

Electronic Supplementary Information

for

Supramolecular Peptide Nanofiber Templated Pd Nanocatalyst for Efficient Suzuki Coupling Reactions in Aqueous Conditions

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Experimental Section

Materials

9-Fluorenylmethoxycarbonyl protected amino acids, MBHA Rink Amide Resin, HBTU (O-Benzotriazole-N,N,N',N'-tetramethyl-uronium-hexafluoro-phosphate) are purchased from Novabiochem, lauric acid is purchased from Merck. All boronic acid derivatives, aryl halides, K_3PO_4 , K_2CO_3 and sodium tetrachloropalladate, L-(+)-ascorbic acid were purchased from Sigma Aldrich. All chemicals were used directly without any further purification.

Peptide Synthesis

In the synthesis of peptide amphiphile, solid phase peptide synthesis method was applied with an automated peptide synthesizer (CS Bio. Company model:136XT). Peptides were constructed on MBHA Rink Amide resin. Amino acid couplings were done with 2 equivalents of fluorenylmethoxycarbonyl (Fmoc) protected amino acid, 1.95 equivalents O-Benzotriazole-N,N,N',N'-tetramethyl-uronium-hexafluoro-phosphate (HBTU) and 3 equivalents of N,N-diisopropylethylamine (DIEA) for 3 h. Fmoc removals were performed with 20% piperidine /dimethylformamide solution for 10 min. Cleavage of the peptides from the resin was carried out with a mixture of trifluoroacetic acid:triisopropylsilane:water in ratio of 95:2.5:2.5 for 3 h. Excess trifluoroacetic acid was removed by rotary evaporation. The remaining viscous peptide solution was triturated with cold ether and the resulting white product was lyophilized.

Liquid Chromatography

For the structural analysis of the peptide Agilent Technologies 6530 Accurate-Mass Q-TOF LC-MS and Zorbax SB-C8 column were used. Concentration of the sample for LC-MS measurement was 0.5

mg/ml. Solvents were water (0.1% formic acid) and acetonitrile (ACN) (0.1% formic acid). LC-MS was run for 25 min for each sample and it started with 2% ACN and 98% H₂O for 5 minutes. Then, gradiently ACN concentration reached to 100% until 20 minutes. Finally, its concentration was dropped to 2% and it kept running for 5 minutes. Solvent flow 0.65 mL/min and 5 µL sample was injected.

Circular Dichroism (CD) Spectroscopy

Secondary structure of peptide amphiphile was analyzed with Jasco J-815 circular dichroism spectrometer. 1 wt% peptide solution was prepared in ddH₂O and gelified with 0.1 M NaOH. Then, peptide gel was diluted with 1 mM NaOH solution and 5x10⁻⁴ M peptide solution was measured from 300 nm to 190 nm with 0.1 data pitch, 100 nm/min scanning speed, 1 nm band width and 4 s D.I.T. Average of three measurements were used and sensitivity was selected as standard.

Rheology

Anton Paar MCR-301 rheometer was used for mechanical characterization of peptide amphiphile gels. I prepared 1% (w/v) peptide solution in distilled water, and added 0.1 M NaOH solution. After sweep measurements, amplitude kept constant as 0.1% and amplitude frequency as 10 rad/s during 60 min. In frequency sweep measurements, angular frequency varied between 0.1 and 100 rad/s while amplitude was 0.1 %. In strain sweep experiments, amplitude varied between 0.001 and 1000% while angular frequency was constant at 10 rad/s. In all rheometer graphs, x and y axes were in logarithmic scale.

Transmission Electron Microscopy

1% (w/v) peptide solution was prepared and alkalified with 0.1 M NaOH solution. Peptide gel was diluted with 1 mM NaOH solution, a small amount of solution was dropped to carbon covered copper grid. To image organic peptide fibers, 2% (w/v) uranyl acetate solution was used. Finally, carbon grid was dried at atmosphere. FEI Tecnai G2 F30 transmission electron microscope (TEM) was used to display peptide amphiphile nanofibers. In the characterization of palladium nanoparticles, samples were dropped to carbon covered copper grids, allowed to dry at atmosphere conditions and imaged with TEM.

Scanning Electron Microscopy/Critical Point Dryer

FEI Quanta 200 FEG environmental scanning electron microscope (SEM) was used to image peptide amphiphile gel after removing solvent with Tousimis Autosamdri-815B, Series C critical point dryer (CPD). 1.5 wt% solution of peptide in distilled water were prepared and 0.1 M NaOH solution was added to peptide solution on metal mesh to adjust the pH around 7. Since critical point dryer can be used with samples in isopropanol, we washed peptide gels with 20%, 40%, 60%, 80% and 100% (v/v) isopropanol solutions. Then, gels were dried with a critical point dryer. Finally, peptide amphiphile network was imaged with SEM.

Synthesis of Palladium Nanostructures

First, 1 wt% peptide was dissolved in hydrogel was prepared at pH 7. 0.5 eq. of Na_2PdCl_4 in 1 mM NaOH solution was added for overnight. Then, 0.5 eq. of Na_2PdCl_4 in 1 mM NaOH solution was added to the sol-gel. After 1 h of incubation for seeding, 0.5 equimolar ascorbic acid in 1 mM NaOH was added. When all of the palladium ions were reduced to Pd^0 (Figure S7), sol-gel was divided into two and while one was kept for further characterization, other one was diluted with same amount of palladium by keeping the final palladium concentration constant but decreasing the peptide concentration to half. After incubation for another hour, ascorbic acid solution was added to reduce palladium ions. This cycle was repeated three times. After each addition and reduction of palladium ions, samples were imaged with TEM. In all characterizations, sample after third addition of palladium ions was used.

Characterization of Pd Nanostructures

To monitor stability of structures, various treatments were applied to nanostructures. Pd nanostructure sample was washed with $3\times\text{H}_2\text{O}$ then $3\times\text{EtOH}$. After evaporation of EtOH, sample was dissolved in EtOH, some amount was poured into Si wafer and heated at $100\text{ }^\circ\text{C}$ for 1 h. Finally, SEM images were taken (FigureS8).

X-Ray Diffractometer

In crystallographic analysis of palladium nanostructures, PANanalytical X'Pert X-ray diffractometer was performed by using Cu $\text{K}\alpha$ radiation. Mylar foil of 6 μm thickness was used as the surface to drop peptide/palladium samples. Rotation time was 16 seconds, scan range was from 30° to 90° , and step size was 0.0525° (Figure S9).

Thermogravimetric Analysis

Thermal gravimetric analysis was performed with TA Q500 instrument. Samples were dried under atmosphere conditions and then analysis was performed under high purity nitrogen purge (40.0 ml/min) with heating the samples from 30 °C to 550 °C with 20 °C/min heating rate (Figure S8).

Suzuki Coupling Reactions

All reactions and manipulations were run under air atmosphere. Under air atmosphere, a reaction tube was charged with aryl iodide (0.5 mmol), aryl boronic acid (0.75 mmol), Pd@Peptide (1.5 mmol%), K₃PO₄ (1 mmol) and deionized water (3 mL). The mixture was stirred at room temperature, it was monitored by GC until aryl iodide was totally reacted. The crude product was characterized by GC-MS analysis (Agilent GCMS-7890A-5975C equipped with a 0.25 mm ×30 m HP-5MS capillary column).

For bromobenzene coupling reactions, typically, under air atmosphere, a reaction tube was charged with aryl bromide (0.5 mmol), aryl boronic acid (0.75 mmol), Pd@Peptide (1.5 mmol %), K₃PO₄ (1 mmol) and deionized water: ethanol into 1:1 ratio (4 mL). The mixture was stirred at 80 °C, it was monitored by GC until aryl bromide was totally reacted. The crude product was characterized by GC-MS analysis (Agilent GCMS-7890A-5975C equipped with a 0.25 mm ×30 m HP-5MS capillary column).

For bromobenzene coupling reactions in neat water at room temperature, typically, under air atmosphere, a reaction tube was charged with aryl bromide (0.5 mmol), aryl boronic acid (0.75 mmol), Pd@Peptide (1.5 mmol %), NaOH (1 mmol) and deionized water (5 mL). The mixture was stirred at room temperature, it was monitored by GC until aryl bromide was totally reacted. The crude product was characterized by GC-MS analysis (Agilent GCMS-7890A-5975C equipped with a 0.25 mm ×30 m HP-5MS capillary column).

For chlorobenzene coupling reaction in neat water at room temperature, typically, under air atmosphere, a reaction tube was charged with chlorobenzene (0.5 mmol), aryl boronic acid (0.75 mmol), Pd@Peptide (1.5 mmol %), NaOH (1 mmol) and deionized water (5 mL). The mixture was stirred at room temperature; it was monitored by GC until aryl bromide was totally reacted. The crude product was characterized by GC-MS analysis (Agilent GCMS-7890A-5975C equipped with a 0.25 mm ×30 m HP-5MS capillary column).

For the recyclability test, Suzuki coupling reaction was performed with bromobenzene (0.5 mmol), 4-methoxyphenylboronic acid (0.75 mmol), Pd@Peptide (1.5 mol% with respect to bromobenzene

concentration), K_3PO_4 (2.0 equiv), water/EtOH (1:1) at 80 °C. Each time, the catalyst was isolated from the reaction solution at the end of catalytic reaction, washed with water and ethanol. The dried catalyst was then reused in a next run.

Supporting Figures and Tables

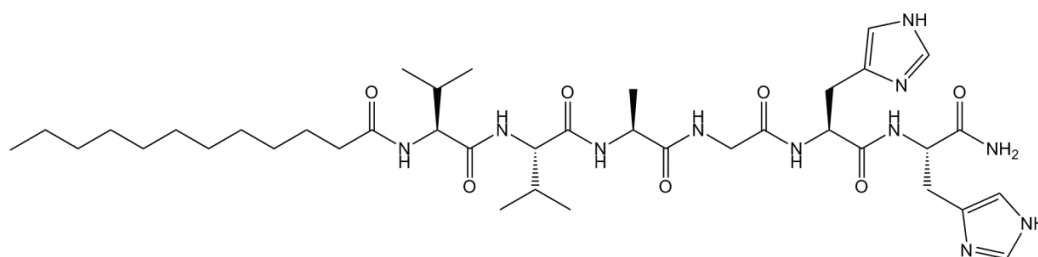


Figure S1. Chemical structure of Lauryl-VVAGHH-Am peptide amphiphile molecule.

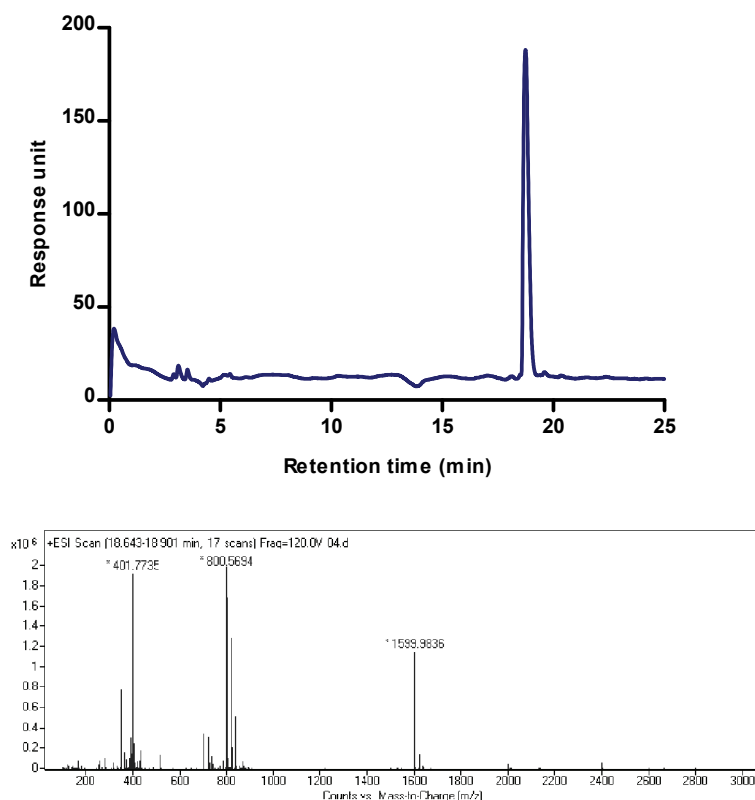


Figure S2. HPLC chromatogram of peptide. Absorbance at 220 nm vs retention time graph (top). Mass spectrometry of peptide after subtracting mass spectra of water sample at that time interval (bottom). $[M+H]^+$ (calculated)=801.00, $[M+H]^+$ (observed)=800.55, $[M/2+H]^+$ (calculated)=401.00, $[M/2+H]^+$ (observed)=401.77.

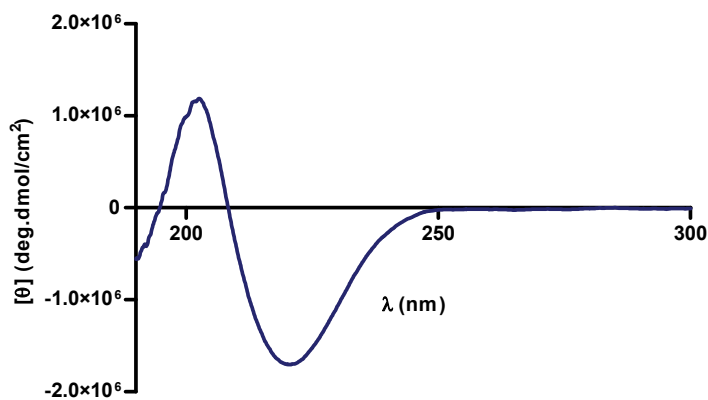


Figure S3. CD spectra of peptide amphiphile

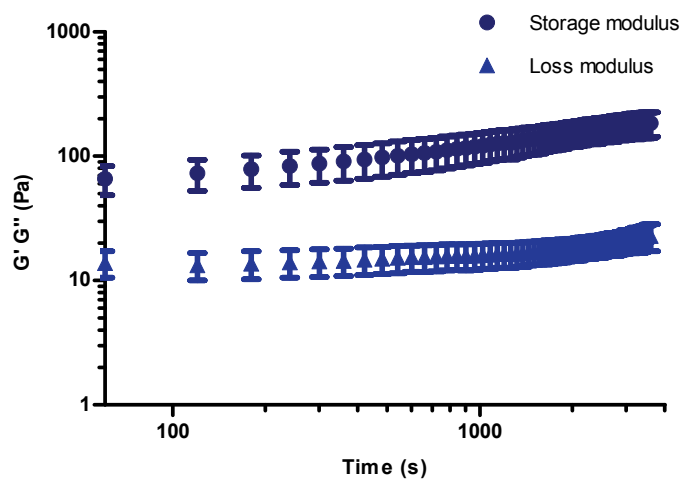


Figure S4. Time sweep graph of peptide amphiphile gel

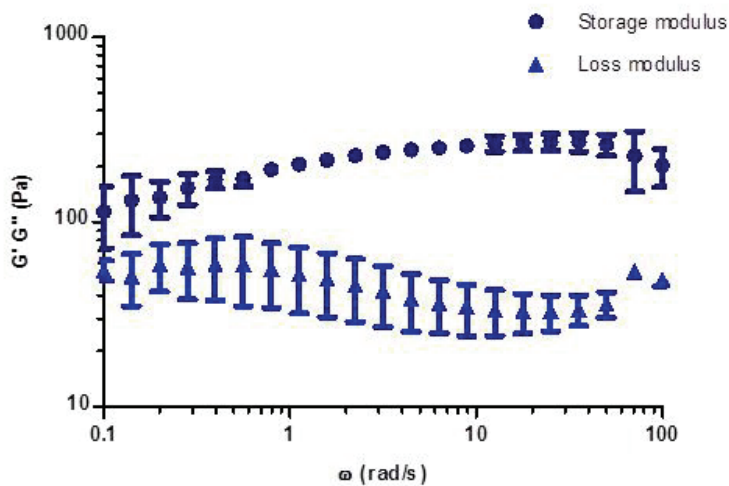


Figure S5. Frequency sweep graph of peptide amphiphile gel

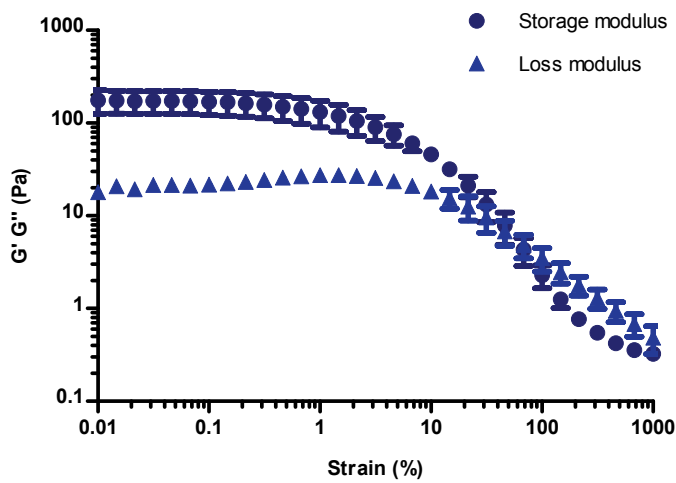


Figure S6. Strain sweep graph of peptide amphiphile gel

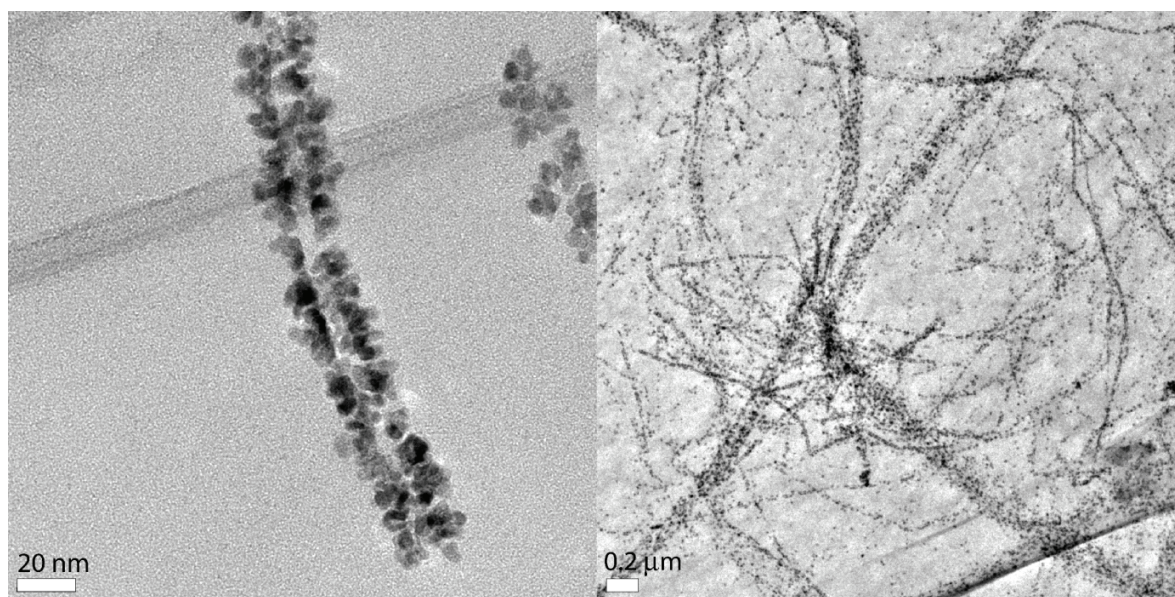


Figure S7. TEM of Pd nanostructures after first reduction cycle.

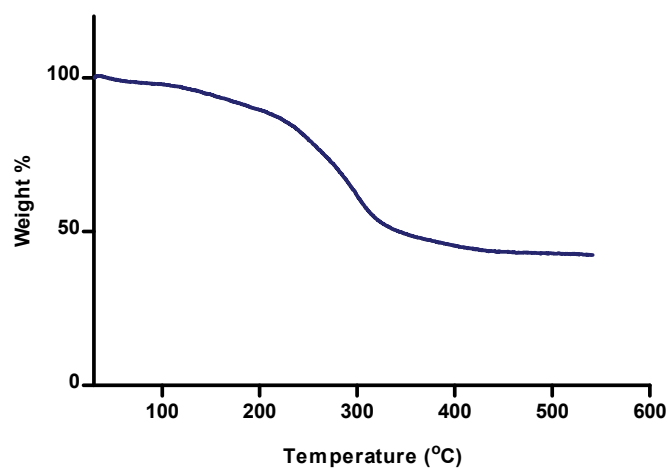


Figure S8. TGA of palladium nanostructures filtered with cellulose ester membranes (42.55% palladium content).

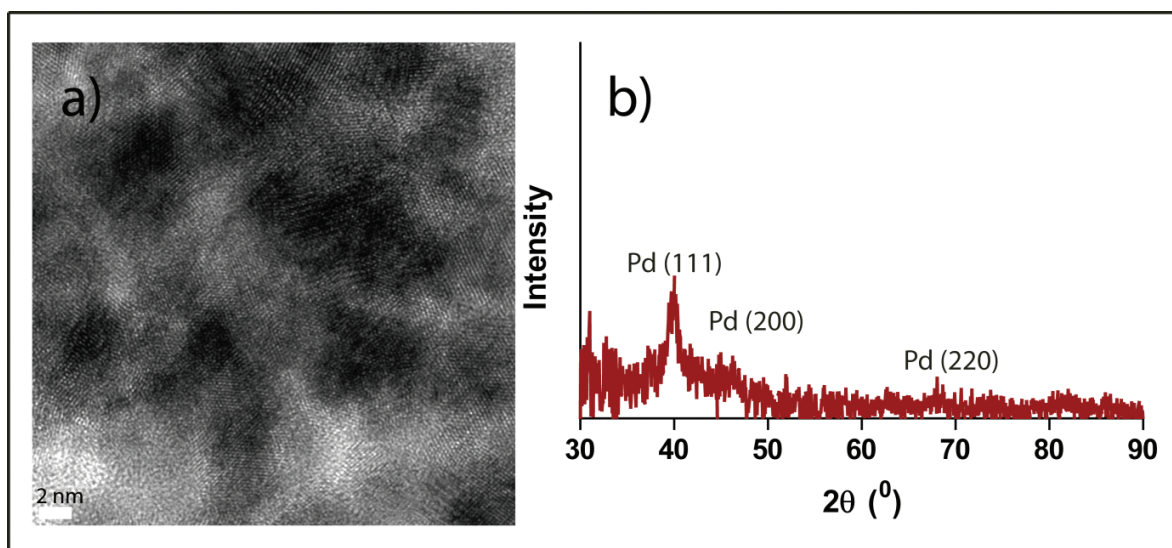


Figure S9. a) HRTEM image of Pd nanostructures b) XRD pattern of Pd nanostructures.

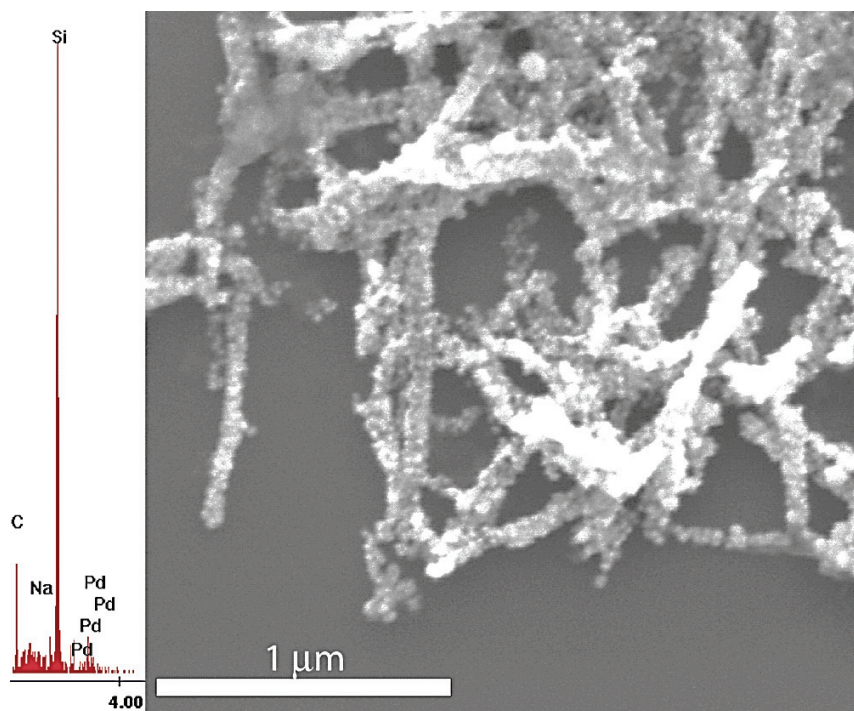


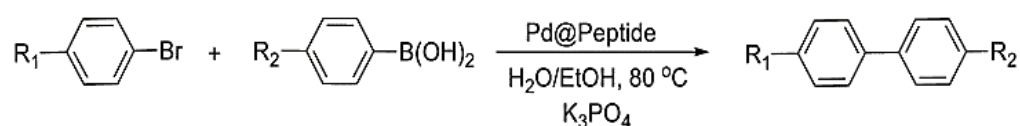
Figure S10. SEM images of Pd nanostructures washed with water and ethanol.

Table S1. Suzuki-Miyaura coupling of aryl halides with Pd@Peptide^[a]

[a] Reaction conditions: aryl halide (0.5 mmol), arylboronic acid (0.75 mmol), Pd@Peptide (1.5 mol% with respect to aryl halide concentration), K₃PO₄ (2.0 equiv), solvent (4 mL). [b] The reaction yield was determined by GC-MS (Figure S11- S20).

Entry	X	Base	Solvent	Time (h)	T [°C]	Conversion (%) ^[b]
1	I	K ₃ PO ₄	H ₂ O	4	25	99
2	I	K ₃ PO ₄	H ₂ O:EtOH	1	25	99
3	Br	K ₃ PO ₄	H ₂ O	10	25	< 3
4	Br	K ₃ PO ₄	H ₂ O	10	80	< 5
5	Br	K ₂ CO ₃	H ₂ O	10	25	0
6	Br	K ₂ CO ₃	H ₂ O	10	80	< 1
7	Br	K ₂ CO ₃	H ₂ O:EtOH	10	25	< 3
8	Br	K ₃ PO ₄	H ₂ O:EtOH	10	25	10
9	Br	K ₃ PO ₄	H ₂ O:EtOH	4	80	99
10	Br	NaOH	H ₂ O	4	25	99
11	Cl	NaOH	H ₂ O	16	25	99

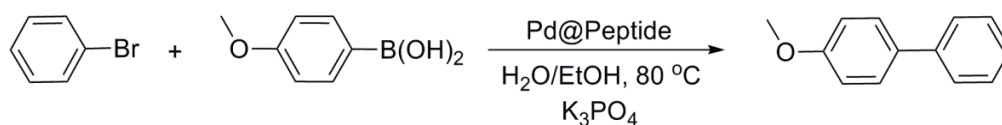
Table S2. Suzuki-Miyaura coupling of aryl bromide with Pd@Peptide^[a]



Entry	R ₁	R ₂	Time [h]	Conversion (%) ^[b]
1	H	H	4	99
2	H	OMe	1.5	99
3	H	COH	2	99
4	H	CH ₂ OH	2	89
5	NO ₂	H	2	85
6	NO ₂	OMe	2	83
7	H	HC=CH	4	58

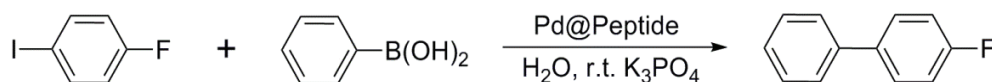
[a] Reaction conditions: aryl bromide (0.5 mmol), arylboronic acid (0.75 mmol), Pd@Peptide (1.5 mol% with respect to aryl bromide concentration), K₃PO₄ (2.0 equiv), water/EtOH (1:1) at 80 °C. [b] The reaction yield was determined by GC-MS (Figure S31- S42).

Table S3. Recyclability test of bromobenzene with 4-methoxyphenylboronic at 80 °C. The GC-MS spectra of the products are given in Figure S51- S60.



Entry	Time [min]	Conversion (%)
1 st	90	99
2 nd	90	97
3 rd	100	97
4 th	100	97
5 th	100	95

Table S4. Catalyst loading experiments of 4-fluoroiodobenzene with phenyl boronic acid in water at room temperature. The GC-MS spectra of the products are given in Figure S61- S66.



Catalyst loading (mol %)	Time [h]	Conversion (%)
1.5	1	99
0.5	5	99
0.1	20	95

GC-MS Chromatograms of the Products

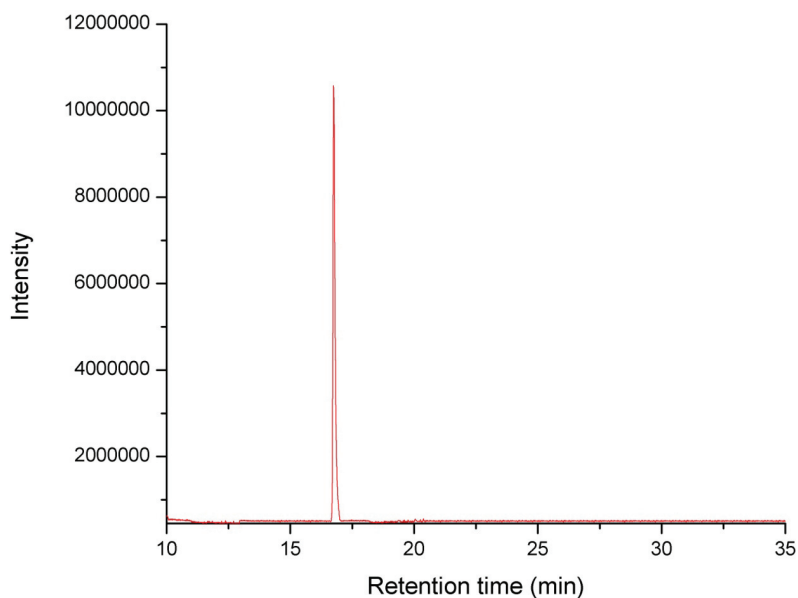


Figure S11. Gas Chromatogram of Biphenyl (Table 1, Entry 1)

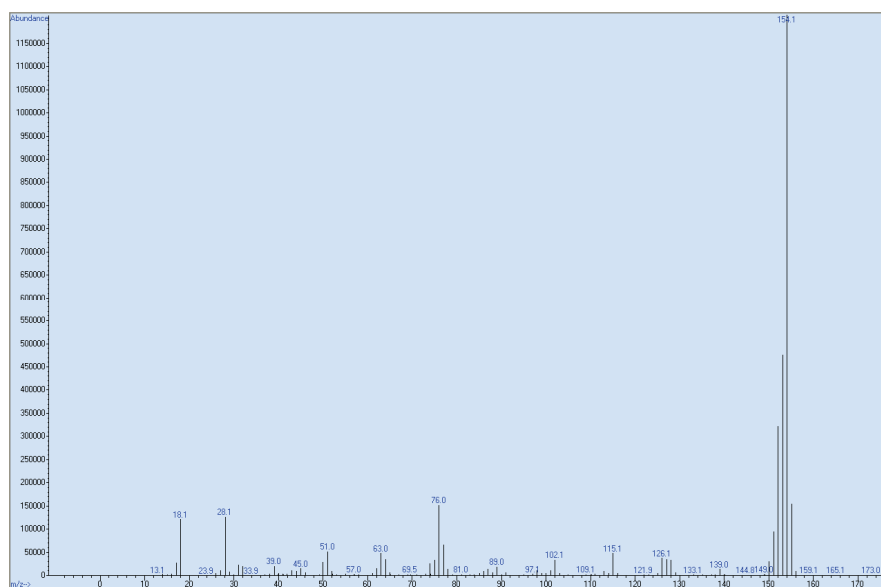


Figure S12. Mass spectrum of Biphenyl (Table 1, Entry 1)

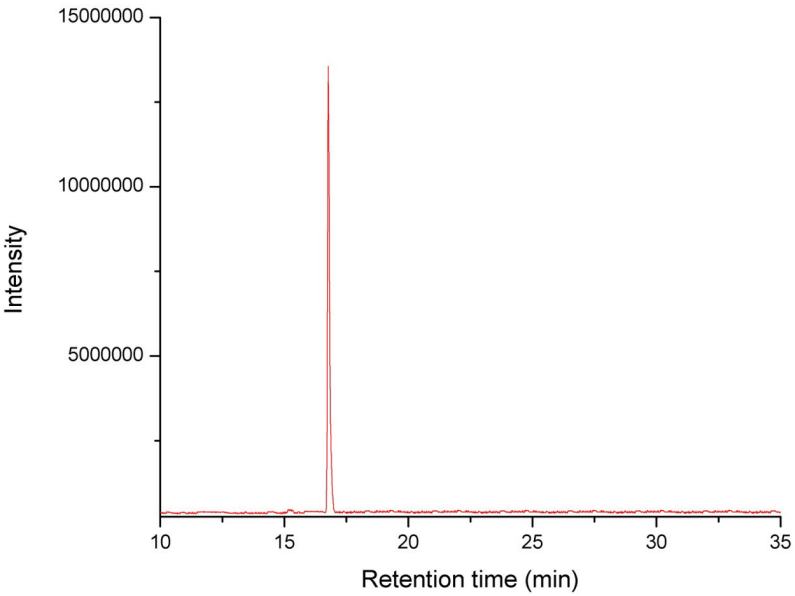


Figure S13. Gas Chromatogram of Biphenyl (Table 1, Entry 2)

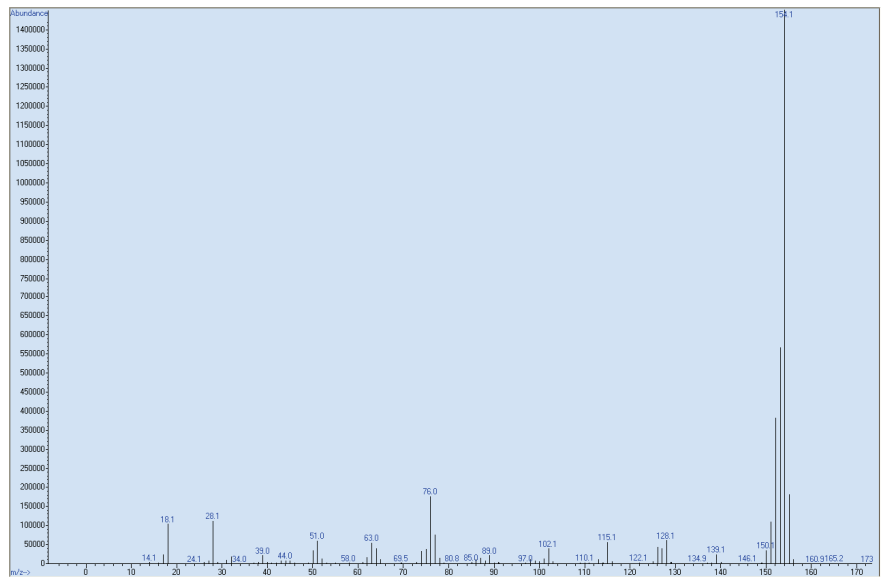


Figure S14. Mass spectrum of Biphenyl (Table 1, Entry 2)

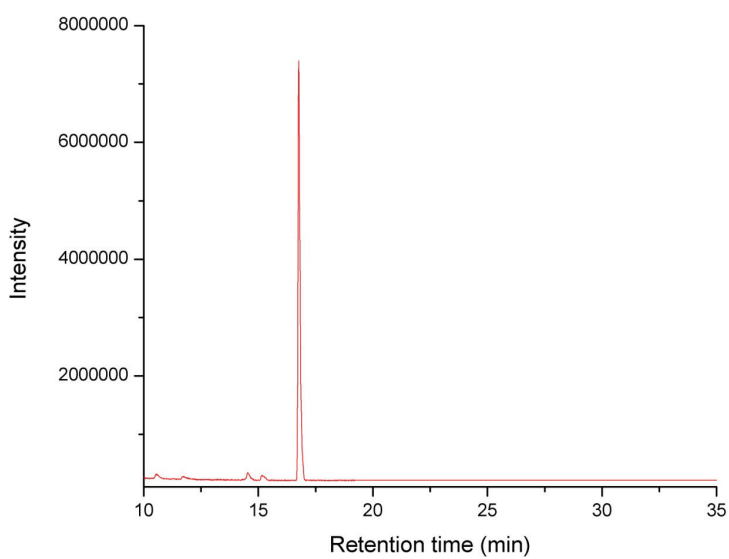


Figure S15. Gas Chromatogram of Biphenyl (Table 1, Entry 9)

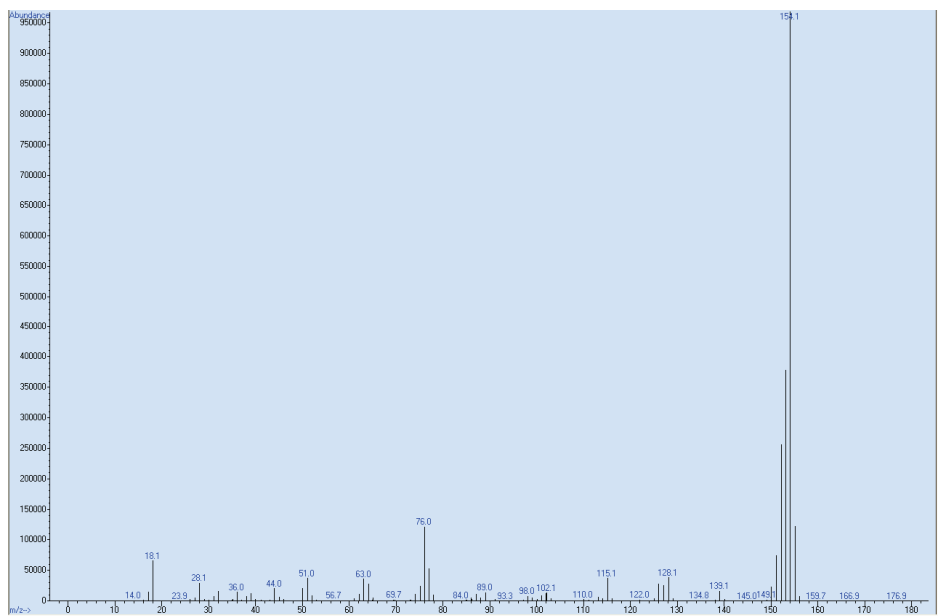


Figure S16. Mass spectrum of Biphenyl (Table 1, Entry 9)

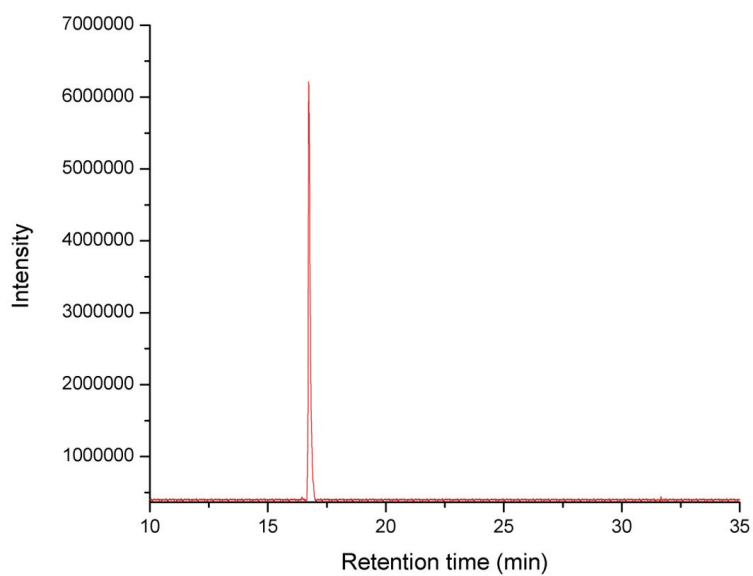


Figure S17. Gas Chromatogram of Biphenyl (Table 1, Entry 10)

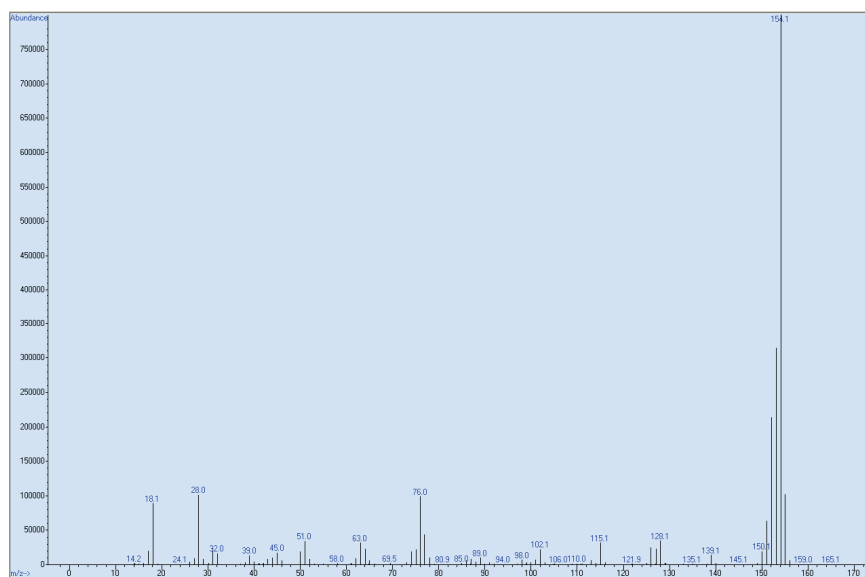


Figure S18. Mass spectrum of Biphenyl (Table 1, Entry 10)

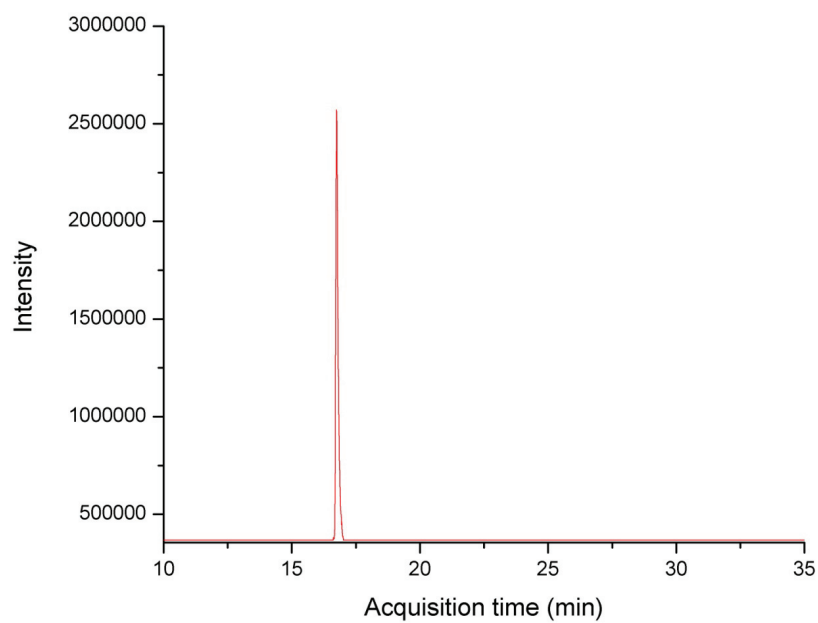


Figure S19. Gas Chromatogram of Biphenyl (Table 1, Entry 11)

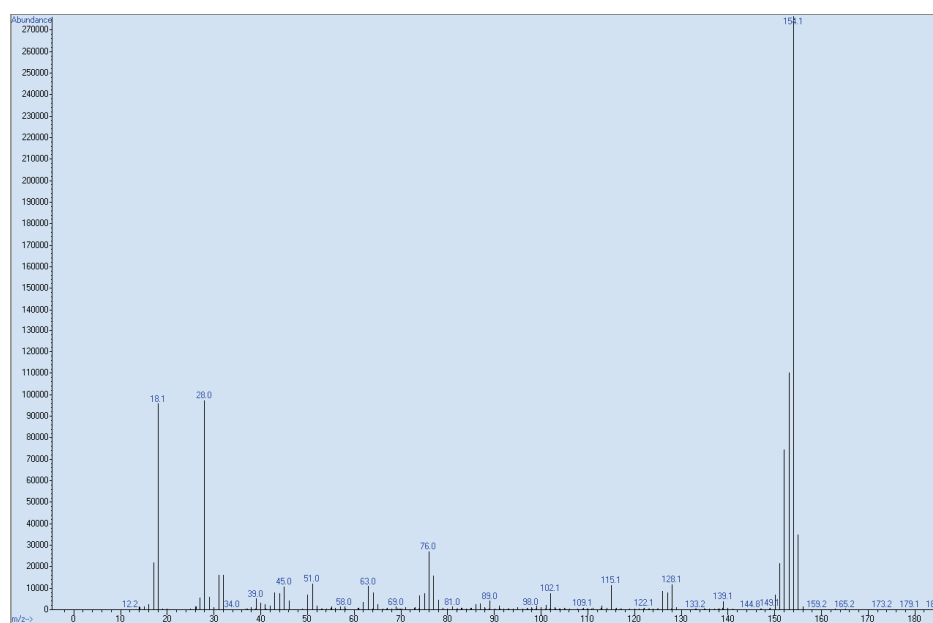


Figure S20. Mass spectrum of Biphenyl (Table 1, Entry 11)

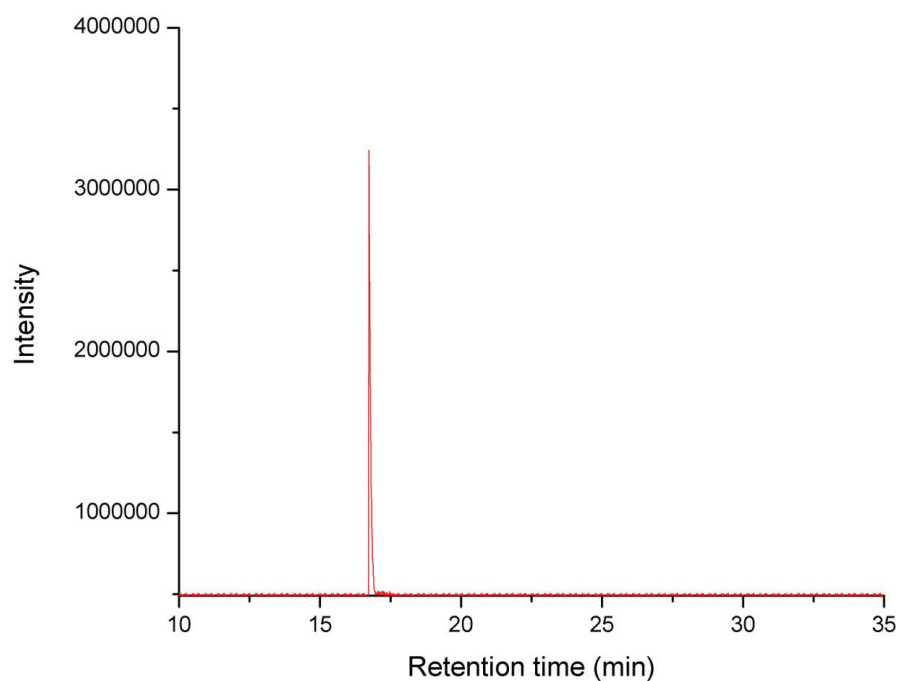


Figure S21. Gas Chromatogram of 4-fluorobiphenyl

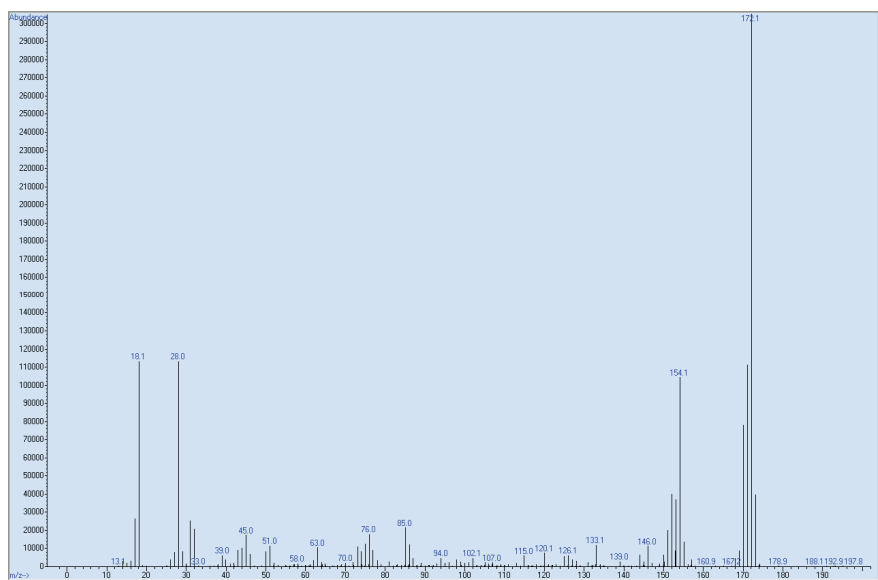


Figure S22. Mass spectrum of 4-fluorobiphenyl

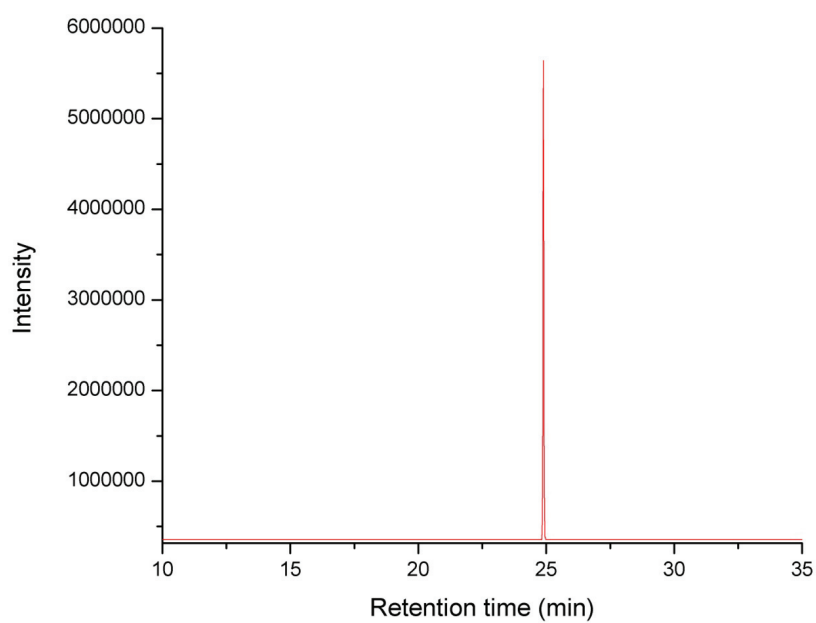


Figure S23. Gas Chromatogram of 4-methoxybiphenyl

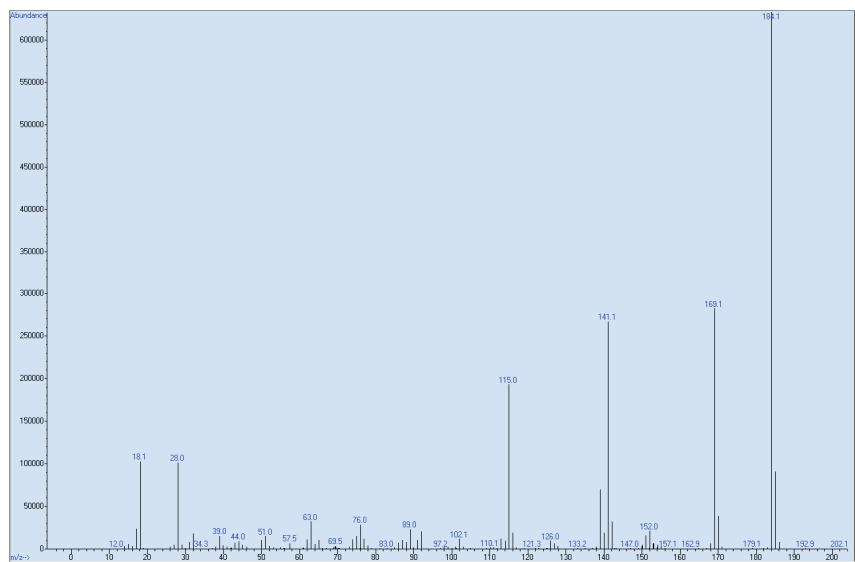


Figure S24. Mass spectrum 4-methoxybiphenyl

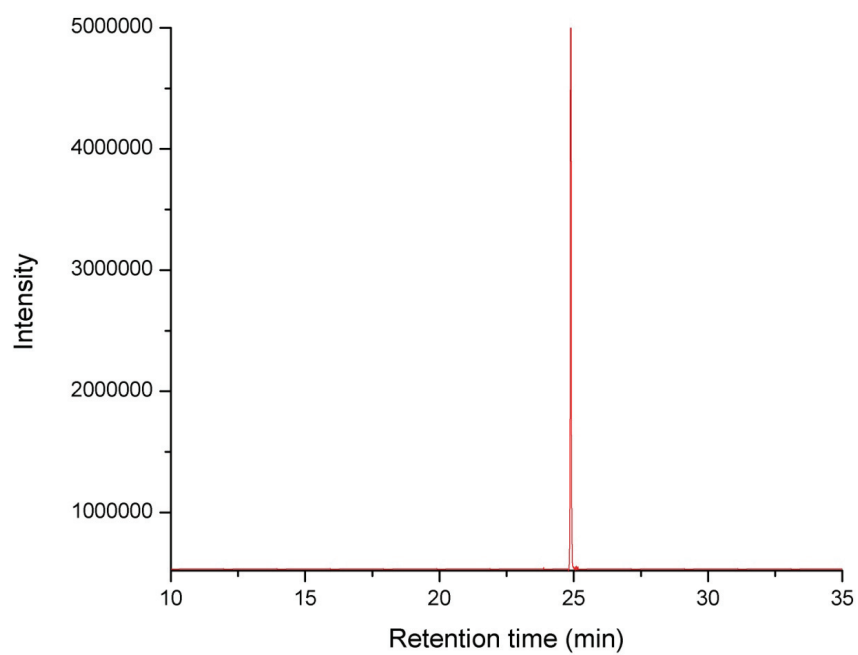


Figure S25. Gas Chromatogram of 4-methoxybiphenyl

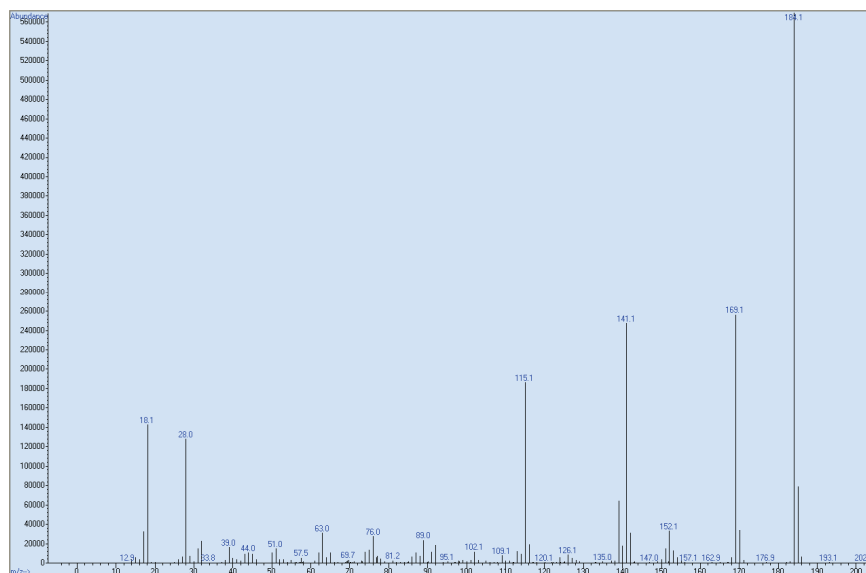


Figure S26. Mass spectrum 4-methoxybiphenyl

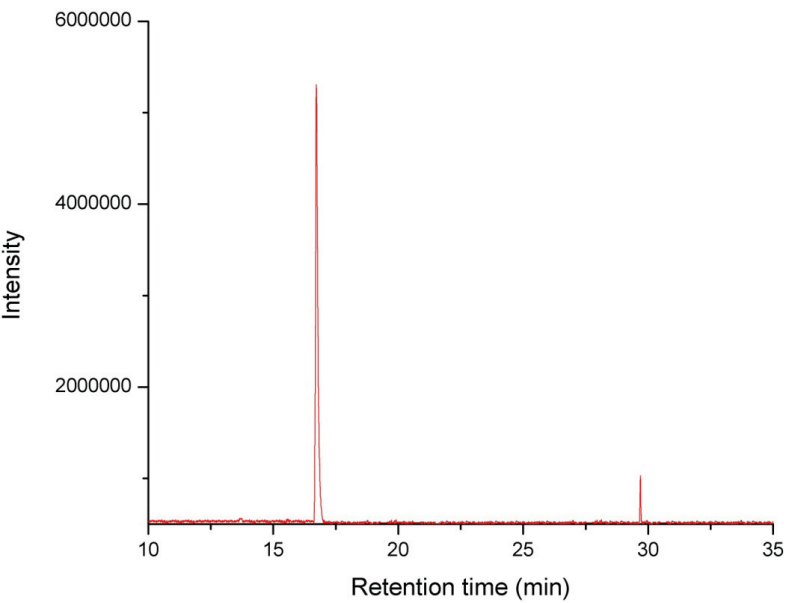


Figure S26. Gas Chromatogram of 4-fluoro-4'-methoxybiphenyl

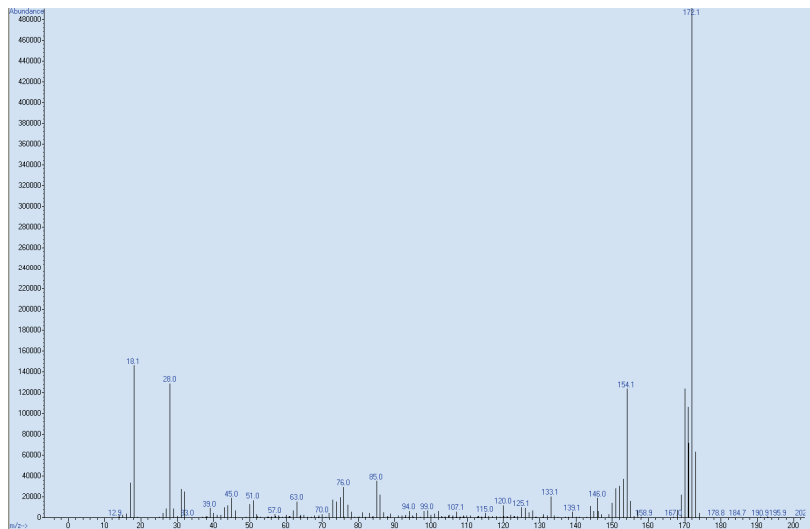


Figure S28. Mass spectrum of 4-fluoro-4'-methoxybiphenyl

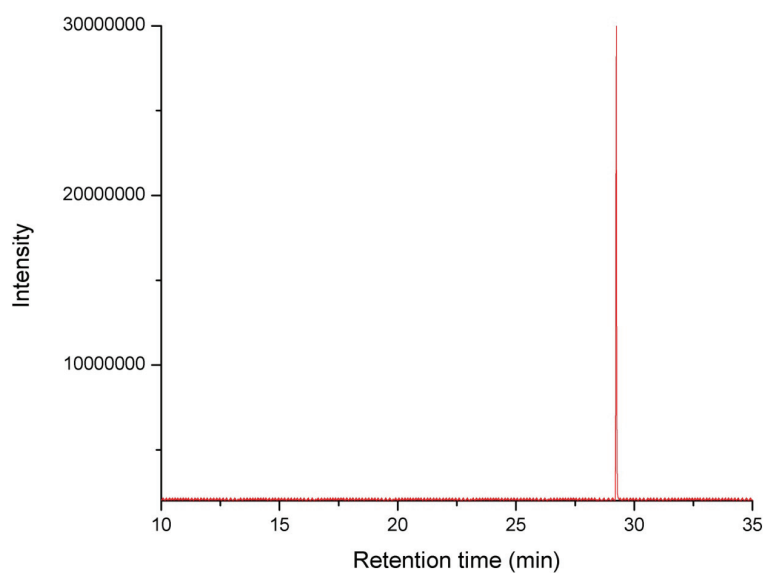


Figure S29. Gas Chromatogram of 4, 4'-dimethoxybiphenyl

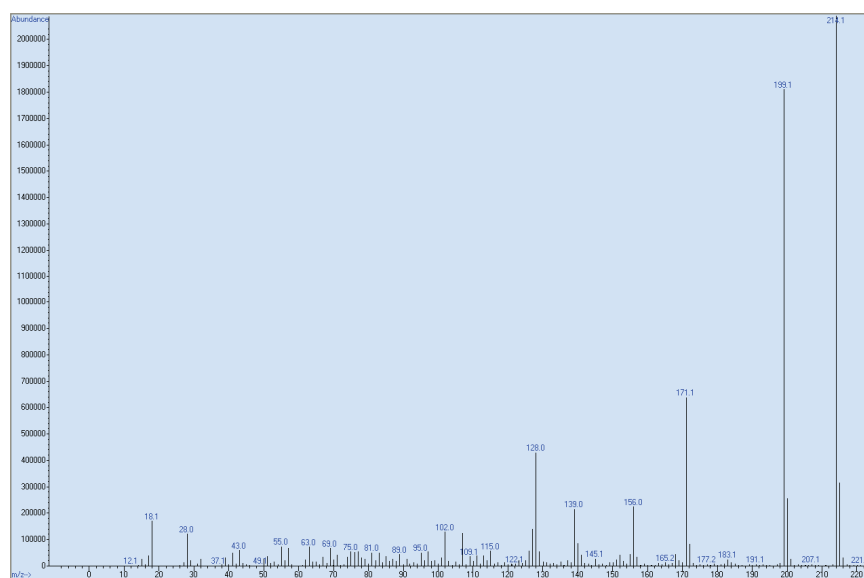


Figure S30. Mass spectrum of 4, 4'-dimethoxybiphenyl

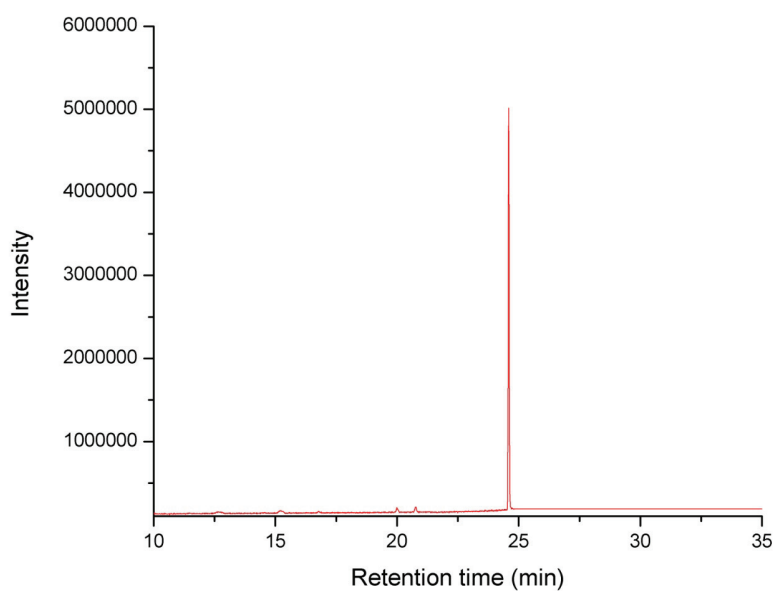


Figure S31. Gas Chromatogram of 4-methoxybiphenyl

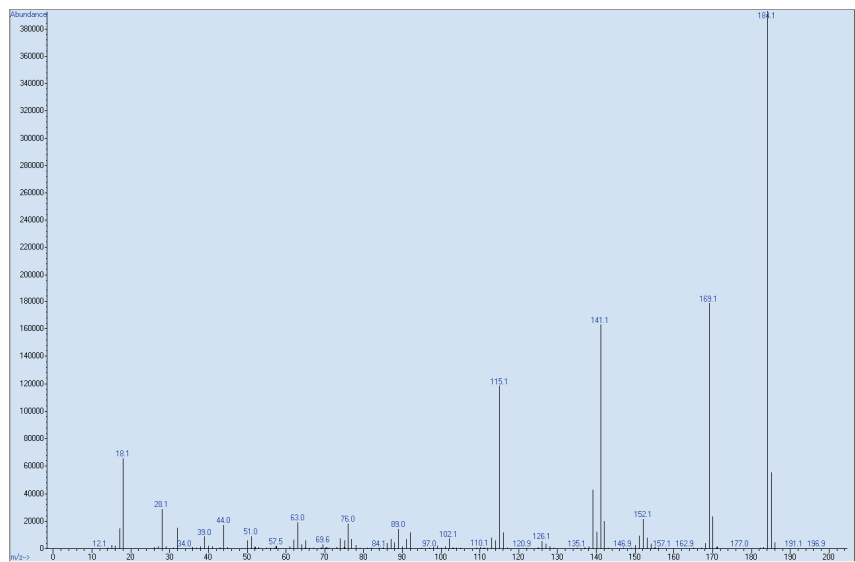


Figure S32. Mass spectrum of 4-methoxybiphenyl

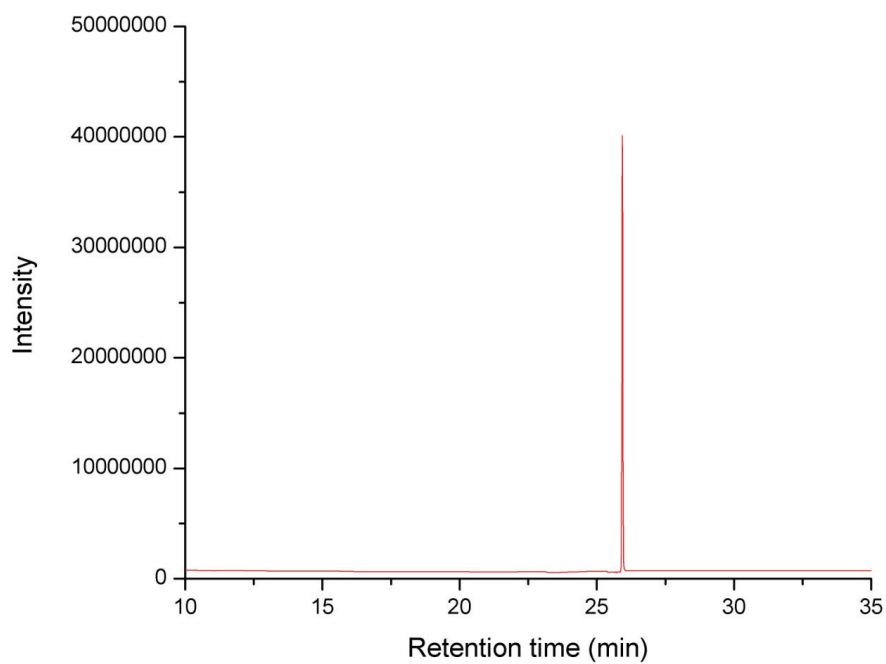


Figure S33. Gas Chromatogram of biphenyl-4-carbaldehyde

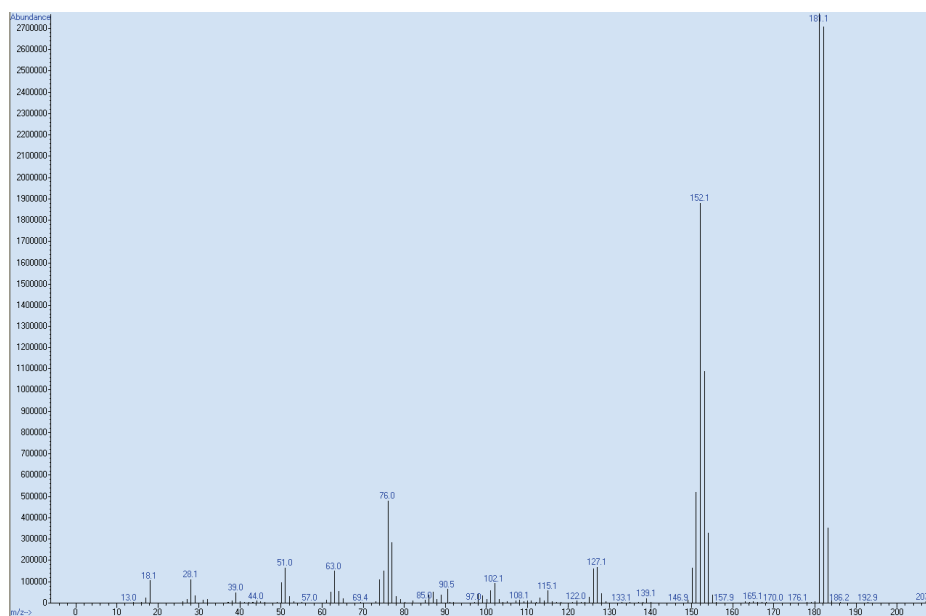


Figure S34. Mass spectrum of biphenyl-4-carbaldehyde

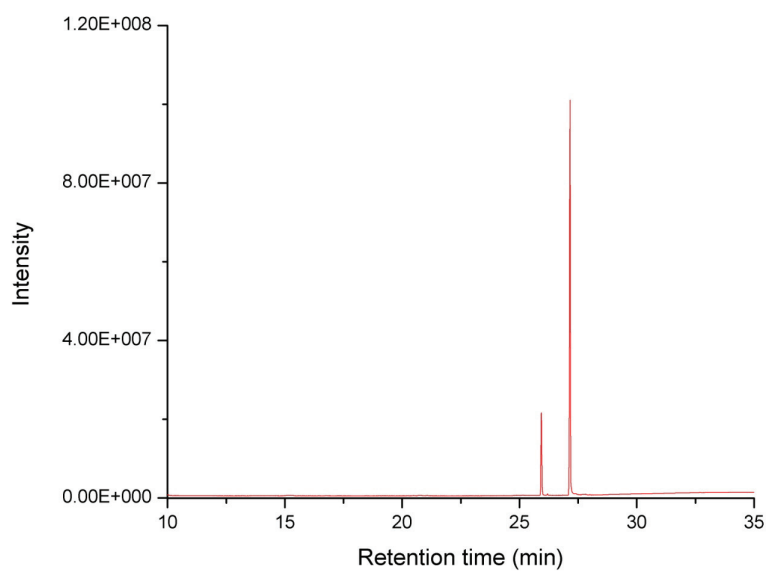


Figure S35. Gas Chromatogram of biphenyl-4-ylmethanol

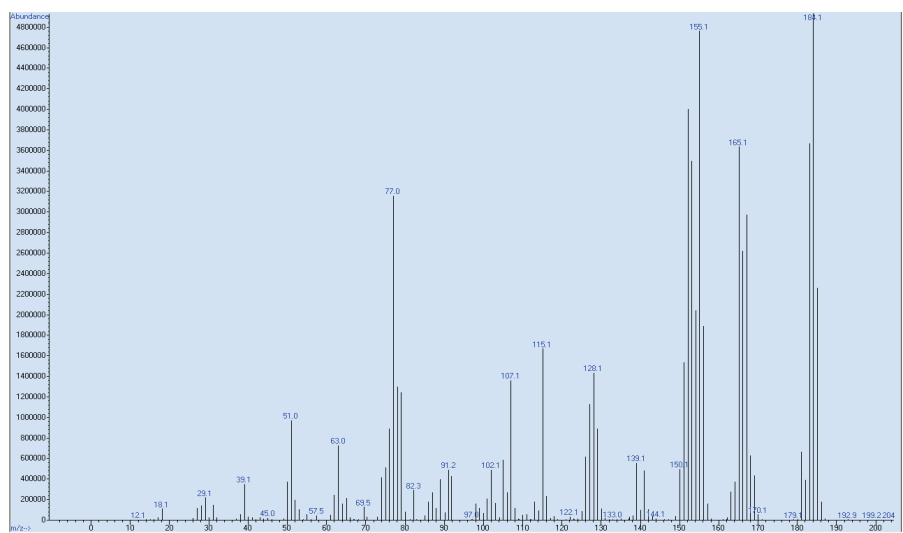


Figure S36. Mass spectrum of biphenyl-4-ylmethanol

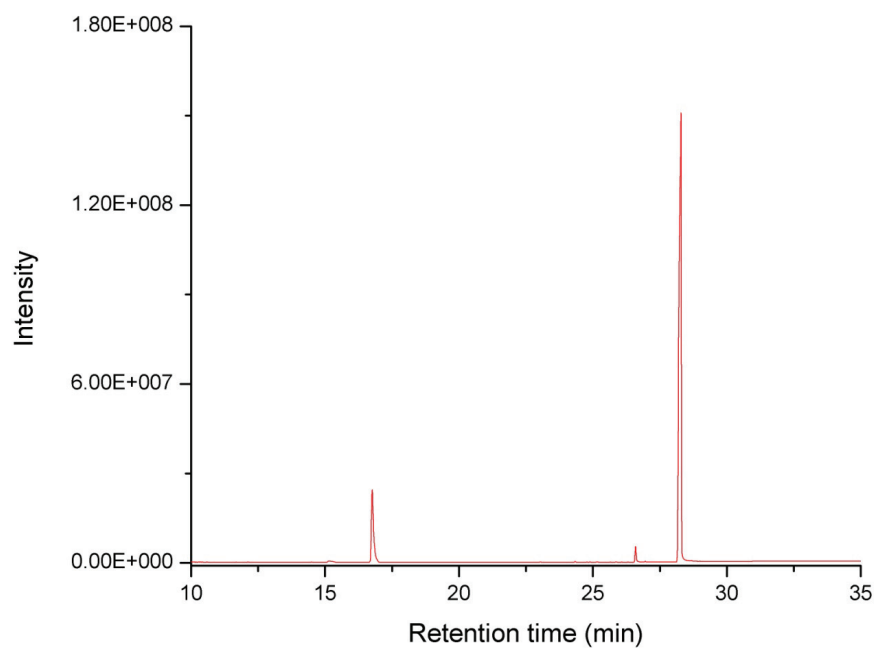


Figure S37. Gas Chromatogram of 4-nitrobiphenyl

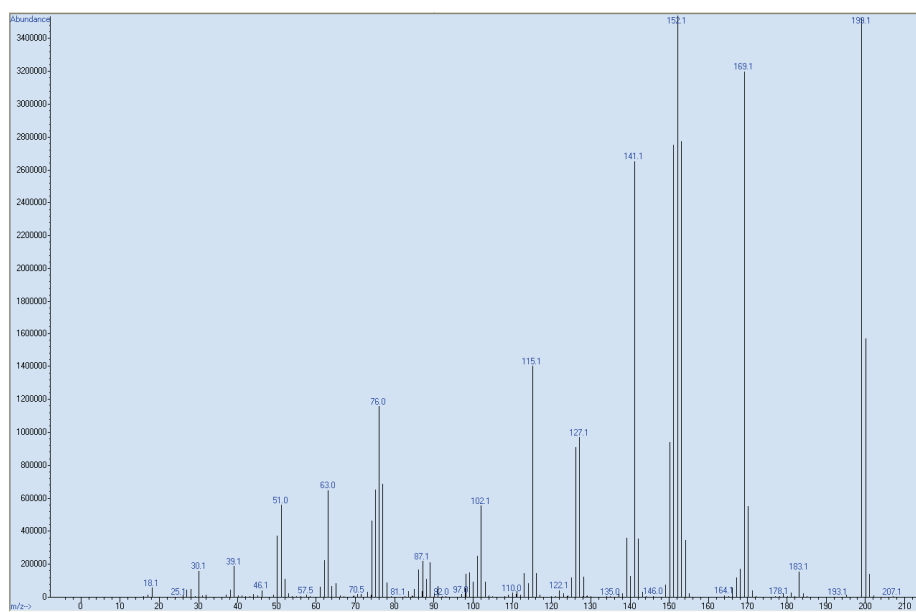


Figure S38. Mass spectrum of 4-nitrobiphenyl

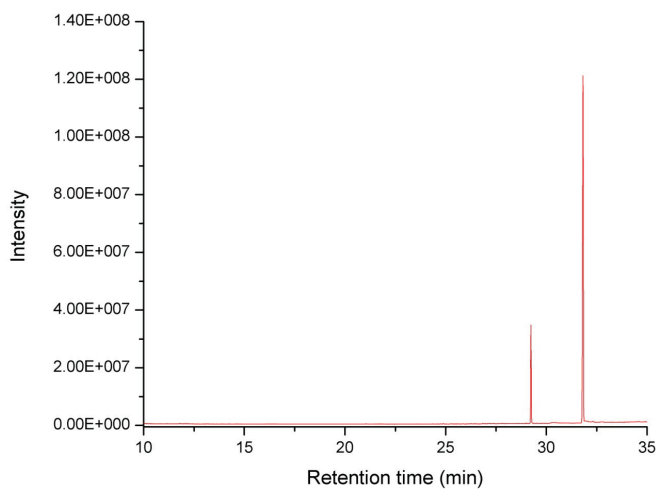


Figure S39. Gas Chromatogram of 4-methoxy-4'-nitrobiphenyl

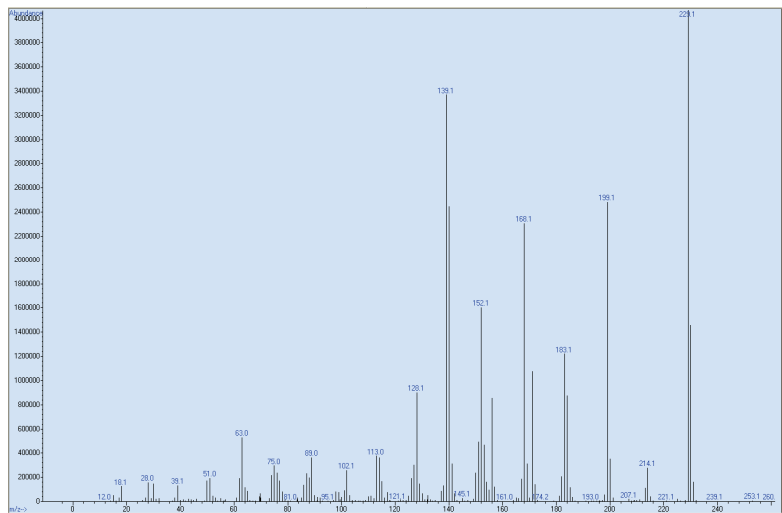


Figure S40. Mass spectrum 4-methoxy-4'-nitrobiphenyl

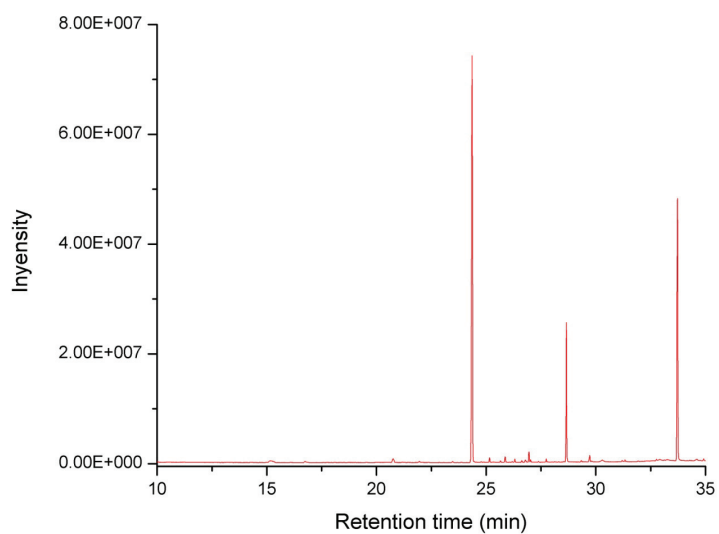


Figure S41. Gas Chromatogram of 4-vinylbiphenyl

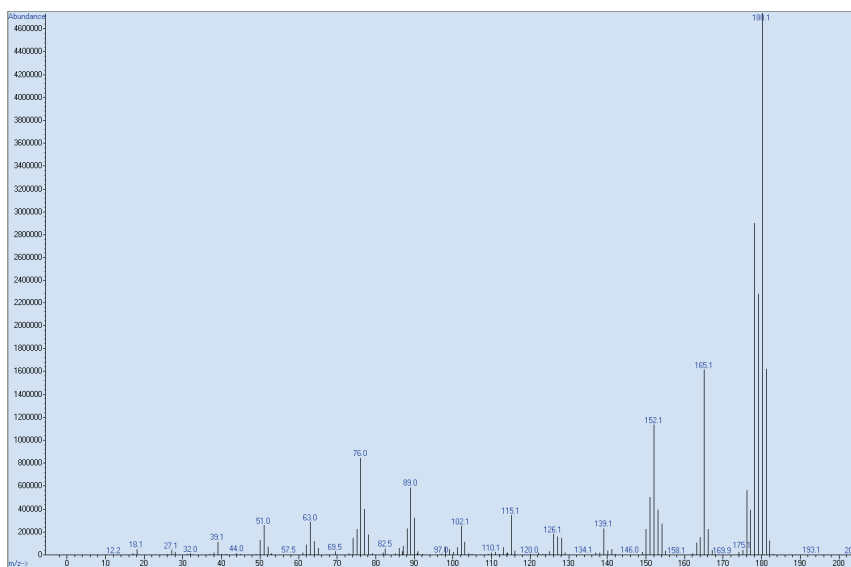


Figure S42. Mass spectrum of 4-vinylbiphenyl

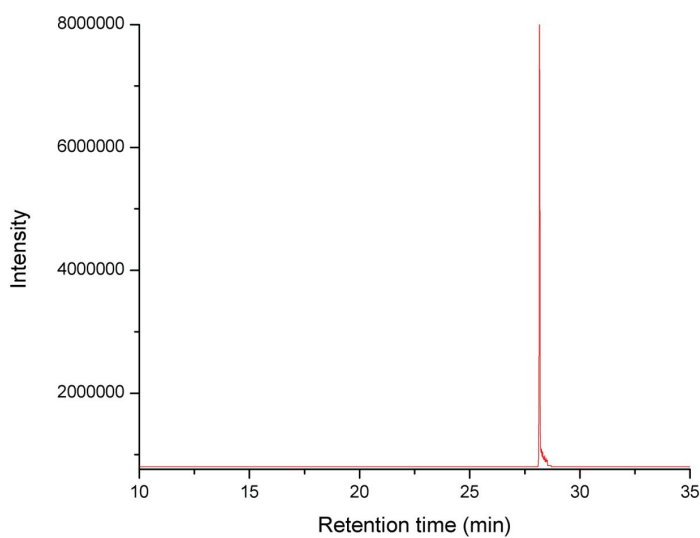


Figure S43. Gas Chromatogram of 4-nitrobiphenyl

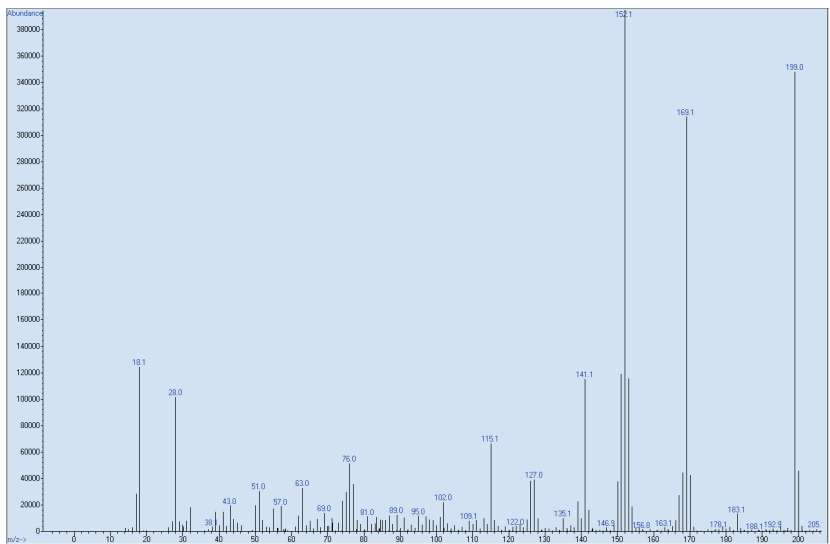


Figure S44. Mass spectrum of 4-nitrobiphenyl

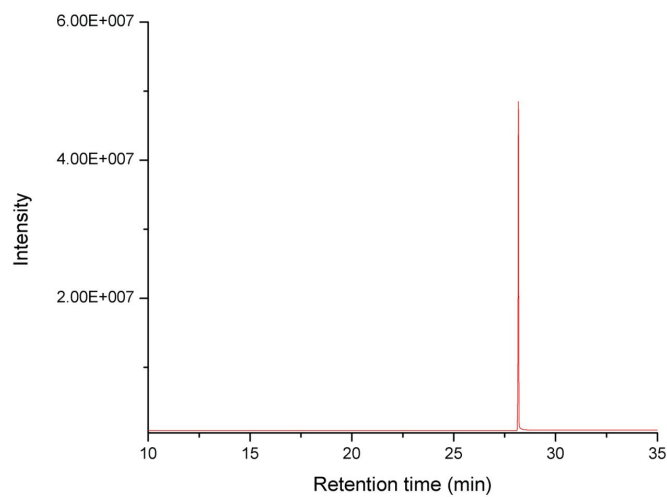


Figure S45. Gas Chromatogram of 4-nitrobiphenyl

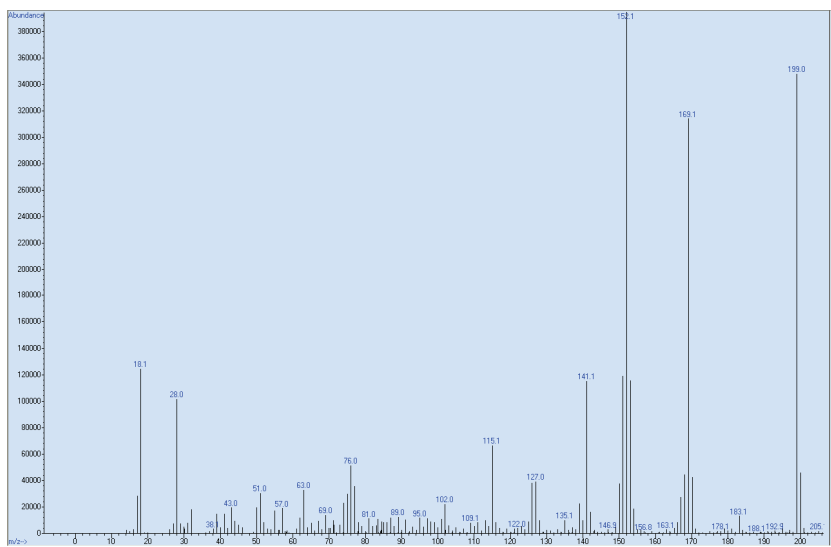


Figure S46. Mass spectrum of 4-nitrobiphenyl

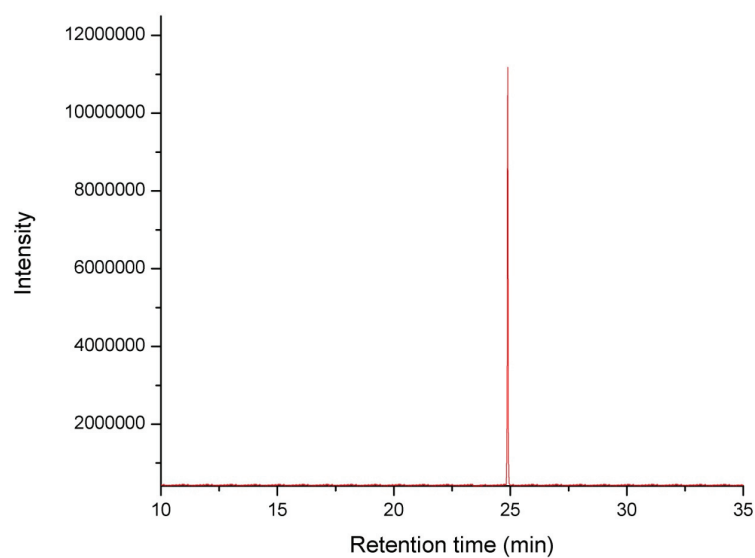


Figure S47. Gas Chromatogram of 4-methoxybiphenyl

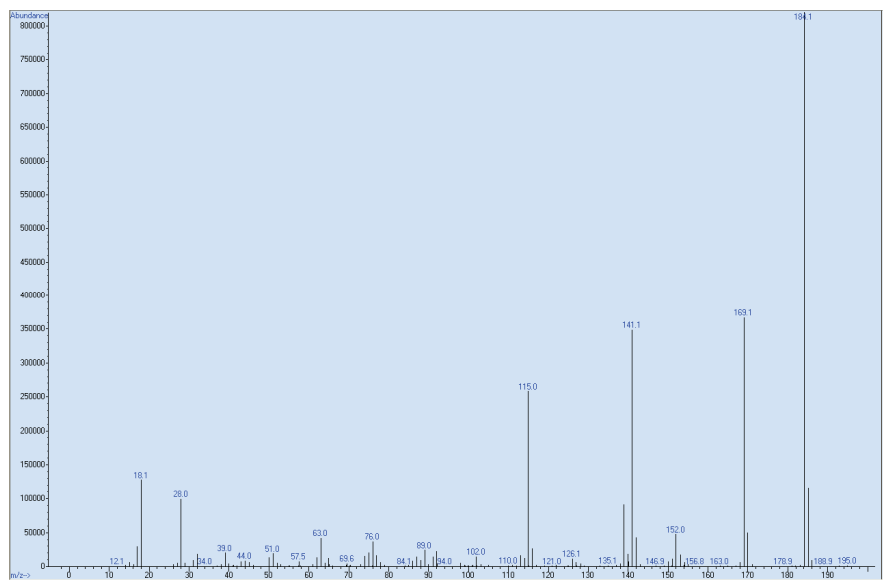


Figure S48. Mass spectrum of of 4-methoxybiphenyl

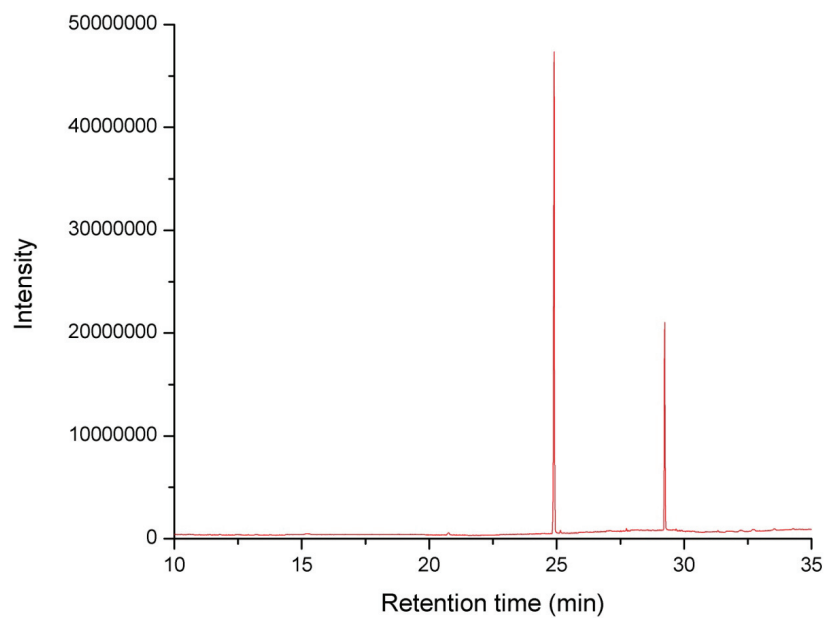


Figure S49. Gas Chromatogram of 4-methoxybiphenyl

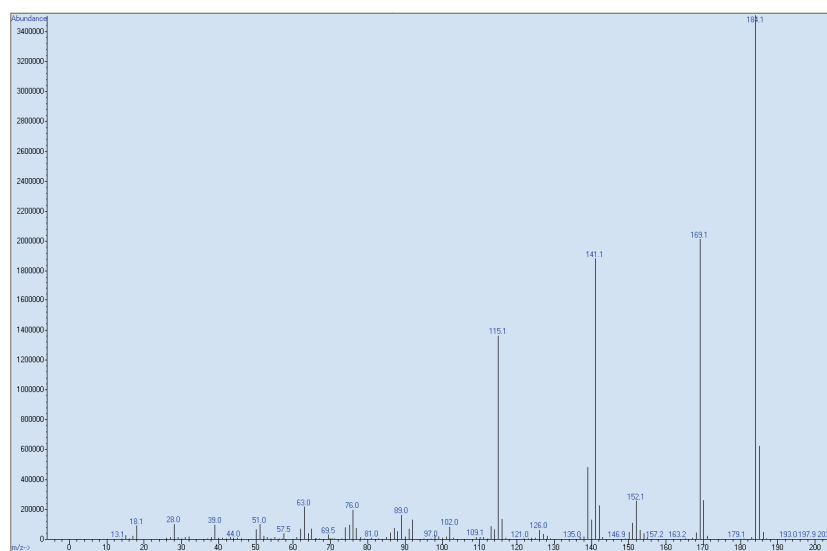


Figure S50. Mass spectrum of of 4-methoxybiphenyl

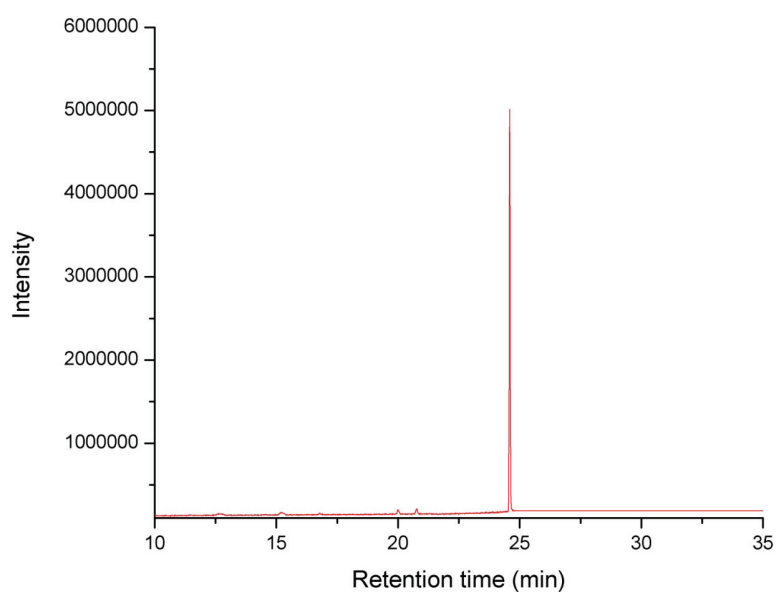


Figure S51. Gas Chromatogram of 4-methoxybiphenyl (first run)

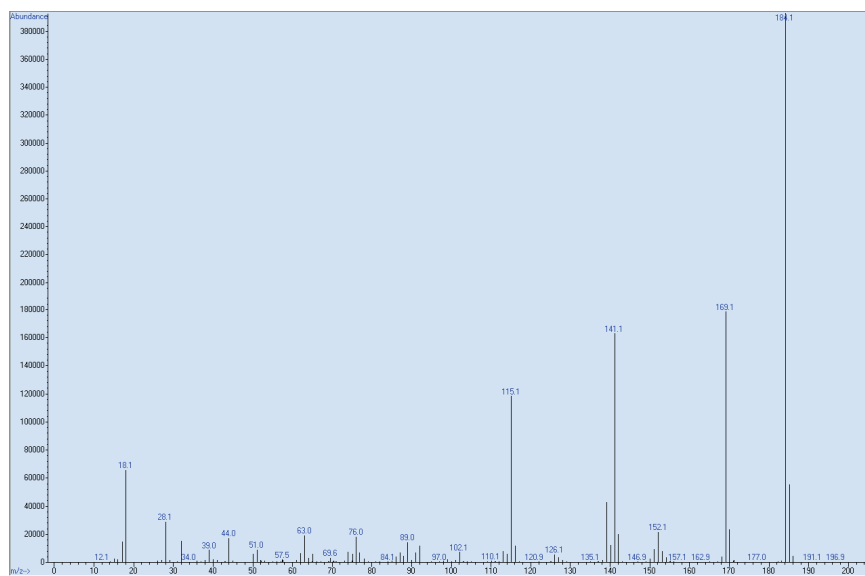


Figure S52. Mass spectrum of 4-methoxybiphenyl (first run)

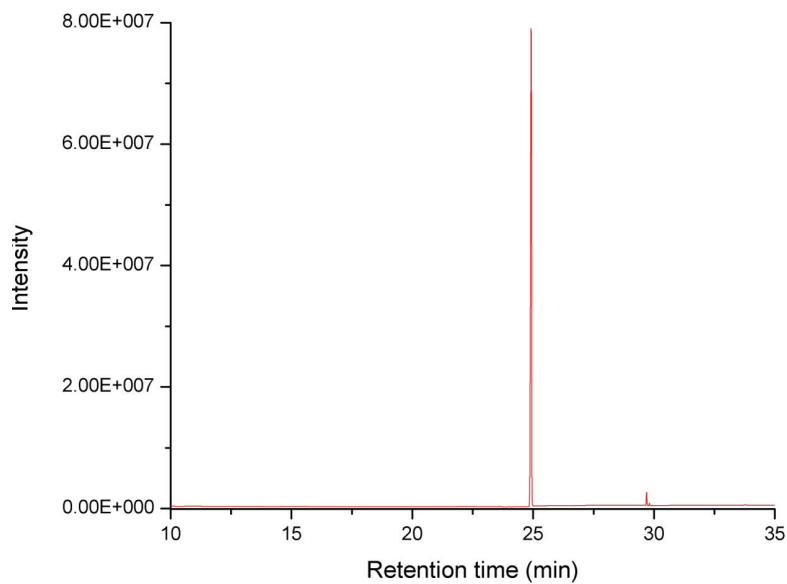


Figure S53. Gas Chromatogram of 4-methoxybiphenyl (second run)

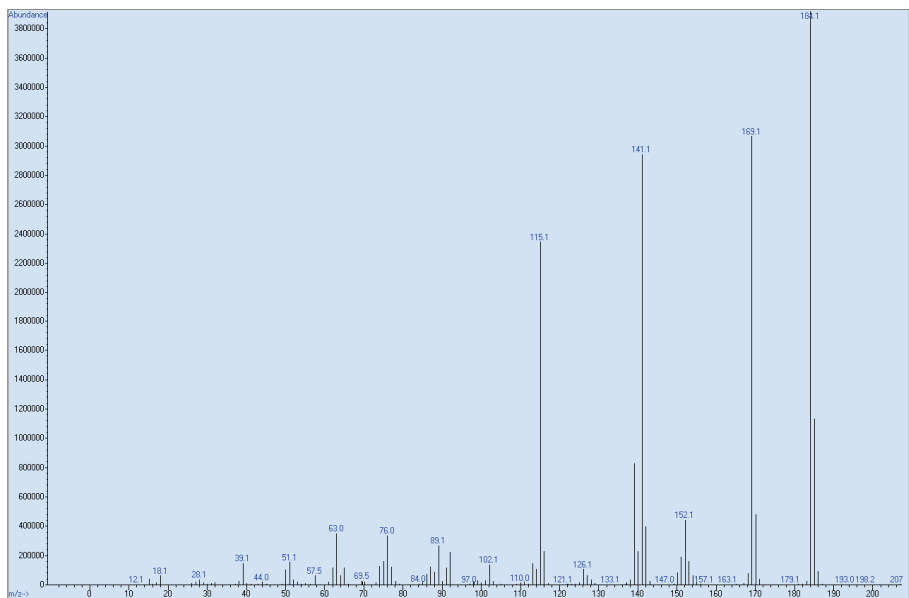


Figure S54. Mass spectrum of 4-methoxybiphenyl (second run)

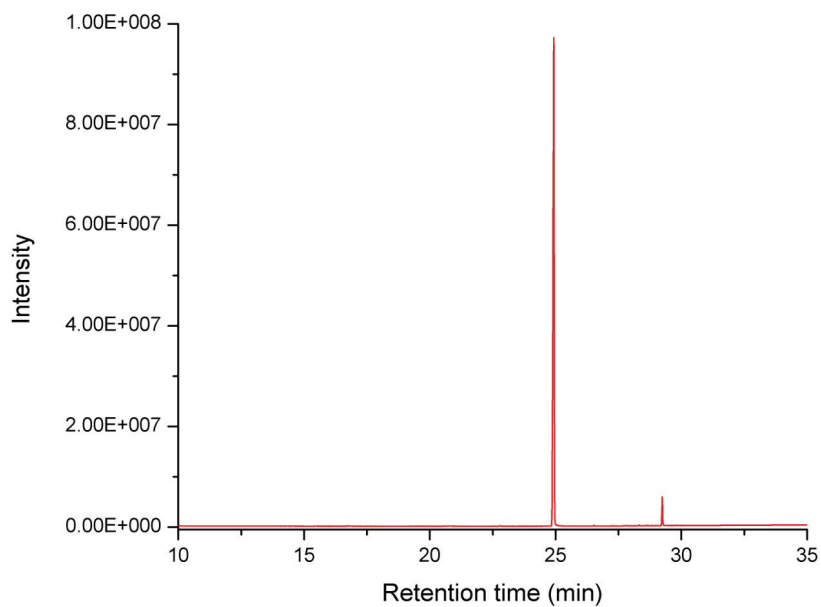


Figure S55. Gas Chromatogram of 4-methoxybiphenyl (third run)

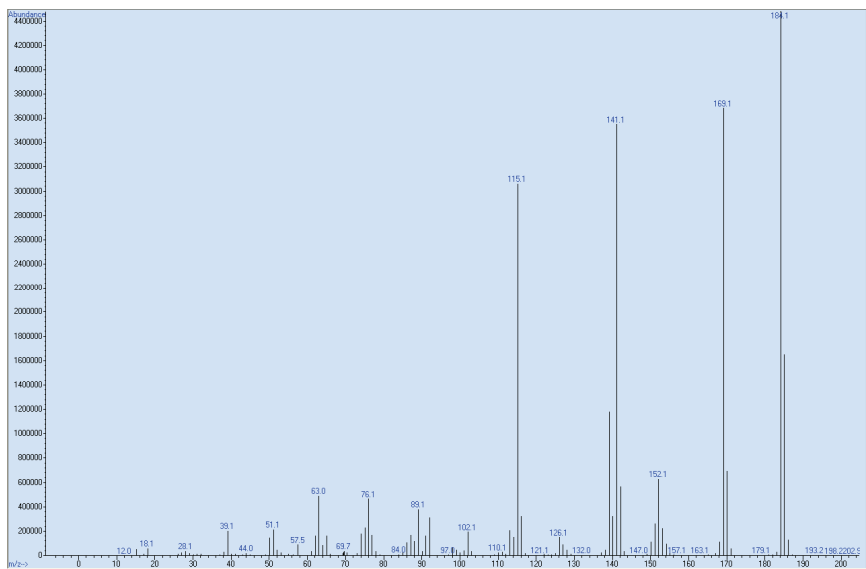
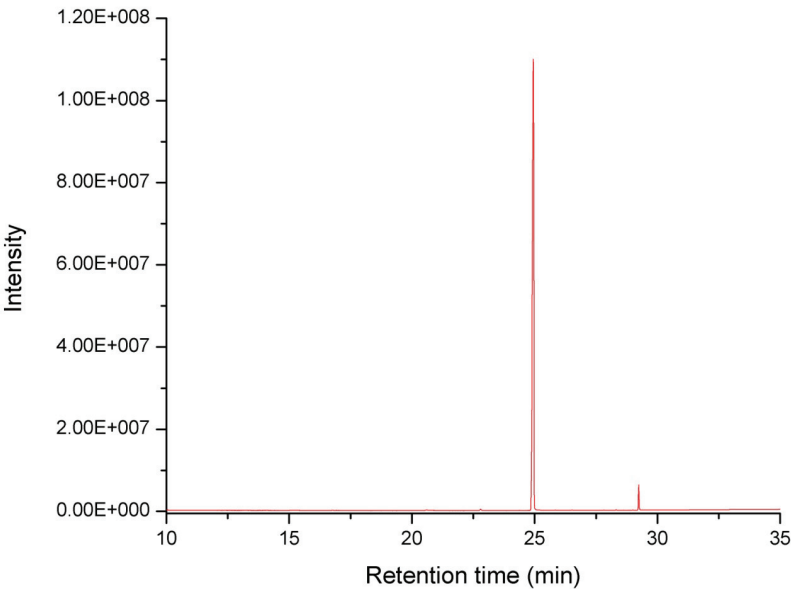


Figure S56. Mass spectrum of 4-methoxybiphenyl (third run)



FigureS57. Gas Chromatogram of 4-methoxybiphenyl (fourth run)

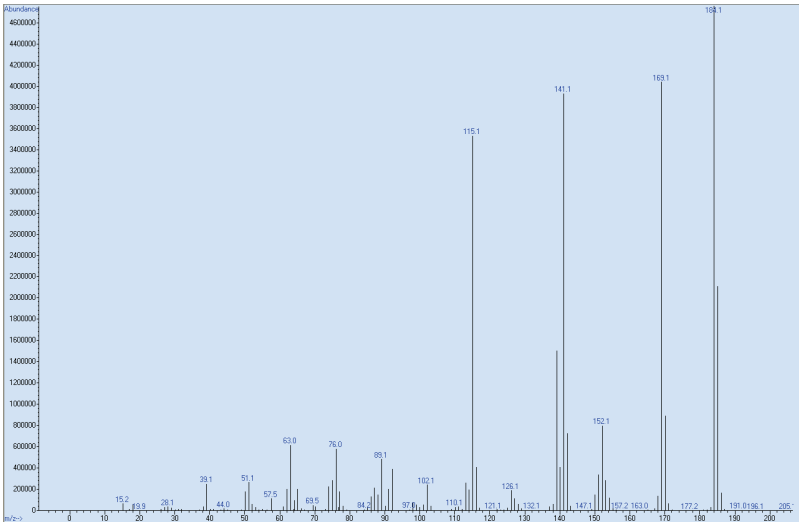


Figure S58. Mass spectrum of 4-methoxybiphenyl (fourth run)

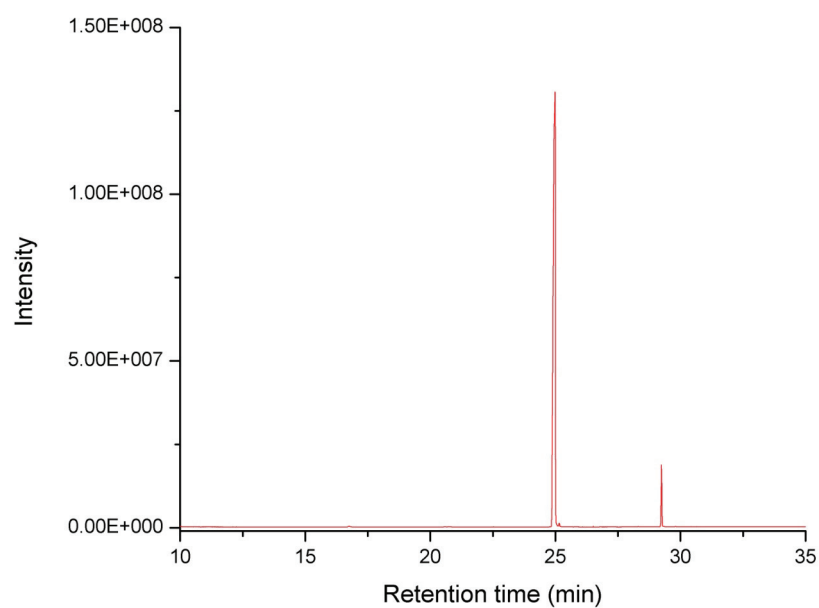


Figure S59. Gas Chromatogram of 4-methoxybiphenyl (fifth run)

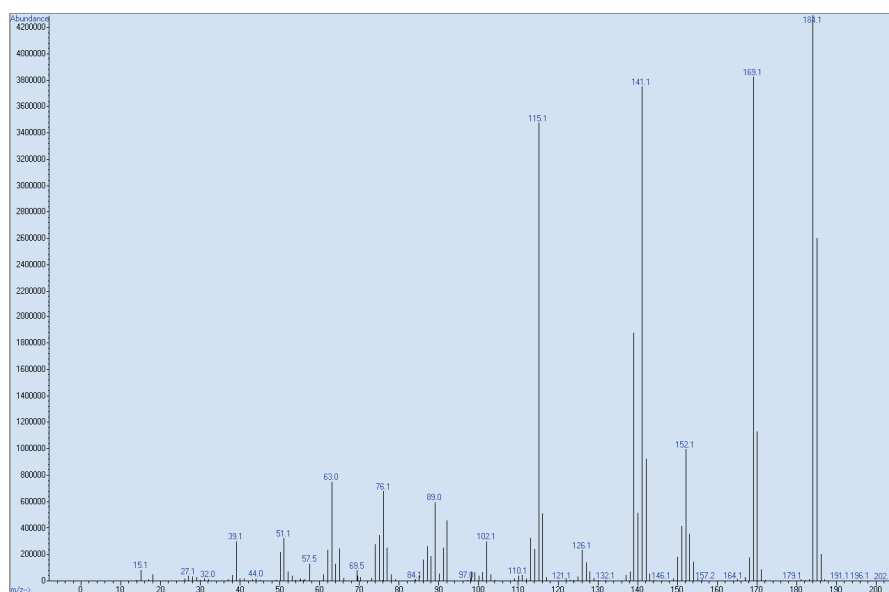


Figure S60. Mass spectrum of 4-methoxybiphenyl (fifth run)

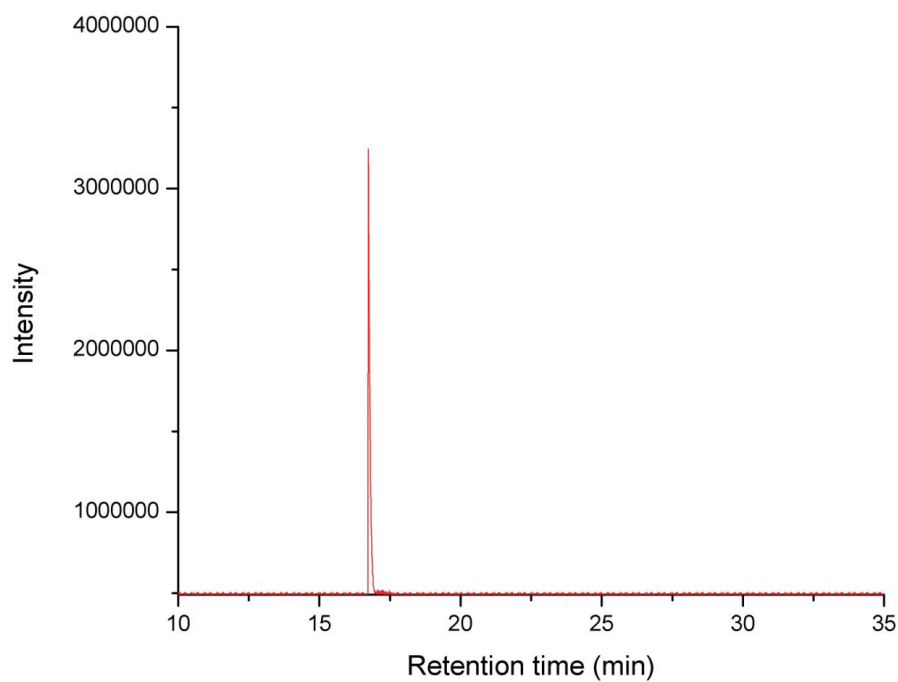


Figure S61. Gas Chromatogram of 4-fluorobiphenyl (1.5 mol % Pd@Peptide)

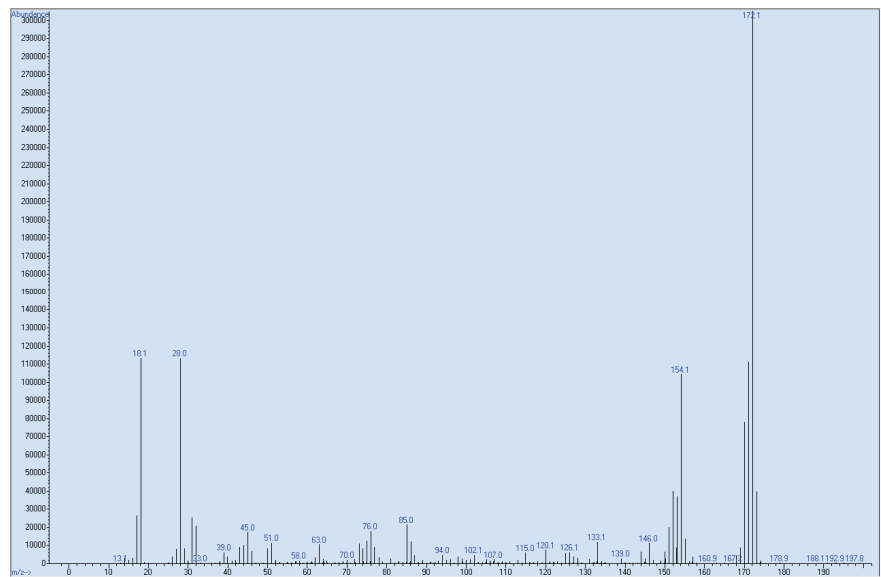


Figure S62. Mass spectrum of 4-fluorobiphenyl.

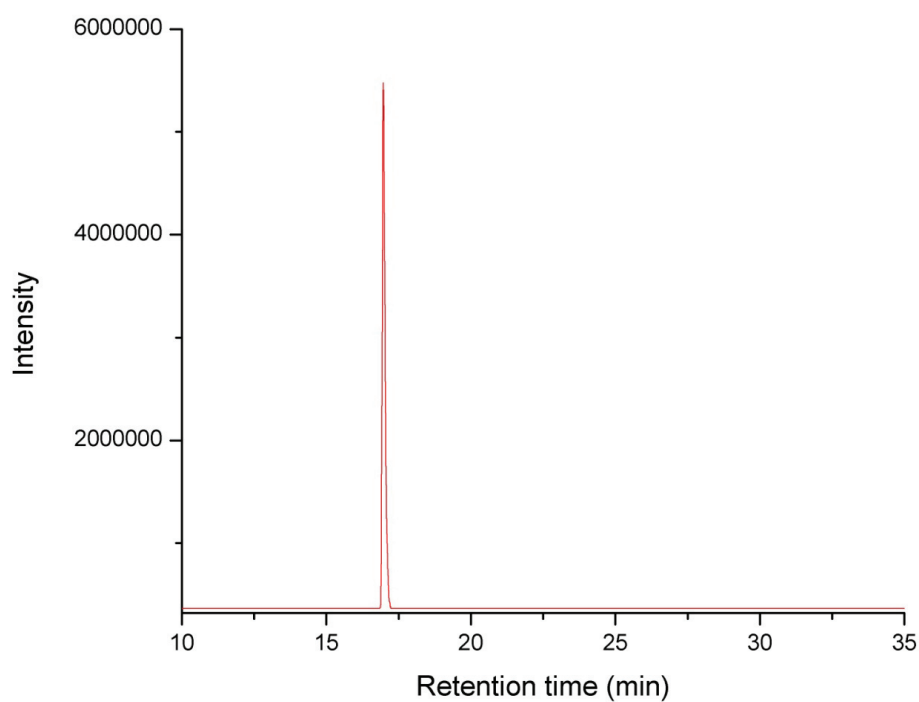


Figure S63. Gas Chromatogram of 4-fluorobiphenyl (0.5 mol % Pd@Peptide)

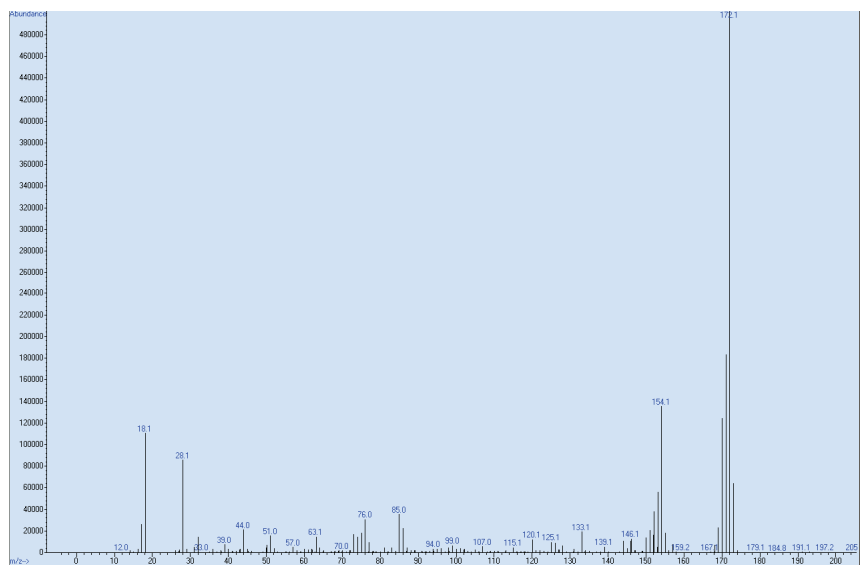


Figure S64. Mass spectrum of 4-fluorobiphenyl

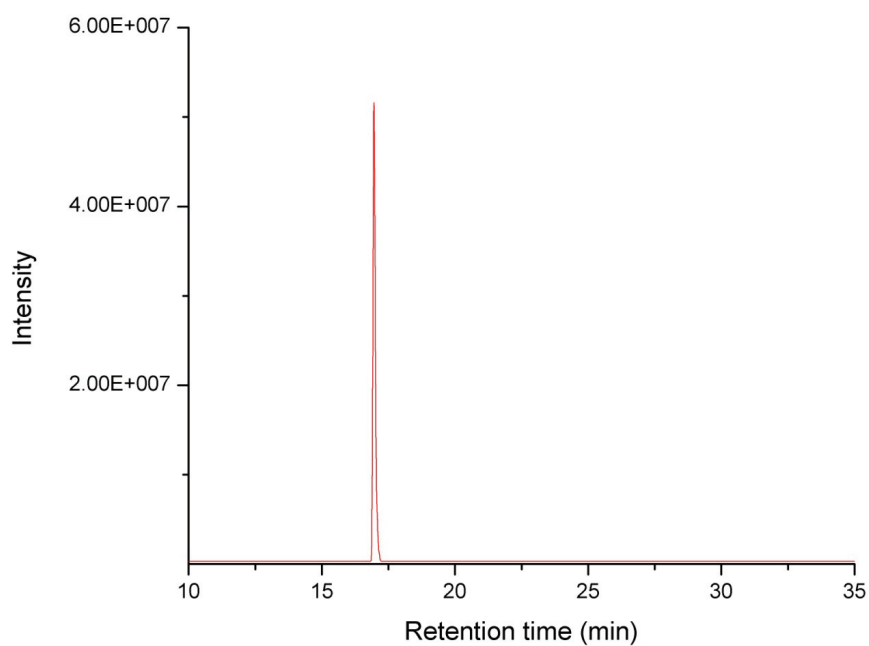


Figure S65. Gas Chromatogram of 4-fluorobiphenyl (0.1 mol % Pd@Peptide)

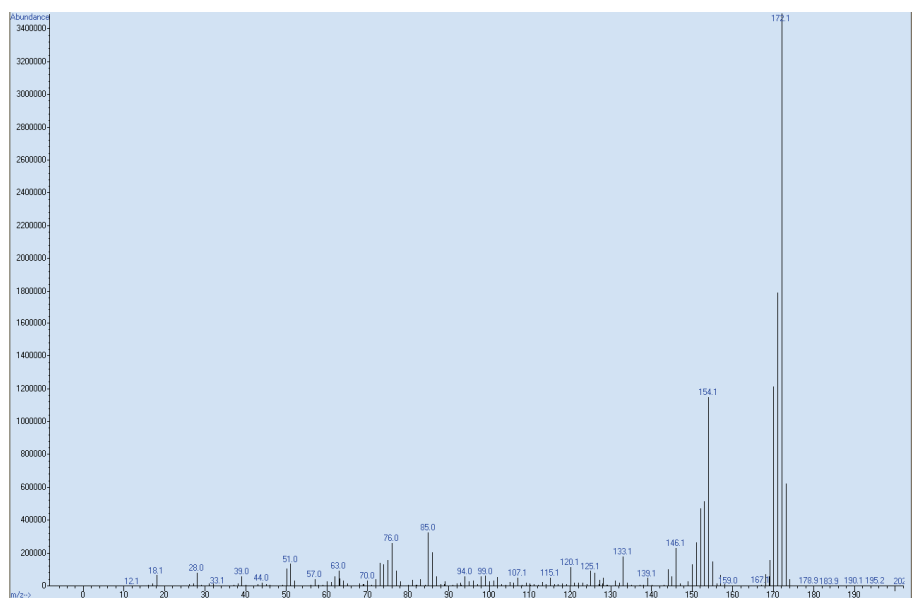


Figure S66. Mass spectrum of 4-fluorobiphenyl