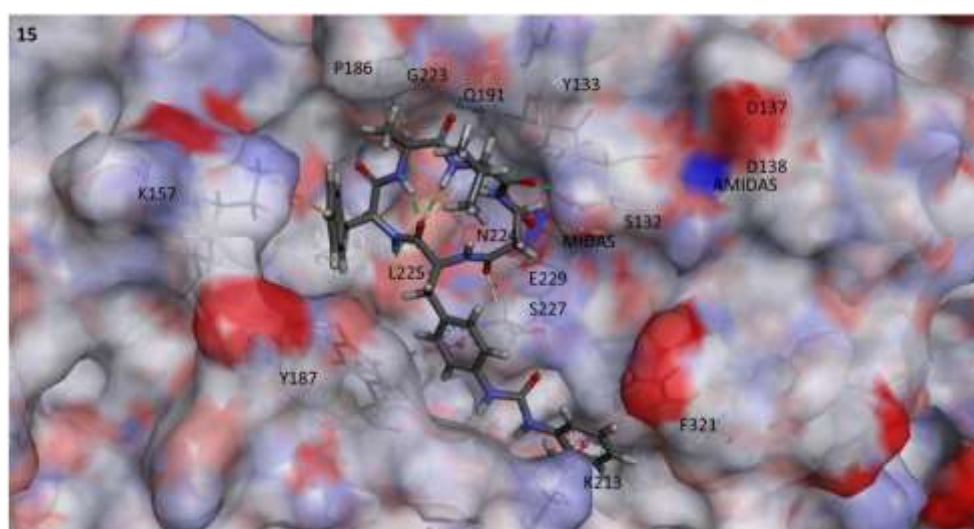


Figure S21. The CPP **15** was obtained from **3a** by replacing Leu² with Phe² and Asp³ with Ala³. The Phu¹MePh group is located between the residues β_1 :F³²¹ and α_4 :K²¹³, with which it interacts giving rise to a π - π stacking interaction and a π -cation interaction (3.19 Å). UreaC=O makes a conventional hydrogen bond with β_1 :S²²⁷OH (2.05 Å), while Phu¹PH makes a π - π stacking interactions with α_4 :Y¹⁸⁷. Phu¹C=O makes two intramolecular hydrogen bonds with Ala³NH (1.72 Å) and Val⁴NH (2.15 Å). Phe²NH makes two hydrogen bonds with β_1 :N²²⁴O (2.87 Å) and with β_1 :L²²⁵O (2.14 Å), while Phe²Ph is held in position by a π -cation interaction with β_1 :K¹⁸²N ζ^+ (4.01 Å). In addition to the intramolecular hydrogen bonds with Phu¹, Ala³ residue makes an hydrogen bond between C=O and β_1 :Gln¹⁹¹He22 (1.89 Å), while the Val⁴C=O forms an hydrogen bond with β_1 :S¹³⁴OH (1.85 Å). The carboxyl group of the isoAsp⁵ residue makes two water-hydrogen bonds with W¹ (2.84 Å) and W³ (2.70 Å), an hydrogen bond with β_1 :Y¹³³NH (2.12 Å) and an hydrogen bond with β_1 :N²²⁴NH (2.30 Å). isoAsp⁵COO⁻ coordinates the magnesium ion in MIDAS (RMSD 0.15).

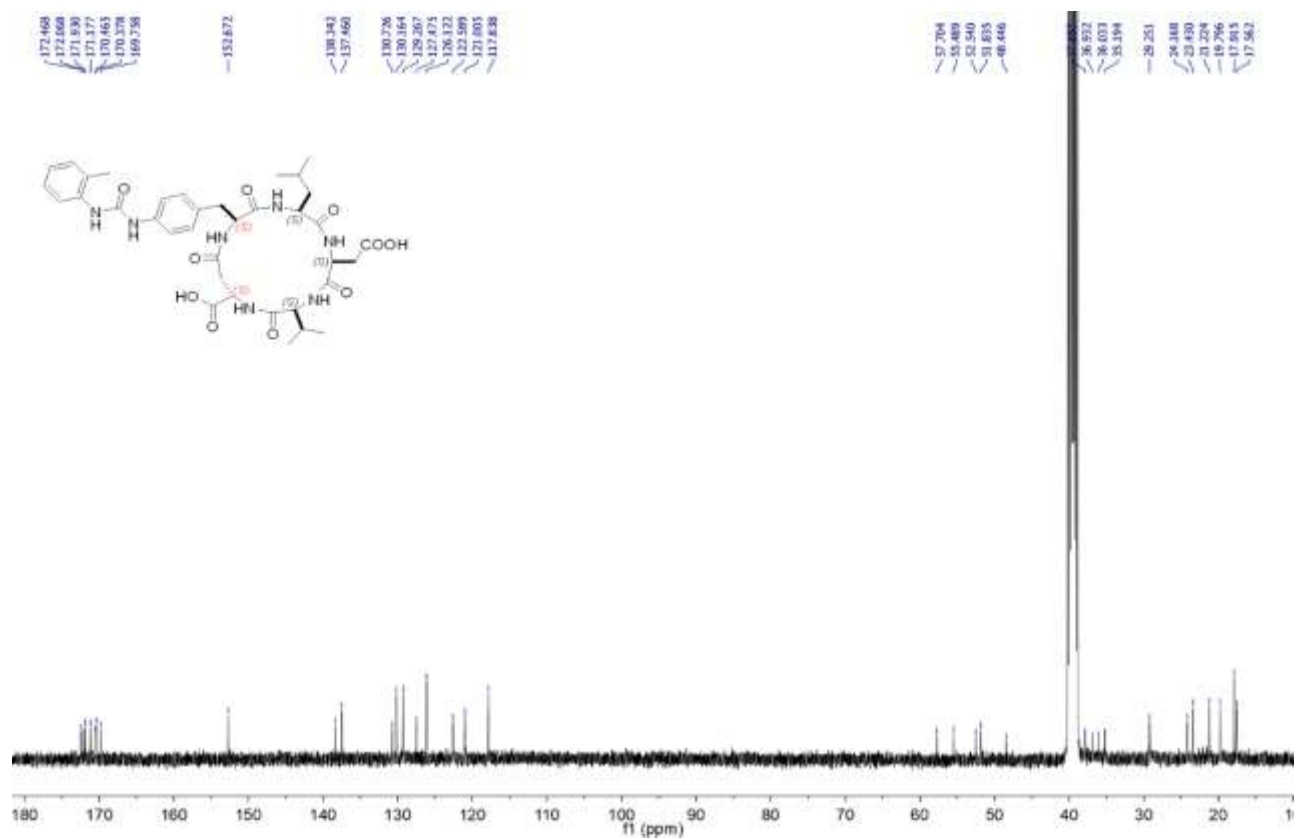
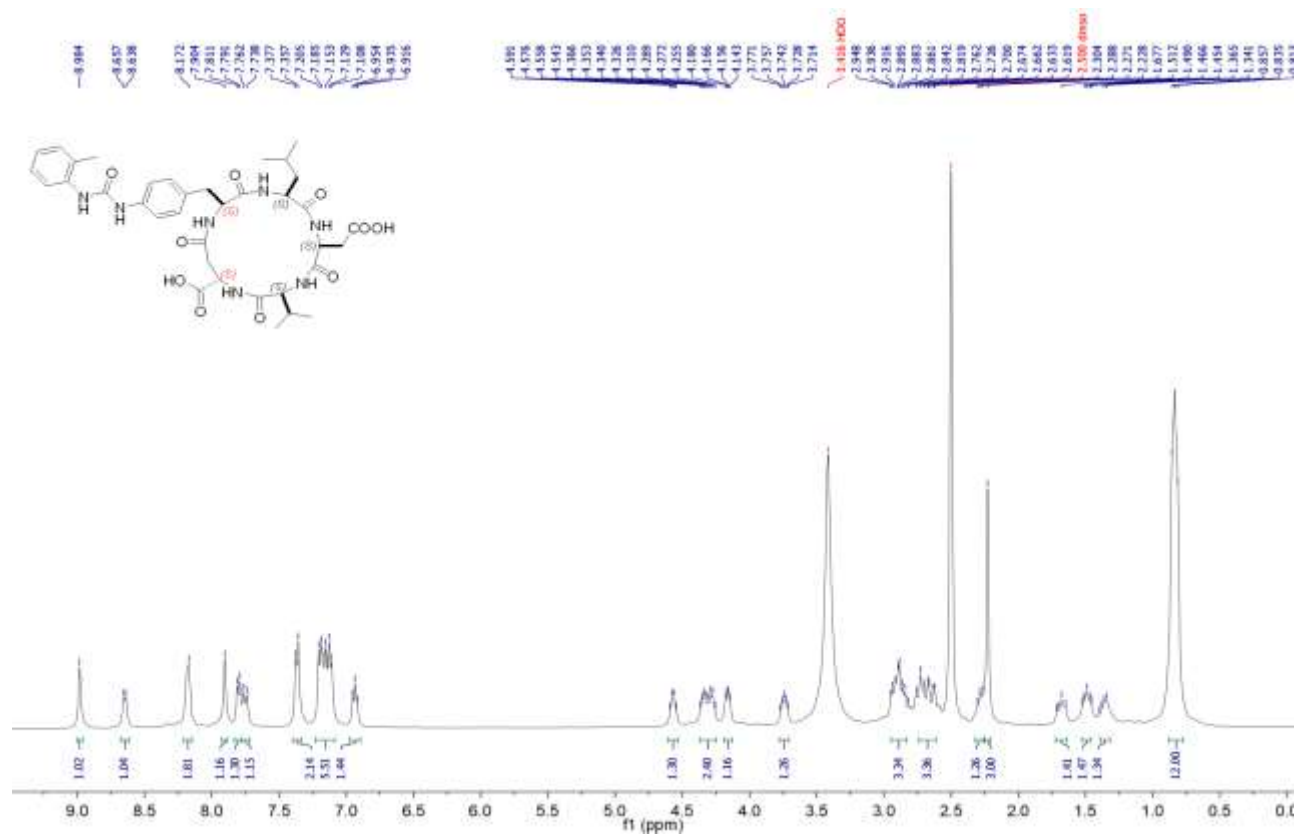


Figure S22. ¹H NMR (8:2 DMSO₆/H₂O at 400 MHz) and ¹³C NMR (DMSO₆, 100 MHz) of 3a.

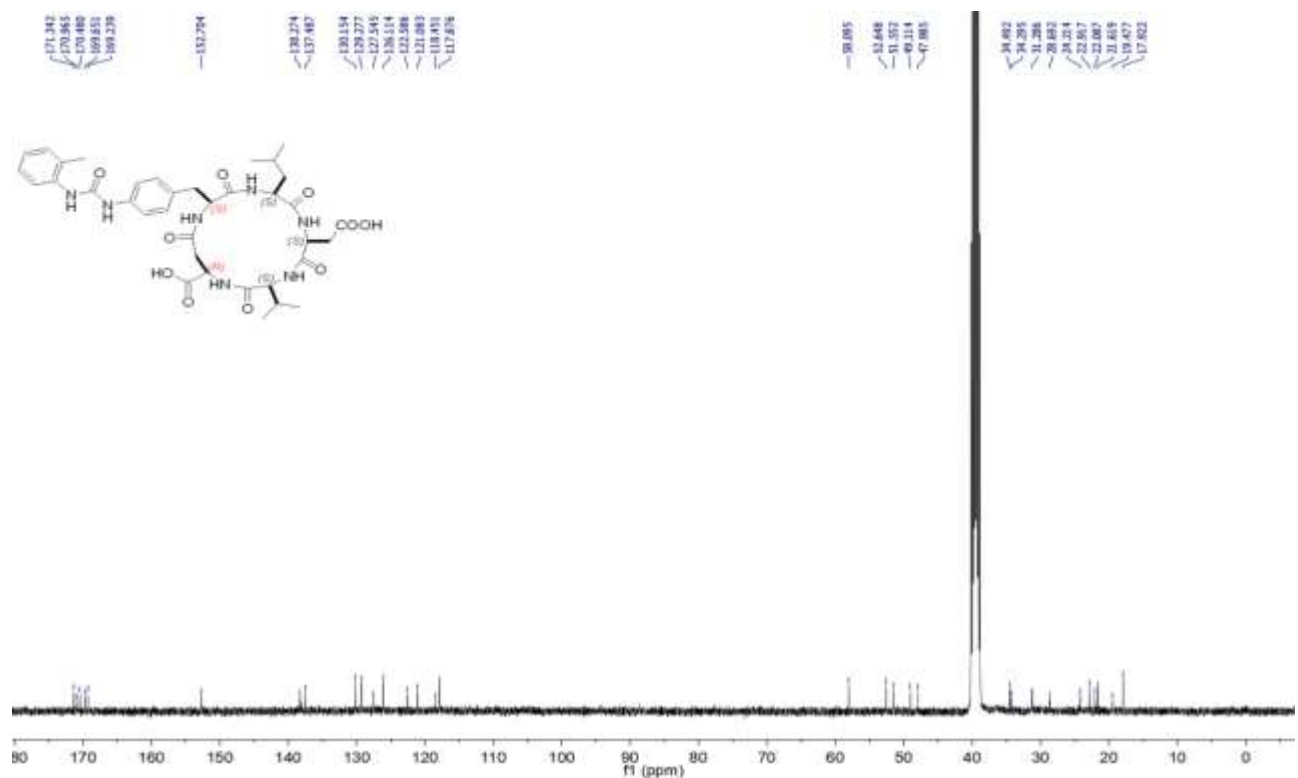
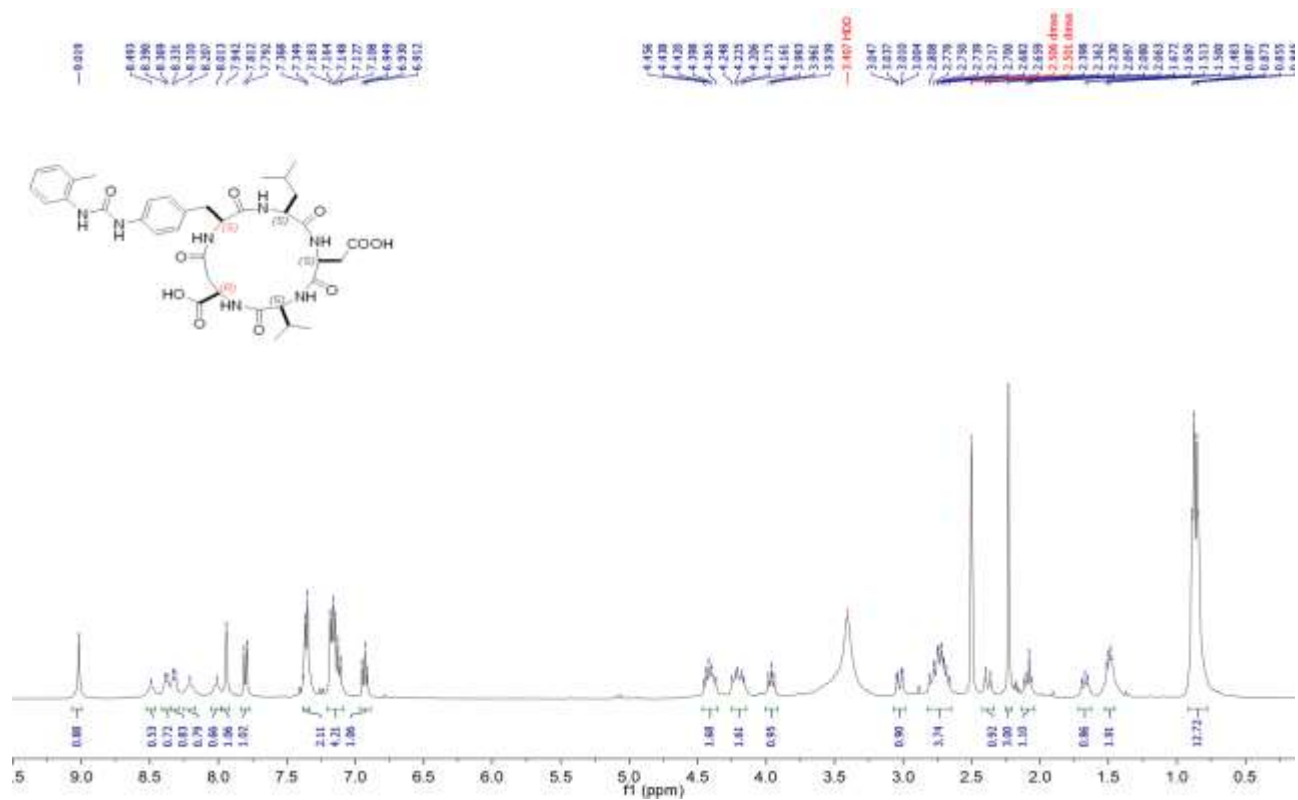


Figure S23. ¹H-NMR (8:2 DMSO₆/H₂O at 400 MHz) and ¹³C-NMR (DMSO₆, 100 MHz) of **3b**.

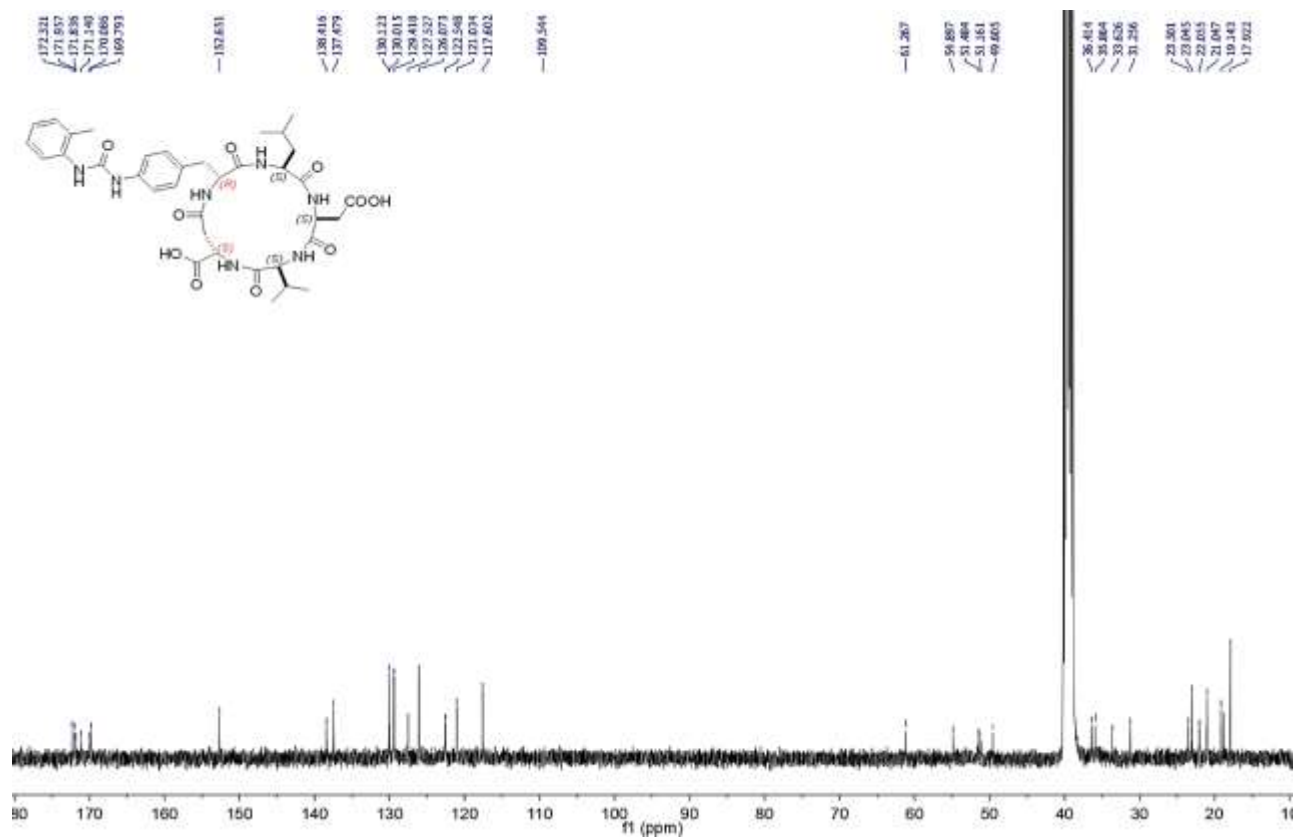
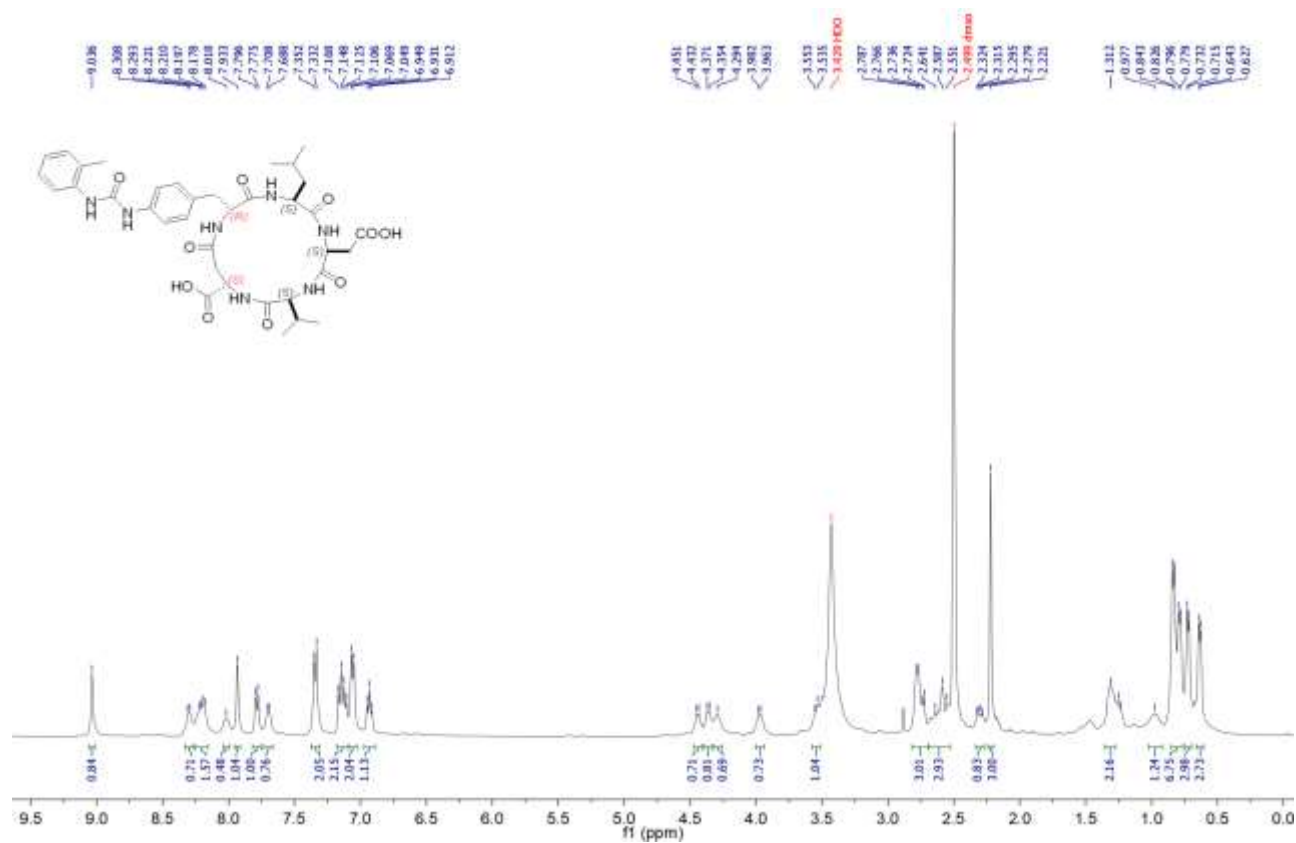


Figure S24. ¹H-NMR (8:2 DMSO₆/H₂O at 400 MHz) and ¹³C-NMR (DMSO₆, 100 MHz) of 3c.

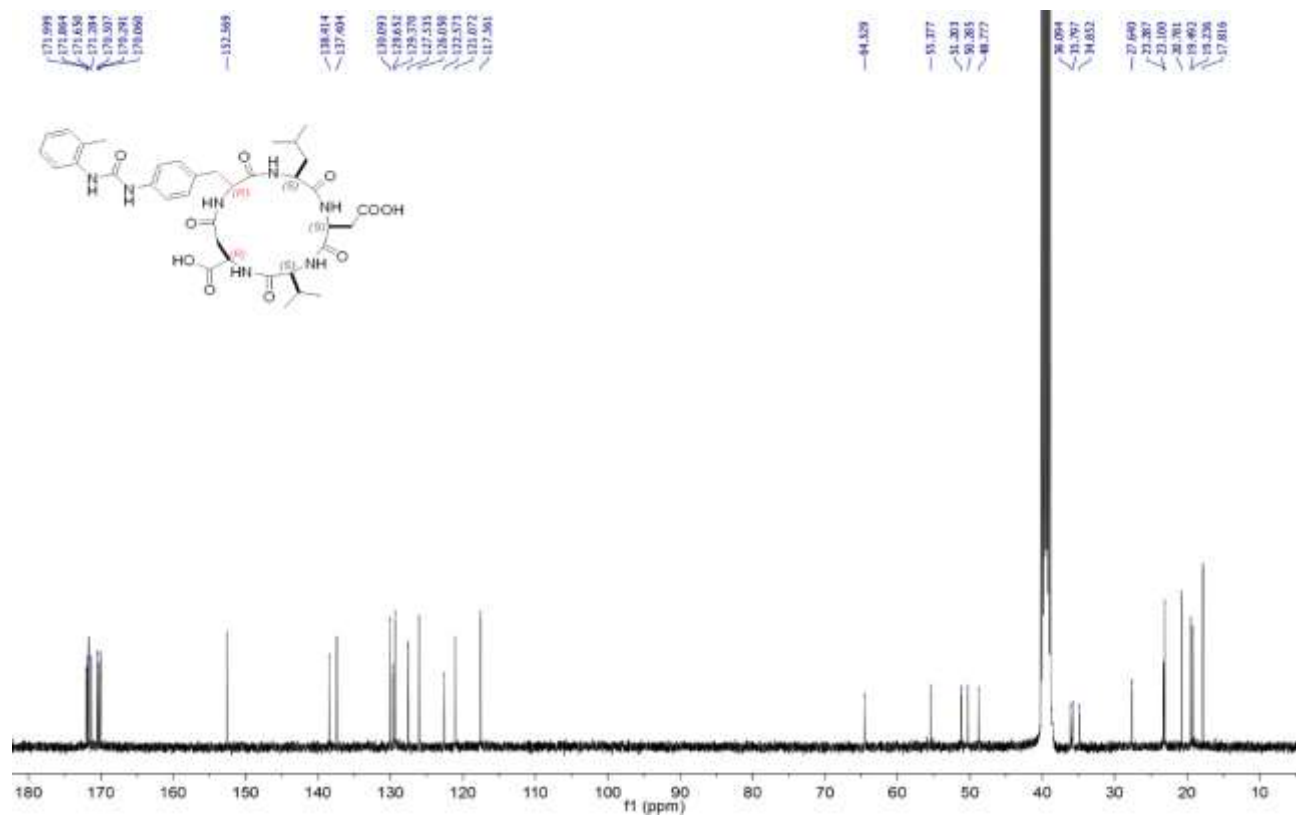
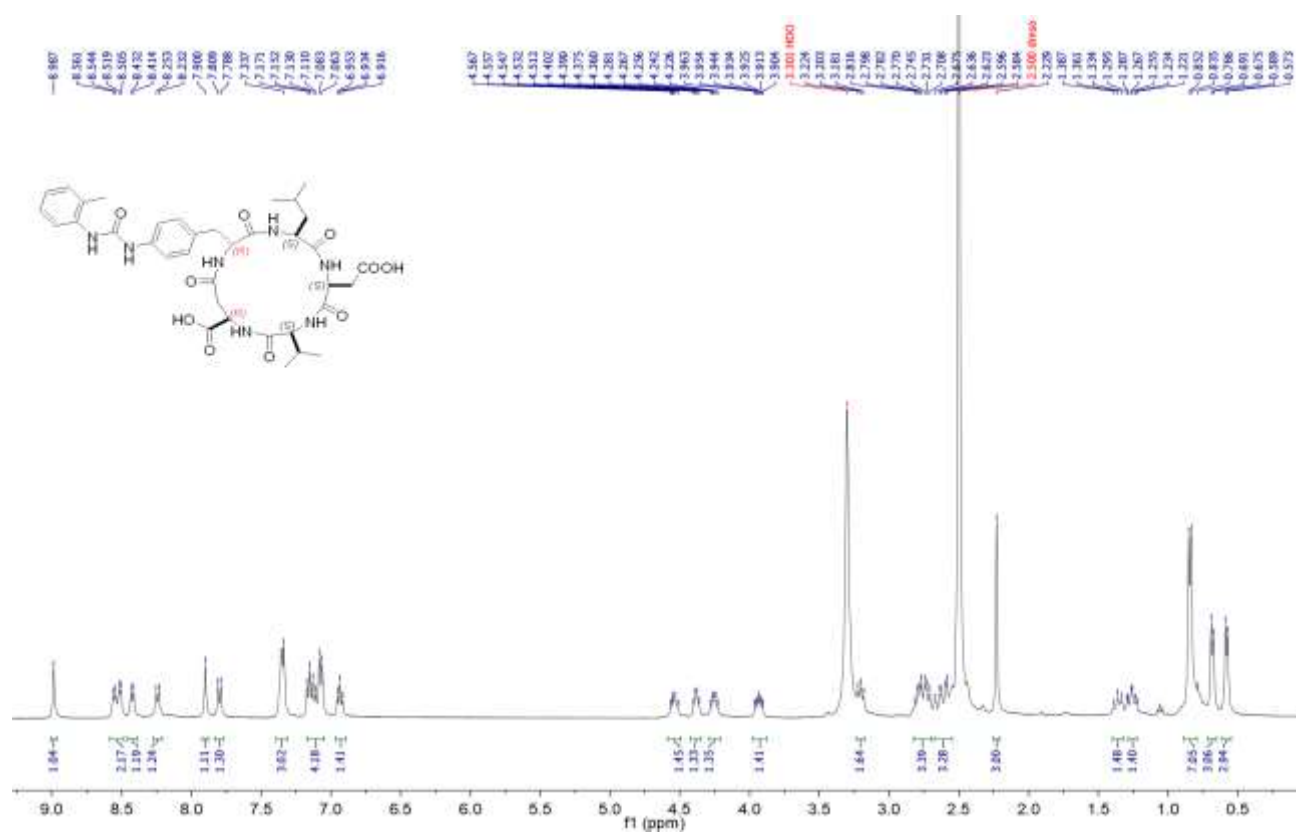


Figure S25. ¹H-NMR (8:2 DMSO₆/H₂O at 400 MHz) and ¹³C-NMR (DMSO₆, 100 MHz) of 3d.

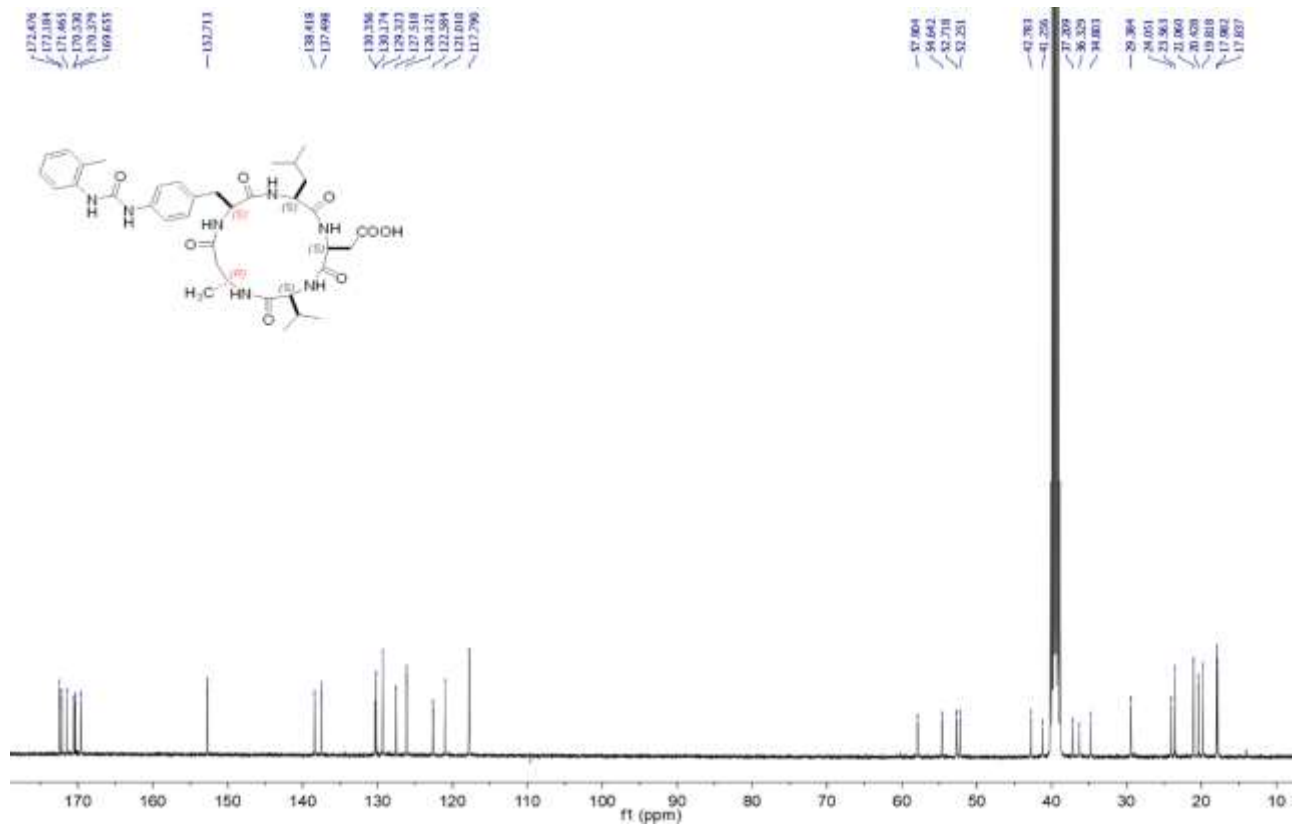
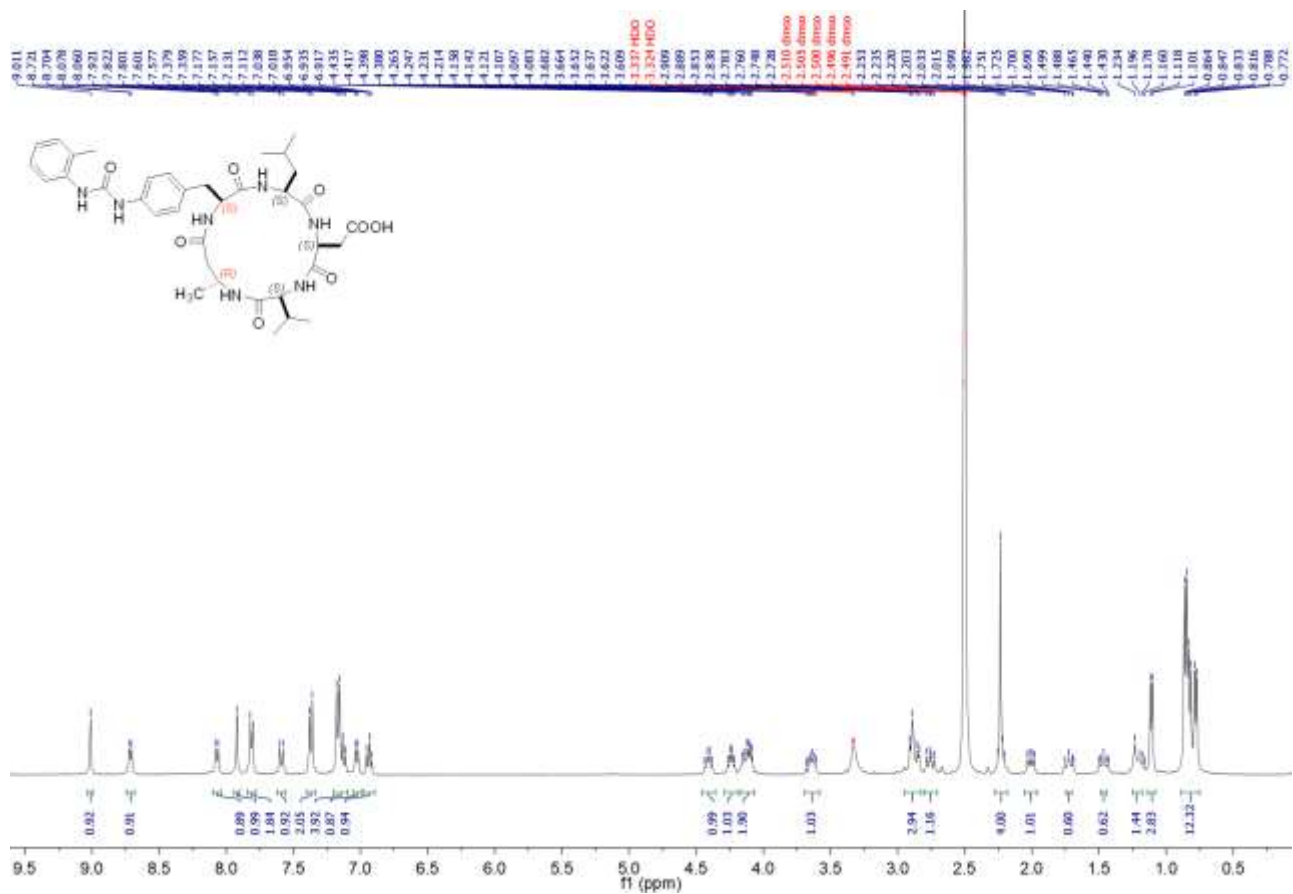


Figure S26. ¹H-NMR (8:2 DMSO₆/H₂O at 400 MHz) and ¹³C-NMR (DMSO₆, 100 MHz) of 11a.

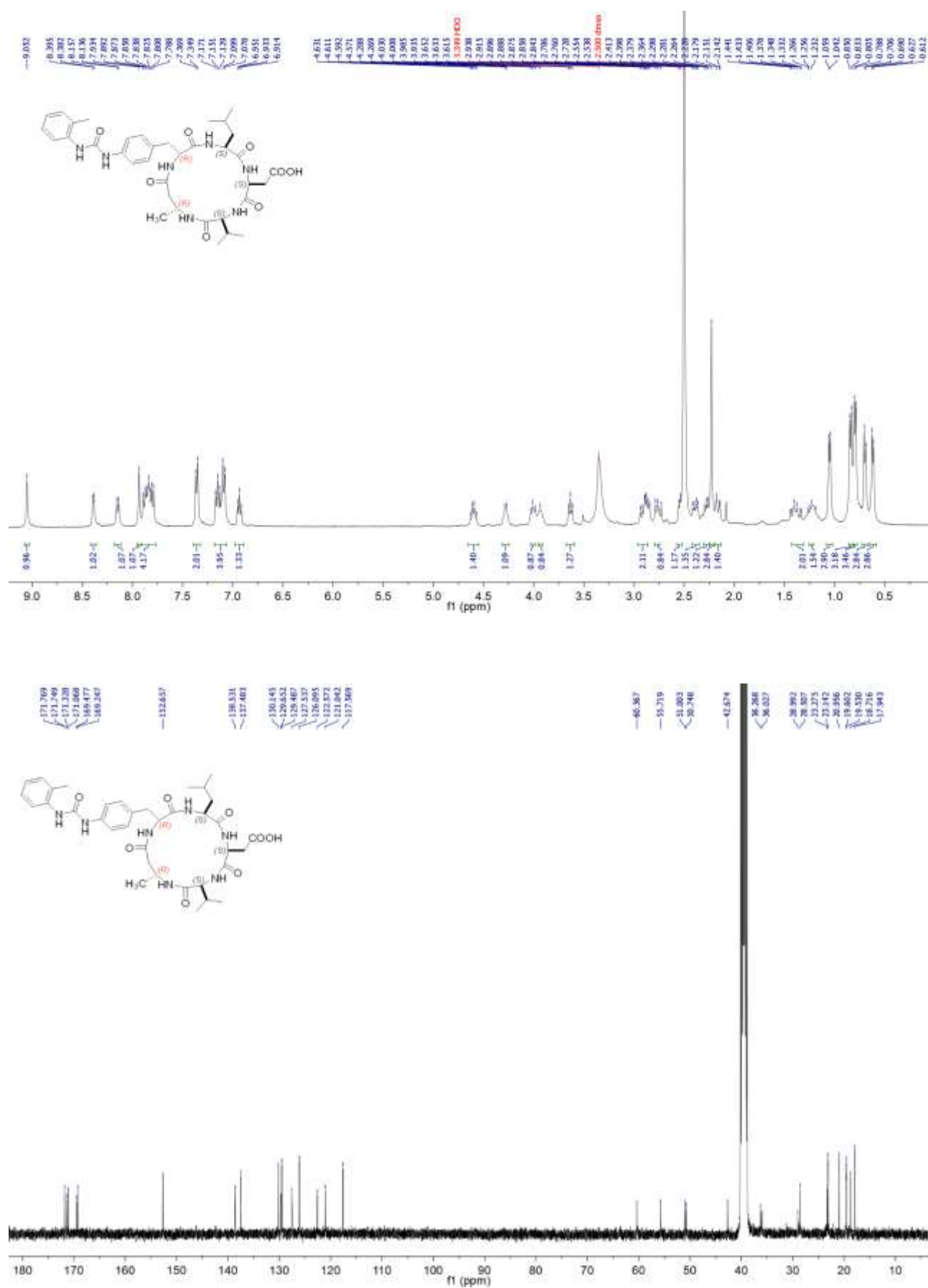


Figure S27. ¹H-NMR (8:2 DMSO₆/H₂O at 400 MHz) and ¹³C-NMR (DMSO₆, 100 MHz) of 11c.

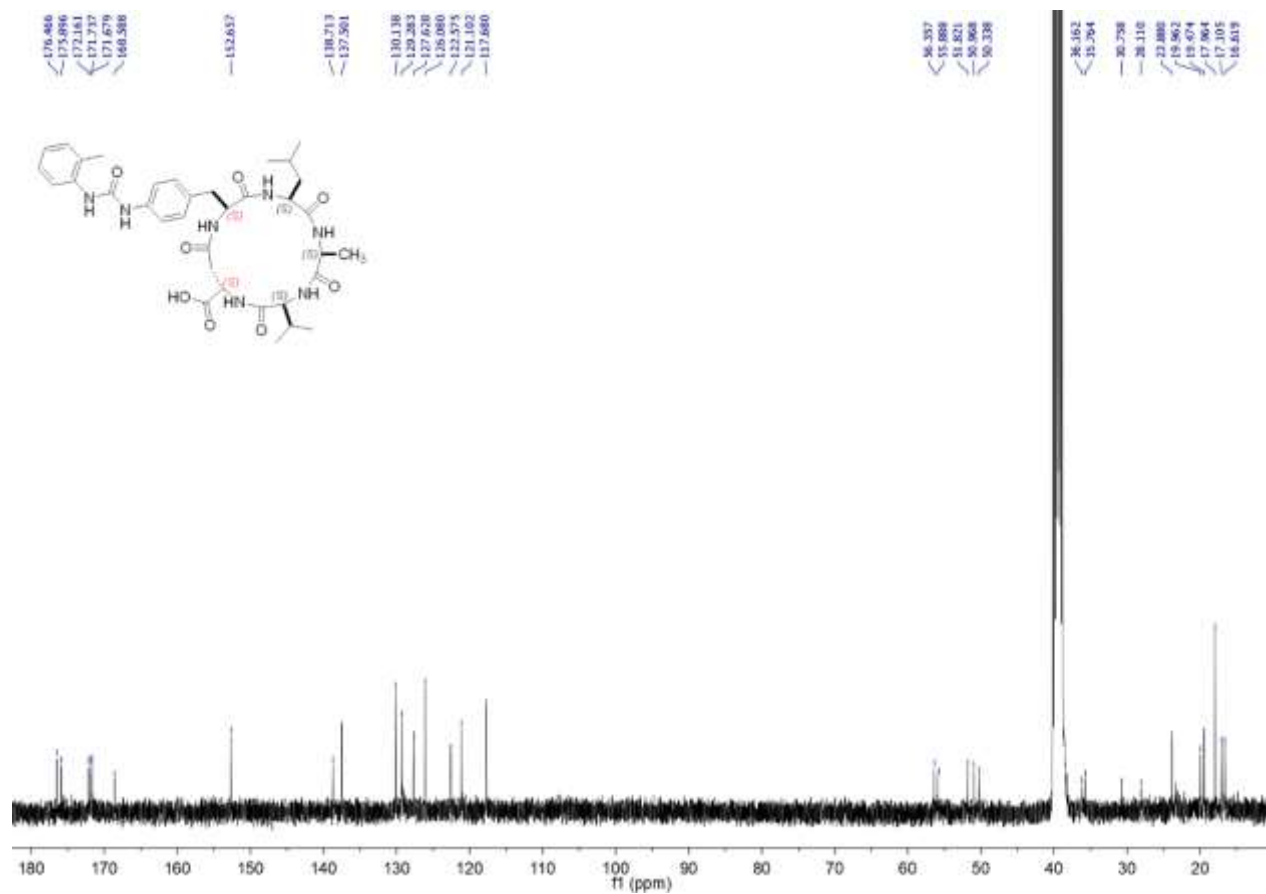
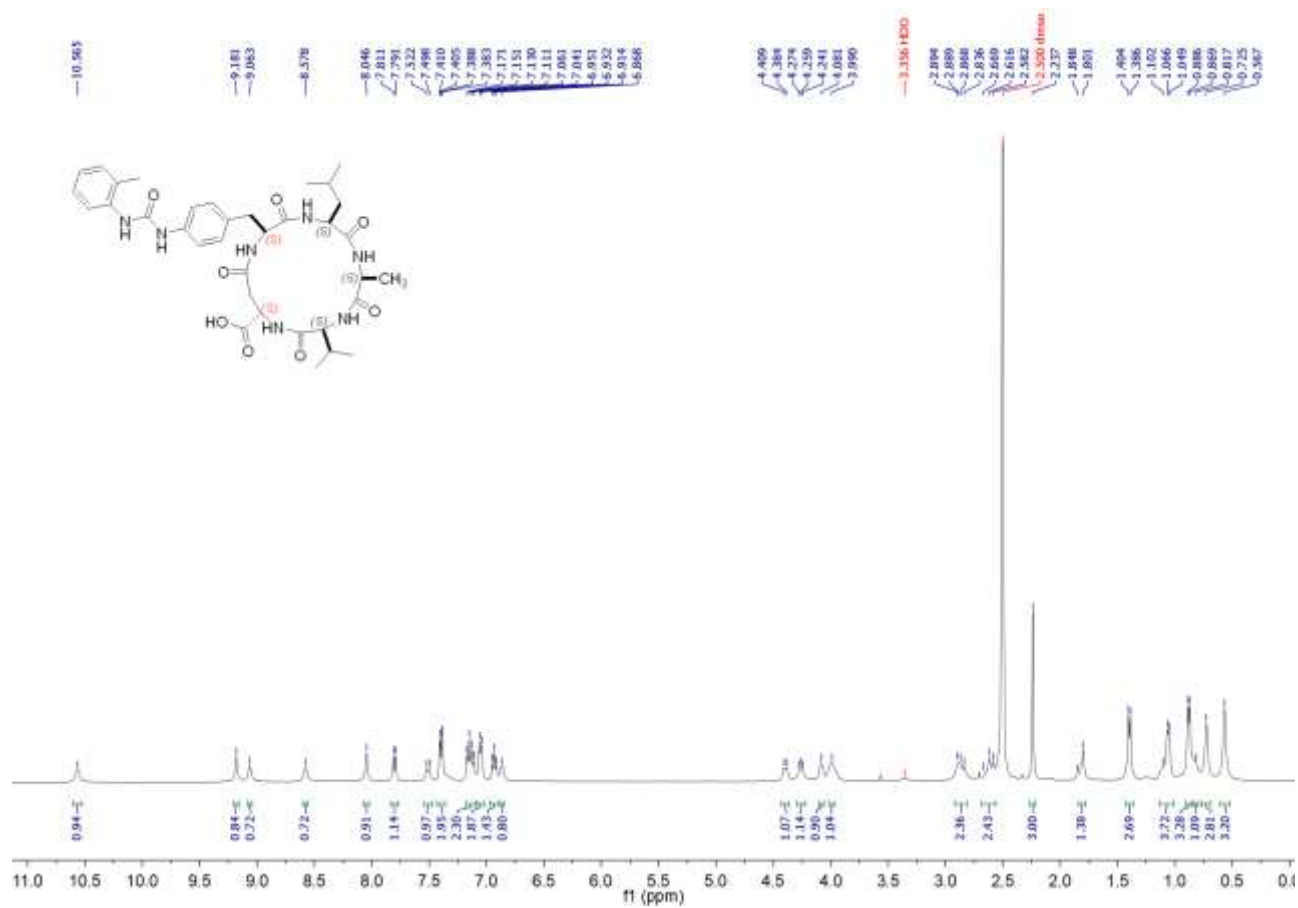


Figure S28. ¹H-NMR (8:2 DMSO₆/H₂O at 400 MHz) and ¹³C-NMR (DMSO₆, 100 MHz) of 12a.

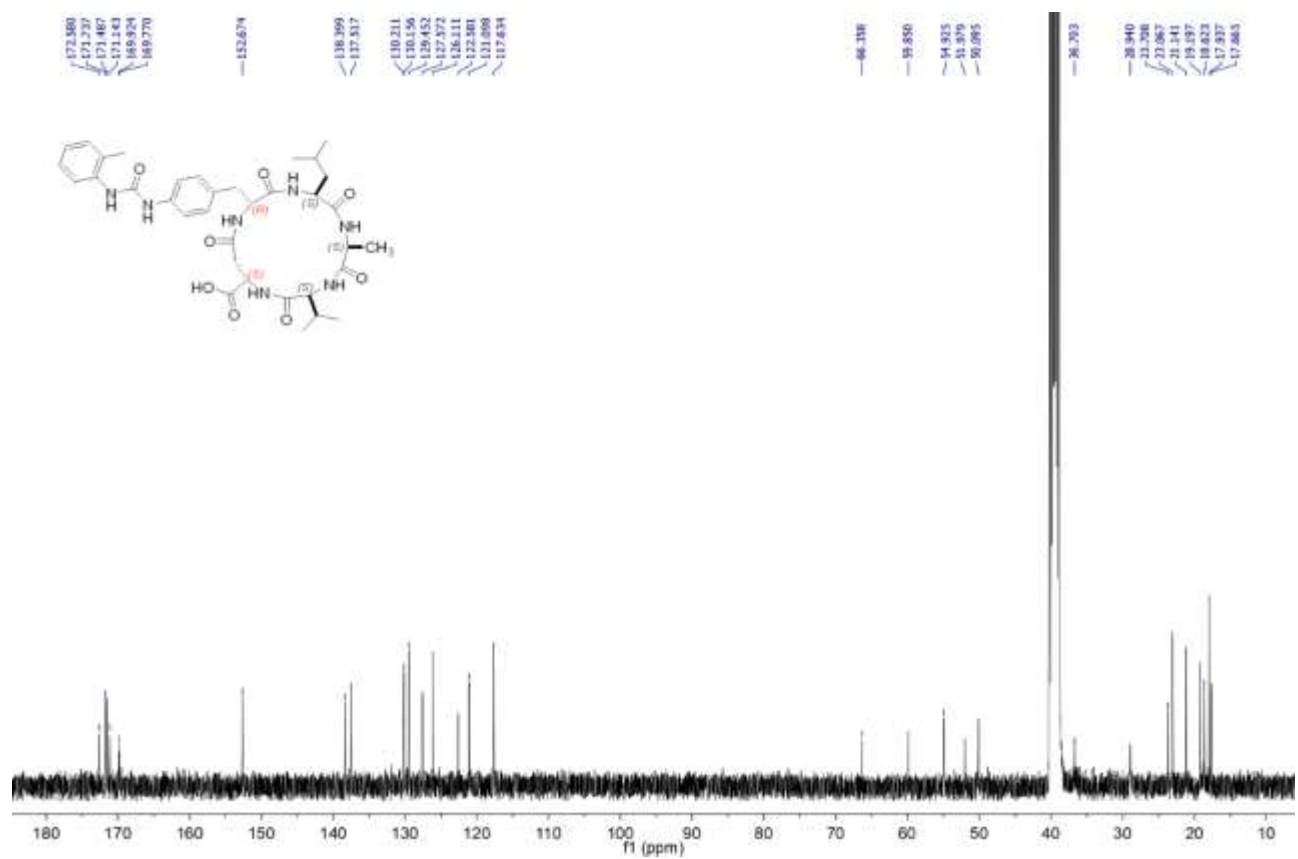
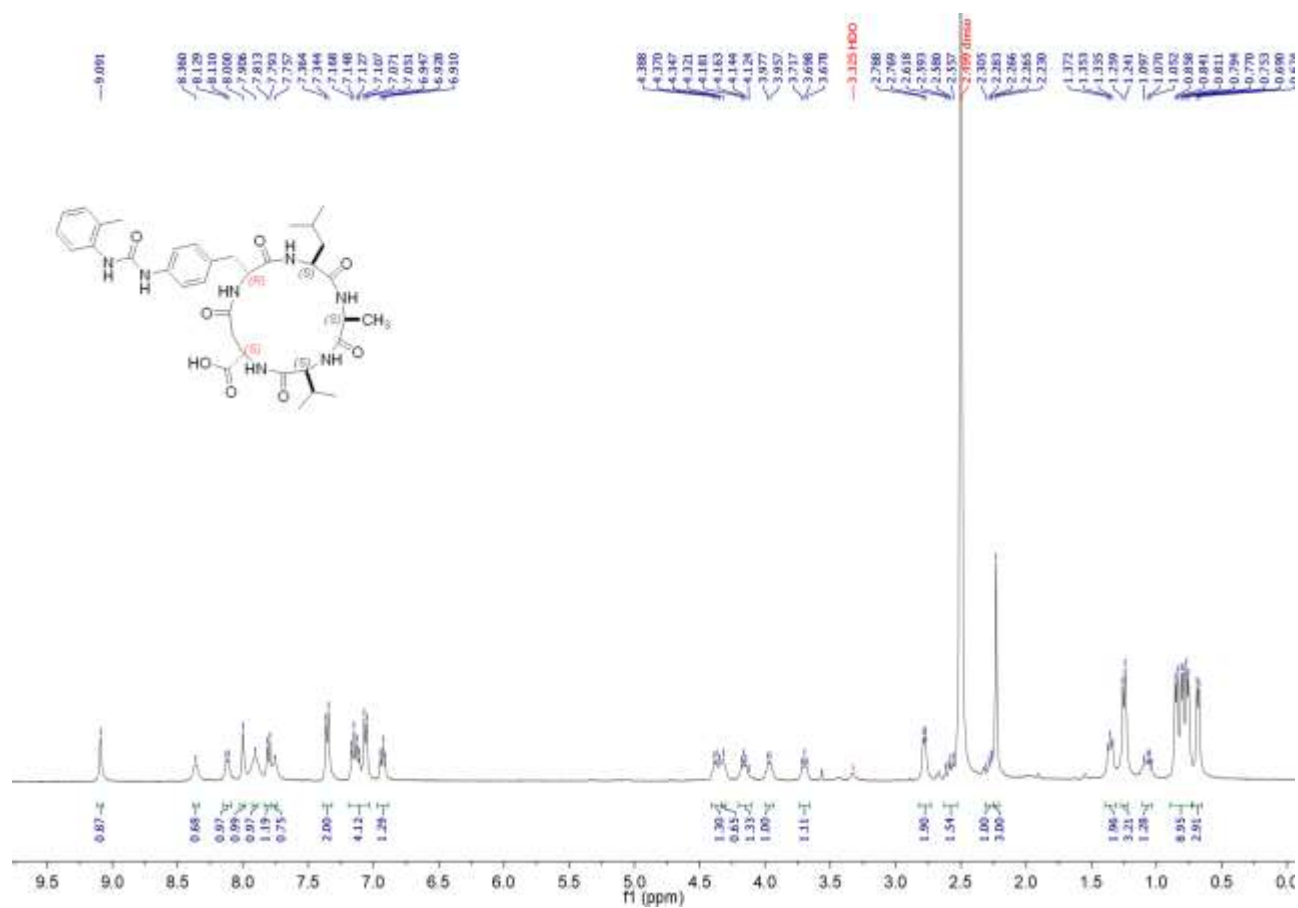


Figure S29. ¹H-NMR (8:2 DMSO₆/H₂O at 400 MHz) and ¹³C-NMR (DMSO₆, 100 MHz) of 12c.

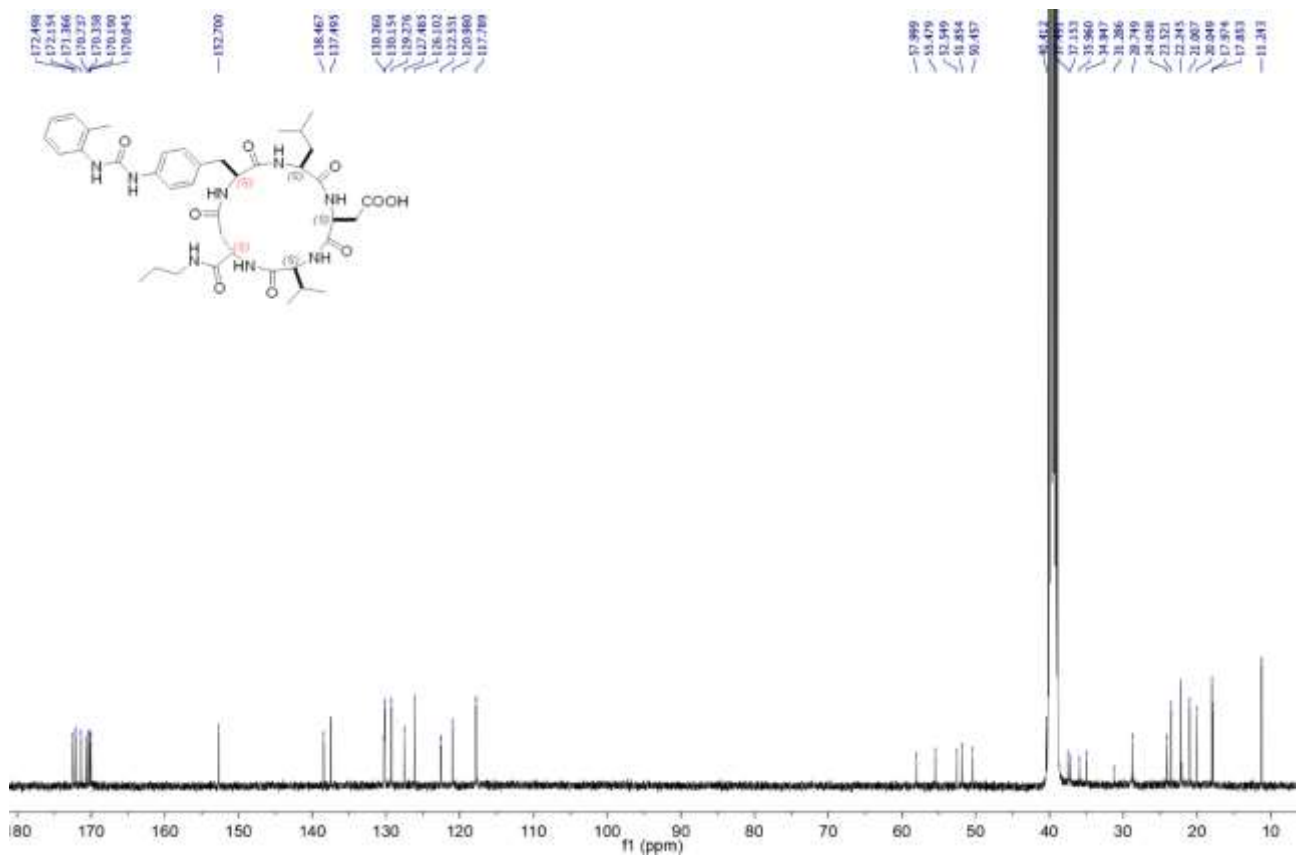
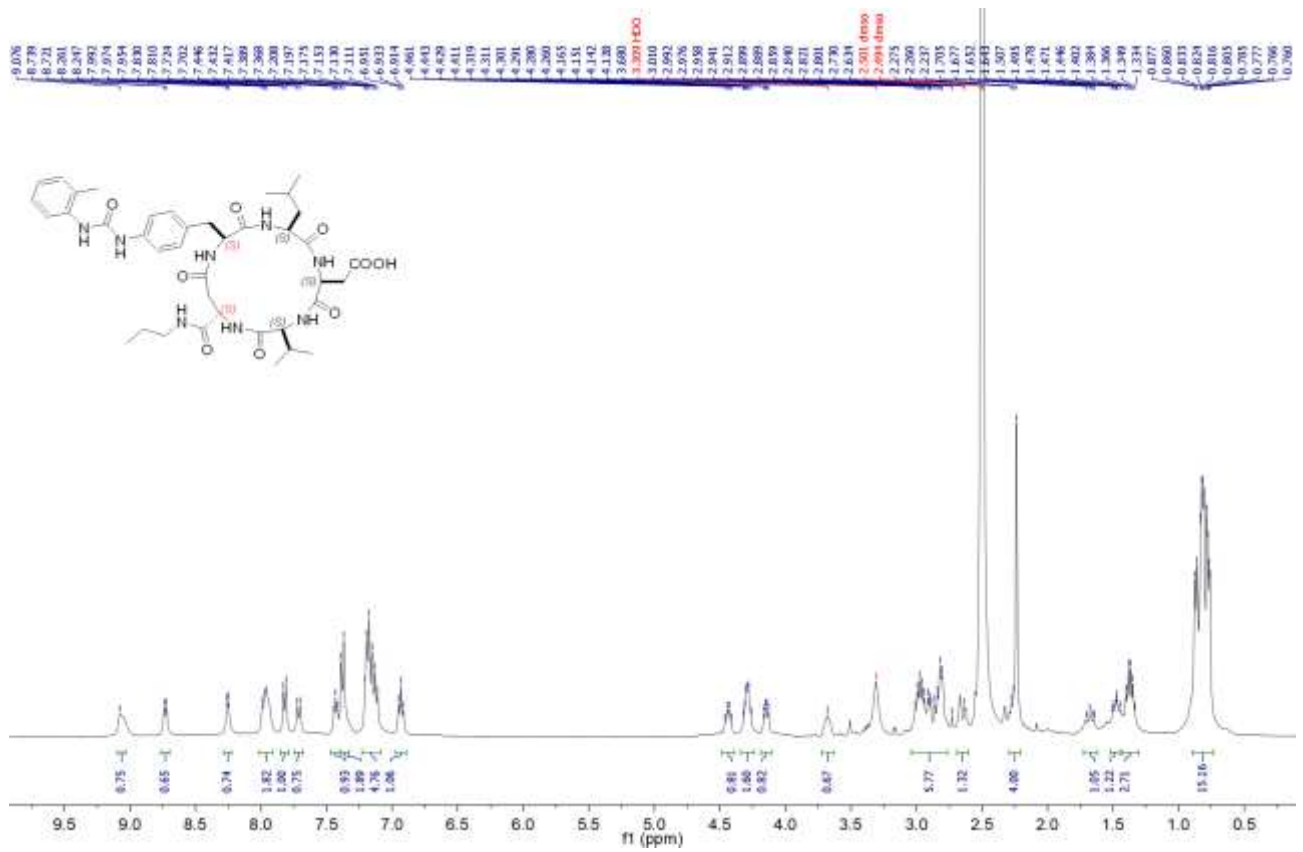


Figure S30. ¹H-NMR (8:2 DMSO₆/H₂O at 400 MHz) and ¹³C-NMR (DMSO₆, 100 MHz) of 13.

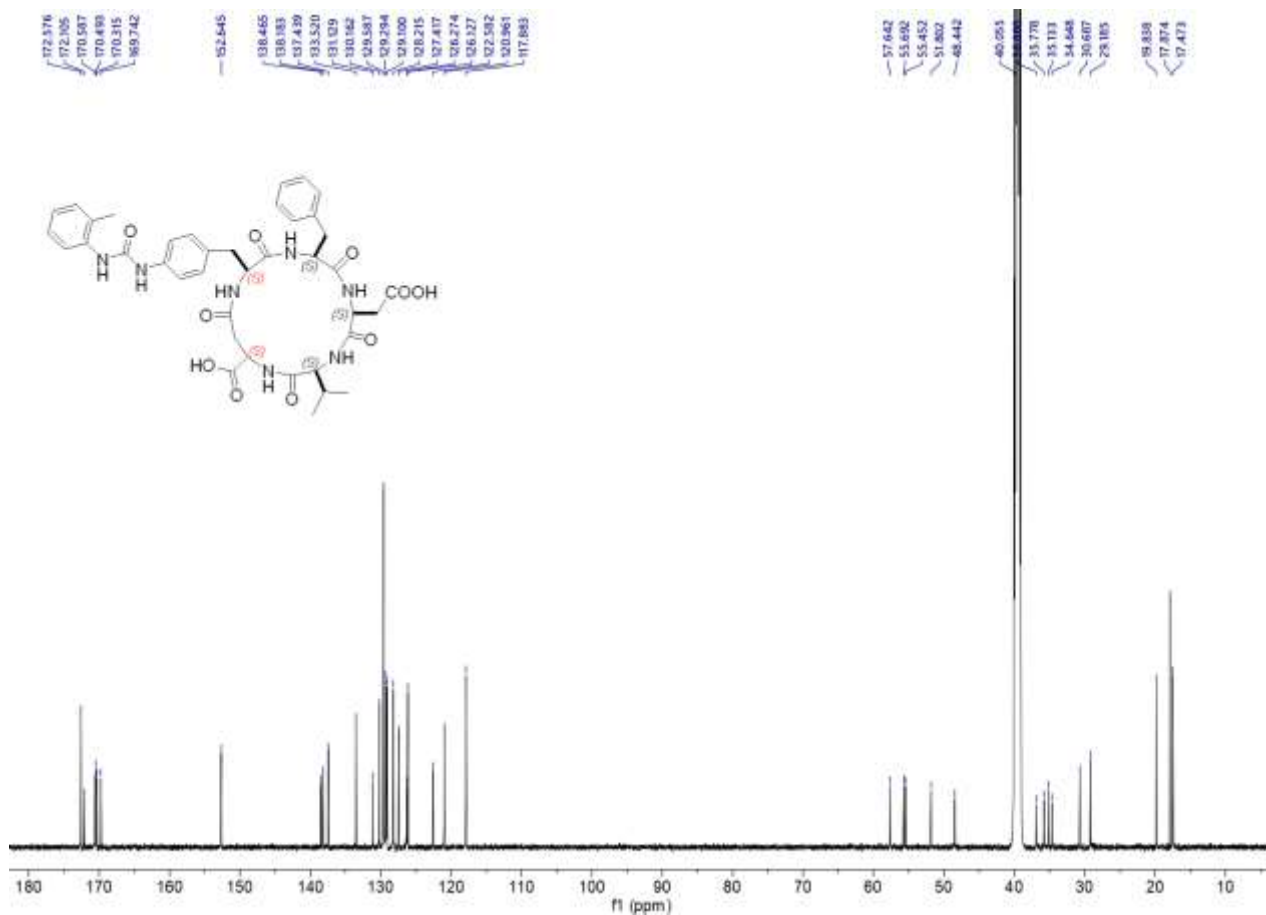
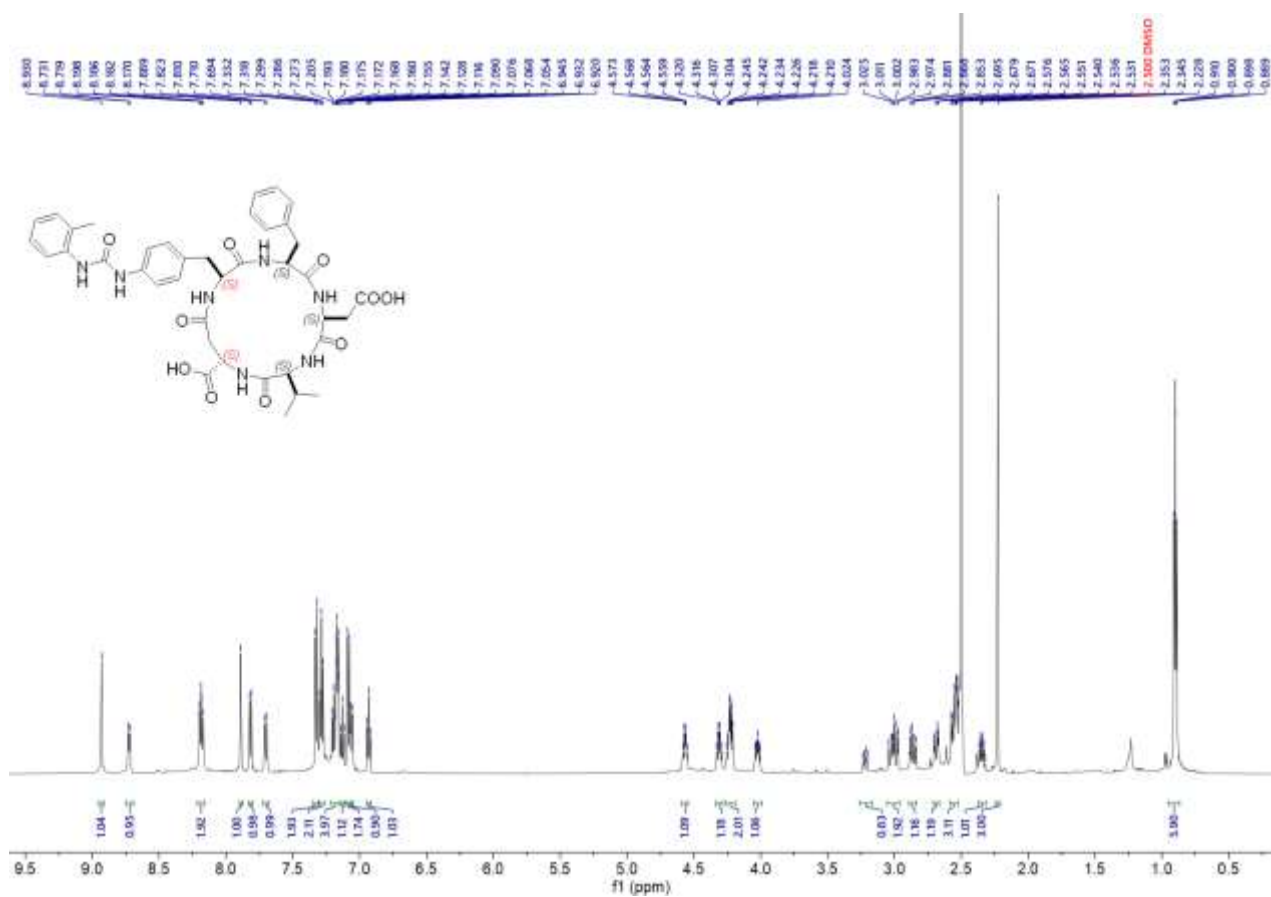


Figure S31. ¹H-NMR (8:2 DMSO₆/H₂O at 600 MHz) and ¹³C-NMR (DMSO₆, 150 MHz) of **14**.

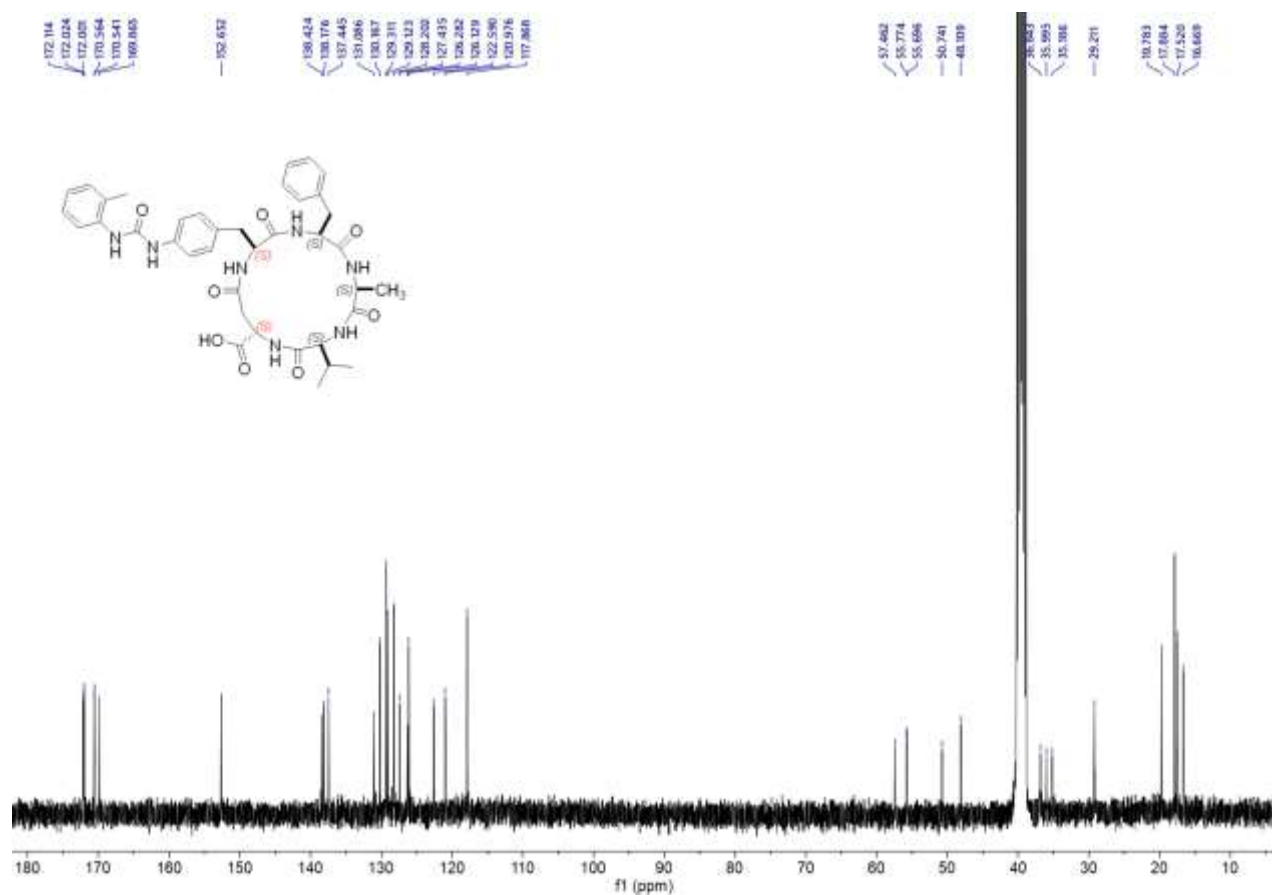
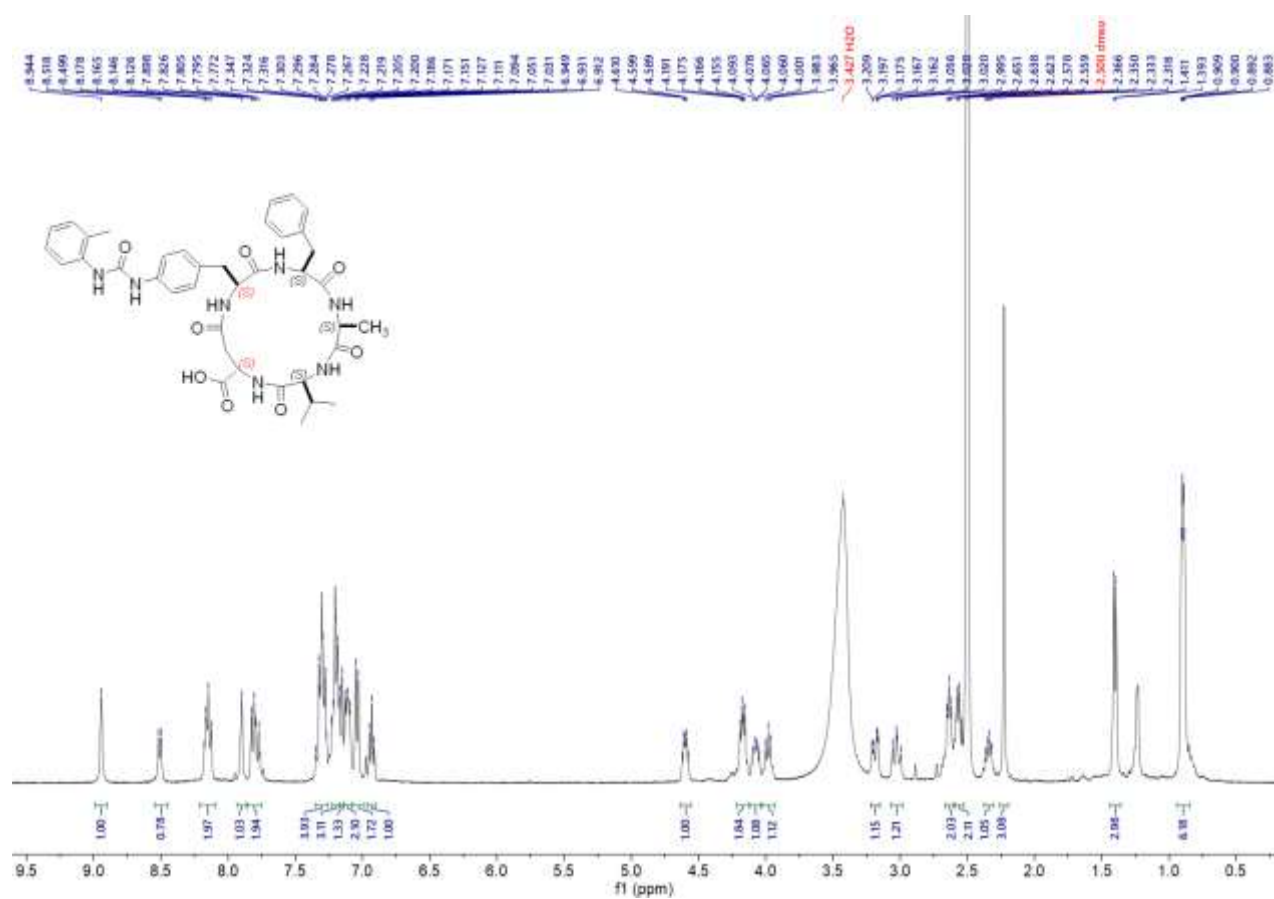


Figure S32. ¹H-NMR (8:2 DMSO₆/H₂O at 400 MHz) and ¹³C-NMR (DMSO₆, 100 MHz) of 15.

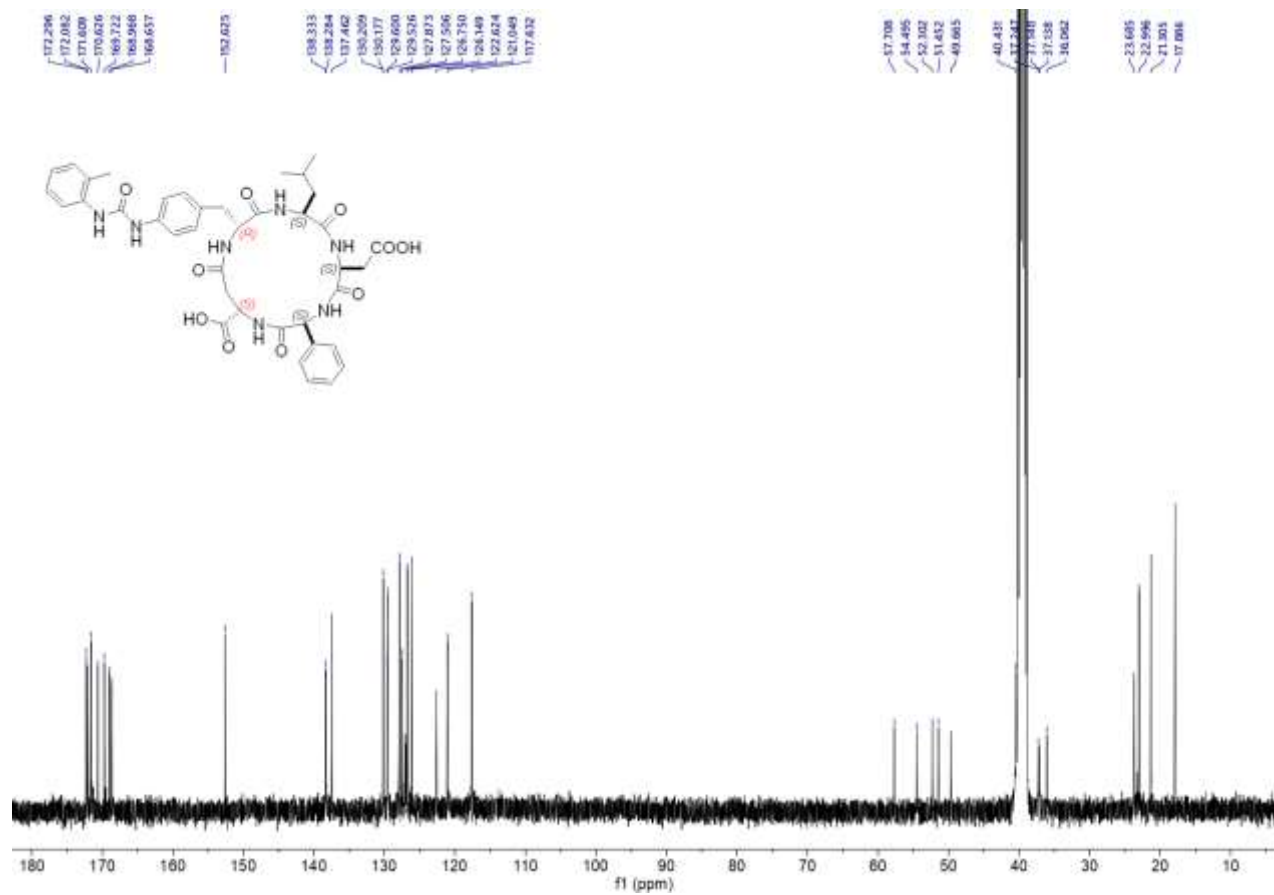
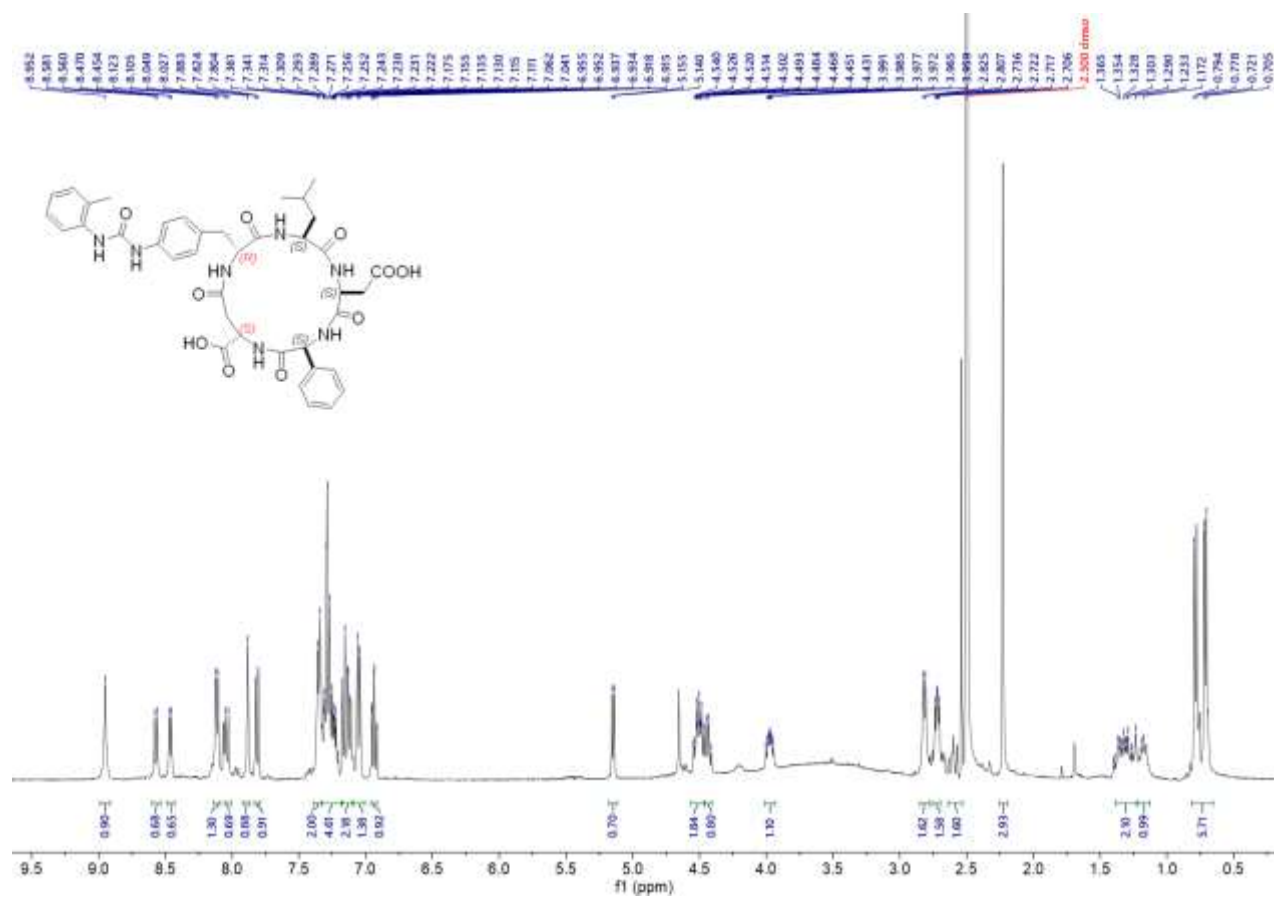


Figure S33. $^1\text{H-NMR}$ (8:2 $\text{DMSO}_d_6/\text{H}_2\text{O}$ at 400 MHz) and $^{13}\text{C-NMR}$ (DMSO_d_6 , 100 MHz) of **16**.

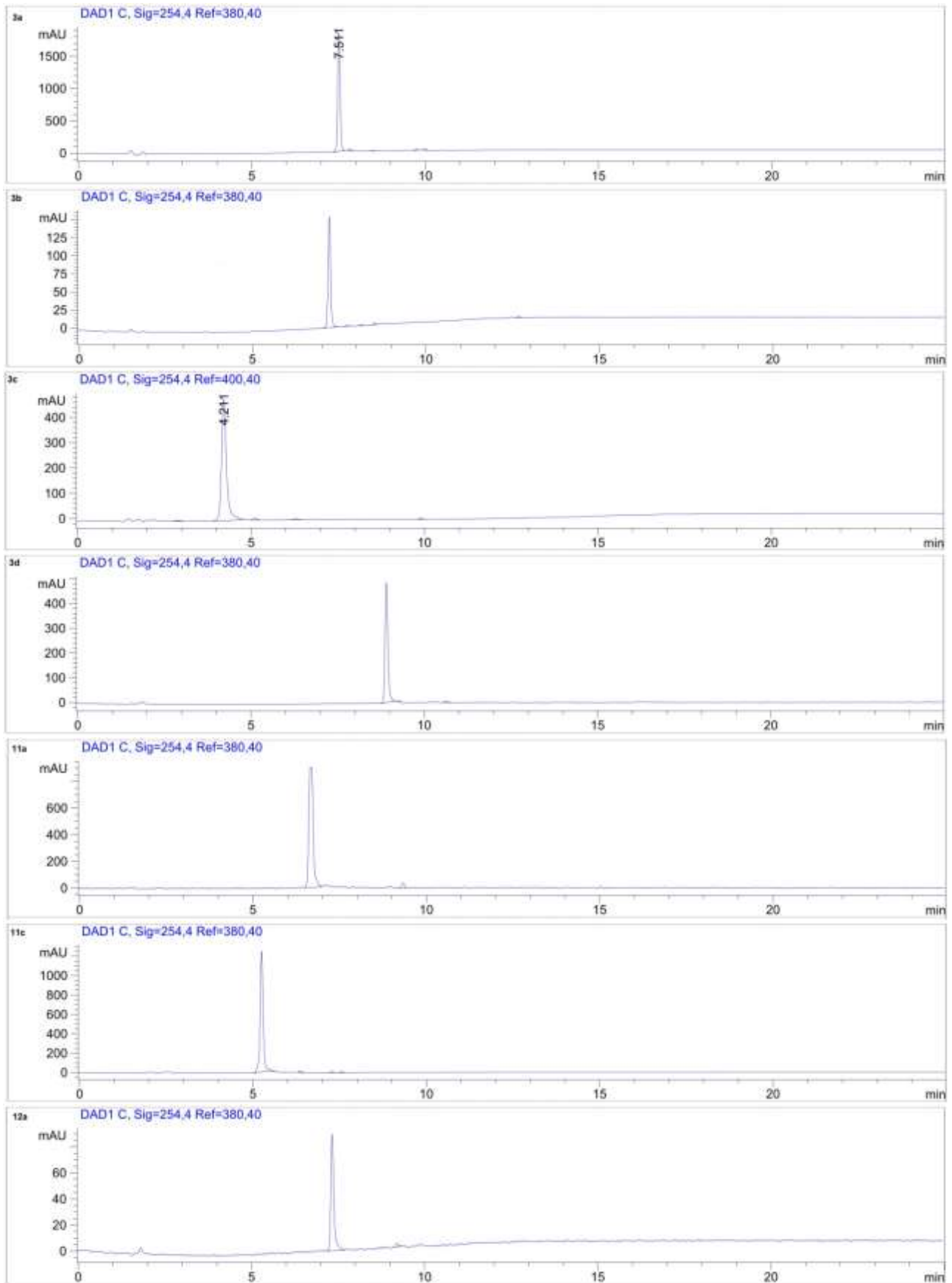


Figure S34. RP HPLC analyses performed on a column Phenomenex mod. Gemini 3 μm C₁₈ 110 Å 100 \times 3.0 mm; mobile phase from 9:1 H₂O/CH₃CN/0.1% HCOOH to 2:8 H₂O/CH₃CN/0.1% HCOOH in 20 min, flow rate of 1.0 mL min⁻¹. DAD 254 nm, unless otherwise specified. For peptide **14**, the analytical flow rate is 0.5 mL min⁻¹.

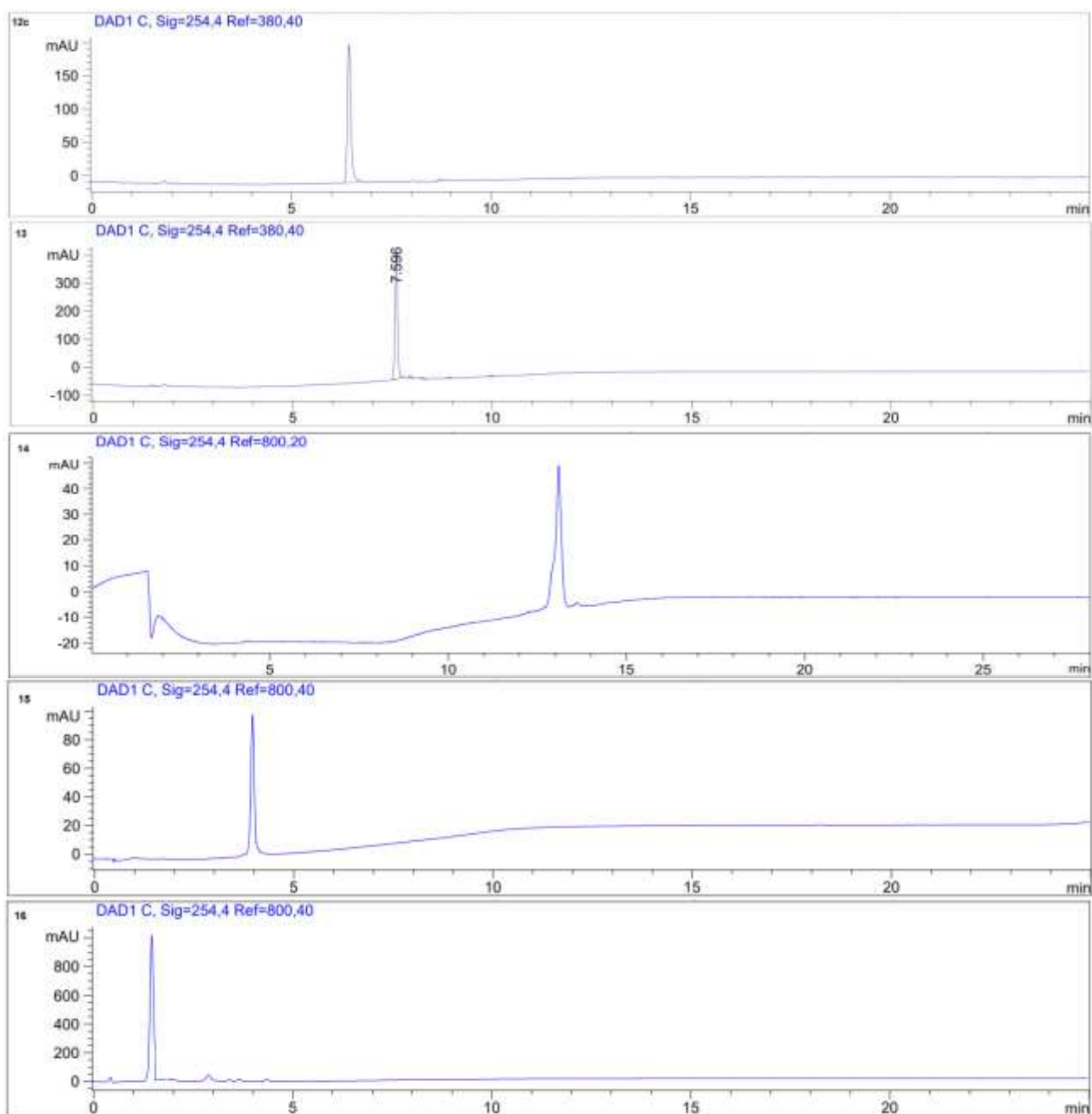


Figure S34-follows. RP HPLC analyses performed on a column Phenomenex mod. Gemini 3 μm C₁₈ 110 Å 100 \times 3.0 mm; mobile phase from 9:1 H₂O/CH₃CN/0.1% HCOOH to 2:8 H₂O/CH₃CN/0.1% HCOOH in 20 min, flow rate of 1.0 mL min⁻¹. DAD 254 nm, unless otherwise specified. For peptide **14**, the analytical flow rate is 0.5 mL min⁻¹.