

Supporting Information for

A tripodal mono-peptide ligand for asymmetric Rh(II) catalysis and the importance of on-bead catalyst development

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1. Experimental procedures and results:

a. General Information:

All rhodium-catalyzed reactions were carried out in 4-mL or 20-mL vials. Flash chromatography was performed with 40-63- μ m particle size silica gel. Optical rotations were measured using a JASCO DIP-370 digital polarimeter.

NMR Spectroscopy: NMR data was acquired with Bruker Avance 400 or Bruker Avance 500 MHz instrument. ^1H and ^{13}C NMR spectra were referenced relative to residual solvent or TMS.

HPLC analysis: Reverse-phase HPLC analyses of the peptides and metallopeptides were performed on a Shimadzu CBM-20A instrument with Phenomenex Jupiter 4 μ Proteo 90A (250 \times 15 mm preparative) and Phenomenex Jupiter 4 μ Proteo 90A (250 \times 4.6 mm analytical) columns. Flow rates of 8 mL/min and 1.5 mL/min were used for the preparative and analytical columns, respectively. The analysis of the peptides and dirhodium complexes was done at two wavelengths (220 nm and 300 nm). Chiral HPLC analyses were performed on a Shimadzu SCL-10ADVP instrument with Phenomenex Lux 5u Cellulose-1 (250 \times 4.6 mm analytical) or a Chiralpak IA (250 \times 2 mm ID analytical) column with a flowrate of 1.6–1.9 mL/min.

Mass Spectrometry: MALDI-MS was performed on a Bruker Daltonics Autoflex MALDI-TOF/TOF mass spectrometer. Ethanolic solutions of analyte were cocrystallized on Bruker Daltonics PAC384 AnchorChip with Alpha-CHC matrix (Agilent technologies). MALDI data analysis was performed using the mMass program.¹ GC-MS was recorded on an Agilent 5975C MSD interfaced to an Agilent 7890A GC System equipped with an Rxi-5sil MS column (30 m \times 0.25 mm in diameter, 0.10 μ m film thickness; Restek). The sample was prepared in a concentration of 1mg/mL of compound in diethylether.

Diffuse Reflectance: Diffuse reflectance measurements were obtained using a UV-Vis spectrometer (Shimadzu UV-2450) equipped with an integrating sphere.

UV-vis spectrometer for Kinetics measurement: The kinetics of the cyclopropanation reactions was monitored by measuring the absorbance of the reaction mixture at 420 nm wavelength at various time intervals using a Varian Cary 50 scan UV-Vis spectrophotometer with a 1cm path length quartz cell.

Peptide Synthesis: *General considerations:* Commercially available L-amino acids were used for peptide synthesis. All peptides were synthesized using standard solid-phase Fmoc protocols.² After peptide synthesis, side-chain protecting groups were cleaved using a cocktail of 25% trifluoroacetic acid, 70% dichloromethane and 5% triisopropylsilane.

Peptide synthesis for solution-phase catalyst generation: Peptides were synthesized manually on Rink amide resin. After peptide synthesis, the peptides were cleaved from the resin using a cocktail of 25% trifluoroacetic acid, 70% dichloromethane and 5% triisopropylsilane. Crude peptides were taken up in trifluoroethanol, and diisopropylethylamine was added dropwise with simultaneous sonication until the peptide dissolved. The purification of peptides was accomplished by direct injection into reverse-phase HPLC with gradients of water-acetonitrile containing 0.1% trifluoroacetic acid, and the peptides were isolated by lyophilization. Analysis and purity assessment was attained by mass spectrometry and analytical HPLC.

Peptide synthesis for library generation: Peptides were synthesized on Novasyn TG amino resin, which contains a linker stable to acid deprotection conditions. The peptides were synthesized in polypropylene 2-ml deep-well square-bottom 96-well filter plate with 25-mm polyethylene frits and long-drip drain ports (AWFP-F20000; Arctic White) fitted with a bottom sealing mat (AWSM-1003DP; Arctic White). Filtration was done using a multiscreen vacuum manifold (Millipore, cat. no. MSVMHTS00) attached to a vacuum trap and an inline waste trap.

Chemicals: The following chemicals were purchased and used as received: L-amino acids (AAPTEC), rink amide MBHA resin with 100-200 mesh (AAPTEC), novasyn TG amino resin (Novabiochem), HATU (AAPTEC), piperidine (Aldrich), diisopropylethylamine (Fisher), Rh₂(OAc)₄ (Pressure Chemical), 2,2,2-trifluoroethanol (Aldrich), phenylacetic acid (Matheson), styrene (Aldrich), ethyl vinyl ether (Aldrich), α -methyl styrene (Aldrich), 4-chlorostyrene (Aldrich), *N*-methyl-*N*-vinylacetamide (Aldrich), 2,3-dihydrofuran (Aldrich), and 1,8-diazabicyclo[5.4.0]undec-7-ene (Acros). All solvents were reagent grade.

Synthesis of known compounds: The dirhodium precursors *cis*-Rh₂(tfa)₂(OAc)₂³ and Rh₂(tfa)₄⁴ were prepared according to published procedures. Diazo substrates methyl α -diazophenylacetate⁵ and *tert*-butyl α -diazophenylacetate⁵ have been previously reported and characterized and were prepared according to the reported protocols. For purpose of ee determination, racemic material was generated using Rh₂(OAc)₄. The absolute configuration of products is assigned by comparison of the optical rotation to previous reports.⁶

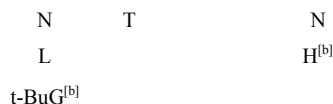
b. Protocol for on-bead library screens:

Library Design:

An arbitrary library of nonapeptide sequences with high diversity was designed in the case of library 3. In all the sequences, *i* and *i*+4 positions were fixed as Asp; the *i*+6 position was fixed as Lys(Z) and from data based on previous results,⁶ the *i*+3 position was fixed as Asn and *i*-1 position was fixed as Gly. A subset of amino acids was chosen to introduce diversity at each of the positions, *i*+1, *i*+2, and *i*+5 (see Table S1 for details). Position *i*-2 was predominantly Lys(Z) with a few sequences containing Ile in this position. Unique nonapeptide sequences were randomly generated from these subset constraints using Excel. Theoretically, for Library 3, there are 420 permutations of sequences that can be generated from the given subsets of amino acids in various positions. However, we biased the library away from His and G^{*t*-Bu} containing sequences, maintaining the number of this amino acid at 5% of the total at each position. Such a bias was also implemented for Ile, restricting it to 25% in the *i*-2 position. This has the effect that 85 of the 95 members of the synthetic library were drawn from the much smaller subset (150 members) of theoretical sequences without a His residue in the *i*+5 position or a G^{*t*-Bu} residue in the *i*+1 position. To avoid confusion during the synthesis, an array for each position was prepared depicting the amino acids to be added to the various wells during each reaction step. The loading of Novasyn TG amino resin was decreased from 0.29 mmol/g to 0.17 mmol/g by a standard capping protocol.⁷

Table S1. Amino acid variation incorporated in Library 3.

i-2	i-1	i	i+1	i+2	i+3	i+4	i+5	i+6
K (Z)	G	D	Y	G	N	D	I	K ^Z
I ^[a]			V	N			M	
			Q	I			Y	
			T	W			T	



[a] This amino acid was constrained to 25% at this position. [b] This amino acid was constrained to 5% at this position. "K^Z" signifies a lysine residue with the side chain amine protected as a benzyloxycarbonyl (Z) carbamate.

In library 4 design, the *i*+1 and *i*+2 positions were widely varied, incorporating amino acids that were left out in the previous library syntheses. Glutamates were introduced in the *i* and *i*+4 positions in 5% of the peptides to study the effect of the long chain carboxylate on ee, and 5% of the sequences incorporated 3-methyl-histidine in the place of histidine. The *i*+5 position was designed to be predominantly histidine, but a number of peptides contained tyrosine and phenylalanine in this position (Table S2). A small percentage (10%) of glutamine and serine were introduced in the *i*+3 position. In this library also, the *i*-2 position was fixed as Ile; the *i*-1 as Gly and the *i*+6 as Lys(Cbz).

Table S2. Amino acid variation incorporated in Library 4.

i-2	i-1	i	i+1	i+2	i+3	i+4	i+5	i+6
I	G	D	L	I	N	D	H	K ^Z
		E ^[a]	N	T	Q ^[b]	E ^[c]	3-Me-H ^[a]	
			Y	W	S ^[b]		Y ^[d]	
			I	L			F ^[d]	
			Q	F				
			S	Y				
			t-BuG ^[a]					

[a] This amino acid was constrained to 5% at this position. [b] This amino acid was constrained to 10% at this position. [c] This amino acid was constrained to 15% at this position [d] This amino acid was constrained to 25% at this position; "K^Z" signifies a lysine residue with the side chain amine protected as a benzyloxycarbonyl (Z) carbamate.

Subsequent design of library 5 was done based on the results obtained from earlier on-bead catalyst screenings (Libraries 1, 2, 3 and 4) to include the *i*+5 histidine-containing peptide counterparts of the peptide sequences yielding enantioselectivities greater than 45%.

General protocol for the synthesis of Library 3:

The peptide library synthesis was conducted by adapting an established protocol.^{6,8} Novasyn TG amino resin with 0.17 mmol loading (1,700 mg) was weighed in a 100-mL round bottom flask and suspended in 3:2 CH₂Cl₂/DMF (50 mL) to form a homogeneous resin suspension and stirred. While stirring, a 500-μL aliquot was transferred into each well of a 2-mL deep-well polypropylene filter plate sealed at the bottom. In this process, roughly an equal amount of resin was distributed in each well (3 μmol, 1 equiv). A small magnetic stir bar was then placed inside each well. The amount of Fmoc-amino acid (9 μmol, 3 equiv per well) required in each coupling step was pre-weighed into separate 20-mL scintillation vials. The bottom sealing matte was removed from the 96-well plate. The plate was then transferred quickly to a vacuum filtration manifold, and the solution in the plate was drained by applying vacuum. The resin in each well was washed by dispensing DMF (roughly 1 mL x 4) from a

squirt bottle. The bottom sealing matte was then fixed in place and Fmoc-deprotection was performed by dispensing 20% piperidine in DMF (250 μ L in each well). The entire plate was placed on an IKA magnetic stir plate and stirred at rt for 7 min. The solution was drained and the deprotection was repeated once again, followed by resin washing with DMF (5×500 μ L for each well). Stock solutions of HATU (0.5 M, 30 mL), *i*-Pr₂NEt (1 M, 30 mL) and Piperidine (20%, v/v) were prepared. Just before coupling, to the vial containing pre-weighed Fmoc-amino acid, pre-made solutions of HATU (18 μ L per well), DMF (150 μ L per well), and *i*-Pr₂NEt (18 μ L per well) were added, and the vial was sonicated until the amino acid dissolved completely. The amino-acid solution (~ 200 μ L per well) was then transferred via pipette to the appropriate wells according to the array prepared earlier. The other wells were filled with the corresponding amino acid solutions in a similar fashion. The entire plate was then stirred for 45 min to allow for amino acid coupling. Then, all the wells were washed with DMF (5×500 μ L per well). The deprotection, wash, coupling and wash steps were repeated until the desired oligomer length was achieved. The Fmoc protecting group from the N-terminal residue was then removed in the final deprotection step and the wells were thoroughly washed with DMF (5×500 μ L per well), and CH₂Cl₂ (5×500 μ L per well). The acetylation cocktail was prepared (708 μ L Ac₂O + 72 μ L pyridine + 15 mL CH₂Cl₂) and this solution (150 μ L per well) was pipetted into each well and stirred for 1 h. The solution was drained and the acetylation process was repeated once again. The wells were washed with CH₂Cl₂ (5×500 μ L per well). Cleavage was accomplished by dispensing 500 μ L of a cocktail containing 25% Trifluoroacetic acid, 5% triisopropylsilane and 70% dichloromethane. The plate was stirred for 3 h inside a fume hood. The bottom sealing matte was then removed and the cleavage solution was filtered off, leaving behind the deprotected peptide ligands attached to the solid support in each well. The resin in each well was washed with CH₂Cl₂ (5×500 μ L per well), *i*-Pr₂NEt in trifluoroethanol (1.5% soln, 2×500 μ L per well), and pure trifluoroethanol (500 μ L per well). In two of the wells in the 96-well plate, the peptides were synthesized on Rink amide resin so that the peptide can be cleaved off from the resin and the sequence confirmed by MALDI. The purity of these two cleaved peptides were checked by HPLC and were found to be >90%.

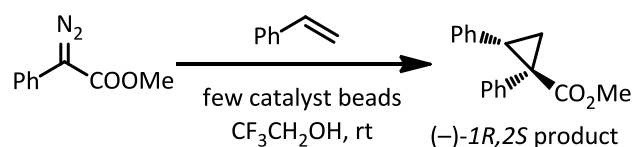
A solution of *i*-Pr₂NEt (470 μ L) in trifluoroethanol (47 mL) and a solution of *cis*-Rh₂(OAc)₂(tfa)₂ (71.75 mg, 0.13 mmol) in trifluoroethanol (47 mL) were prepared separately. A 500 μ L aliquot of the *i*-Pr₂NEt solution followed by a 500 μ L aliquot of the *cis*-Rh₂(OAc)₂(tfa)₂ solution were added to each well of a 96-well plate containing peptide on Novasyn TG resin, and the wells were stirred at 50 °C for 24 h. The beads in wells containing sequences devoid of histidine and methionine turned blue, indicating complexation of dirhodium to the peptide. The beads were of burgundy color in wells containing sequences with Met and green in wells containing sequences with His. The catalyst in each well is then washed thoroughly with trifluoroethanol (2×500 μ L/well) to remove unreacted *cis*-Rh₂(OAc)₂(tfa)₂.

General protocol for catalyst screening from Library 1:

A few beads (~ 0.15 μ mol, $\sim 10\%$ of total resin estimated by eye) from each well in the 2-mL deep-well polypropylene plate were transferred to the corresponding well in a new 500- μ L capacity 96-well polypropylene plate manually via spatula taking care not to contaminate the various wells. The new 96-well plate had been pre-treated with trifluoroethanol (50 μ L) and the spatula tip containing the beads was dipped into the solvent to facilitate bead transfer. A solution of styrene (1.3 mL, 10 equiv) in trifluoroethanol (10 mL) was prepared and an aliquot (100 μ L) was dispensed into each well of the 96-well plate containing catalyst beads. Then, a solution of methyl α -phenyl diazoacetate (200 mg) in trifluoroethanol (10 mL) was prepared

and this solution (100 μ L, 1 equiv) was added to each well. The entire plate was then placed on a shaker and shaken until the diazo compound reacted fully as seen from the disappearance of yellow color of the diazo compound. After completion of the reaction, the trifluoroethanol was removed under a gentle stream of nitrogen. The plate was then placed under vacuum to remove residual styrene and solvent. Hexane (400 μ L) was added to each well and the plate was placed in an HPLC autosampler for ee determination. The reactions go to full conversion and the cyclopropane products from the crude reactions were subjected directly to ee determination by chiral hplc. In most of the reactions, there was a small overlapping peak with the minor enantiomer. The pure product was isolated in reactions where the crude mixture product was \geq 80% ee to obtain a true measure of the enantiomeric excess.

c. Complete results for libraries 3, 4 and 5:



ligand	<i>i</i> -2	<i>i</i> -1	<i>i</i>	<i>i</i> +1	<i>i</i> +2	<i>i</i> +3	<i>i</i> +4	<i>i</i> +5	<i>i</i> +6	% ee
Library 3										
L3.01	I	G	D	L	G	N	D	H	K ^Z	60
L3.02	I	G	D	N	I	N	D	H	K ^Z	86
L3.03	K ^Z	G	D	Q	N	N	D	H	K ^Z	63
L3.04	I	G	D	Q	T	N	D	H	K ^Z	74
L3.05	I	G	D	L	W	N	D	H	K ^Z	79
L3.06	K ^Z	G	D	L	G	N	D	I	K ^Z	47
L3.07	K ^Z	G	D	N	G	N	D	I	K ^Z	38
L3.08	I	G	D	Q	G	N	D	I	K ^Z	18
L3.09	I	G	D	V	G	N	D	I	K ^Z	25
L3.10	K ^Z	G	D	Y	G	N	D	I	K ^Z	45
L3.11	K ^Z	G	D	N	I	N	D	I	K ^Z	45
L3.12	I	G	D	Q	I	N	D	I	K ^Z	30
L3.13	K ^Z	G	D	Q	I	N	D	I	K ^Z	29
L3.14	K ^Z	G	D	N	N	N	D	I	K ^Z	45
L3.15	I	G	D	Q	N	N	D	I	K ^Z	21
L3.16	I	G	D	T	N	N	D	I	K ^Z	28
L3.17	K ^Z	G	D	T	N	N	D	I	K ^Z	29
L3.18	K ^Z	G	D	G ^{t-Bu}	N	N	D	I	K ^Z	12
L3.19	K ^Z	G	D	N	T	N	D	I	K ^Z	48
L3.20	K ^Z	G	D	T	T	N	D	I	K ^Z	24

L3.21	K ^Z	G	D	Y	T	N	D	I	K ^Z	45
L3.22	K ^Z	G	D	Q	W	N	D	I	K ^Z	35
L3.23	K ^Z	G	D	Y	W	N	D	I	K ^Z	43
L3.24	K ^Z	G	D	Q	G	N	D	M	K ^Z	27
L3.25	K ^Z	G	D	V	G	N	D	M	K ^Z	35
L3.26	K ^Z	G	D	L	I	N	D	M	K ^Z	48
L3.27	K ^Z	G	D	N	I	N	D	M	K ^Z	49
L3.28	I	G	D	N	N	N	D	M	K ^Z	43
L3.29	K ^Z	G	D	Q	N	N	D	M	K ^Z	34
L3.30	K ^Z	G	D	V	N	N	D	M	K ^Z	35
L3.31	I	G	D	Y	N	N	D	M	K ^Z	50
L3.32	K ^Z	G	D	L	T	N	D	M	K ^Z	53
L3.33	K ^Z	G	D	N	T	N	D	M	K ^Z	51
L3.34	I	G	D	T	T	N	D	M	K ^Z	34
L3.35	K ^Z	G	D	T	T	N	D	M	K ^Z	37
L3.36	K ^Z	G	D	G ^{t-Bu}	T	N	D	M	K ^Z	30
L3.37	I	G	D	N	W	N	D	M	K ^Z	43
L3.38	K ^Z	G	D	T	W	N	D	M	K ^Z	39
L3.39	K ^Z	G	D	L	G	N	D	N	K ^Z	48
L3.40	K ^Z	G	D	Q	G	N	D	N	K ^Z	24
L3.41	I	G	D	T	G	N	D	N	K ^Z	12
L3.42	K ^Z	G	D	T	G	N	D	N	K ^Z	11
L3.43	K ^Z	G	D	G ^{t-Bu}	G	N	D	N	K ^Z	13
L3.44	K ^Z	G	D	V	G	N	D	N	K ^Z	28
L3.45	I	G	D	T	I	N	D	N	K ^Z	42
L3.46	K ^Z	G	D	N	N	N	D	N	K ^Z	44
L3.47	K ^Z	G	D	Q	N	N	D	N	K ^Z	33
L3.48	K ^Z	G	D	V	N	N	D	N	K ^Z	39
L3.49	K ^Z	G	D	Y	N	N	D	N	K ^Z	50
L3.50	K ^Z	G	D	N	T	N	D	N	K ^Z	47
L3.51	K ^Z	G	D	T	T	N	D	N	K ^Z	25
L3.52	K ^Z	G	D	Y	T	N	D	N	K ^Z	51
L3.53	K ^Z	G	D	L	W	N	D	N	K ^Z	49
L3.54	K ^Z	G	D	G ^{t-Bu}	W	N	D	N	K ^Z	26
L3.55	K ^Z	G	D	V	W	N	D	N	K ^Z	44
L3.56	I	G	D	L	G	N	D	T	K ^Z	50
L3.57	K ^Z	G	D	L	G	N	D	T	K ^Z	49
L3.58	K ^Z	G	D	T	G	N	D	T	K ^Z	18
L3.59	K ^Z	G	D	V	G	N	D	T	K ^Z	26
L3.60	K ^Z	G	D	Y	G	N	D	T	K ^Z	47
L3.61	K ^Z	G	D	L	N	N	D	T	K ^Z	51

L3.62	I	G	D	V	N	N	D	T	K ^Z	37
L3.63	K ^Z	G	D	V	N	N	D	T	K ^Z	35
L3.64	K ^Z	G	D	L	T	N	D	T	K ^Z	55
L3.65	K ^Z	G	D	N	T	N	D	T	K ^Z	50
L3.66	K ^Z	G	D	Q	T	N	D	T	K ^Z	32
L3.67	K ^Z	G	D	T	T	N	D	T	K ^Z	29
L3.68	K ^Z	G	D	V	T	N	D	T	K ^Z	34
L3.69	I	G	D	Y	T	N	D	T	K ^Z	46
L3.70	K ^Z	G	D	L	W	N	D	T	K ^Z	53
L3.71	K ^Z	G	D	N	W	N	D	T	K ^Z	52
L3.72	I	G	D	V	W	N	D	T	K ^Z	37
L3.73	K ^Z	G	D	V	W	N	D	T	K ^Z	39
L3.74	I	G	D	Q	G	N	D	Y	K ^Z	12
L3.75	I	G	D	V	G	N	D	Y	K ^Z	24
L3.76	K ^Z	G	D	V	G	N	D	Y	K ^Z	24
L3.77	K ^Z	G	D	Y	G	N	D	Y	K ^Z	50
L3.78	K ^Z	G	D	N	I	N	D	Y	K ^Z	46
L3.79	K ^Z	G	D	T	I	N	D	Y	K ^Z	23
L3.80	I	G	D	Y	I	N	D	Y	K ^Z	48
L3.81	K ^Z	G	D	Y	I	N	D	Y	K ^Z	48
L3.82	I	G	D	N	N	N	D	Y	K ^Z	37
L3.83	K ^Z	G	D	Q	N	N	D	Y	K ^Z	15
L3.84	I	G	D	T	N	N	D	Y	K ^Z	17
L3.85	K ^Z	G	D	V	N	N	D	Y	K ^Z	23
L3.86	I	G	D	Y	N	N	D	Y	K ^Z	42
L3.87	K ^Z	G	D	Y	N	N	D	Y	K ^Z	44
L3.88	K ^Z	G	D	Q	T	N	D	Y	K ^Z	21
L3.89	K ^Z	G	D	Y	T	N	D	Y	K ^Z	42
L3.90	K ^Z	G	D	L	W	N	D	Y	K ^Z	43
L3.91	K ^Z	G	D	N	W	N	D	Y	K ^Z	44
L3.92	K ^Z	G	D	Q	W	N	D	Y	K ^Z	29
L3.93	K ^Z	G	D	T	W	N	D	Y	K ^Z	24
L3.94	I	G	D	G ^{t-Bu}	W	N	D	Y	K ^Z	21
L3.95	K ^Z	G	D	V	W	N	D	Y	K ^Z	32
L3.96	K ^Z	G	D	I	A	N	D	Y	K ^Z	n.d. ^a
Library 4										
L4.01	I	G	D	N	I	N	D	3-Me-H	K ^Z	69
L4.02	I	G	D	N	G ^{t-Bu}	N	D	3-Me-H	K ^Z	68
L4.03	I	G	D	L	W	N	D	3-Me-H	K ^Z	54
L4.04	I	G	D	L	F	N	D	F	K ^Z	38

L4.05	I	G	D	Q	F	N	D	F	K ^Z	35
L4.06	I	G	D	I	I	N	D	F	K ^Z	37
L4.07	I	G	D	N	I	N	D	F	K ^Z	47
L4.08	I	G	D	S	I	N	D	F	K ^Z	37
L4.09	I	G	D	I	L	N	D	F	K ^Z	32
L4.10	I	G	D	Y	L	N	D	F	K ^Z	49
L4.11	I	G	D	I	T	N	D	F	K ^Z	31
L4.12	I	G	D	L	T	N	D	F	K ^Z	36
L4.13	I	G	D	Q	T	N	D	F	K ^Z	29
L4.14	I	G	D	S	T	N	D	F	K ^Z	45
L4.15	I	G	D	Y	T	N	D	F	K ^Z	45
L4.16	I	G	D	L	G ^{<i>t</i>-Bu}	N	D	F	K ^Z	41
L4.17	I	G	D	Y	G ^{<i>t</i>-Bu}	N	D	F	K ^Z	47
L4.18	I	G	D	N	W	N	D	F	K ^Z	39
L4.19	I	G	D	Y	W	N	D	F	K ^Z	40
L4.20	I	G	D	N	Y	N	D	F	K ^Z	49
L4.21	I	G	D	N	I	Q	D	F	K ^Z	37
L4.22	I	G	D	N	W	Q	D	F	K ^Z	30
L4.23	I	G	D	Y	W	Q	D	F	K ^Z	38
L4.24	I	G	D	Y	T	S	D	F	K ^Z	27
L4.25	I	G	D	Y	W	S	D	F	K ^Z	25
L4.26	I	G	D	Y	Y	S	D	F	K ^Z	26
L4.27	I	G	D	I	F	N	D	H	K ^Z	74
L4.28	I	G	D	L	F	N	D	H	K ^Z	76
L4.29	I	G	D	I	I	N	D	H	K ^Z	n.d. ^b
L4.30	I	G	D	L	I	N	D	H	K ^Z	74
L4.31	I	G	D	N	I	N	D	H	K ^Z	68
L4.32	I	G	D	Q	I	N	D	H	K ^Z	70
L4.33	I	G	D	S	I	N	D	H	K ^Z	69
L4.34	I	G	D	Y	I	N	D	H	K ^Z	67
L4.35	I	G	D	L	L	N	D	H	K ^Z	67
L4.36	I	G	E	L	L	N	D	H	K ^Z	25
L4.37	I	G	D	N	L	N	D	H	K ^Z	69
L4.38	I	G	E	N	I	N	D	H	K ^Z	13
L4.39	I	G	D	Y	L	N	D	H	K ^Z	68
L4.40	I	G	D	I	T	N	D	H	K ^Z	58
L4.41	I	G	D	L	T	N	D	H	K ^Z	62
L4.42	I	G	D	N	T	N	D	H	K ^Z	55
L4.43	I	G	D	S	T	N	D	H	K ^Z	53
L4.44	I	G	D	Y	T	N	D	H	K ^Z	n.d. ^b
L4.45	I	G	E	Y	T	N	D	H	K ^Z	24

L4.46	I	G	D	N	G ^{t-Bu}	N	D	H	K ^Z	76
L4.47	I	G	D	I	W	N	D	H	K ^Z	71
L4.48	I	G	D	N	W	N	D	H	K ^Z	68
L4.49	I	G	D	Q	W	N	D	H	K ^Z	78
L4.50	I	G	D	S	W	N	D	H	K ^Z	71
L4.51	I	G	D	Y	W	N	D	H	K ^Z	70
L4.52	I	G	D	Q	Y	N	D	H	K ^Z	78
L4.53	I	G	D	S	Y	N	D	H	K ^Z	72
L4.54	I	G	D	Y	Y	N	D	H	K ^Z	69
L4.55	I	G	D	I	F	Q	D	H	K ^Z	35
L4.56	I	G	D	I	I	Q	D	H	K ^Z	19
L4.57	I	G	D	N	I	Q	D	H	K ^Z	12
L4.58	I	G	D	Y	I	Q	D	H	K ^Z	20
L4.59	I	G	D	N	I	S	D	H	K ^Z	13
L4.60	I	G	D	L	L	S	D	H	K ^Z	20
L4.61	I	G	D	N	L	S	D	H	K ^Z	6
L4.62	I	G	D	I	T	S	D	H	K ^Z	21
L4.63	I	G	D	L	L	N	E	H	K ^Z	25
L4.64	I	G	D	N	I	N	E	H	K ^Z	30
L4.65	I	G	D	L	T	N	E	H	K ^Z	32
L4.66	I	G	D	Y	T	N	E	H	K ^Z	18
L4.67	I	G	D	Y	W	N	E	H	K ^Z	16
L4.68	I	G	D	Q	Y	N	E	H	K ^Z	24
L4.69	I	G	D	S	Y	N	E	H	K ^Z	18
L4.70	I	G	D	Y	Y	Q	E	H	K ^Z	18
L4.71	I	G	D	L	L	S	E	H	K ^Z	19
L4.72	I	G	D	Y	F	N	D	Y	K ^Z	44
L4.73	I	G	D	I	I	N	D	Y	K ^Z	34
L4.74	I	G	D	L	I	N	D	Y	K ^Z	39
L4.75	I	G	E	N	I	N	D	Y	K ^Z	-1
L4.76	I	G	D	Q	I	N	D	Y	K ^Z	24
L4.77	I	G	D	S	I	N	D	Y	K ^Z	31
L4.78	I	G	D	I	L	N	D	Y	K ^Z	31
L4.79	I	G	D	L	L	N	D	Y	K ^Z	29
L4.80	I	G	D	Y	L	N	D	Y	K ^Z	39
L4.81	I	G	D	I	T	N	D	Y	K ^Z	36
L4.82	I	G	D	L	T	N	D	Y	K ^Z	38
L4.83	I	G	D	N	T	N	D	Y	K ^Z	31
L4.84	I	G	E	Q	T	N	D	Y	K ^Z	1
L4.85	I	G	D	I	W	N	D	Y	K ^Z	34
L4.86	I	G	D	I	Y	N	D	Y	K ^Z	37

L4.87	I	G	D	S	Y	N	D	Y	K ^Z	31
L4.88	I	G	D	Y	F	Q	D	Y	K ^Z	32
L4.89	I	G	D	Y	L	Q	D	Y	K ^Z	33
L4.90	I	G	D	N	I	S	D	Y	K ^Z	14
L4.91	I	G	D	I	W	S	D	Y	K ^Z	14
L4.92	I	G	D	Y	I	N	E	Y	K ^Z	37
L4.93	I	G	D	L	L	N	E	Y	K ^Z	33
L4.94	I	G	D	Y	T	N	E	Y	K ^Z	45
L4.95	I	G	D	I	W	N	E	Y	K ^Z	18
L4.96	I	G	D	I	Y	N	D	Y	K ^Z	n.d. ^a
Library 5										
L5.01	I	Q	D	N	A	N	D	1-Me-H	K ^Z	66
L5.02	I	G	D	L	F	N	D	1-Me-H	K ^Z	77
L5.03	I	G	D	N	I	N	D	1-Me-H	K ^Z	75
L5.04	I	G	D	N	G ^{t-Bu}	N	D	1-Me-H	K ^Z	76
L5.05	I	G	D	Q	W	N	D	1-Me-H	K ^Z	63
L5.06	I	G	D	Q	Y	N	D	1-Me-H	K ^Z	74
L5.07	I	Q	D	N	A	N	D	3-Me-H	K ^Z	80
L5.08	I	G	D	L	F	N	D	3-Me-H	K ^Z	65
L5.09	I	G	D	N	I	N	D	3-Me-H	K ^Z	77
L5.10	I	G	D	N	G ^{t-Bu}	N	D	3-Me-H	K ^Z	81
L5.11	I	G	D	Q	W	N	D	3-Me-H	K ^Z	76
L5.12	I	G	D	Q	Y	N	D	3-Me-H	K ^Z	77
L5.13	I	Q	D	N	A	N	D	F	K ^Z	50
L5.14	I	G	D	L	F	N	D	F	K ^Z	46
L5.15	I	G	D	N	I	N	D	F	K ^Z	57
L5.16	I	G	D	N	G ^{t-Bu}	N	D	F	K ^Z	63
L5.17	I	G	D	Q	W	N	D	F	K ^Z	36
L5.18	I	G	D	Q	Y	N	D	F	K ^Z	41
L5.19	I	G	D	I	A	N	D	H	K ^Z	63
L5.20	I	N	D	I	A	N	D	H	K ^Z	63
L5.21	I	W	D	I	A	N	D	H	K ^Z	82
L5.22	I	G	D	L	A	N	D	H	K ^Z	65
L5.23	I	N	D	L	A	N	D	H	K ^Z	77
L5.24	I	Q	D	L	A	N	D	H	K ^Z	88
L5.25	I	W	D	L	A	N	D	H	K ^Z	88
L5.26	I	G	D	N	A	N	D	H	K ^Z	74
L5.27	I	N	D	N	A	N	D	H	K ^Z	67
L5.28	I	Q	D	N	A	N	D	H	K ^Z	83
L5.29	I	W	D	N	A	N	D	H	K ^Z	79

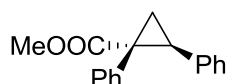
L5.30	I	I	D	W	A	N	D	H	K ^Z	52
L5.31	I	V	D	Y	A	N	D	H	K ^Z	66
L5.32	I	N	D	I	F	N	D	H	K ^Z	86
L5.33	I	G	D	L	F	N	D	H	K ^Z	86
L5.34	I	N	D	L	F	N	D	H	K ^Z	86
L5.35	I	N	D	N	F	N	D	H	K ^Z	87
L5.36	I	Q	D	N	F	N	D	H	K ^Z	90
L5.37	I	G	D	Y	F	N	D	H	K ^Z	87
L5.38	I	N	D	Y	F	N	D	H	K ^Z	88
L5.39	I	Q	D	Y	F	N	D	H	K ^Z	90
L5.40	I	V	D	I	G	N	D	H	K ^Z	29
L5.41	I	Q	D	L	G	N	D	H	K ^Z	71
L5.42	I	V	D	L	G	N	D	H	K ^Z	32
L5.43	I	F	D	N	G	N	D	H	K ^Z	40
L5.44	I	F	D	Y	G	N	D	H	K ^Z	56
L5.45	I	G	D	Y	G	N	D	H	K ^Z	48
L5.46	I	G	D	I	I	N	D	H	K ^Z	84
L5.47	I	G	D	N	I	N	D	H	K ^Z	88
L5.48	I	Q	D	N	I	N	D	H	K ^Z	94
L5.49	I	G	D	W	I	N	D	H	K ^Z	81
L5.50	I	G	D	A	L	N	D	H	K ^Z	80
L5.51	I	W	D	T	L	N	D	H	K ^Z	91
L5.52	I	G	D	W	L	N	D	H	K ^Z	73
L5.53	I	G	D	L	N	N	D	H	K ^Z	69
L5.54	I	Q	D	Q	N	N	D	H	K ^Z	83
L5.55	I	G	D	Y	N	N	D	H	K ^Z	72
L5.56	I	F	D	I	S	N	D	H	K ^Z	76
L5.57	I	F	D	L	S	N	D	H	K ^Z	76
L5.58	I	F	D	N	S	N	D	H	K ^Z	77
L5.59	I	F	D	Y	S	N	D	H	K ^Z	83
L5.60	I	Q	D	L	T	N	D	H	K ^Z	95
L5.61	I	Q	D	N	T	N	D	H	K ^Z	92
L5.62	I	G	D	Y	T	N	D	H	K ^Z	77
L5.63	I	Q	D	I	G ^{<i>t</i>-Bu}	N	D	H	K ^Z	92
L5.64	I	Q	D	L	G ^{<i>t</i>-Bu}	N	D	H	K ^Z	96
L5.65	I	G	D	N	G ^{<i>t</i>-Bu}	N	D	H	K ^Z	90
L5.66	I	Q	D	N	G ^{<i>t</i>-Bu}	N	D	H	K ^Z	96
L5.67	I	Q	D	Y	G ^{<i>t</i>-Bu}	N	D	H	K ^Z	97
L5.68	I	W	D	I	V	N	D	H	K ^Z	88
L5.69	I	W	D	L	V	N	D	H	K ^Z	90
L5.70	I	W	D	T	V	N	D	H	K ^Z	90

L5.71	I	W	D	Y	V	N	D	H	K ^Z	89
L5.72	I	Q	D	L	W	N	D	H	K ^Z	93
L5.73	I	Q	D	N	W	N	D	H	K ^Z	94
L5.74	I	G	D	Q	W	N	D	H	K ^Z	84
L5.75	I	Q	D	Q	W	N	D	H	K ^Z	95
L5.76	I	G	D	W	W	N	D	H	K ^Z	81
L5.77	I	G	D	Q	Y	N	D	H	K ^Z	88
L5.78	I	Q	D	Q	Y	N	D	H	K ^Z	96
L5.79	I	G	D	W	Y	N	D	H	K ^Z	82
L5.80	I	Q	D	N	A	N	D	M	K ^Z	49
L5.81	I	G	D	L	F	N	D	M	K ^Z	66
L5.82	I	G	D	N	I	N	D	M	K ^Z	58
L5.83	I	G	D	N	G ^{t-Bu}	N	D	M	K ^Z	58
L5.84	I	G	D	Q	W	N	D	M	K ^Z	53
L5.85	I	G	D	Q	Y	N	D	M	K ^Z	62
L5.86	I	Q	D	H	A	N	D	T	K ^Z	81
L5.87	I	H	D	N	A	N	D	T	K ^Z	48
L5.88	I	Q	D	N	A	N	D	T	K ^Z	62
L5.89	I	G	D	N	H	N	D	T	K ^Z	42
L5.90	I	Q	D	N	H	N	D	T	K ^Z	50
L5.91	K ^Z	N	D	A	A	I	D	A	K ^Z	n.d. ^a
L5.92	K ^Z	T	D	A	A	I	D	A	K ^Z	n.d. ^a
L5.93	K ^Z	N	D	A	A	I	D	A	K ^Z	n.d. ^a
L5.94	K ^Z	T	D	A	A	I	D	A	K ^Z	n.d. ^a
L5.95	I	G	D	N	I	N	D	H	K ^Z	n.d. ^a
L5.96	I	Q	D	N	A	N	D	H	K ^Z	n.d. ^a

^a peptide synthesized on Rink amide resin; purity and mass by MALDI and RP-HPLC

^b defective wells. No metallopeptide catalyst prepared

d. General procedure for Rh-catalyzed cyclopropanations: (1*R*,2*S*)-methyl 1,2-diphenylcyclopropanecarboxylate (2a)



A few beads of the catalyst Rh₂(**L5.78**)(OAc)₂ (~0.15 μmol, 10% of total resin) in trifluoroethanol (100 μL) was stirred at rt in a 4-mL vial. A stock solution of methyl α-diazophenylacetate (5mg in 500 μL 2,2,2-trifluoroethanol) was prepared. Styrene (5.9 mg, 56.8 μmol) was added to the vial containing the catalyst, followed by methyl α-diazophenylacetate solution (100 μL of stock solution, 1 mg, 5.7 μmol). The reaction mixture was allowed to stir at rt until the diazo compound reacted fully. A stock solution of an external standard, bibenzyl

(12.5 mg in 1 mL CHCl₃) was prepared. After the completion of the reaction observed from the complete disappearance of the yellow color, the bibenzyl standard (16.6 µL of stock solution, 0.207 mg, 1.1 µmol) was added and stirred for 10 min. The mixture was concentrated under reduced pressure to remove solvent and excess alkene. The yield (quantitative, ≥ 99%) was then determined by ¹H NMR. Purification by silica gel chromatography using a gradient from pure hexane to 5:95 diethylether/hexane afforded cyclopropane **2a** in 96% enantiomeric excess. Characterization data is consistent with previously published data.^{6,9}

¹H NMR (500 MHz, CDCl₃) δ 7.13–7.11 (m, 3H), 7.07–7.01 (m, 5H), 6.77–6.75 (m, 2H), 3.66 (s, 3H), 3.11 (dd, *J* = 9.5, 7.5 Hz, 1H), 2.14 (dd, *J* = 9.5, 5 Hz, 1H), 1.88 (dd, *J* = 7.5, 5 Hz, 1H)

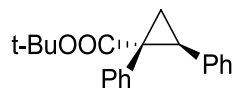
GC-MS *t*_R 16.6 min, (> 95%) *m/z*: [M]⁺ calcd for C₁₇H₁₆O₂: 252.3; found: 252.1

Enantiomeric excess determined by HPLC; Chiralpak IA column, eluting with 97:3 hexanes/CH₂Cl₂, 1.5 mL/min, detection wavelength: 220 nm

(1*R*,2*S*)-methyl 1,2-diphenylcyclopropanecarboxylate *t*_R = 6.7 min and

(1*S*,2*R*)-methyl 1,2-diphenylcyclopropanecarboxylate *t*_R = 7.6 min

(1*R*,2*S*)-*tert*-butyl 1,2-diphenylcyclopropanecarboxylate (2b)



A few beads of the catalyst Rh₂(**L5.78**)(OAc)₂ (ca. 0.15 mol%) in trifluoroethanol (1 mL) was stirred at rt in a 4-mL vial. A mixture of *t*-butyl α-diazophenylacetate (25 mg, 0.115 mmol) and styrene (119.4 mg, 1.15 mmol) in trifluoroethanol (1 mL) were stirred at the same temperature in another 4-mL vial. The suspended on-bead catalyst in solvent was then quickly transferred to the vial containing the substrates and the reaction mixture was allowed to stir at rt until the diazo compound reacted fully. The mixture was concentrated under reduced pressure without further workup and purification of the product by flash chromatography on silica gel using a gradient from 1:99 to 1:9 diethylether/hexane gave 32.9 mg (98%) of the desired (1*R*,2*S*) product. The enantiomeric excess was determined to be 92%. Characterization data is consistent with previously published data.⁶

¹H NMR (500 MHz, CDCl₃) δ 7.10–7.00 (m, 8H), 6.78–6.76 (m, 2H), 3.01 (dd, *J* = 9.0, 7.0 Hz, 1H), 2.06 (dd, *J* = 9.0, 5.0 Hz, 1H), 1.81 (dd, *J* = 7.0, 5.0 Hz, 1H), 1.39 (s, 9H)

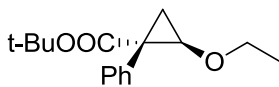
GC-MS *t*_R 17.1 min, (> 95%) *m/z*: [M + H – *t*-Bu]⁺ calcd for C₁₆H₁₄O₂: 238.3; found: 238.1

Enantiomeric excess determined by HPLC; Phenomenex Lux 5u Cellulose-1 column, eluting with 99.75:0.25 hexanes/*i*-PrOH, 1.9 mL/min, detection wavelength: 220 nm

(1*R*,2*S*)-*tert*-butyl 1,2-diphenylcyclopropanecarboxylate *t*_R = 7.3 min and

(1*S*,2*R*)-*tert*-butyl 1,2-diphenylcyclopropanecarboxylate *t*_R = 4.9 min

(1*S*,2*R*)-*tert*-butyl 2-ethoxy-1-phenylcyclopropanecarboxylate (2c)

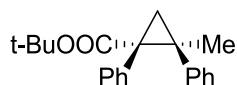


The general procedure was employed using *t*-butyl α -diazophenylacetate on a 4.6 μ mol scale to afford the (1*S*,2*R*) product in quantitative yield and 89% ee. Characterization data is consistent with previously published data.⁶

¹H NMR (500 MHz, CDCl₃) δ 7.34–7.29 (m, 4H), 7.25–7.22 (m, 1H), 3.86 (dd, *J* = 7.0, 4.5 Hz, 1H), 3.58–3.53 (m, 2H), 1.70 (dd, *J* = 7.0, 5.5 Hz, 1H), 1.58–1.56 (m, 1H), 1.38 (s, 9H), 0.98 (t, *J* = 7.0 Hz, 3H)

GC-MS *t*_R 13.4 min, (> 95%) *m/z*: [M + H – *t*-Bu]⁺ calcd for C₁₂H₁₄O₃: 206.2; found: 206.1
Enantiomeric excess determined by HPLC; Phenomenex Lux 5u Cellulose-1 column, eluting with 99.95:0.05 hexanes/*i*-PrOH, 1.9 mL/min, detection wavelength: 220 nm
(1*S*,2*R*)-*tert*-butyl 2-ethoxy-1-phenylcyclopropanecarboxylate *t*_R = 12.8 min and
(1*R*,2*S*)-*tert*-butyl 2-ethoxy-1-phenylcyclopropanecarboxylate *t*_R = 11.1 min

(1*S*,2*S*)-*tert*-butyl 2-methyl-1,2-diphenylcyclopropanecarboxylate (2d)

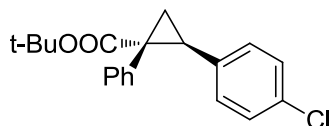


The general procedure was employed using *t*-butyl α -diazophenylacetate on a 4.6 μ mol scale to afford the (1*S*,2*S*) product in quantitative yield and 99% ee. Purification was conducted by preparative tlc (silica gel; 1:9 ether/hexane eluent). Characterization data is consistent with previously published data.⁶

¹H NMR (500 MHz, CDCl₃) δ 7.18–7.16 (m, 2H), 7.09–6.96 (m, 8H), 2.01 (d, *J* = 5.5 Hz, 1H), 1.83 (d, *J* = 5.5 Hz, 1H), 1.68 (s, 3H), 1.44 (s, 9H)

GC-MS *t*_R 17.5 min, (> 95%) *m/z*: [M + H – *t*-Bu]⁺ calcd for C₁₇H₁₆O₂: 252.3; found: 252.1
Enantiomeric excess determined by HPLC; Phenomenex Lux 5u Cellulose-1 column, eluting with 99.9925:0.0075 hexanes/*i*-PrOH, 1.9 mL/min, detection wavelength: 220 nm
(1*S*,2*S*)-*tert*-butyl 2-methyl-1,2-diphenylcyclopropanecarboxylate *t*_R = 11.1 min and
(1*R*,2*R*)-*tert*-butyl 2-methyl-1,2-diphenylcyclopropanecarboxylate *t*_R = 11.9 min

(1*R*,2*S*)-*tert*-butyl 2-(4-chlorophenyl)-1-phenylcyclopropanecarboxylate (2e)



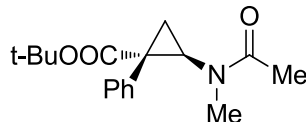
The general procedure was employed using *t*-butyl α -diazophenylacetate on a 4.6 μ mol scale to afford the (1*R*,2*S*) product in quantitative yield and 95% ee. Characterization data is consistent with previously published data.⁶

¹H NMR (500 MHz, CDCl₃) δ 7.14–7.11 (m, 3H), 7.03–6.99 (m, 4H), 6.69–6.67 (m, 2H), 2.97 (dd, *J* = 9.0, 7.0 Hz, 1H), 2.06 (dd, *J* = 9.0, 5.0 Hz, 1H), 1.76 (dd, *J* = 7.0, 5.0 Hz, 1H), 1.38 (s, 9H)

GC-MS *t*_R 18.9 min, (> 95%) *m/z*: [M + H – *t*-Bu]⁺ calcd for C₁₆H₁₃ClO₂: 272.7; found: 272.1
Enantiomeric excess determined by HPLC; Phenomenex Lux 5u Cellulose-1 column, eluting with 99.9:0.1 hexanes/*i*-PrOH, 1.9 mL/min, detection wavelength: 220 nm
(1*R*,2*S*)-*tert*-butyl 2-(4-chlorophenyl)-1-phenylcyclopropanecarboxylate *t*_R = 5.92 min and

(1*S*,2*R*)-*tert*-butyl 2-(4-chlorophenyl)-1-phenylcyclopropanecarboxylate $t_R = 7.06$ min

(1*S*,2*R*)-*tert*-butyl 2-(*N*-methylacetamido)-1-phenylcyclopropanecarboxylate (2f):



A few beads of the catalyst $\text{Rh}_2(\text{L5.67})(\text{OAc})_2$ (12 mg, ca. 0.15 mol%) in trifluoroethanol (4.5 mL) was stirred at rt in a 20-mL vial. A mixture of *t*-butyl α -diazophenylacetate (218 mg, 1 mmol) and *N*-methyl-*N*-vinylacetamide (991 mg, 10 mmol) in trifluoroethanol (4.5 mL) were stirred at the same temperature in another 20-mL vial. The suspended on-bead catalyst in solvent was then quickly transferred to the vial containing the substrates and the reaction mixture was allowed to stir at rt until the diazo compound reacted fully. The mixture was concentrated under reduced pressure without further workup and purification of the product by flash chromatography on silica gel using a gradient from 2:8 to 7:3 diethylether/hexane gave 267 mg (92%) of the desired (1*S*,2*R*) product. The enantiomeric excess was determined to be 95%. Characterization data is consistent with previously published data.⁶

Characterization data as a 56:44 mixture of amide rotamers:

¹H NMR (400 MHz, CDCl₃) δ 7.32–7.22 (m, 5H), 3.89 (dd, $J = 8.0, 4.0$ Hz, 0.43H), 3.71 (dd, $J = 8.0, 4.0$ Hz, 0.55H), 2.37, 2.35 (s, 3H), 2.29 (s, 1.57H), 2.04–1.94 (m, 1.56H), 1.91 (s, 1.32H), 1.81–1.73 (m, 0.64H), 1.40, 1.39 (s, 9H)

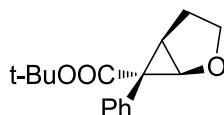
¹³C NMR (400 MHz, CDCl₃) δ 172.6, 172.6, 171.8, 171.3, 134.9, 133.7, 131.4, 130.6, 128.6, 128.0, 127.8, 127.4, 81.7, 81.2, 46.3, 44.5, 35.3, 35.1, 35.0, 31.6, 28.1, 22.9, 22.5, 19.3, 18.0

GC-MS t_R 17.4 min, (> 95%) m/z : [M + H – *t*-Bu]⁺ calcd for C₁₃H₁₅NO₃: 233.2; found: 233.1

Enantiomeric excess determined by HPLC; Chiralpak IA column, eluting with 70:30 hexanes/CH₂Cl₂, 1.7 mL/min, detection wavelength: 254 nm

(1*S*,2*R*)-*tert*-butyl 2-(*N*-methylacetamido)-1-phenylcyclopropanecarboxylate $t_R = 12.4$ min and (1*R*,2*S*)-*tert*-butyl 2-(*N*-methylacetamido)-1-phenylcyclopropanecarboxylate $t_R = 11.27$ min.

(1*R*,5*R*,6*S*)-*tert*-butyl 6-phenyl-2-oxa-bicyclo[3.1.0]hexane-6-carboxylate (2g)



The general procedure was employed using *t*-butyl α -diazophenylacetate on a 4.6 μmol scale to afford the (1*R*,6*S*) product in quantitative yield and 94% ee. Characterization data is consistent with previously published data.⁶

¹H NMR (500 MHz, CDCl₃) δ 7.36–7.27 (m, 5H), 4.46 (d, $J = 5.5$ Hz, 1H), 3.79–3.74 (m, 1H), 2.56 (dd, $J = 6.0, 6.0$ Hz, 1H), 2.41 (ddd, $J = 9.0, 9.0, 9.0$ Hz, 1H), 2.24–2.20 (m, 1H), 1.87–1.82 (m, 1H), 1.32 (s, 9H)

GC-MS t_R 14.6 min, (> 95%) m/z : [M + H – *t*-Bu]⁺ calcd for C₁₂H₁₂O₃: 204.2; found: 204.1

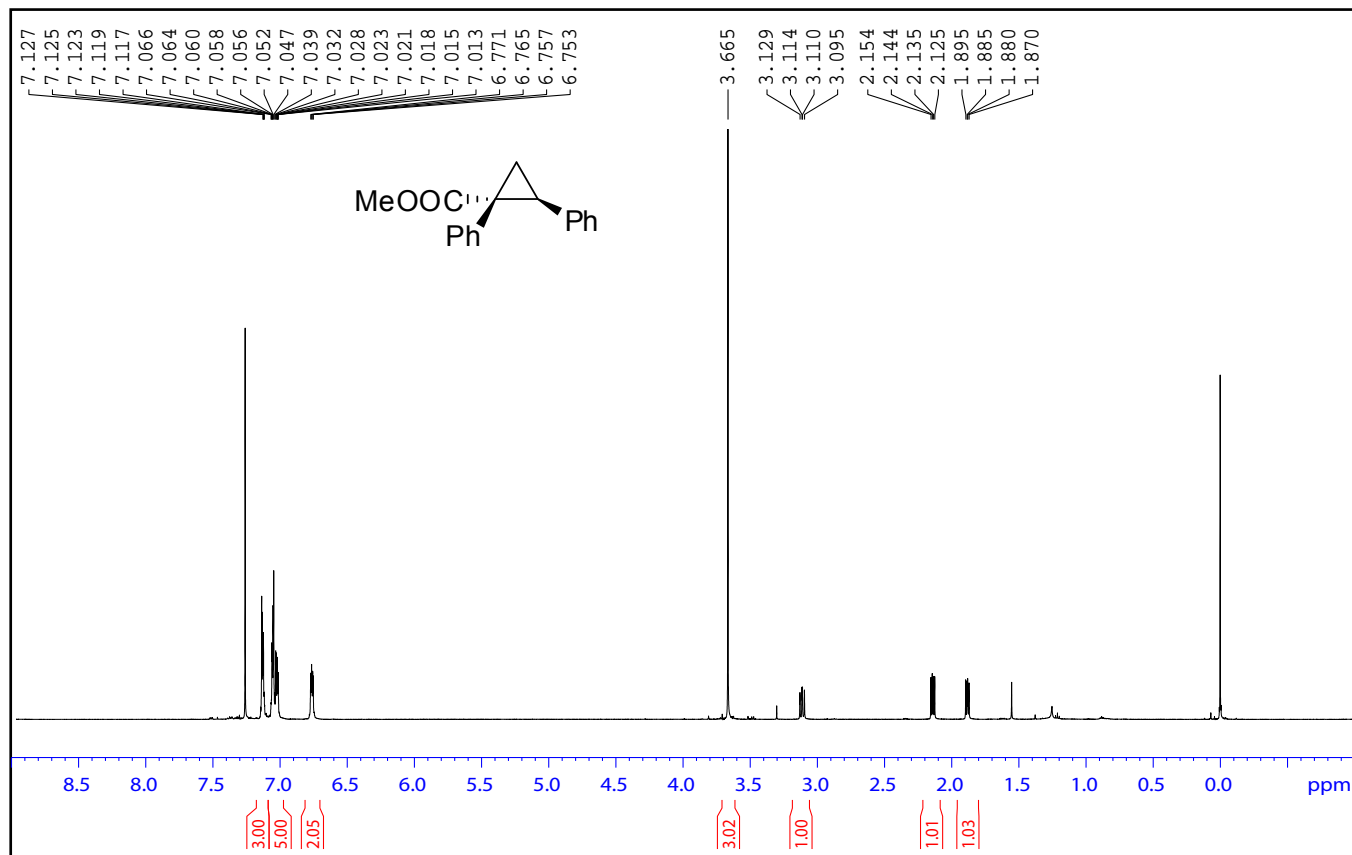
Enantiomeric excess determined by HPLC; Chiralpak IA column, eluting with 99.9925:0.0075 hexanes/*i*-PrOH, 1.7 mL/min, detection wavelength: 220 nm

(1*R*,6*S*)-*tert*-butyl 6-phenyl-2-oxa-bicyclo[3.1.0]hexane-6-carboxylate $t_R = 13.9$ min and

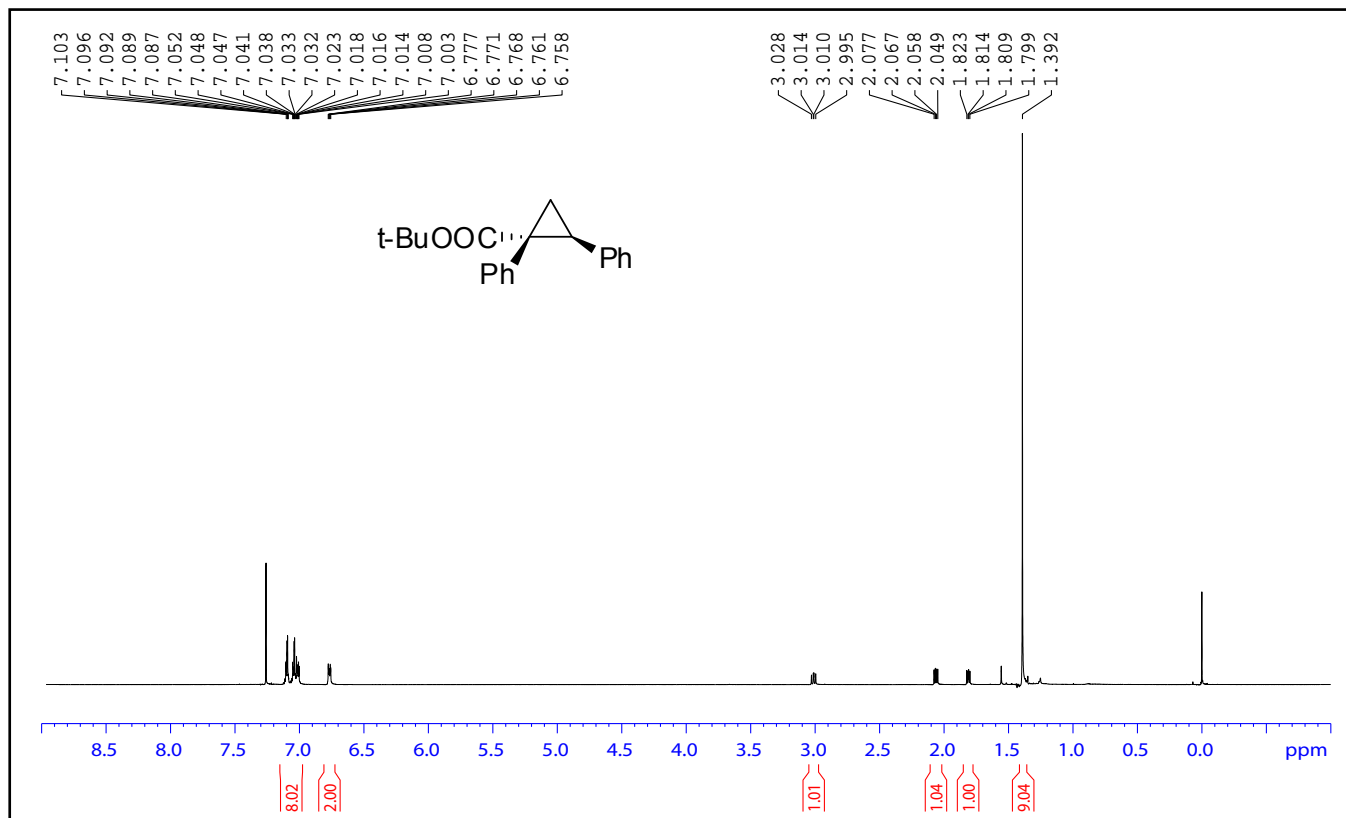
(1*S*,6*R*)-*tert*-butyl 6-phenyl-2-oxa-bicyclo[3.1.0]hexane-6-carboxylate $t_R = 17.6$ min

e. NMR spectra of cyclopropane products:

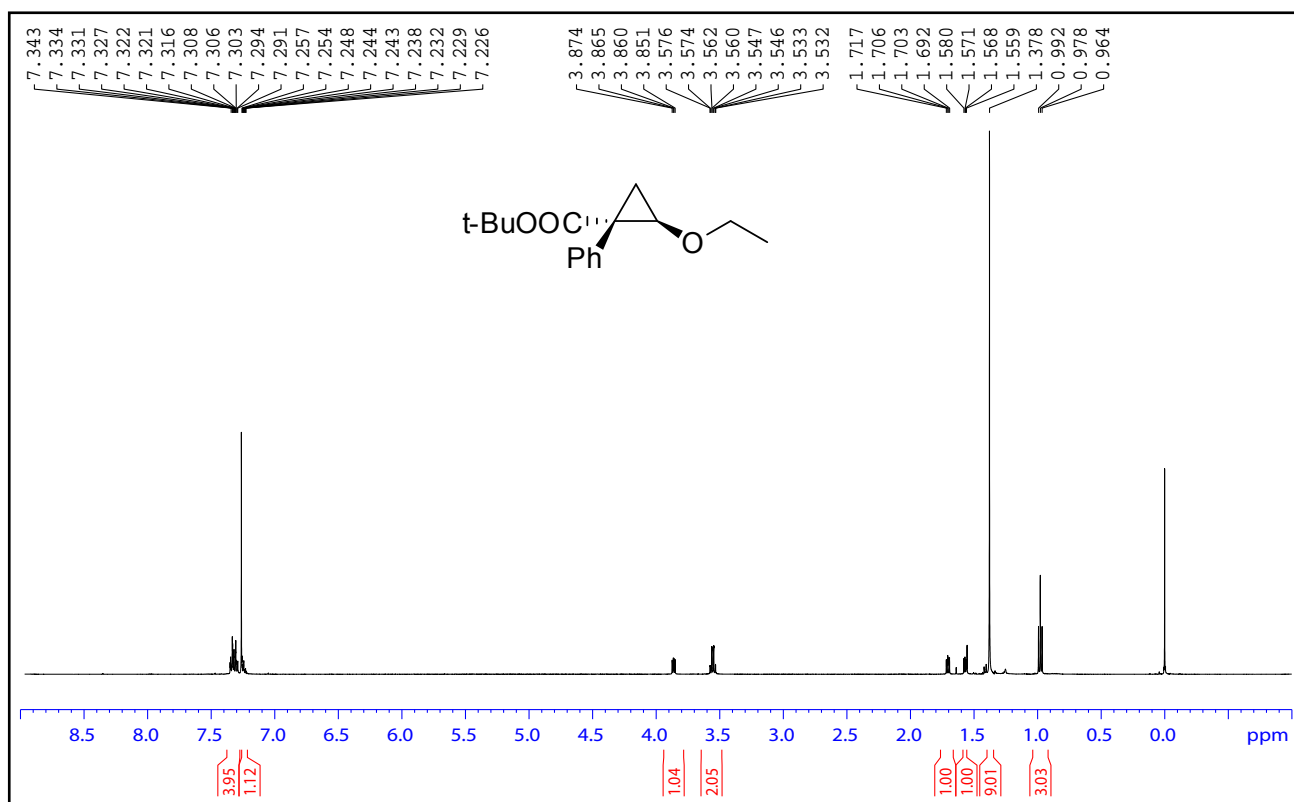
(1*R*,2*S*)-methyl 1,2-diphenylcyclopropanecarboxylate (**2a**)



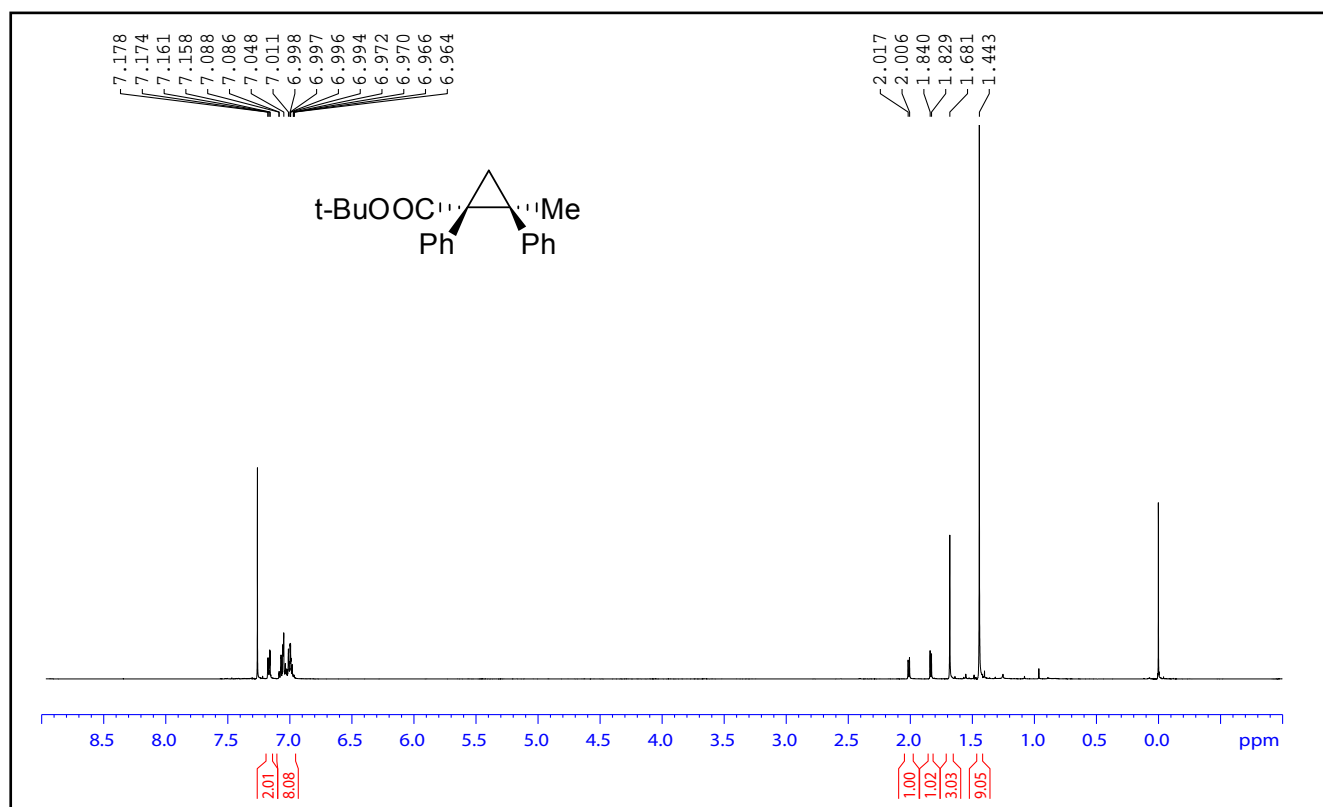
(1*R*,2*S*)-tert-butyl 1,2-diphenylcyclopropanecarboxylate (**2b**)



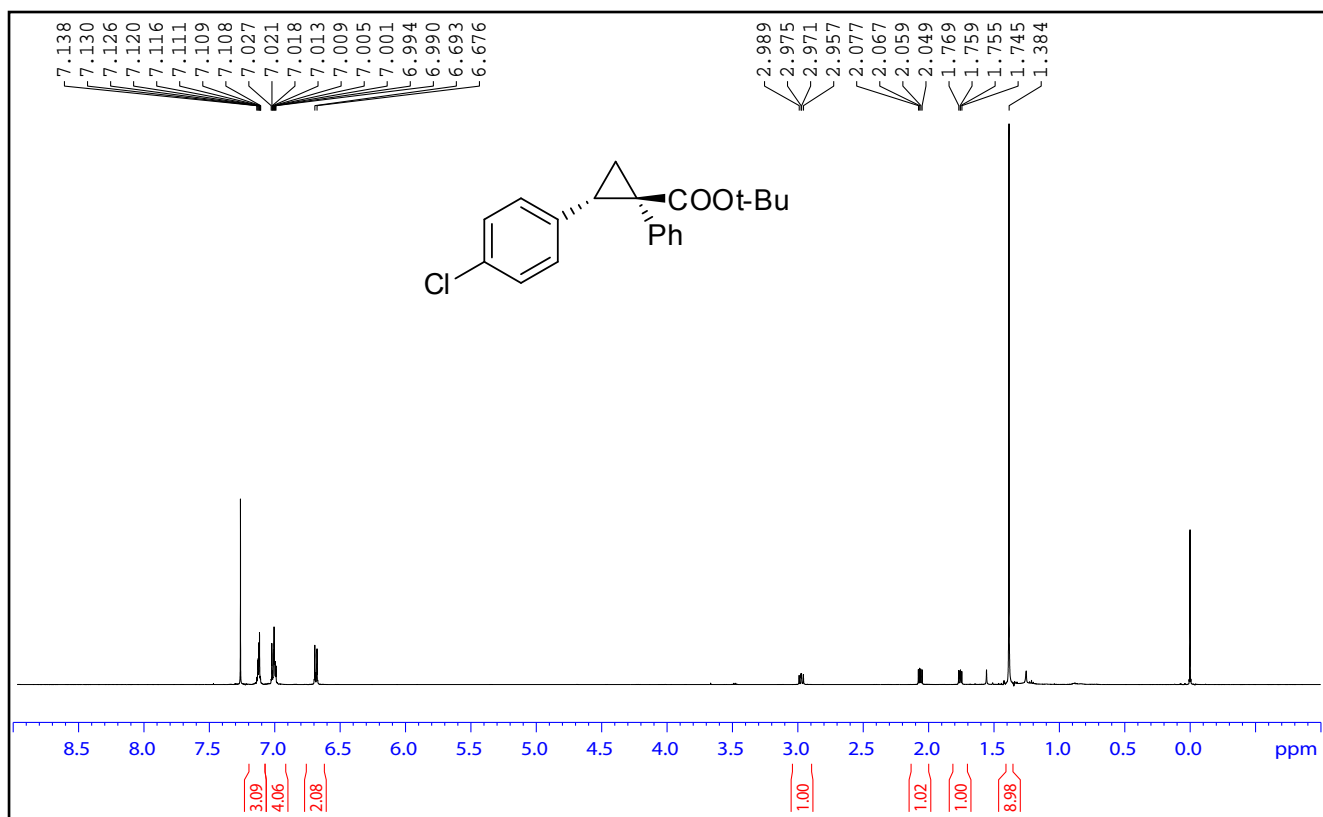
(1*S*,2*R*)-*tert*-butyl 2-ethoxy-1-phenylcyclopropanecarboxylate (**2c**)



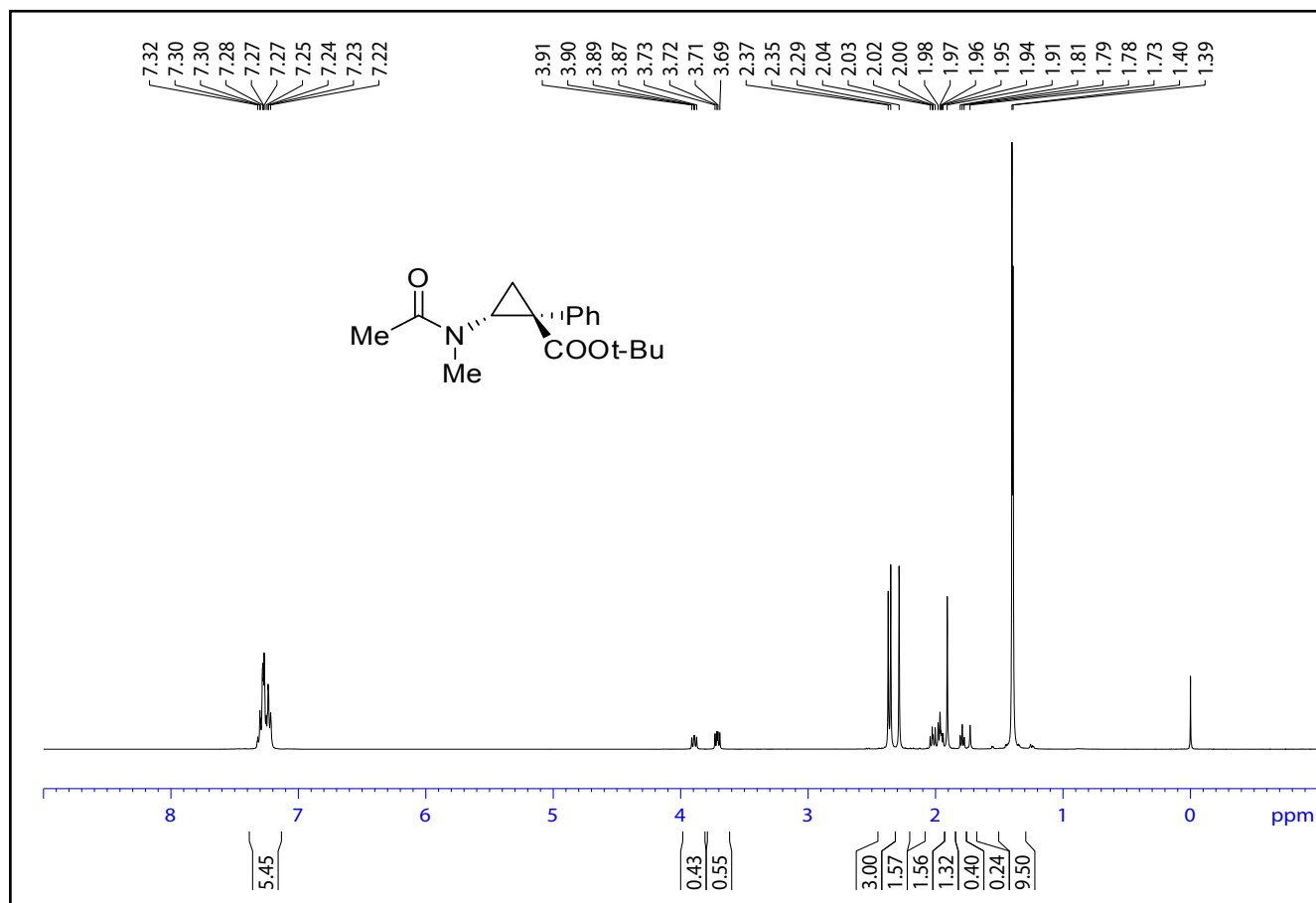
(1*S*,2*S*)-*tert*-butyl 2-methyl-1,2-diphenylcyclopropanecarboxylate (**2d**)



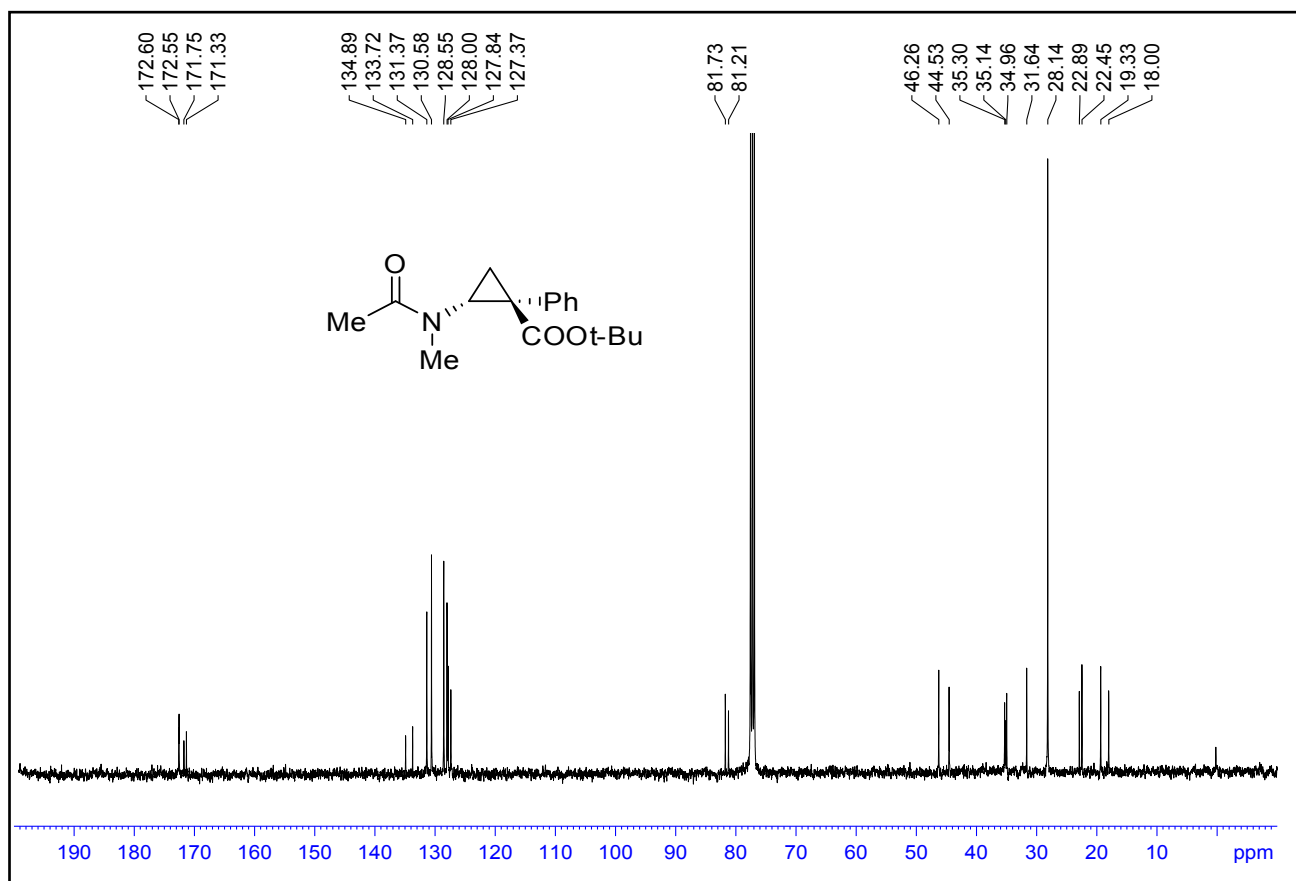
(1*R*,2*S*)-*tert*-butyl 2-(4-chlorophenyl)-1-phenylcyclopropanecarboxylate (**2e**)



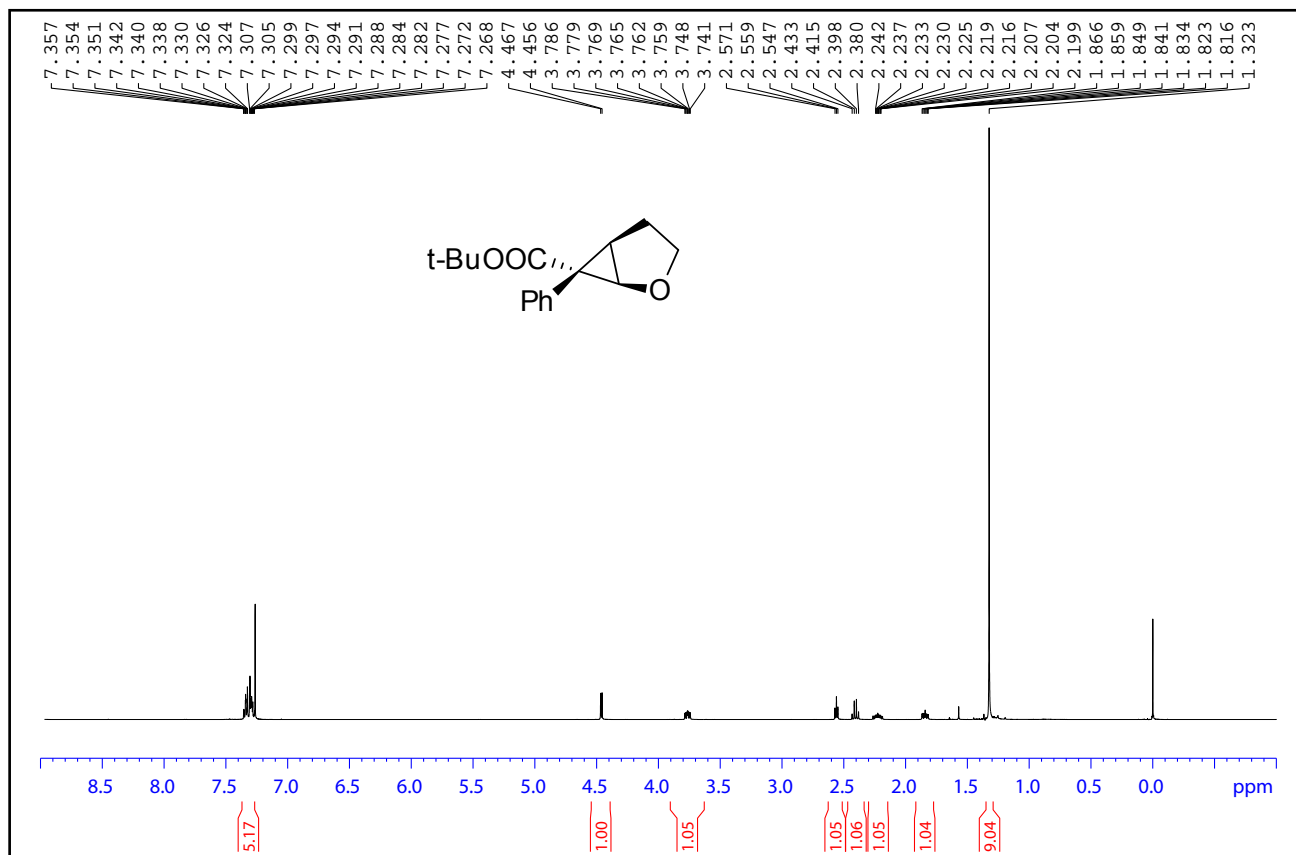
(1*S*,2*R*)-*tert*-butyl 2-(*N*-methylacetamido)-1-phenylcyclopropanecarboxylate (**2f**)



(1*S*,2*R*)-*tert*-butyl 2-(*N*-methylacetamido)-1-phenylcyclopropanecarboxylate (**2f**)

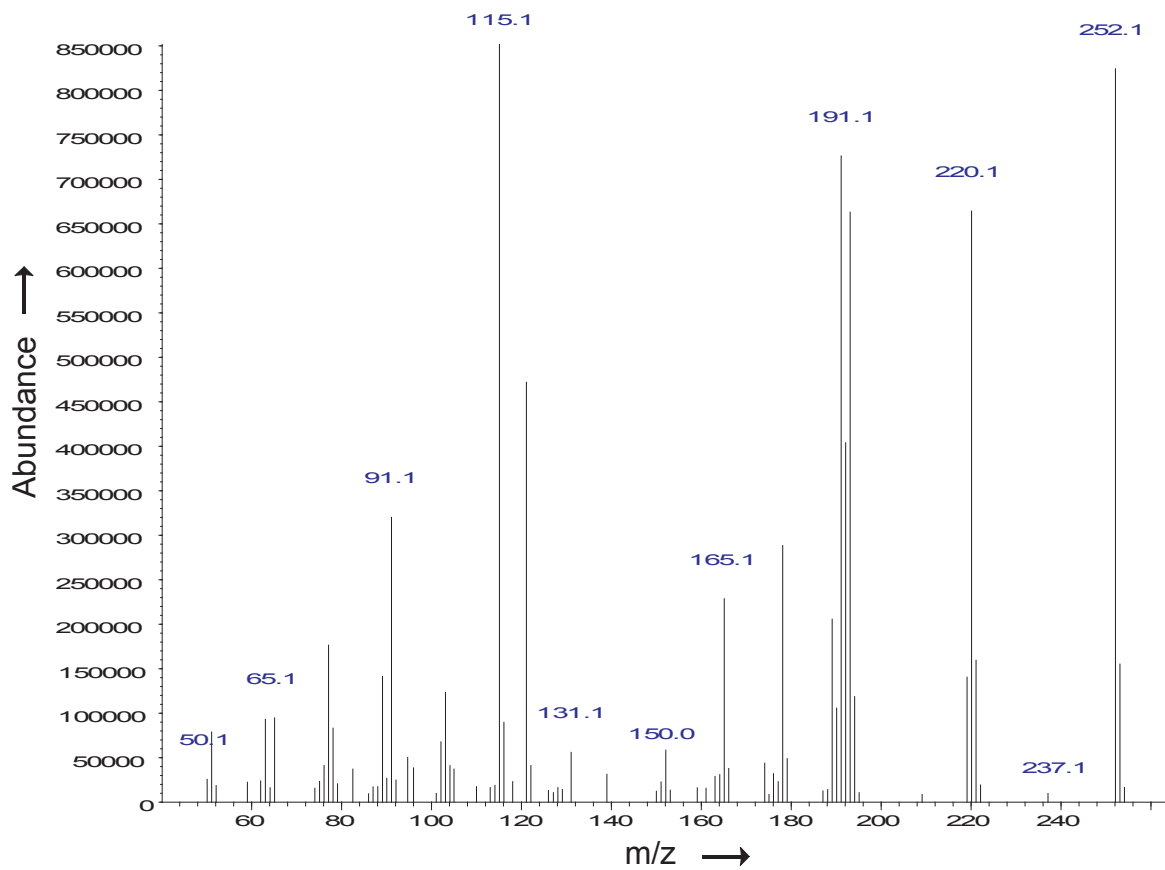
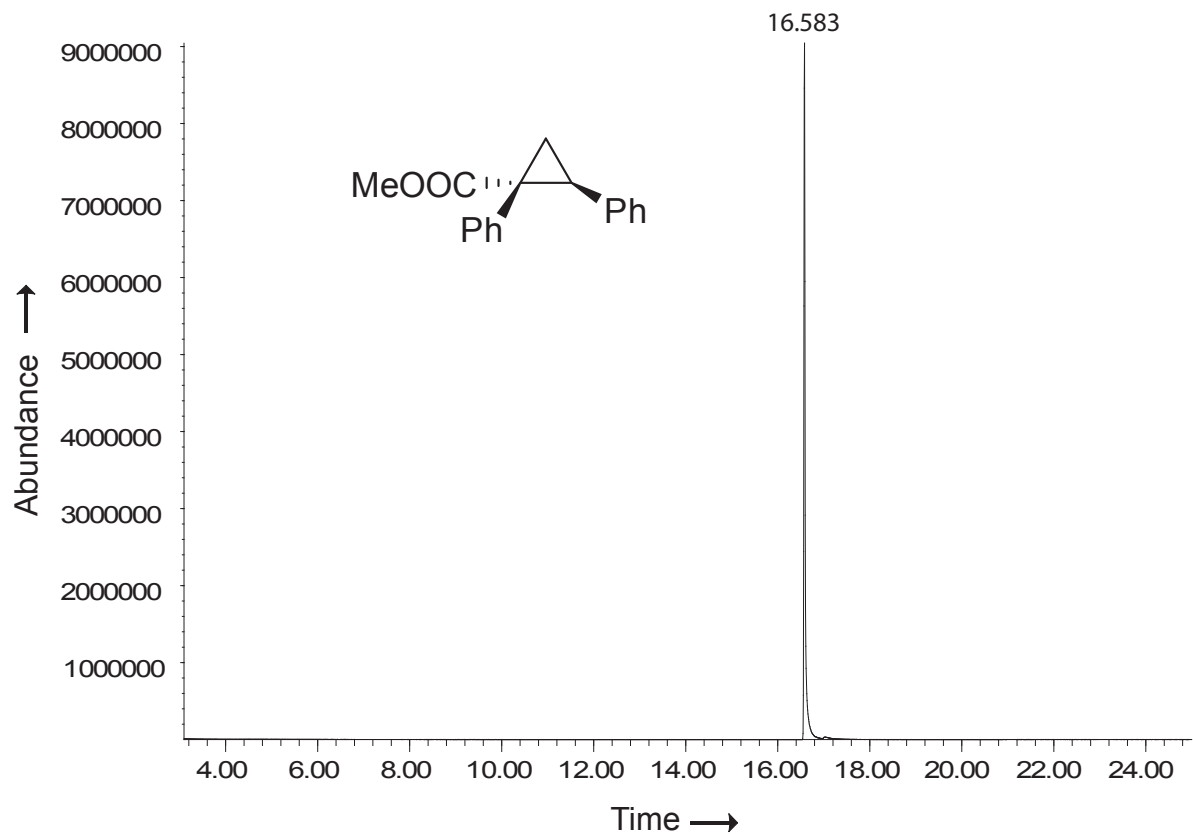


(1*R*,5*R*,6*S*)-*tert*-butyl 6-phenyl-2-oxabicyclo[3.1.0]hexane-6-carboxylate (**2g**)

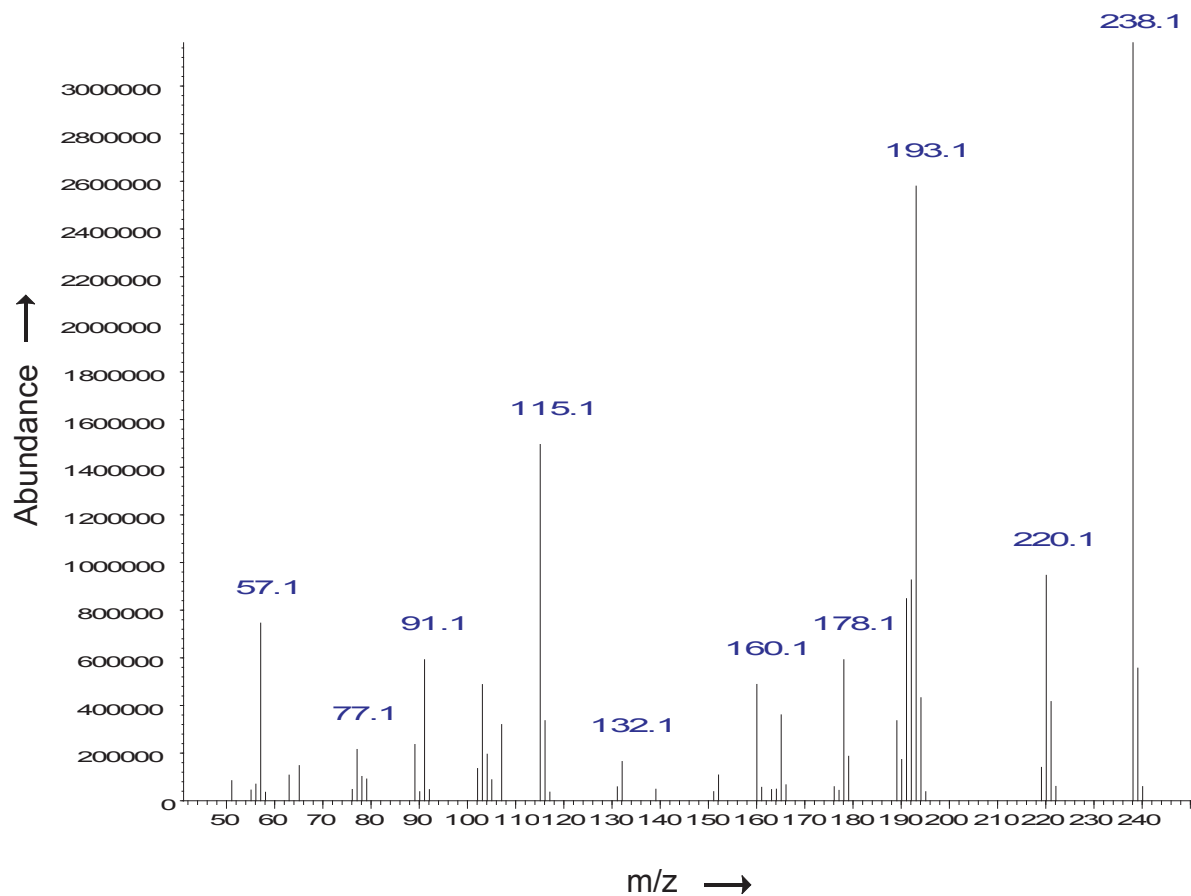
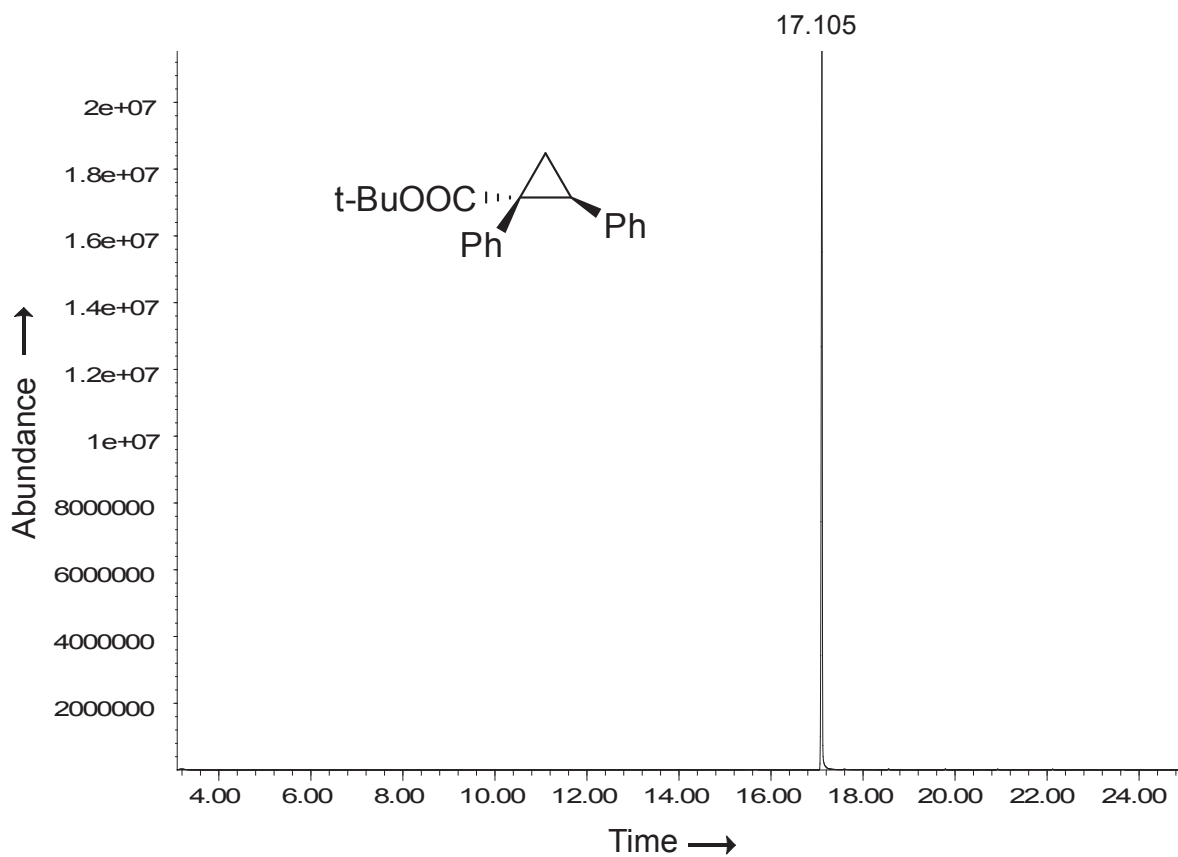


f. GC-MS spectra of cyclopropane products:

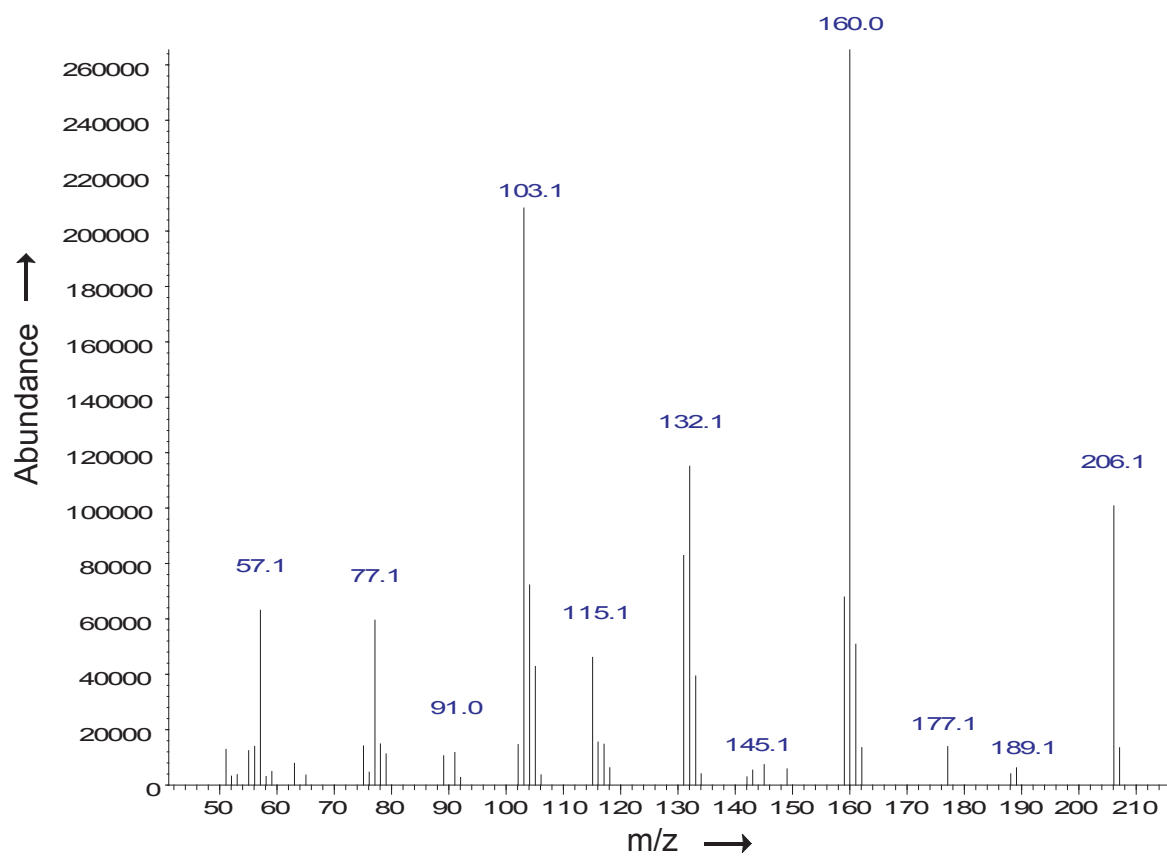
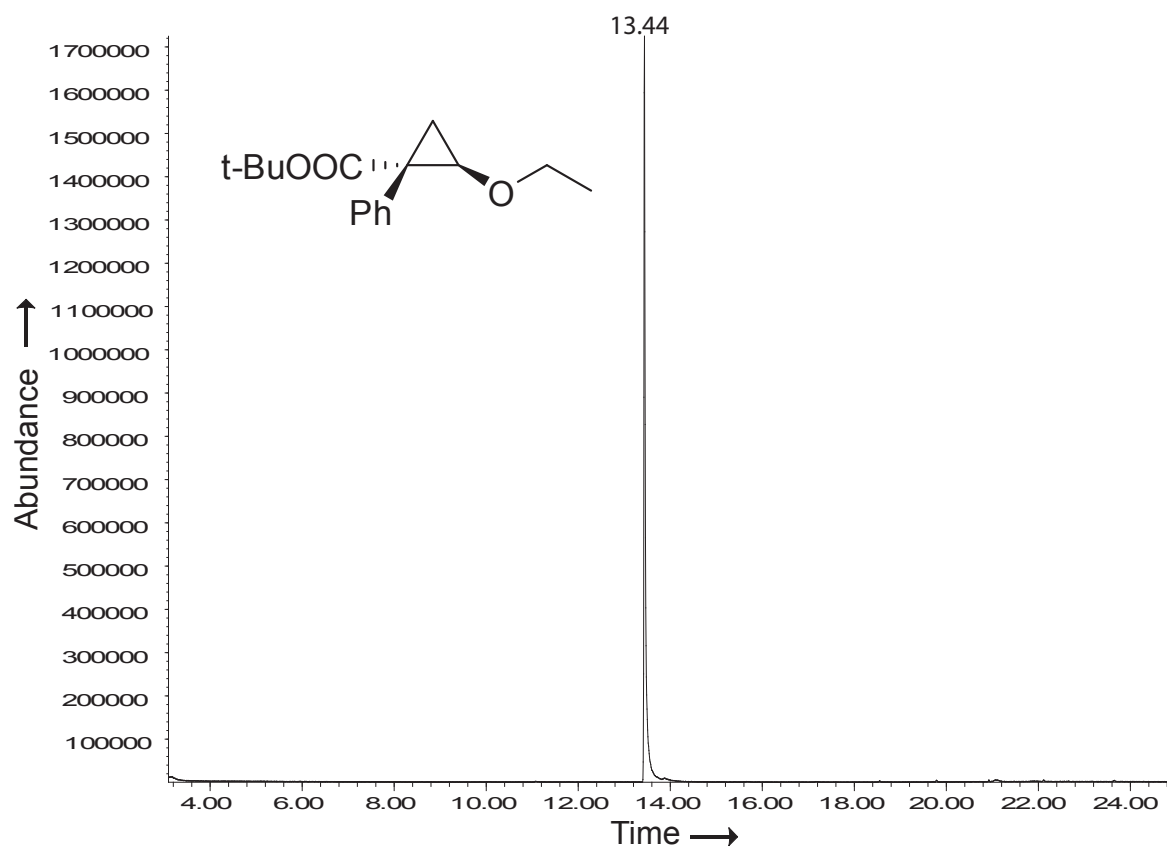
(1*R*,2*S*)-methyl 1,2-diphenylcyclopropanecarboxylate (**2a**)



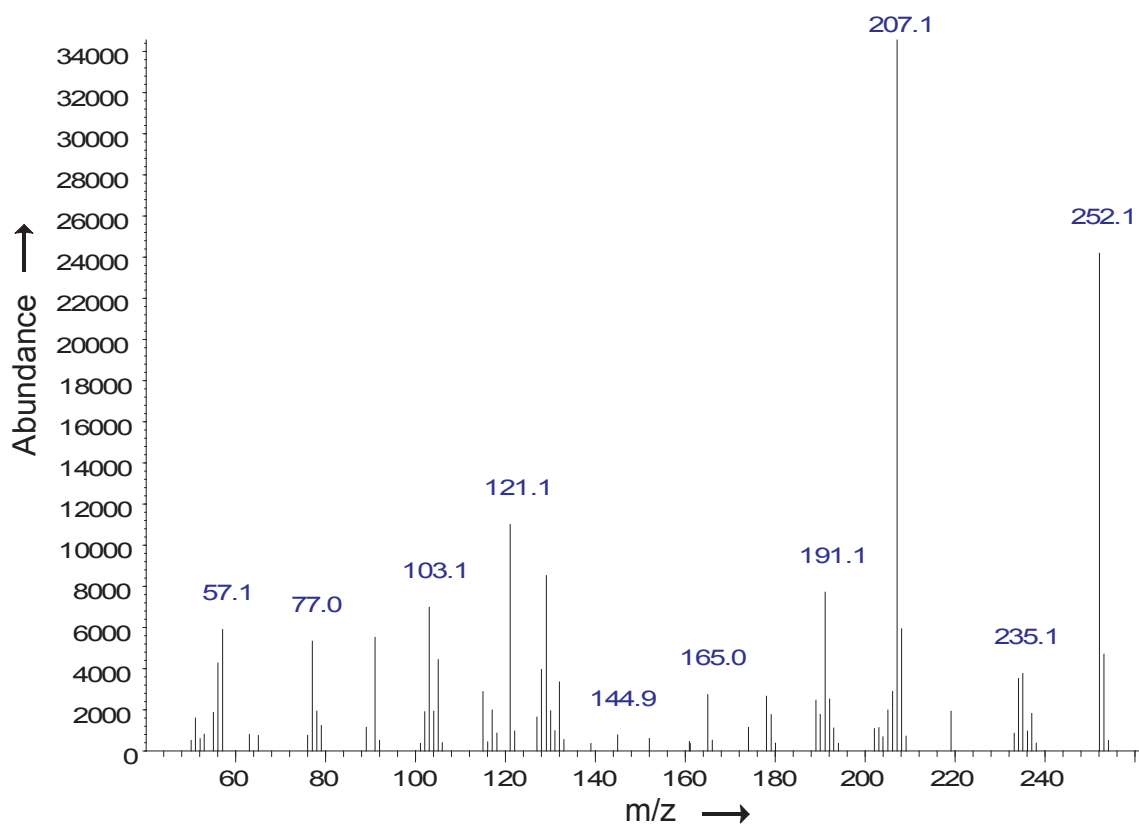
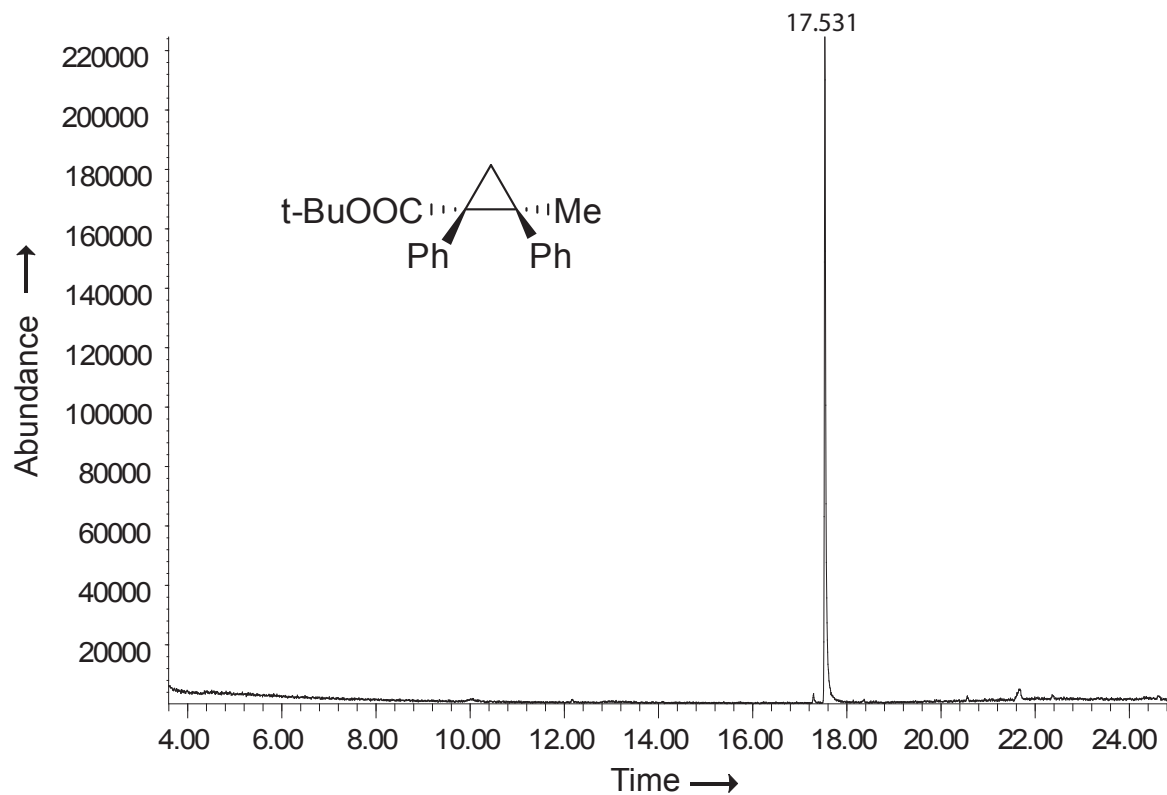
(1*R*,2*S*)-*tert*-butyl 1,2-diphenylcyclopropanecarboxylate (**2b**)



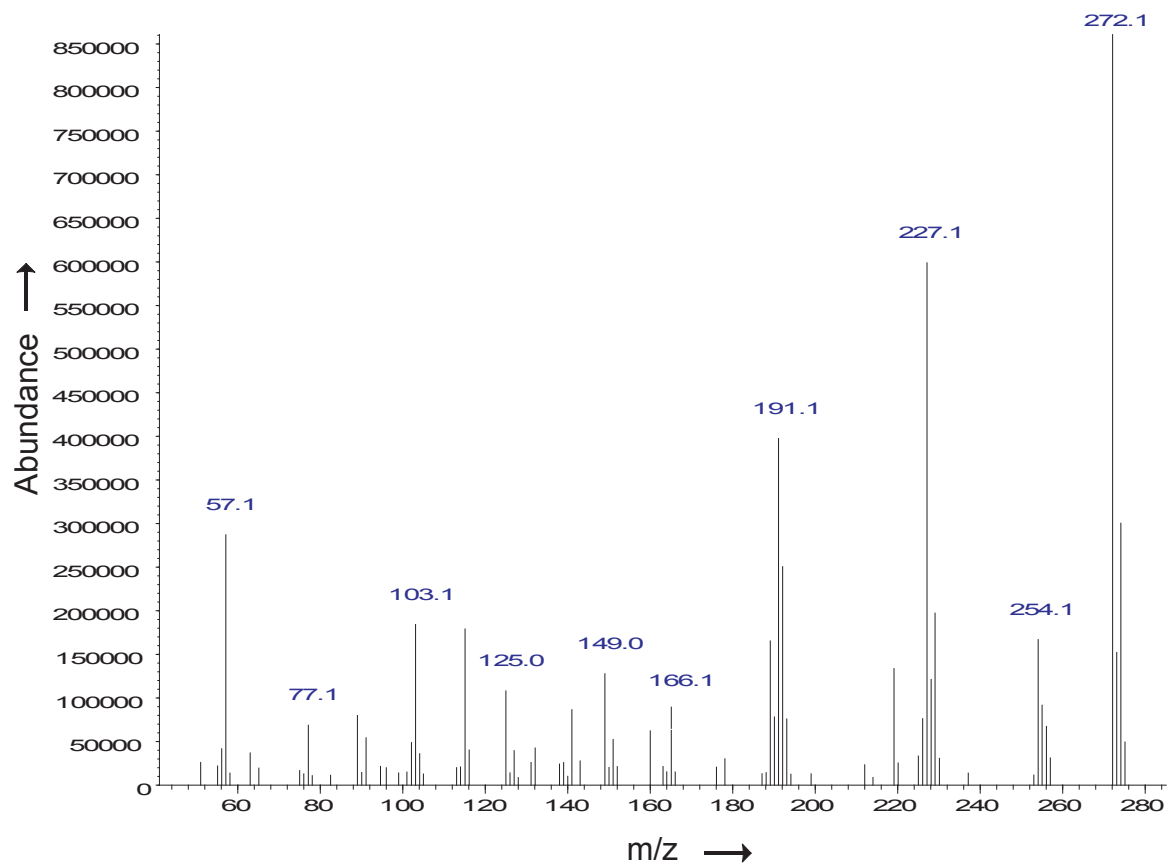
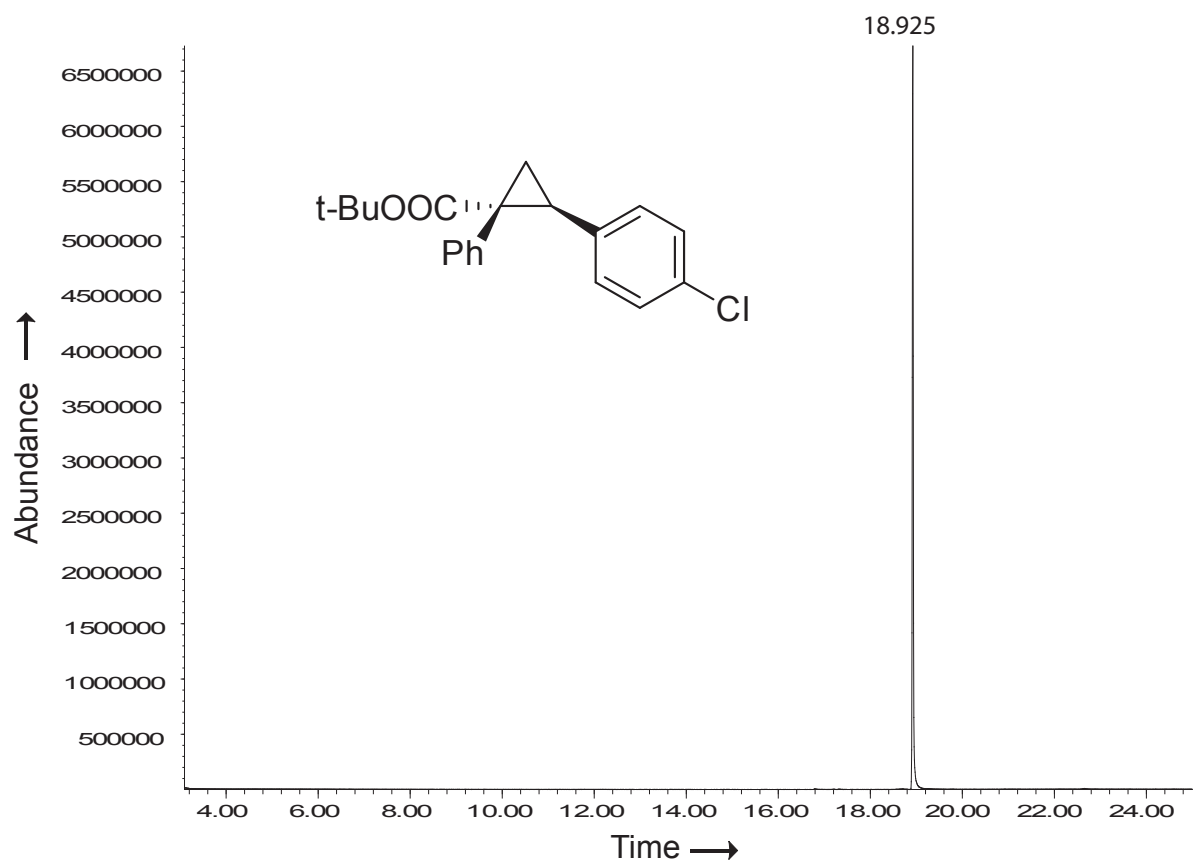
(1*S*,2*R*)-*tert*-butyl 2-ethoxy-1-phenylcyclopropanecarboxylate (**2c**)



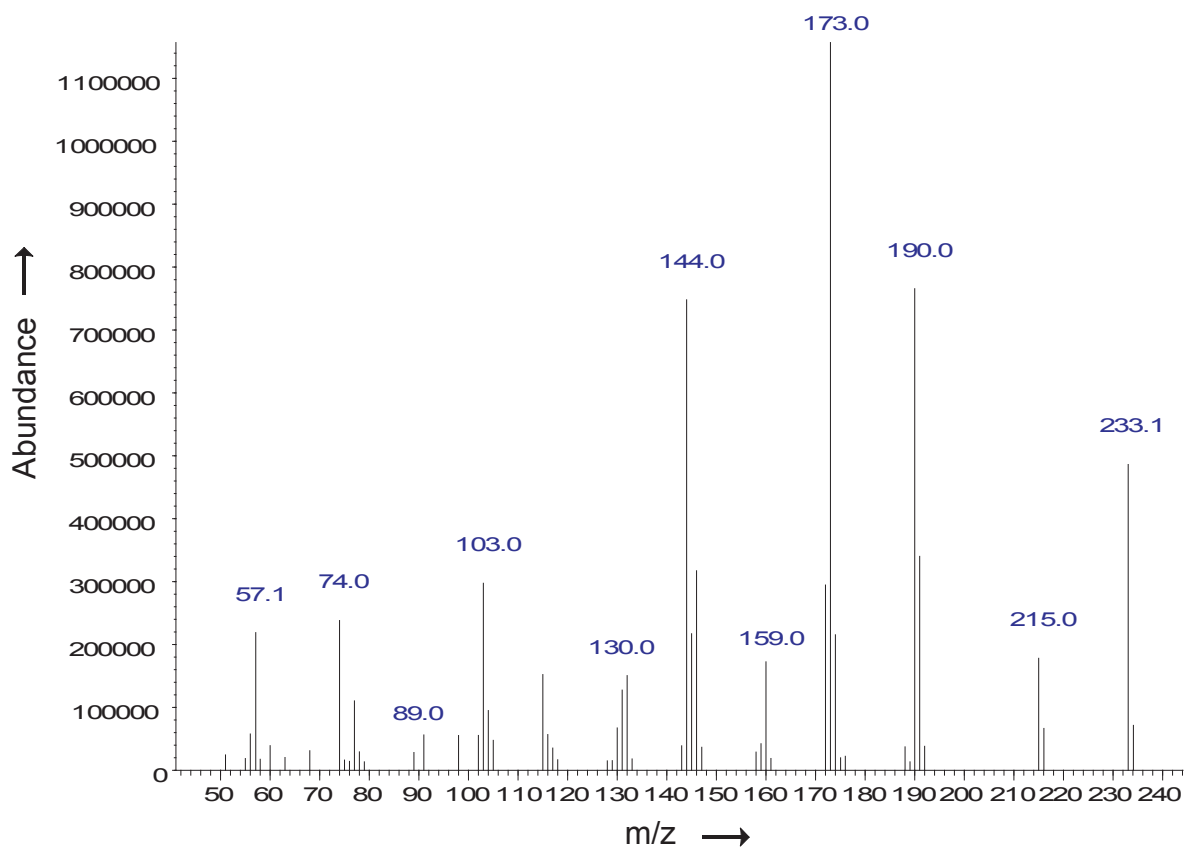
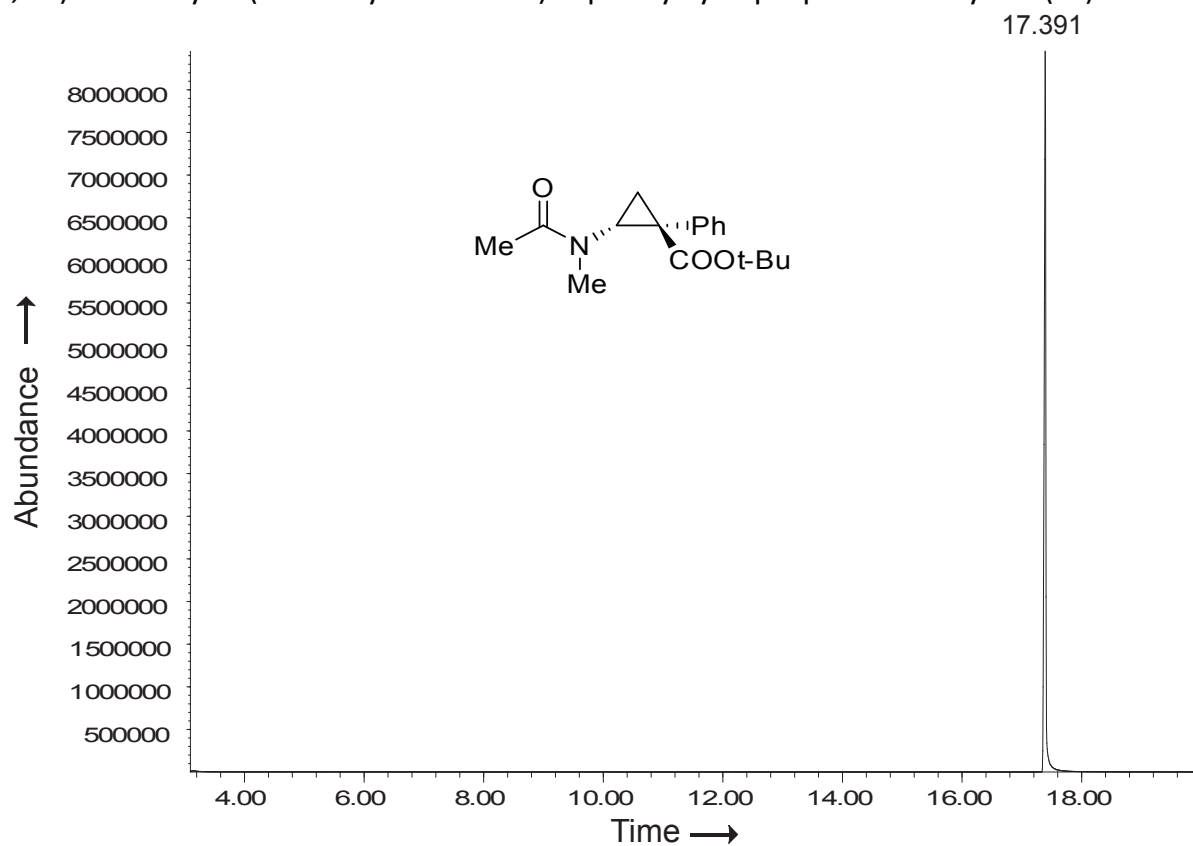
(1*S*,2*S*)-*tert*-butyl 2-methyl-1,2-diphenylcyclopropanecarboxylate (**2d**)



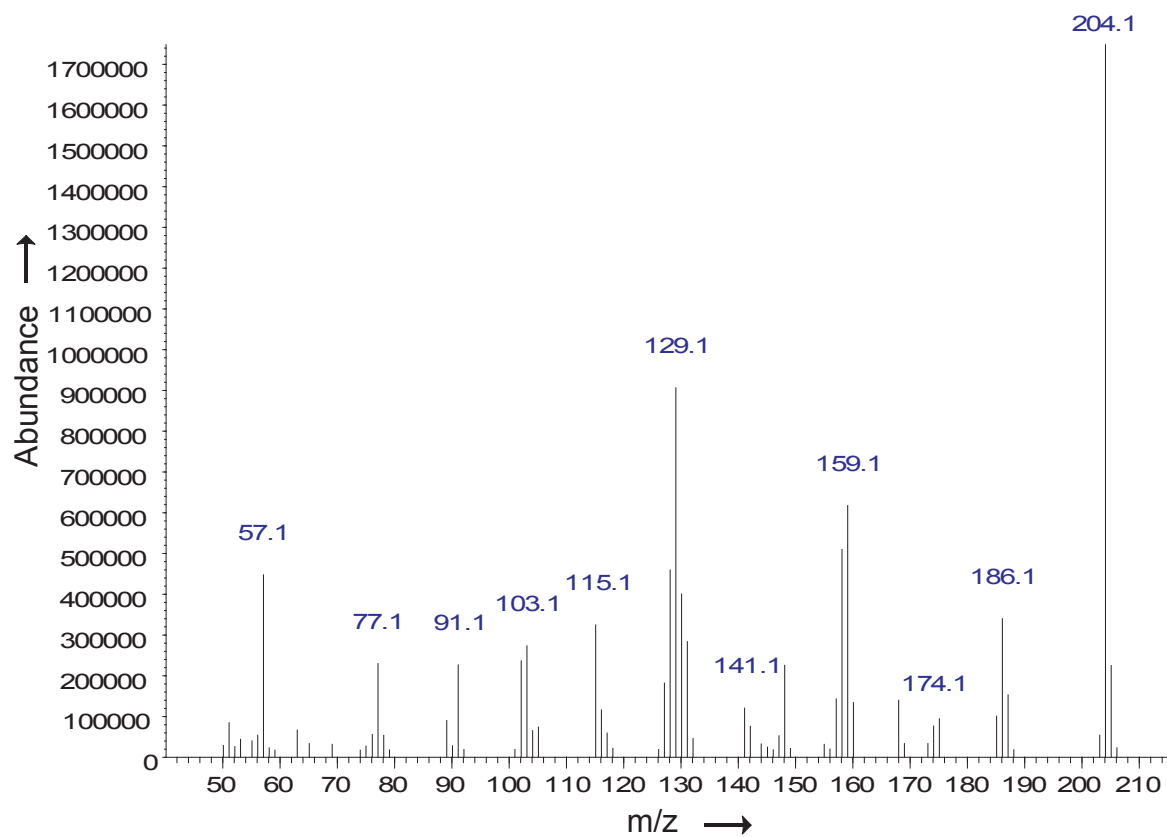
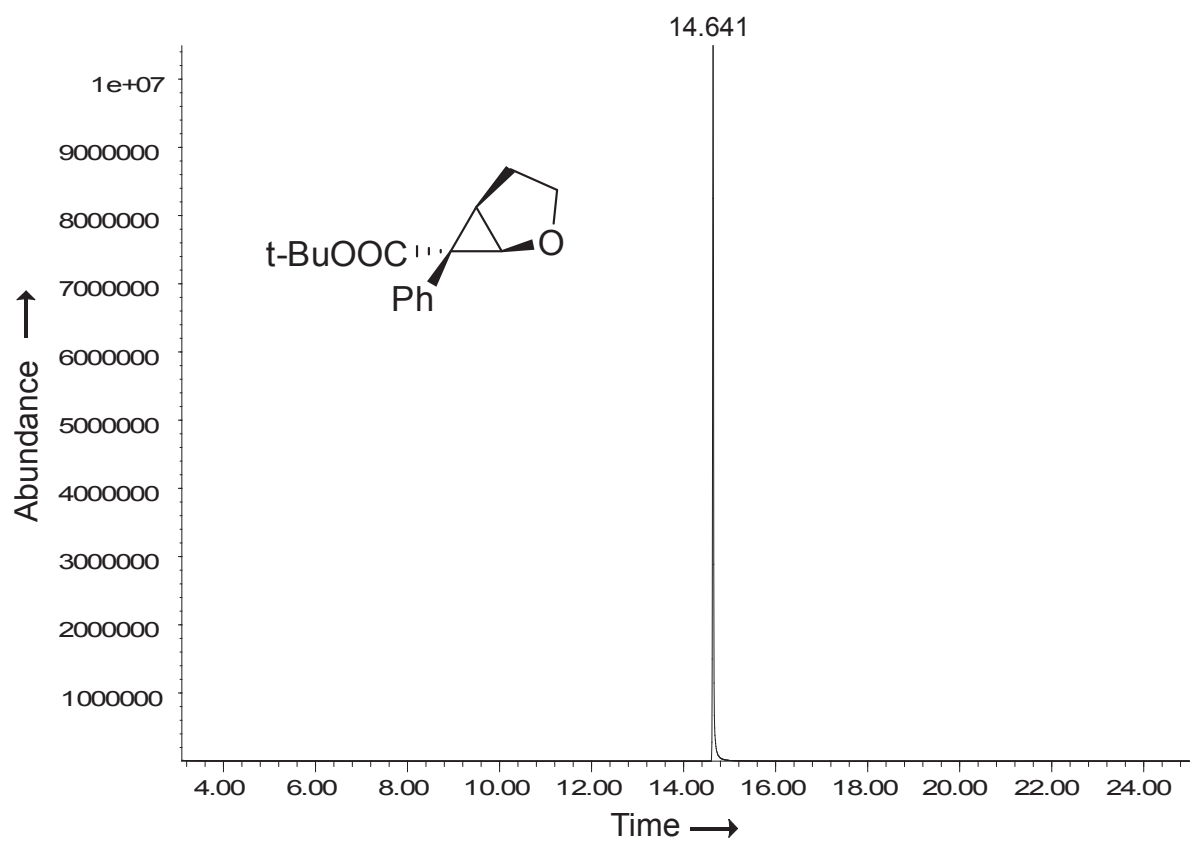
(1*R*,2*S*)-*tert*-butyl 2-(4-chlorophenyl)-1-phenylcyclopropanecarboxylate (**2e**)



(1*S*,2*R*)-*tert*-butyl 2-(*N*-methylacetamido)-1-phenylcyclopropanecarboxylate (**2f**)

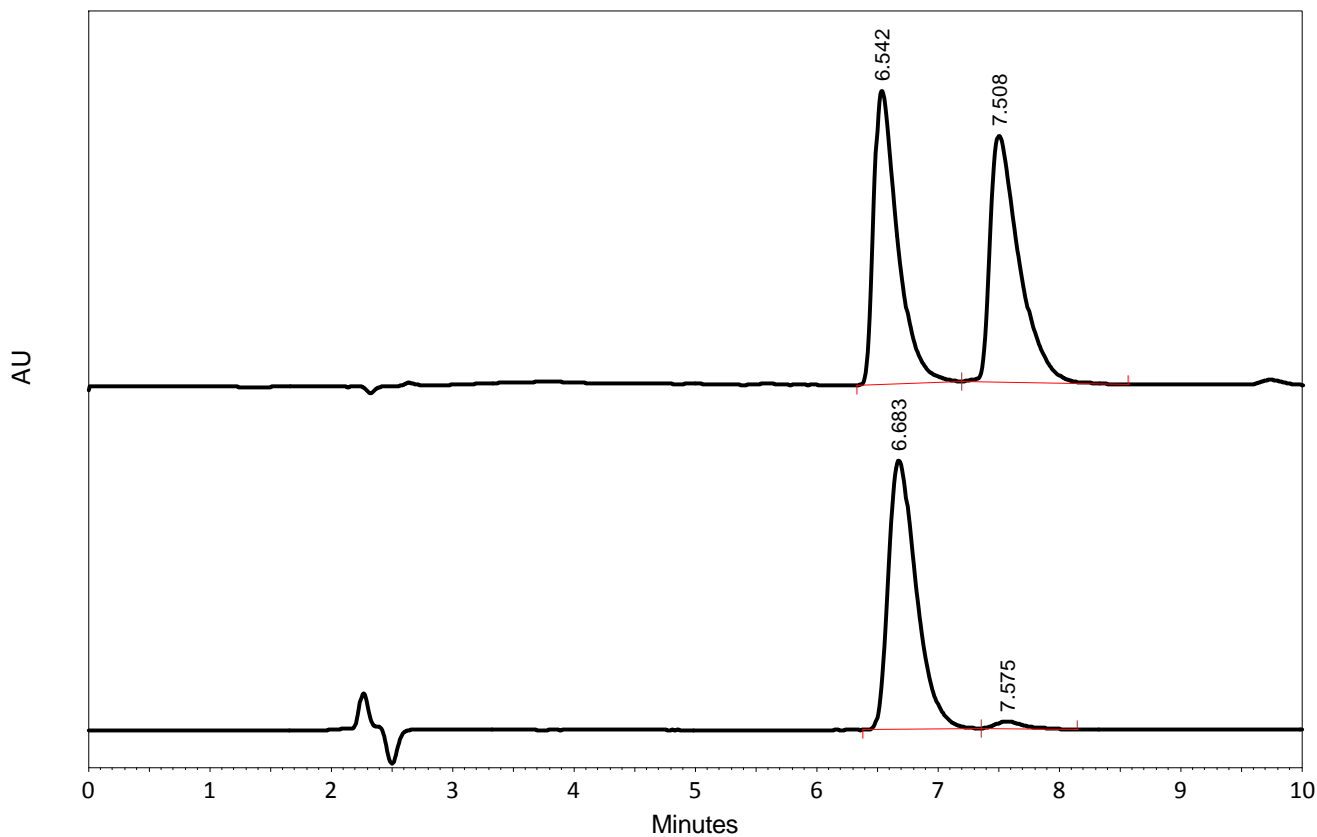
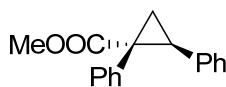


(1*R*,5*R*,6*S*)-*tert*-butyl 6-phenyl-2-oxabicyclo[3.1.0]hexane-6-carboxylate (**2g**)



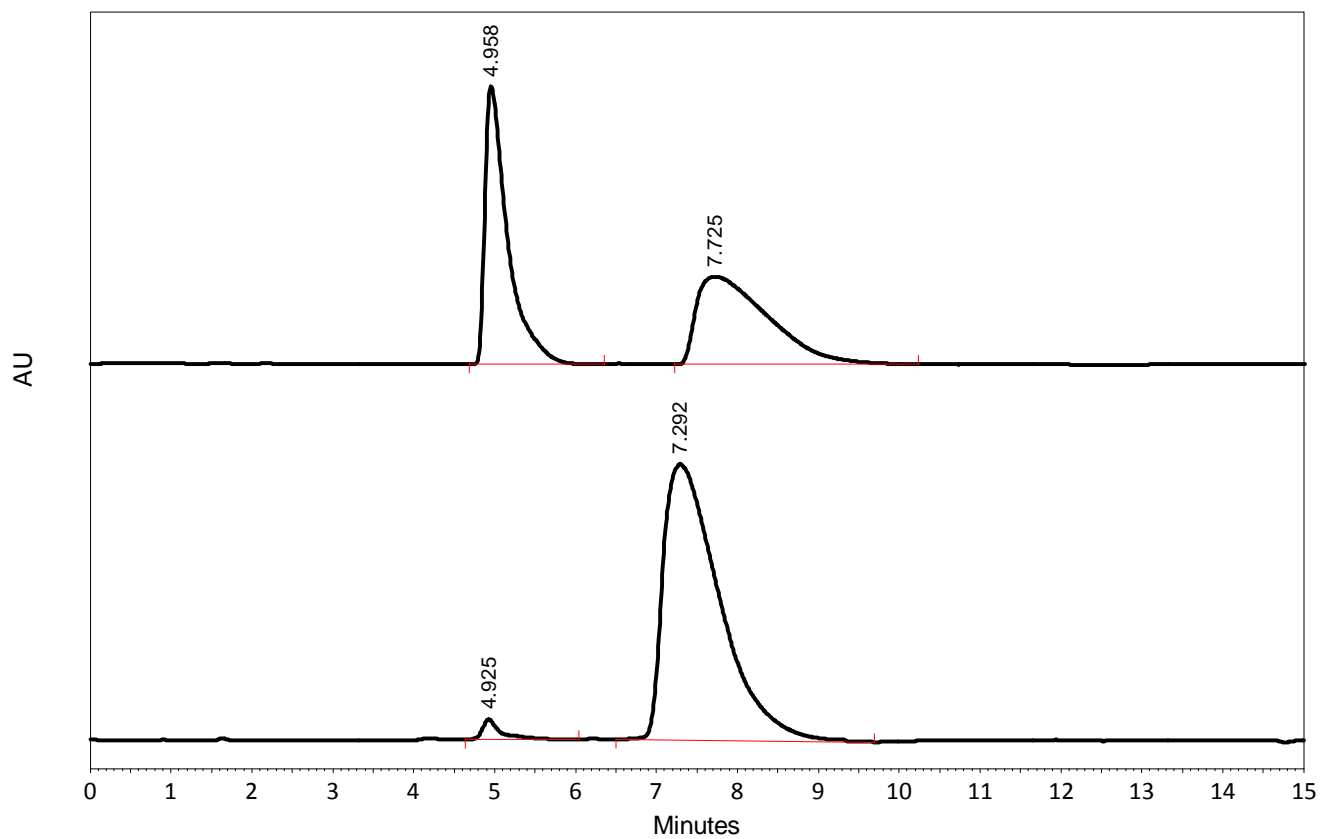
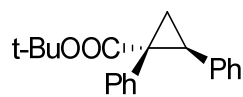
g. HPLC traces of cyclopropane products:

(1*R*,2*S*)-methyl 1,2-diphenylcyclopropanecarboxylate (**2a**)



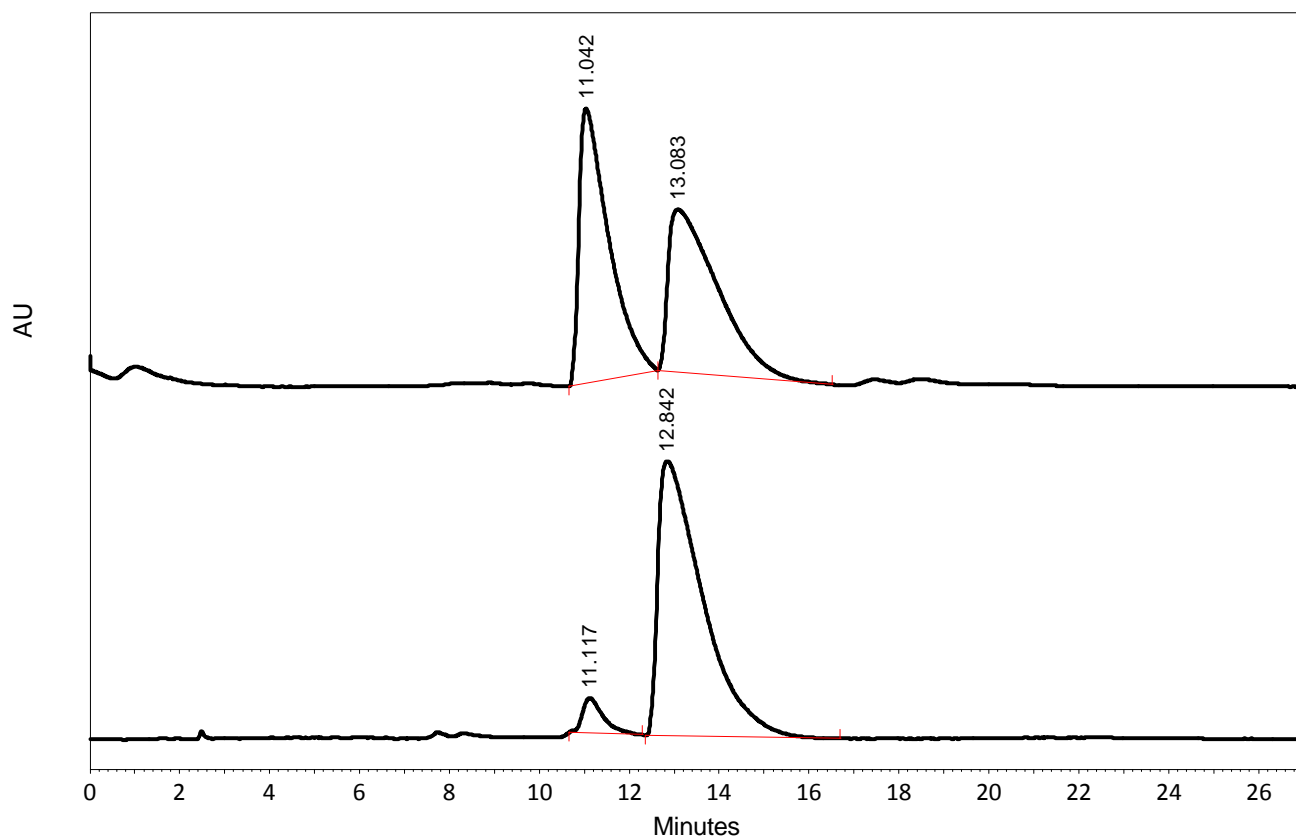
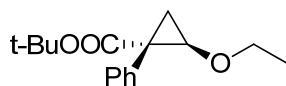
Peak	RT	Area	% Area	Height
1	6.683	5290875	97.303	328469
2	7.575	146670	2.697	8959

(1*R*,2*S*)-*tert*-butyl 1,2-diphenylcyclopropanecarboxylate (**2b**)



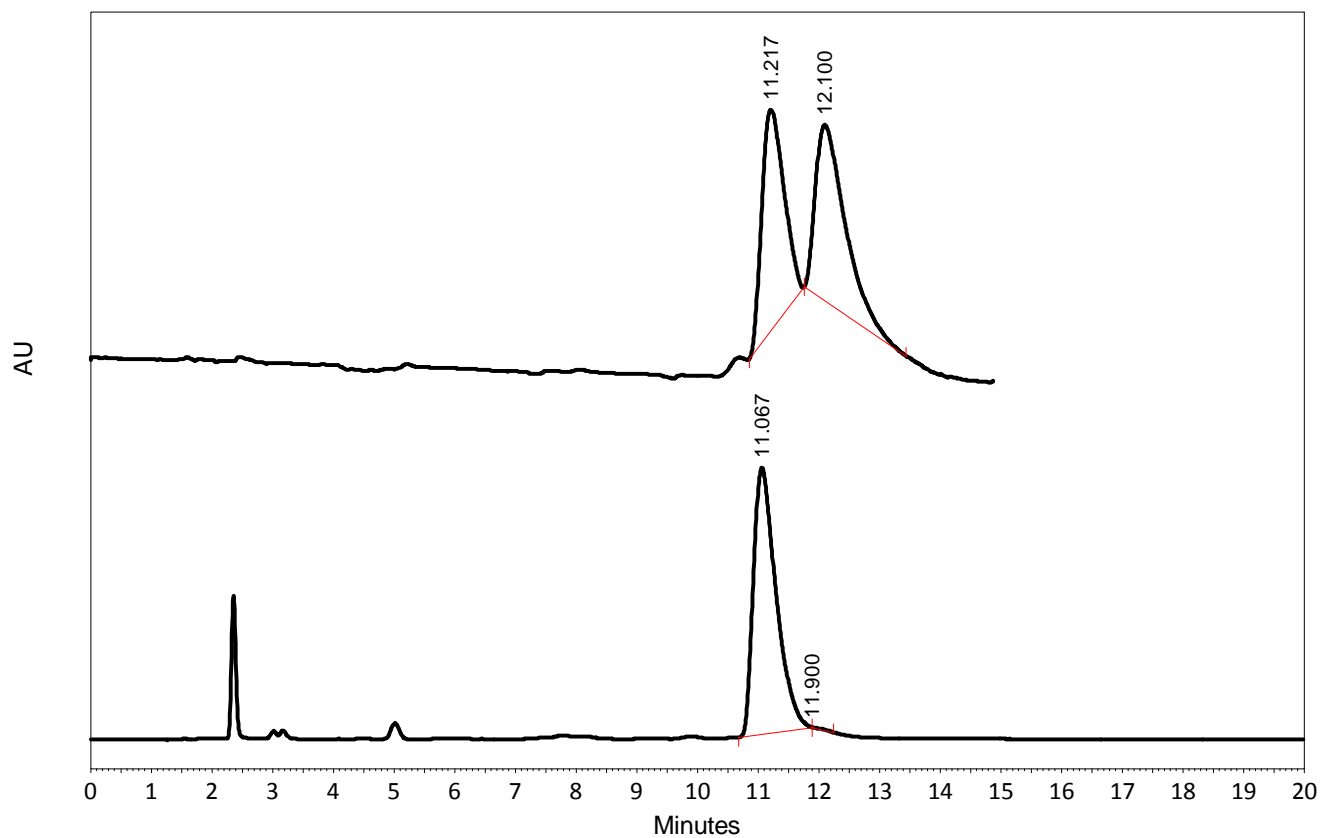
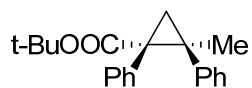
Peak	RT	Area	% Area	Height
1	4.925	53282	2.318	3361
2	7.292	2245222	97.682	46317

(1*S*,2*R*)-*tert*-butyl 2-ethoxy-1-phenylcyclopropanecarboxylate (**2c**)



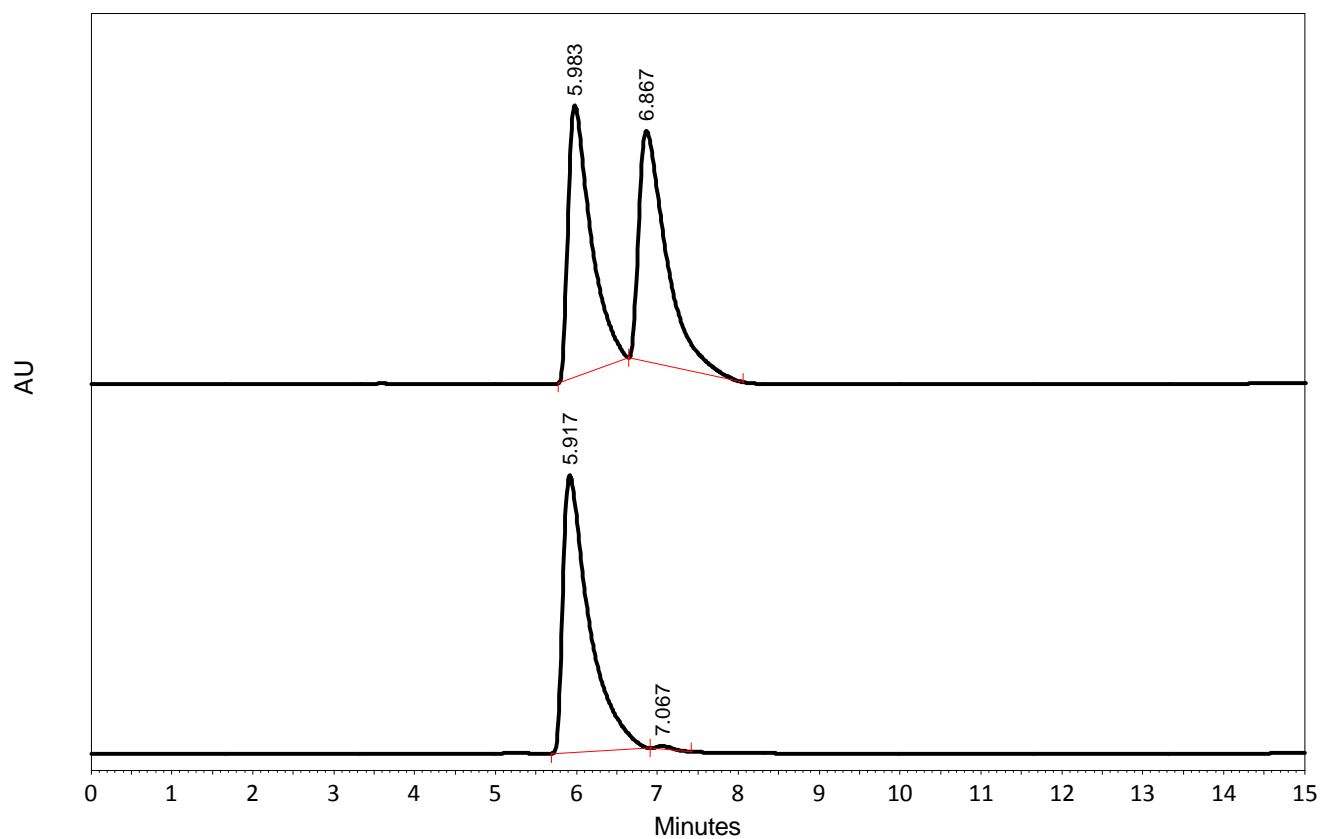
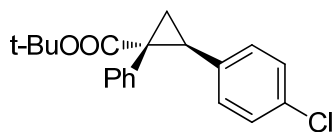
Peak	RT	Area	% Area	Height
1	11.117	250497	5.722	7708
2	12.842	4127561	94.278	59868

(1*S*,2*S*)-*tert*-butyl 2-methyl-1,2-diphenylcyclopropanecarboxylate (**2d**)



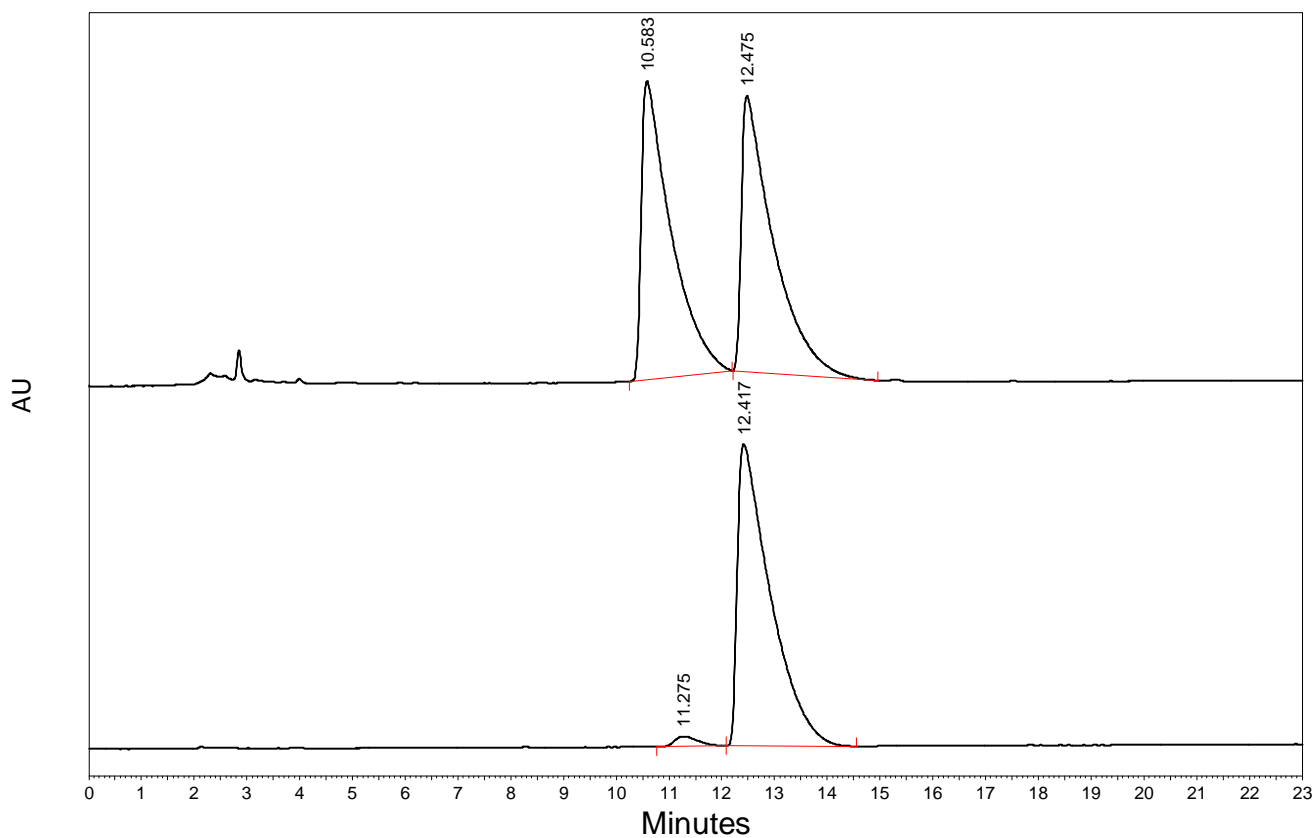
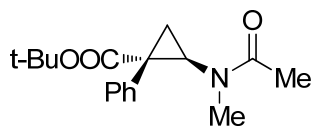
Peak	RT	Area	% Area	Height
1	11.067	1779135	99.886	68189
2	11.900	2034	0.114	1

(1*R*,2*S*)-*tert*-butyl 2-(4-chlorophenyl)-1-phenylcyclopropanecarboxylate (**2e**)



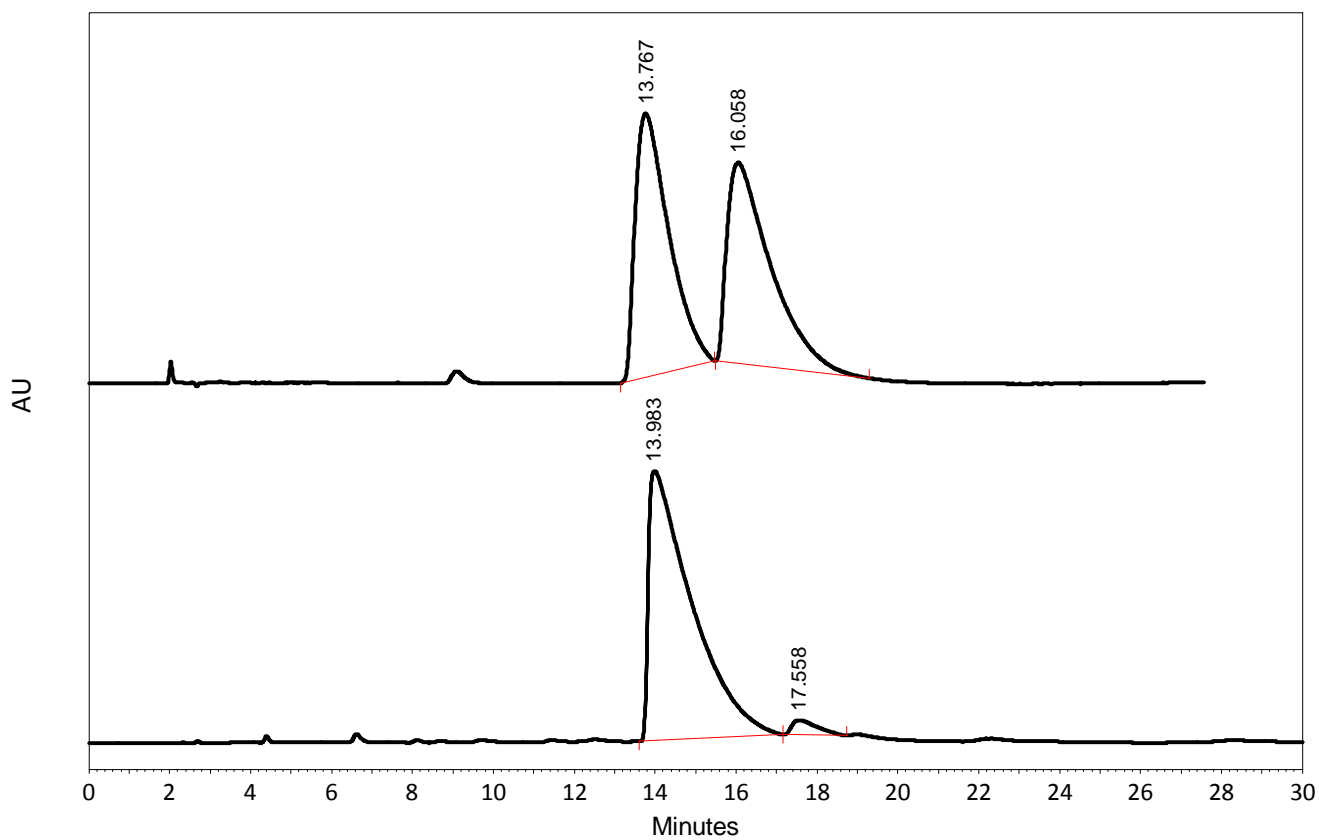
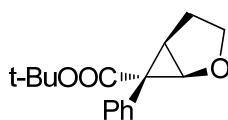
Peak	RT	Area	% Area	Height
1	5.917	18451467	99.365	814376
2	7.067	117964	0.635	9733

(1*S*,2*R*)-*tert*-butyl 2-(*N*-methylacetamido)-1-phenylcyclopropanecarboxylate (**2f**)



Peak	RT	Area	% Area	Height
1	11.275	15862	2.368	511
2	12.417	653886	97.632	15115

(1*R*,5*R*,6*S*)-*tert*-butyl 6-phenyl-2-oxabicyclo[3.1.0]hexane-6-carboxylate (**2g**)

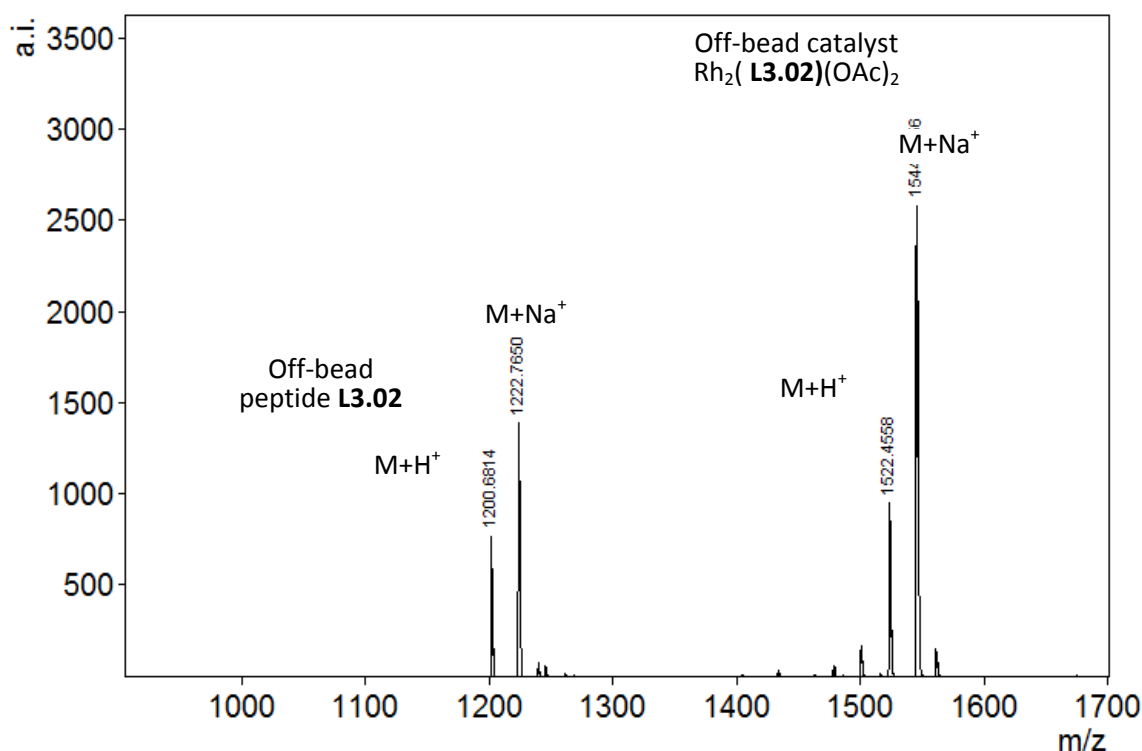


Peak	RT	Area	% Area	Height
1	13.983	25394631	96.923	341932
2	17.558	806076	3.077	18446

h. Comparative kinetics:

A few beads of the catalyst $\text{Rh}_2(\text{L3.02})(\text{OAc})_2$ (~3.0 mg, 0.03 mol%) was weighed in a 3.5-mL cuvette with 1 cm path length. Trifluoroethanol (1.5 mL), a small stirbar and a solution of styrene (29.6 mg, 0.284 mmol) in trifluoroethanol (0.5 mL) were added and stirred well at room temperature. Blank absorbance was measured after which a solution of methyl α -diazophenylacetate (5 mg, 0.0284 mmol) in trifluoroethanol (0.5 mL) was added and the absorbance of the solution was measured at a time interval of one minute over a period of 35 minutes. All absorbances were measured at a wavelength of 420 nm. This protocol was followed for reactions with catalysts $\text{Rh}_2(\text{L4.07})(\text{OAc})_2$ and $\text{Rh}_2(\text{L3.27})(\text{OAc})_2$.

i. MALDI spectrum of off-bead complexation with L3.02:



j. Molecular Dynamics calculations:

In order to study the stable states of the free peptide, Molecular Dynamics (MD) simulation was run on the peptide with the sequence IGDNINDHK (L3.02; the Cbz group was omitted for simplicity) in implicit solvent with Generalized Born formalism. The software package used for MD simulation is Gromacs v4.5.4.⁹ A total of 18 simulations (each 500 ns long) were performed and the data was recorded every 100 ps. 90,000 frames of configurations were collected from the simulation.

To analyze these configurations and get the stable states, a recently developed nonlinear dimensionality reduction method, locally-scaled diffusion map, LSDMap,¹⁰ was used to extract

the slowest conformational changes of the system. The LSDMap method is based on obtaining numerical approximations for the eigenfunctions of the Fokker-Planck equation from the discrete MD data set. The solution of the Fokker-Planck equation can be casted as an eigenvalue problem, and in systems for which there is a separation of timescales between $m+1$ slow collective modes and the remaining faster ones, the first m collective degrees of freedom can be used to describe the dynamics on the long timescales. The details of LSDMap method can be found in the recent work.¹⁰ For the peptide system in this manuscript, only the first two LSDMap coordinates are enough to reveal five stable states on the free energy landscape (Fig. 5).

To obtain the peptide structure bound to the Rh(II) complex, a steered MD simulation¹¹ was used to push the binding site of the peptide to the perfect binding position. The software package to perform steered MD is Gromacs v4.5.4.⁹ A total of 18 simulations (each 500 ns long) was performed with the Plumed plug-in.¹² The collective variable used in the steered MD is the root mean square deviation (RMSD) to the perfect binding configuration, considering only the position of the three binding sites: the two carboxylate groups and the nitrogen in the histidine residues. One starting configuration was chosen from each of the five stable states with the smallest RMSD to the perfect binding configuration considering the position of the three binding sites. 100 steered MD simulations were run from each of the starting configurations with spring constant 5000 kJ/mol/nm² and velocity 0.03 nm/ps until the RMSD was close to 0 nm, indicating that the perfect binding configuration for the peptide was reached. 500 configurations were generated from the steered MD.

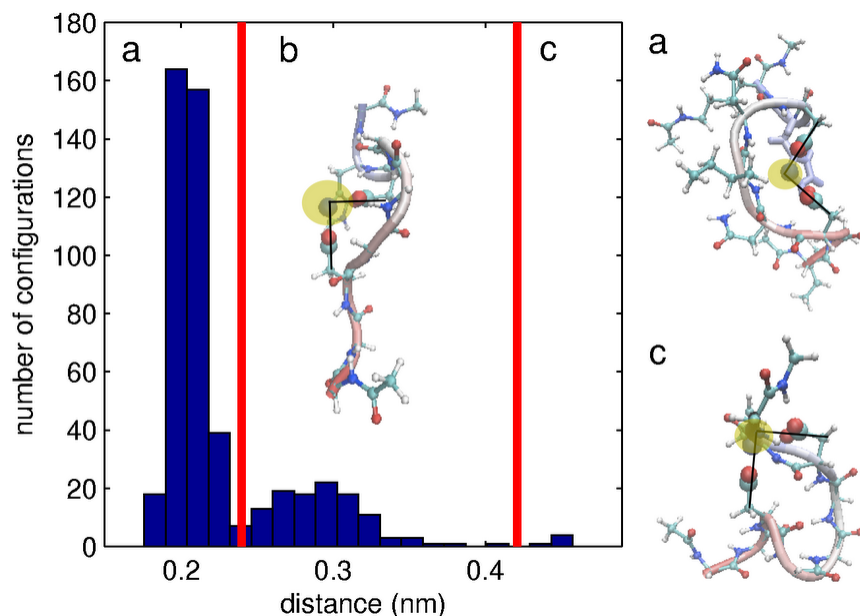


Fig S1: The distribution of the distance between the center of mass of the two carboxylate groups in the side chains of the two Asp residues and the center of mass of the backbone of the two Asp residues computed over the configurations obtained from steered MD. The yellow dots indicate the potential binding position of Rh(II). The two black lines indicate the carboxylate groups. The red lines divide the configurations into three groups according to this distance: a, b and c. Typical configurations of these clusters are marked with the corresponding letters.

To refine the results from steered MD, we calculated the distances between the center of mass of the two carboxylate groups in the side chains of the two Asp residues and the center of mass of the backbone of the two Asp residues. The distribution of these distances is shown in Fig. S1. This distance indicates how far the position of the potential binding site is from the cavity formed by the backbone of the peptide. We clustered the configurations into three groups according to this distance and found that only the configurations in the medium range of the distance (group b in Fig. S1) could accommodate the binding of Rh(II). Therefore, configurations in group b were selected. A RMSD-clustering was performed to group together configurations structurally very similar. 22 candidate binding configurations resulted from this procedure and were used for quantum chemistry calculation.

k. Density Functional Theory calculations:

Spin-restricted density functional theory (RDFT) calculations were performed with the Gaussian 03 (G03) program.¹³ Geometry optimization and normal mode analysis was performed using the B3LYP functional.^{14,15} A combination of the double-zeta Stuttgart RSC 1997 ECP (ECP28MWB) for Rh,¹⁶ obtained from the EMSL Basis Set Library,^{17,18} and the 6-31G(d) basis set for all other atoms were used. The identified stationary point exceeded all default G03 convergence criteria. A frequency calculation was performed at the optimized geometry using the same basis sets to confirm that the optimized geometry had zero negative eigenvalues.

Calculation results at DFT-optimized geometry:

Total Energy ~ -4611.42712138 AU

SCF Convergence ~ 0.1955E-08

Three lowest frequencies (cm⁻¹) ~ 8.3, 13.9, 18.1

XYZ coordinate for DFT-optimized Rh₂ metallopeptide – 165 atoms:

C	7.063203	-5.545295	2.061646	H	0.325968	6.930173	0.792458	H	-8.169843	-1.324429	2.125338
H	7.994243	-5.106516	2.434837	C	0.443240	6.968522	2.940561	C	-6.093706	-1.396739	2.722994
H	6.670656	-6.229404	2.822557	H	-0.518743	6.468552	3.087961	H	-5.829064	-0.334729	2.694974
H	7.274273	-6.136518	1.167270	H	1.110362	6.650040	3.750586	H	-5.193128	-1.954431	2.435283
C	5.995521	-4.514888	1.727880	H	0.274497	8.044517	3.044167	C	-6.502665	-1.777931	4.151981
O	5.022755	-4.787872	1.039112	C	2.355443	7.436453	1.315921	H	-6.831478	-2.828063	4.180288
N	6.211995	-3.254617	2.248334	H	2.839524	7.054834	0.409317	H	-7.372998	-1.177581	4.451563
H	6.948520	-3.161918	2.936206	H	3.052703	7.238153	2.142747	C	-5.400363	-1.575799	5.205164
C	5.173481	-2.225250	2.246778	C	2.152121	8.948034	1.158369	H	-5.816067	-1.749634	6.206976
H	4.298074	-2.668143	1.759426	H	3.102952	9.442134	0.929236	H	-5.046034	-0.542030	5.185469
C	4.749520	-1.783839	3.674842	H	1.458591	9.168036	0.337451	N	-4.255850	-2.456765	5.011865
H	3.998010	-1.001619	3.521259	H	1.753786	9.411506	2.067454	H	-4.446705	-3.453364	5.001291
C	4.075001	-2.947874	4.414016	C	0.081628	4.263052	1.841366	C	-3.027976	-2.163491	4.476913
H	3.229725	-3.334421	3.835401	O	0.061781	3.622095	2.884440	O	-2.283986	-3.074720	4.113632
H	4.775467	-3.773918	4.592744	N	-0.969389	4.297450	0.968721	C	-2.623215	-0.702564	4.373695
H	3.688338	-2.624782	5.385058	H	-0.851567	4.737901	0.060227	H	-2.768104	-0.172791	5.321976
C	5.916828	-1.158378	4.469080	C	-1.992430	3.260673	0.956242	H	-1.569052	-0.665496	4.094584
H	6.442741	-0.436984	3.828811	H	-1.571037	2.344946	1.382991	H	-3.200519	-0.177995	3.602995
H	6.651241	-1.935939	4.734995	C	-3.227021	3.648084	1.800672	C	-7.271852	0.501058	0.382791
C	5.480295	-0.437153	5.750749	H	-3.659338	4.584251	1.427491	O	-7.662252	1.072361	1.411495
H	5.017483	-1.121723	6.469289	H	-2.863466	3.840787	2.817865	N	-7.048313	1.144761	-0.782587
H	6.339079	0.029879	6.245875	C	-4.292532	2.551107	1.872262	H	-6.600324	0.652904	-1.551449
H	4.753916	0.351872	5.524042	O	-4.022471	1.356480	1.673522	C	-7.234618	2.575631	-0.946316
C	5.539373	-1.013154	1.379059	N	-5.539835	2.959377	2.189094	H	-7.912641	2.930662	-0.168637
O	4.834447	0.006086	1.368354	H	-5.754721	3.942300	2.271775	H	-6.283704	3.117243	-0.870101
N	6.639946	-1.111630	0.600319	H	-6.320556	2.301099	2.105561	H	-7.670000	2.776239	-1.929519
H	7.138431	-1.991028	0.615631	C	-2.303151	3.024995	-0.537955	Rh	0.071720	-2.617797	-1.401900
C	7.146418	-0.005180	-0.199523	O	-1.957760	3.847743	-1.391596	Rh	1.111026	-1.014913	0.125575
H	8.222275	-0.128504	-0.335143	N	-2.908190	1.856433	-0.856248	O	1.175322	-4.112074	-0.492326
H	6.975216	0.921226	0.360814	H	-3.135477	1.226493	-0.090221	O	-1.376227	-2.881554	0.047369
C	6.553903	0.203516	-1.605856	C	-2.919462	1.410126	-2.250274	O	-0.413326	-1.380684	1.456806
O	7.265135	0.647728	-2.498992	H	-3.308929	2.231721	-2.855211	O	2.136436	-2.615219	0.931178
N	5.227192	-0.072787	-1.749932	C	-1.462114	1.161504	-2.736785	O	2.086564	0.351070	1.695452
H	4.674888	-0.349542	-0.947489	H	-0.964406	2.129739	-2.708707	C	1.957009	-3.777399	0.441836
C	4.518560	0.231015	-2.982720	H	-1.484016	0.803949	-3.770709	C	-1.259761	-2.270079	1.159006
H	5.286441	0.340159	-3.751814	C	-0.688900	0.153285	-1.903690	H	3.052396	0.171349	1.672737
C	3.582743	-0.920083	-3.418390	O	-0.877045	-1.052452	-2.286960	H	2.032182	1.302898	1.479698
H	4.186672	-1.806721	-3.646130	O	0.023358	0.508459	-0.922315	H	2.568399	-4.574313	0.880191
H	3.075396	-0.639818	-4.347984	C	-3.964239	0.279598	-2.433609	H	-1.962837	-2.554083	1.950125
C	2.523998	-1.325577	-2.396732	O	-5.088611	0.562454	-2.852921				
O	1.660789	-2.187724	-2.739832	N	-3.614971	-0.977159	-2.048747				
O	2.601378	-0.749680	-1.261783	H	-2.618961	-1.179873	-1.977382				
C	3.799385	1.606691	-2.997765	C	-4.478701	-2.129841	-2.308464				
O	3.608165	2.164138	-4.085539	H	-4.818530	-2.100235	-3.350259				
N	3.411555	2.130551	-1.812848	C	-3.715584	-3.460962	-2.054820				
H	3.546007	1.624412	-0.943951	H	-4.484177	-4.240578	-2.018970				
C	2.789712	3.435431	-1.684841	H	-3.233440	-3.429247	-1.074533				
H	3.527791	4.199835	-1.968452	C	-2.689410	-3.854407	-3.093622				
C	1.526077	3.614317	-2.584049	N	-1.308723	-3.834709	-2.899365				
H	0.611551	3.559009	-1.990721	C	-0.764364	-4.306007	-4.004191				
H	1.509481	2.825771	-3.333481	H	0.296467	-4.408220	-4.181722				
C	1.603819	4.984430	-3.231347	N	-1.718236	-4.635261	-4.912808				
O	1.309567	6.010735	-2.611164	H	-1.556530	-5.024723	-5.830112				
N	2.088172	4.980778	-4.499295	C	-2.945221	-4.357657	-4.347680				
H	2.568473	4.147372	-4.825196	H	-3.873193	-4.555225	-4.862950				
H	2.336096	5.870962	-4.911599	C	-5.796946	-2.104840	-1.502736				
C	2.440147	3.662755	-0.198640	O	-6.759942	-2.744385	-1.908847				
O	2.781278	2.848241	0.663628	N	-5.818625	-1.352758	-0.362434				
N	1.754339	4.795426	0.072378	H	-4.977647	-0.859412	-0.091828				
H	1.492374	5.404087	-0.710317	C	-7.064735	-1.034391	0.332857				
C	1.307805	5.119656	1.432426	H	-7.850863	-1.441507	-0.314035				
H	2.096235	4.813228	2.125268	C	-7.217923	-1.682616	1.717189				
C	1.053939	6.642982	1.568182	H	-7.316394	-2.765382	1.569296				

2. References:

- (1) Strohm, M.; Hassman, M.; Košata, B.; Kodíček, M. *Rapid Commun. Mass Spectrom.* **2008**, *22*, 905.
- (2) Wellings, D. A.; Atherton, E. In *Methods in Enzymology*; Gregg, B. F., Ed.; Academic Press: **1997**; Vol. 289, p 44.
- (3) Lou, Y.; Remarchuk, T. P.; Corey, E. J. *J. Am. Chem. Soc.* **2005**, *127*, 14223.
- (4) Johnson, S. A.; Hunt, H. R.; Neumann, H. M. *Inorg. Chem.* **1963**, *2*, 960.
- (5) Davies, H. M. L.; Hansen, T.; Churchill, M. R. *J. Am. Chem. Soc.* **2000**, *122*, 3063.
- (6) Sambasivan, R.; Ball, Z. T. *Angew. Chem. Int. Ed.* **2012**, *51*, 8568.
- (7) Liu, G.; Lam, K. S. In *Combinatorial Chemistry: A Practical Approach*; Fenniri, H., Ed.; Oxford University Press: **2000**, p 33.
- (8) Murray, J. K.; Gellman, S. H. *Nat. Protocols* **2007**, *2*, 624.
- (9) Davies, H. M. L.; Lee, G. H. *Org. Lett.* **2004**, *6*, 1233.
- (10) Hess, B.; Kutzner, C.; van der Spoel, D.; Lindahl, E. *J. Chem. Theory Comput.* **2008**, *4*, 435.
- (11) Rohrdanz, M. A.; Zheng, W.; Maggioni, M.; Clementi, C. *J. Chem. Phys.* **2011**, *134*, 124116.
- (12) Izrailev, S.; Stepaniants, S.; Balsera, M.; Oono, Y.; Schulten, K. *Biophys. J.* **1997**, *72*, 1568.
- (13) Bonomi, M.; Branduardi, D.; Bussi, G.; Camilloni, C.; Provasi, D.; Raiteri, P.; Donadio, D.; Marinelli, F.; Pietrucci, F.; Broglia, R. A.; Parrinello, M. *Comput. Phys. Commun.* **2009**, *180*, 1961.
- (14) Frisch, M. J.; Trucks, G. W.; Schlegel, H. B.; Scuseria, G. E.; Robb, M. A.; Cheeseman, J. R.; Montgomery, J. A.; Vreven, T.; Kudin, K. N.; Burant, J. C.; Millam, J. M.; Iyengar, S. S.; Tomasi, J.; Barone, V.; Mennucci, B.; Cossi, M.; Scalmani, G.; Rega, N.; Petersson, G. A.; Nakatsuji, H.; Hada, M.; Ehara, M.; Toyota, K.; Fukuda, R.; Hasegawa, J.; Ishida, M.; Nakajima, T.; Honda, Y.; Kitao, O.; Nakai, H.; Klene, M.; Li, X.; Knox, J. E.; Hratchian, H. P.; Cross, J. B.; Bakken, V.; Adamo, C.; Jaramillo, J.; Gomperts, R.; Stratmann, R. E.; Yazyev, O.; Austin, A. J.; Cammi, R.; Pomelli, C.; Ochterski, J. W.; Ayala, P. Y.; Morokuma, K.; Voth, G. A.; Salvador, P.; Dannenberg, J. J.; Zakrzewski, V. G.; Dapprich, S.; Daniels, A. D.; Strain, M. C.; Farkas, O.; Malick, D. K.; Rabuck, A. D.; Raghavachari, K.; Foresman, J. B.; Ortiz, J. V.; Cui, Q.; Baboul, A. G.; Clifford, S.; Cioslowski, J.; Stefanov, B. B.; Liu, G.; Liashenko, A.; Piskorz, P.; Komaromi, I.; Martin, R. L.; Fox, D. J.; Keith, T.; Laham, A.; Peng, C. Y.; Nanayakkara, A.; Challacombe, M.; Gill, P. M. W.; Johnson, B.; Chen, W.; Wong, M. W.; Gonzalez, C.; Pople, J. A.; Gaussian, Inc.: Wallingford CT, **2004**.
- (15) Becke, A. D. *J. Chem. Phys.* **1993**, *98*, 1372.
- (16) Lee, C.; Yang, W.; Parr, R. G. *Phys. Rev. B: Condens. Matter* **1988**, *37*, 785.
- (17) Andrae, D.; Häußermann, U.; Dolg, M.; Stoll, H.; Preuß, H. *Theor. Chim. Acta* **1990**, *77*, 123.
- (18) Schuchardt, K. L.; Didier, B. T.; Elsethagen, T.; Sun, L.; Gurumoorthi, V.; Chase, J.; Li, J.; Windus, T. L. *J. Chem. Inf. Model.* **2007**, *47*, 1045.
- (19) Feller, D. J. *Comput. Chem.* **1996**, *17*, 1571.