

Supplementary information

Biocatalyzed asymmetric reduction of benzils to either benzoin or hydrobenzoin: pH dependent switch

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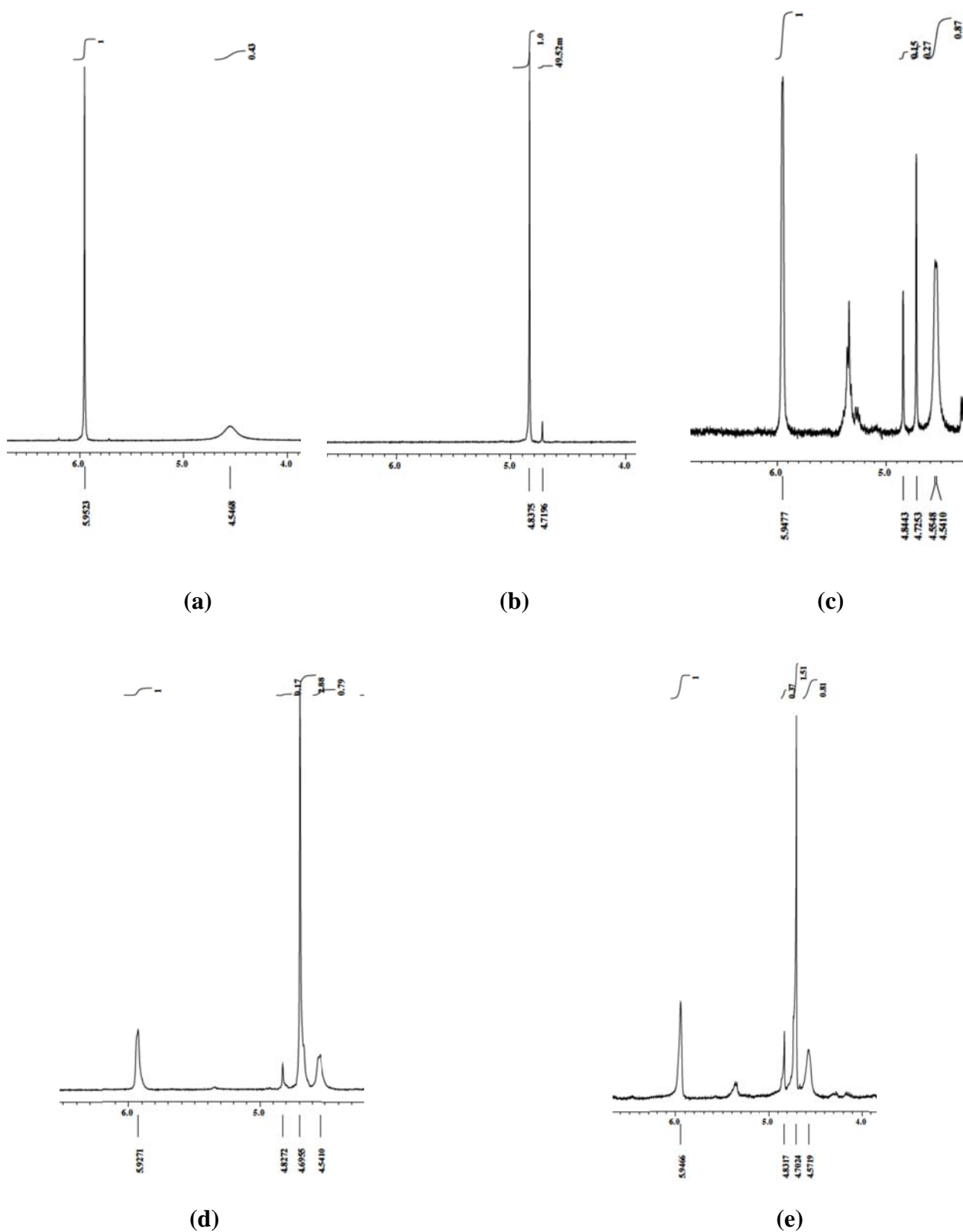


Figure 1S: ^1H NMR showing selected portion of a) *rac*-benzoin (**2a**) b) *dl/meso*-hydrobenzoin (**3a**) prepared by NaBH_4 reduction and biocatalyzed mixture of **2a/3a** by (c) *Penicillium sp.* (d) *Alternaria alternata* and (e) *Talaromyces flavus*

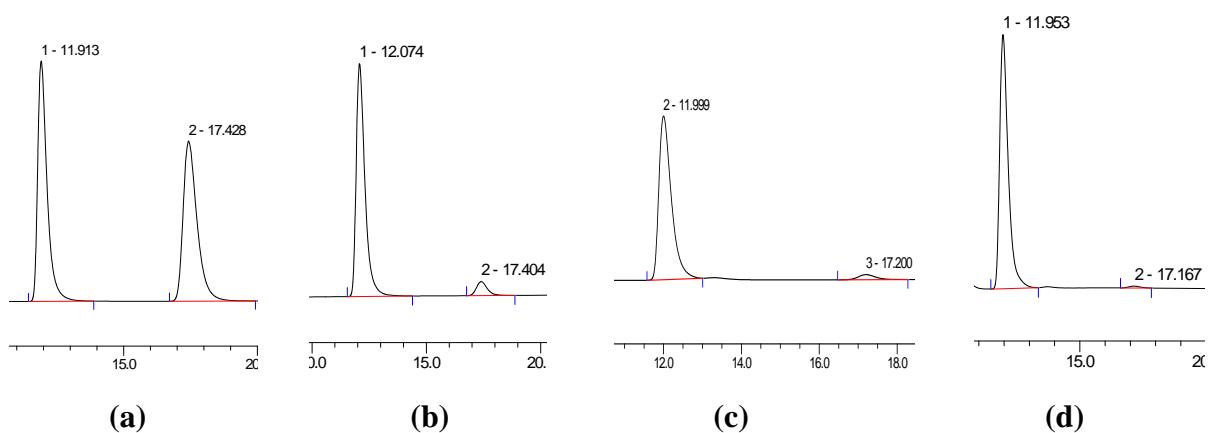


Figure 2S: HPLC profiles of (a) *rac*-benzoin (**2a**) and biocatalyzed (*S*)-benzoin (**2a**) by (b) *Penicillium sp.* (c) *Alternaria alternata* and (d) *Talaromyces flavus*

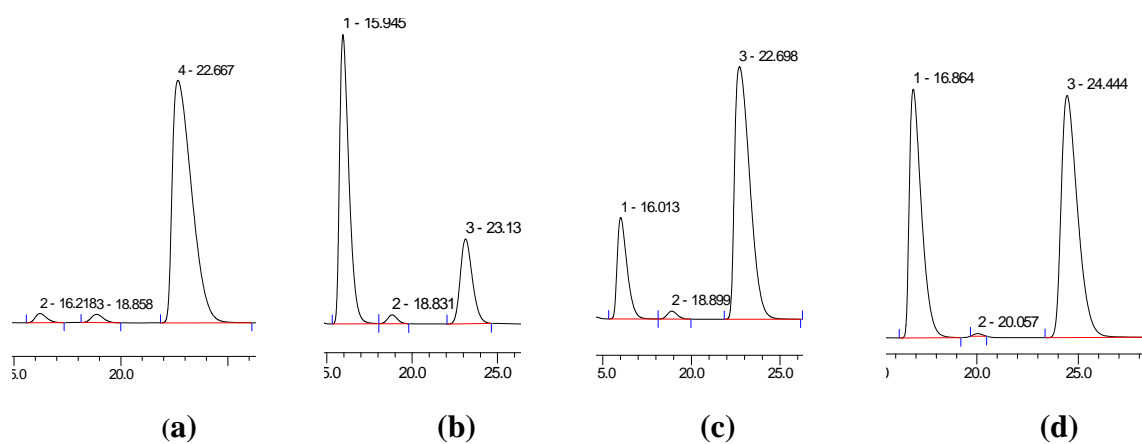


Figure 3S: HPLC profiles of **3a** obtained from (a) borohydride reduction (b) *Penicillium sp.* (c) *Alternaria alternata* and (d) *Talaromyces flavus* catalyzed reduction

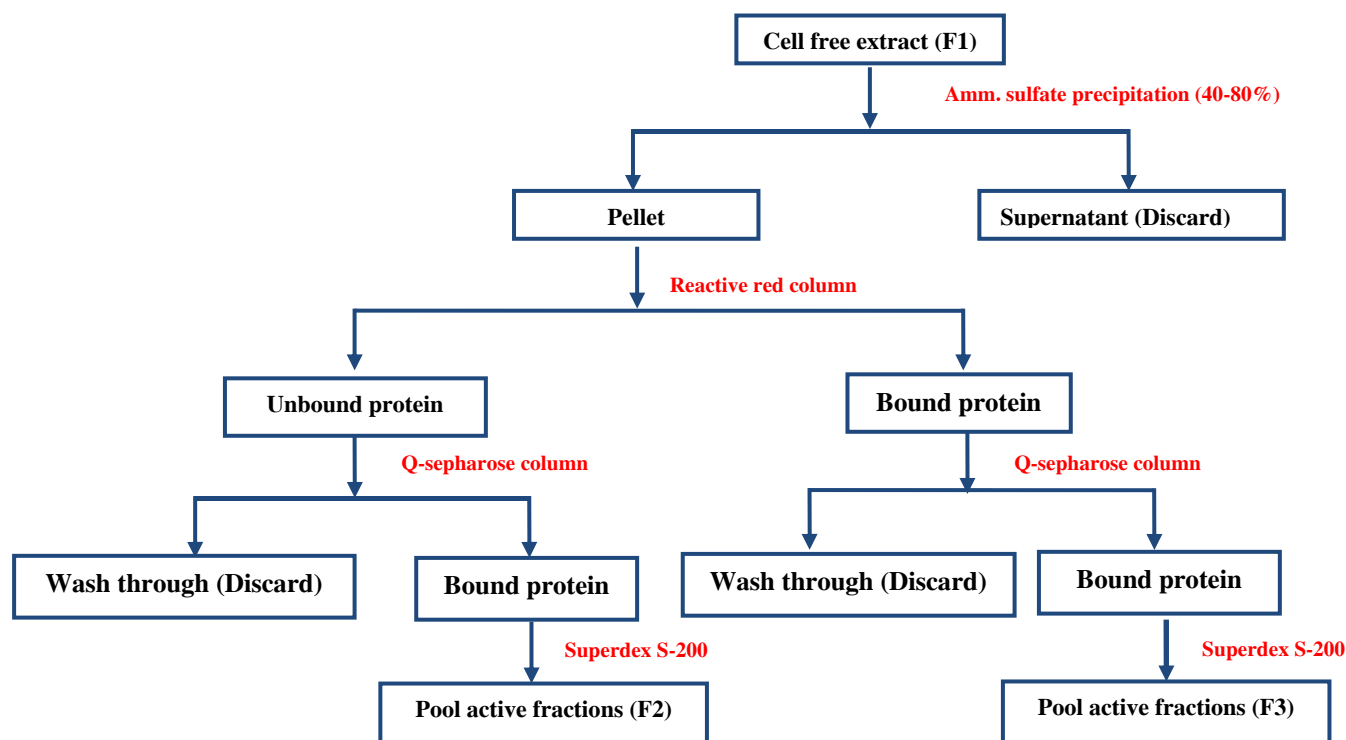


Figure 4S: Summary of attempted fractionation of proteins of *T. flavus*. Fraction 1 to 3 were used for asymmetric reduction of benzil (**1a**), *rac*-benzoin (**2a**) and (*S*)-benzoin (**2a**)

Table 1S: Summary of the 5-step protein purification procedure

Entry	Protein purification Step	Total protein (mg)	Total activity (μmolmin^{-1})	Specific activity ($\mu\text{molmin}^{-1}\text{mg}^{-1}$ protein)	Fold purification
1	Cell free extract	487	114.5	0.235	1
2	(40-80%) amm. sulfate pellet	192	95.6	0.497	2.11
3	Reactive red	7.6	11.7	1.54	6.55
4	Q-sepharose	1.08	3.2	2.96	12.59
5	Gel filtration	0.4	1.9	4.75	20.2

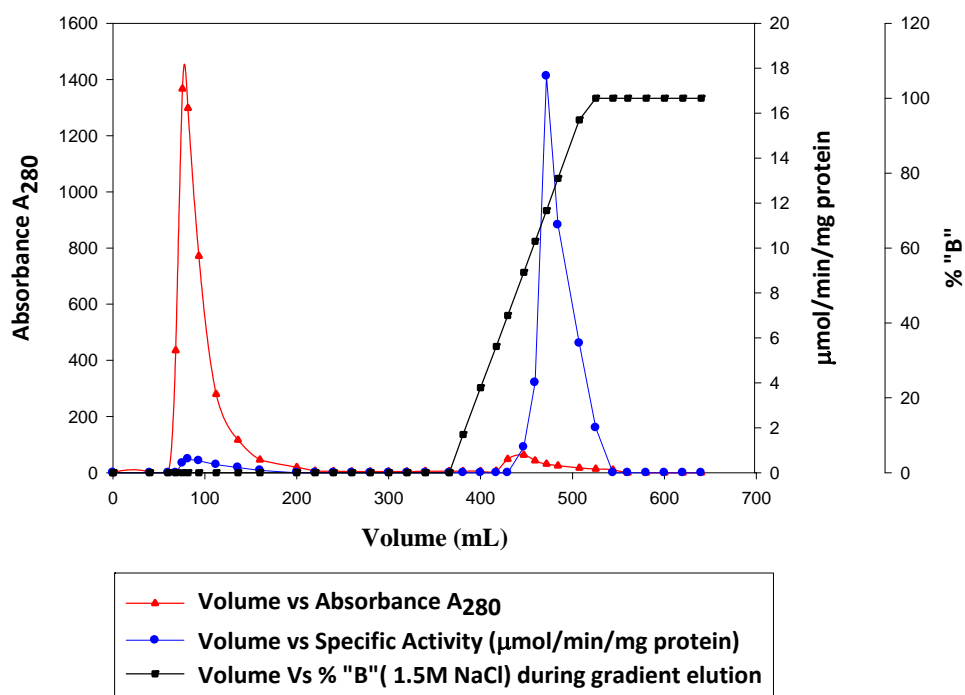


Figure 5S: Purification profile of dehydrogenase of *T. flavus* on reactive red column. The reactive red column (2×13 cm) was pre-equilibrated with phosphate buffer (10 mM, pH 8.0). The bound proteins were eluted with linear gradient of 0-1.5 M NaCl in phosphate buffer (10 mM, pH 6.5) at a flow rate of 1 mL/min. Fractions were analyzed for amount of protein by Bradford method. The enzyme activity was determined by monitoring the decrease in absorbance of NADPH at 340 nm spectrophotometrically. The active fractions were pooled and concentrated in an ultrafiltration cell using a 10 kDa membrane

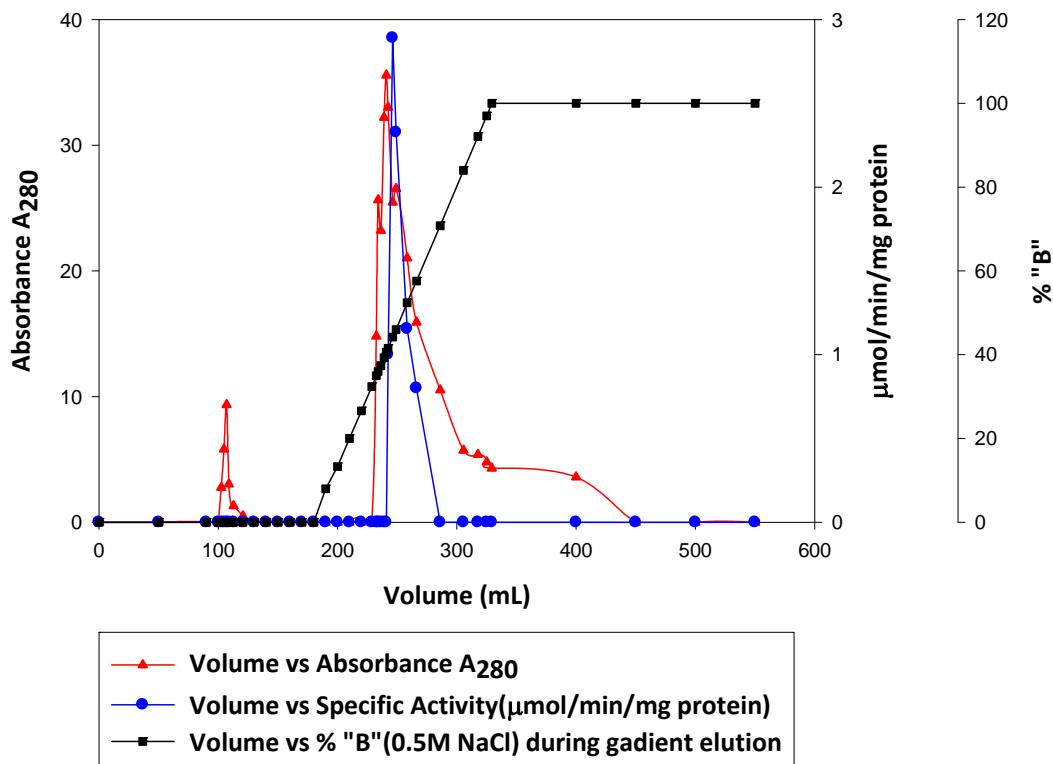


Figure 6S: Purification profile of dehydrogenase of *T. flavus* on Q-Sepharose column. The Q-sepharose column (2×5 cm) was pre-equilibrated with Tris-HCl buffer (10 mM, pH 8.0). The bound proteins were eluted with linear gradient of 0-0.5 M NaCl in with Tris-HCl buffer (10 mM, pH 8.0) at a flow rate of 1 mL/min. Fractions were analyzed for amount of protein by Bradford method. The enzyme activity was determined by monitoring the decrease in absorbance of NADPH at 340 nm spectrophotometrically. The active fractions were pooled and concentrated in an ultrafiltration cell using a 10 kDa membrane.

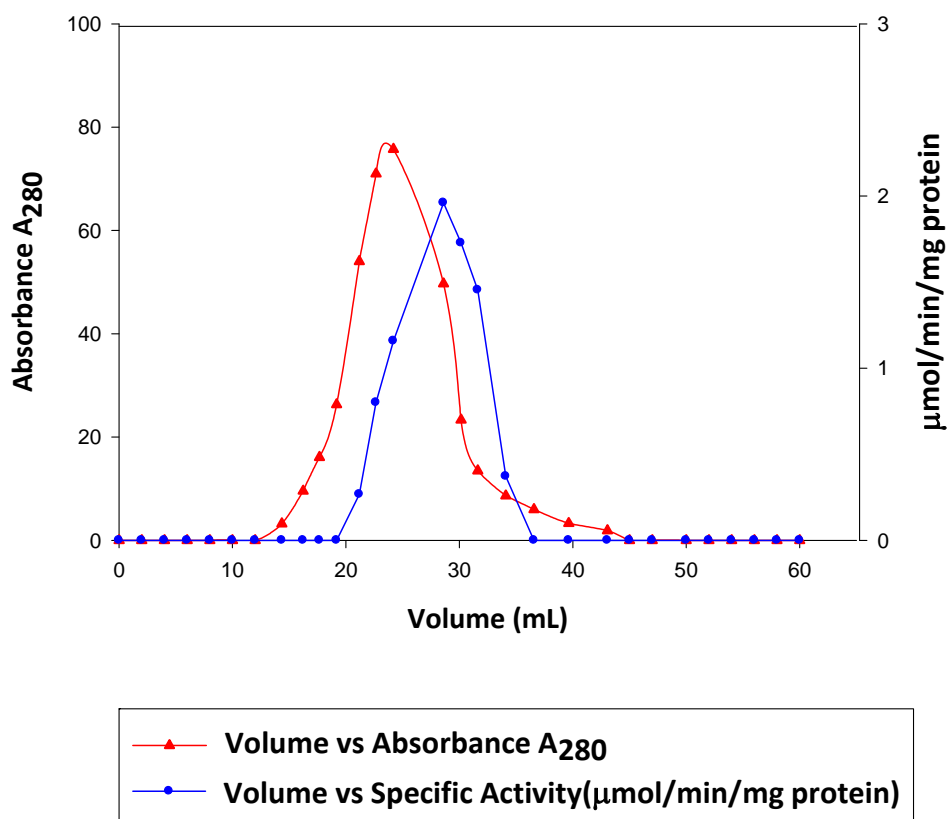
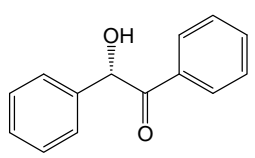
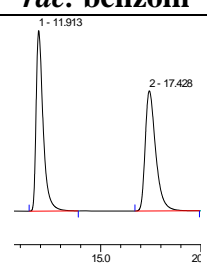
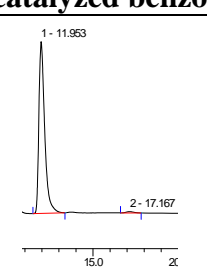
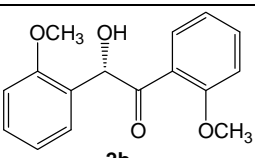
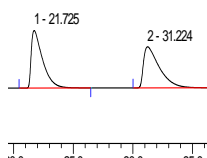
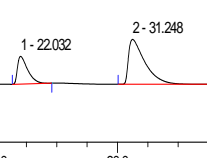
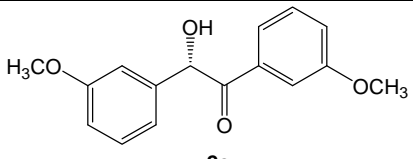
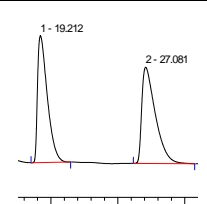
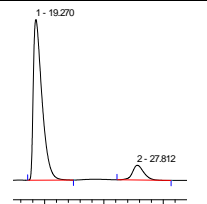
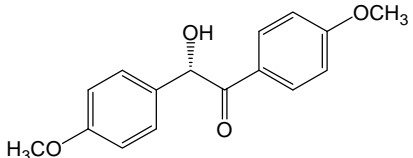
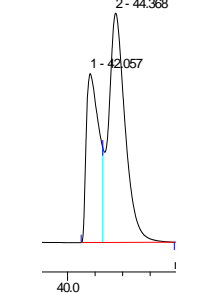
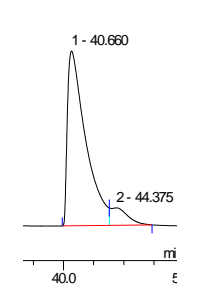
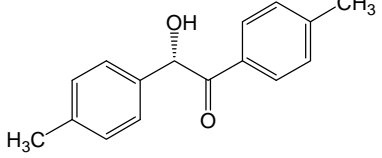
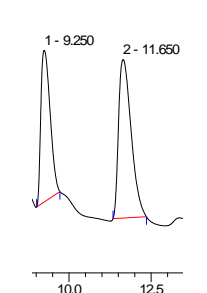
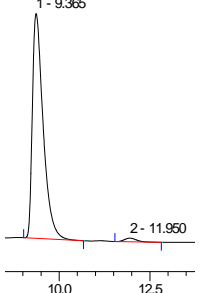
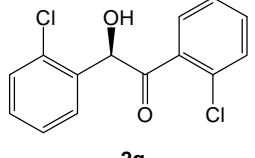
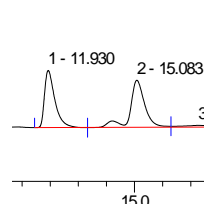
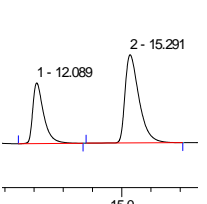


Figure 7S: Purification profile of dehydrogenase of *T. flavus* on superdex S-200 column. 0.5 mL of concentrated protein sample from Q-sepharose chromatography step was loaded on a superdex S-200 column (2×60 cm, 43 mL bed volume) previously equilibrated with Tris-HCl buffer (50 mM, pH 7.5) containing 0.15 M NaCl. The enzyme was eluted with same buffer at flow rate of 0.5 mL/min and active fractions were pooled and concentrated in an ultra filtration cell using a 10 kDa membrane. The enzyme activity was determined by monitoring the decrease in absorbance of NADPH at 340 nm spectrophotometrically.

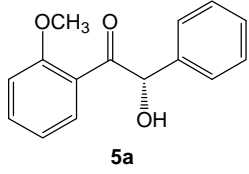
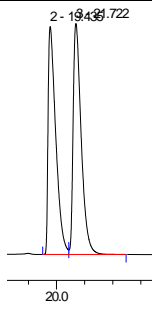
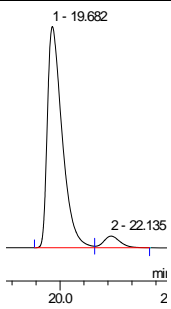
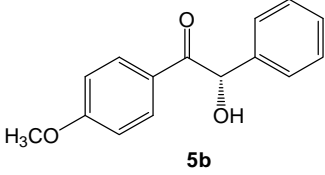
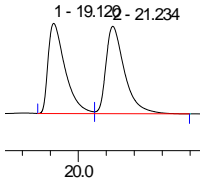
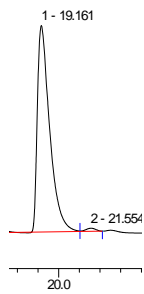
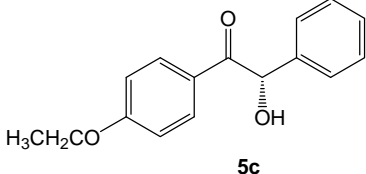
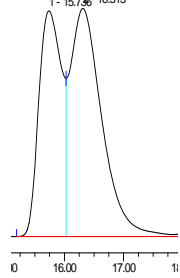
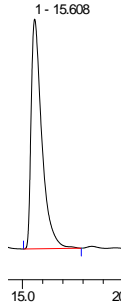
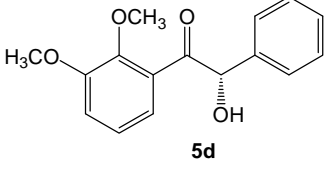
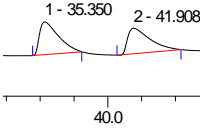
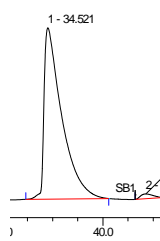
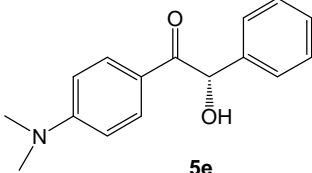
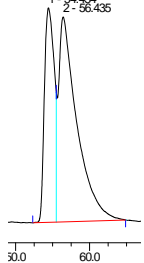
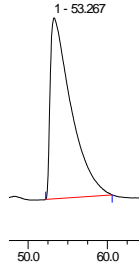
HPLC traces for biocatalyzed products

Table 2S. HPLC profiles of the products obtained from asymmetric reduction of symmetrical benzil derivatives with *T. flavus* at pH 5.0^{a,b}

Entry	Biocatalyzed product	<i>rac.</i> benzoin	biocatalyzed benzoin
1	 2a		
2	 2b		
3	 2c		
4	 2d		
5	 2e		
6	 2g		

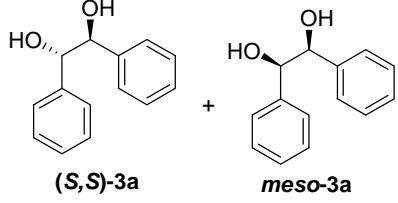
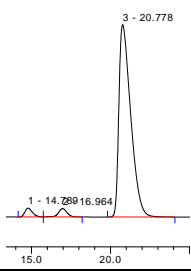
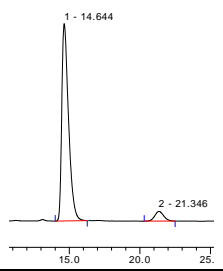
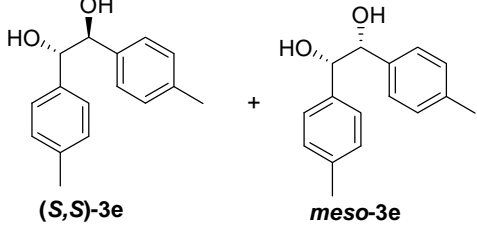
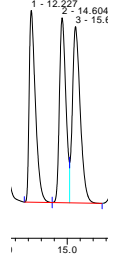
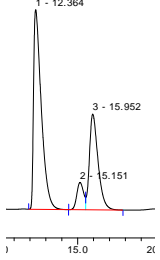
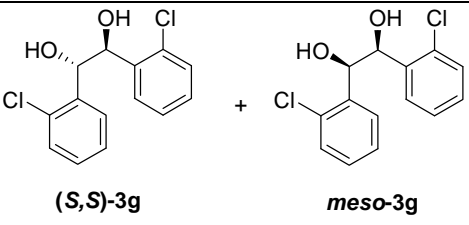
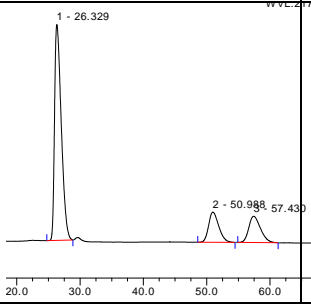
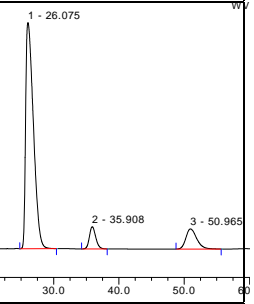
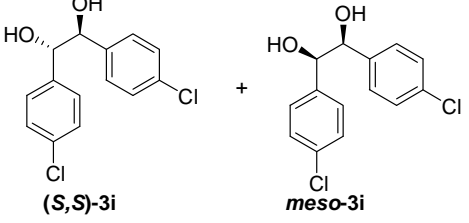
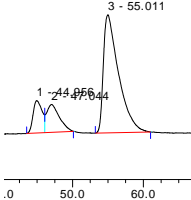
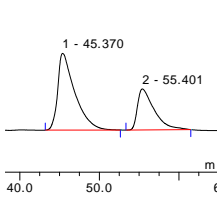
^ae.e. was determined by chiral HPLC on Chiralcel OD-H (Diacel, Japan) column. ^bAbsolute configuration was assigned based on comparison of sign of optical rotation with literature.

Table 3S. HPLC profiles of the products obtained from asymmetric reduction of unsymmetrical benzil derivatives with *T. flavus* at pH 5.0^{a,b}

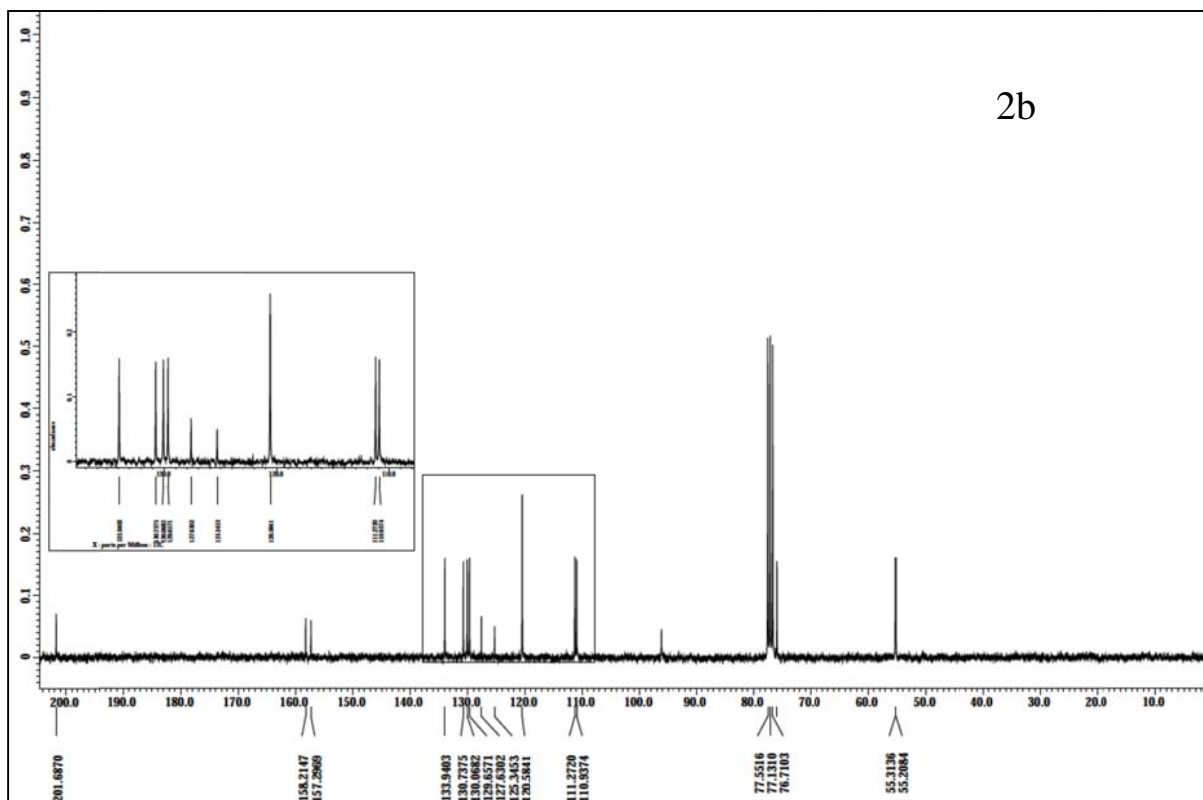
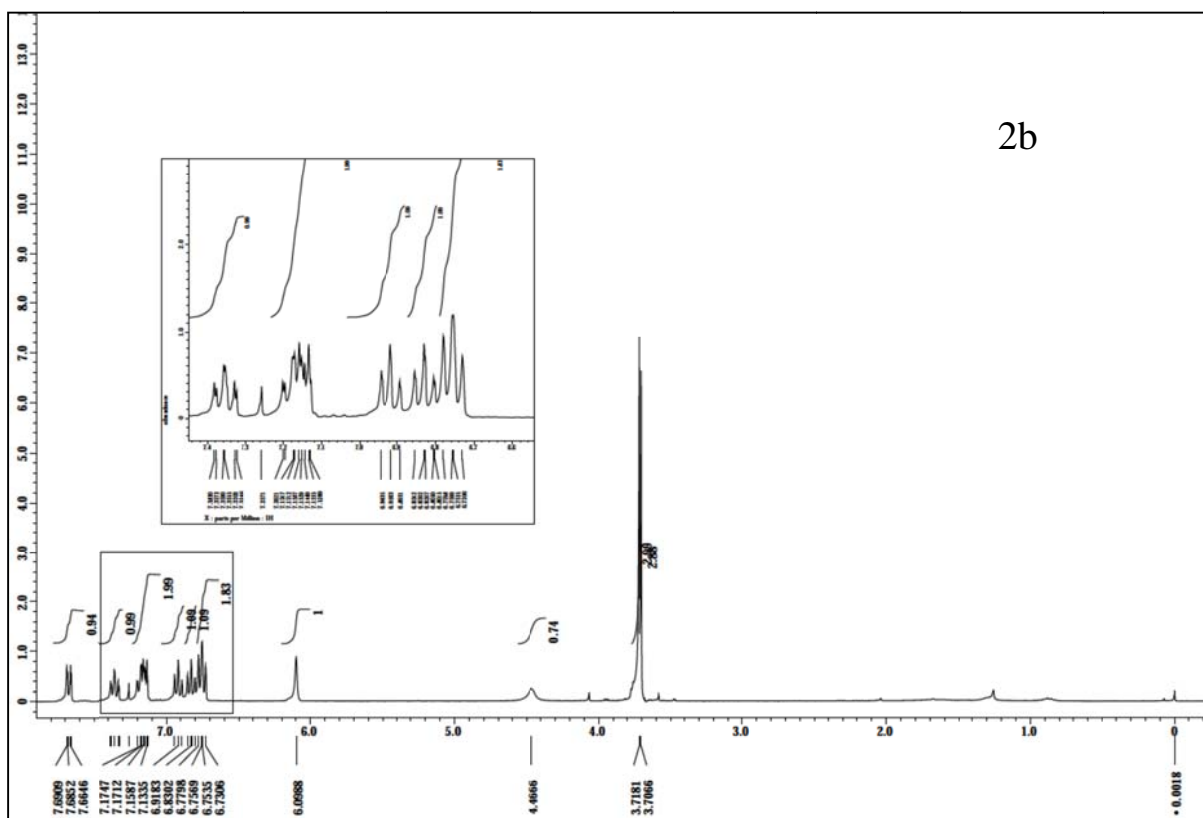
Entry	Biocatalyzed product	<i>rac.</i> benzoin	biocatalyzed benzoin
1	 <p>5a</p>	 <p>2 - 19.436 1 - 19.722</p>	 <p>1 - 19.682 2 - 22.135</p>
2	 <p>5b</p>	 <p>1 - 19.120 2 - 21.234</p>	 <p>1 - 19.161 2 - 21.554</p>
3	 <p>5c</p>	 <p>1 - 15.738 2 - 16.313</p>	 <p>1 - 15.608</p>
4	 <p>5d</p>	 <p>1 - 35.350 2 - 41.908</p>	 <p>1 - 34.521 SB1 2</p>
5	 <p>5e</p>	 <p>1 - 54.434 2 - 56.435</p>	 <p>1 - 53.267</p>

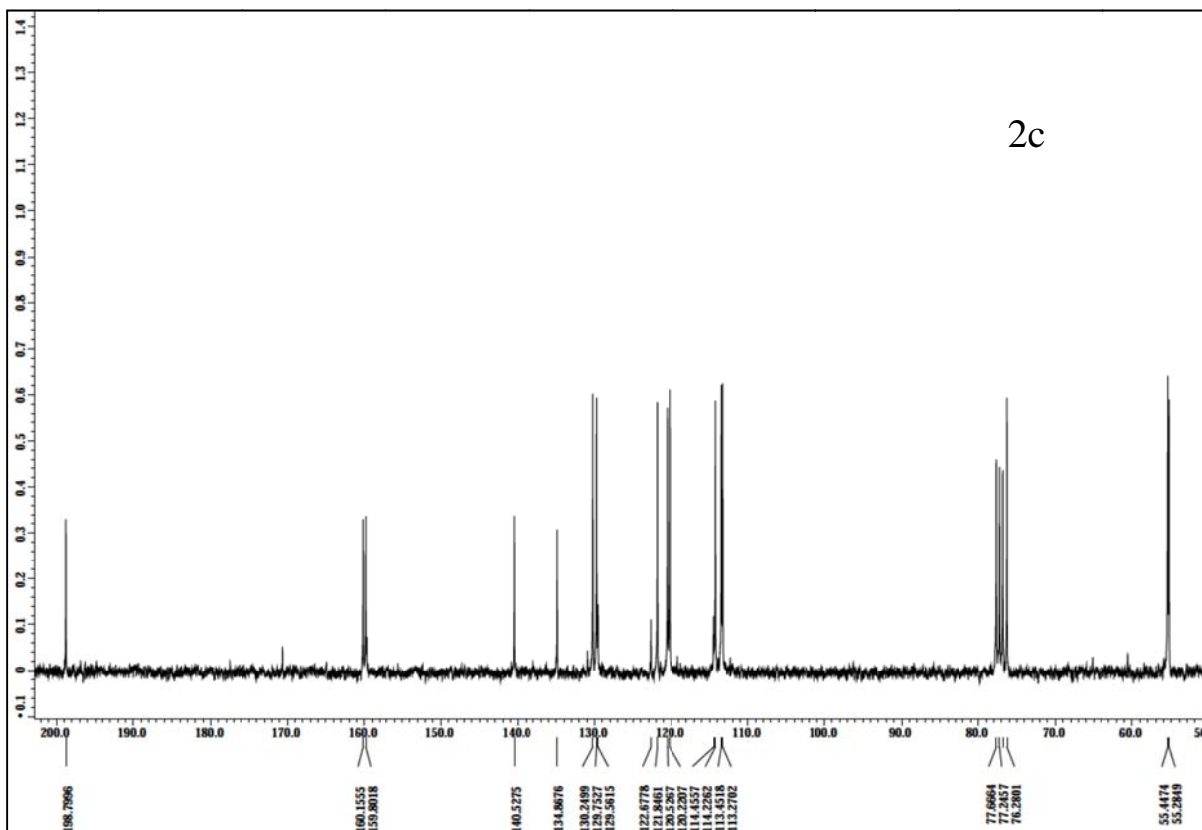
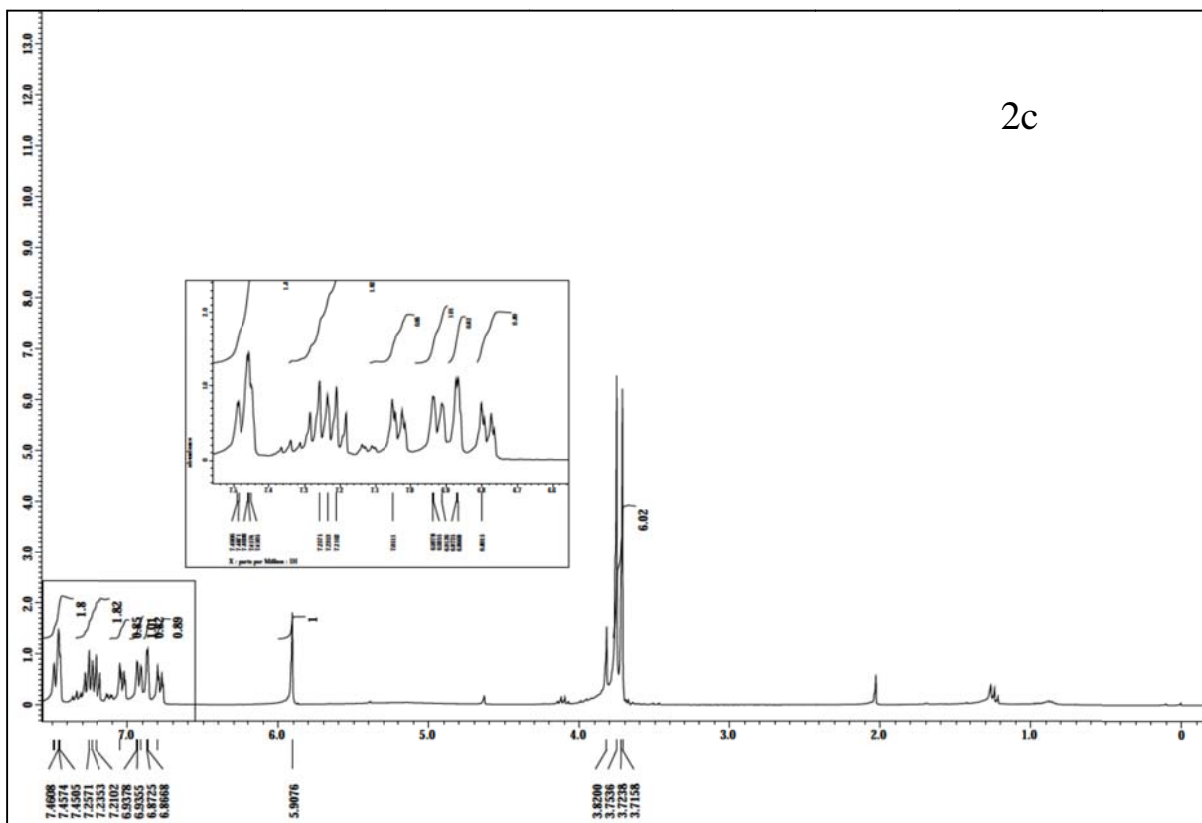
^ae.e. was determined by chiral HPLC on Chiralcel OD-H (Diacel, Japan) column. ^b Configuration tentative

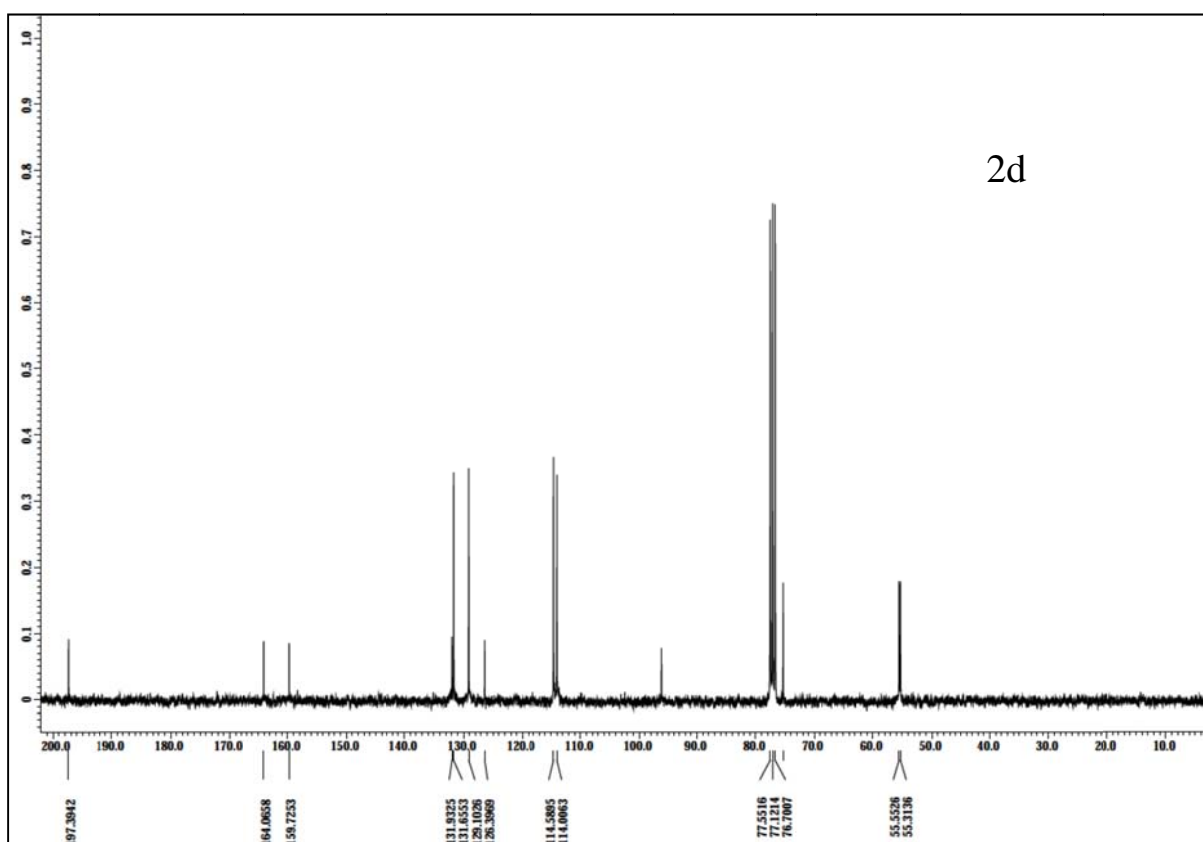
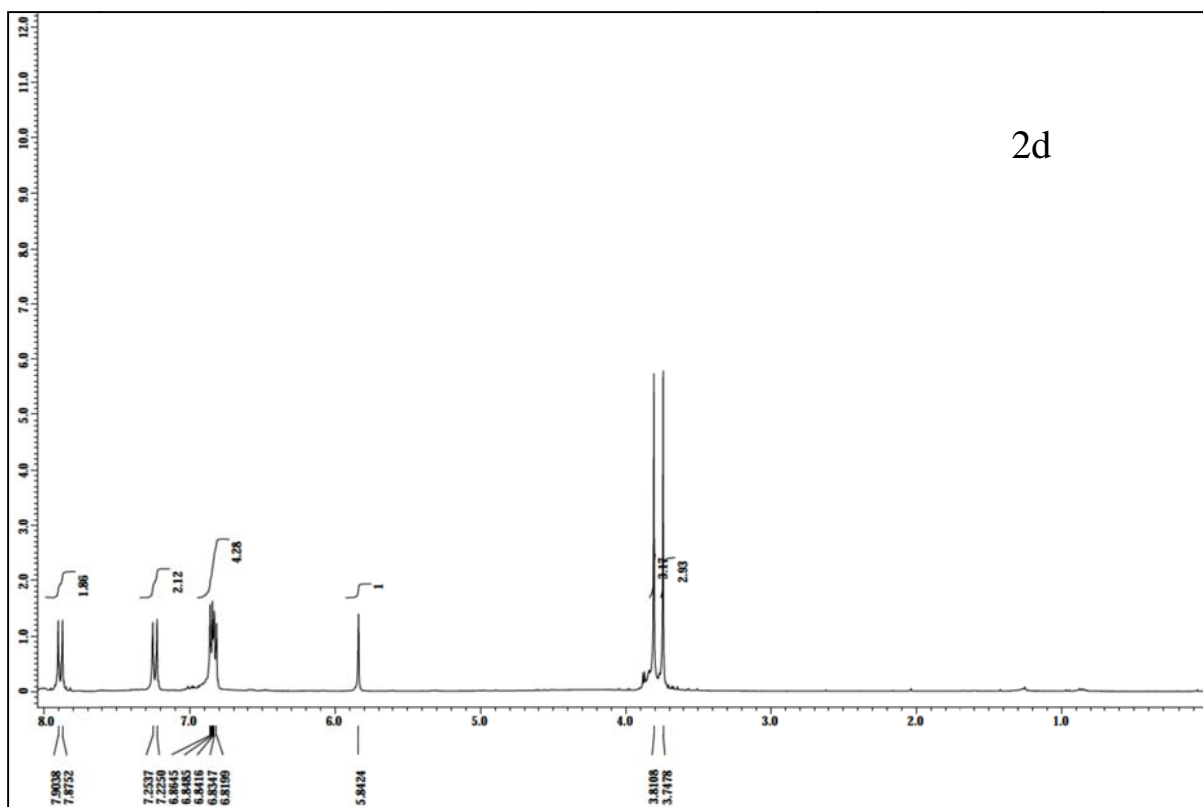
Table 4S. HPLC profiles of the products obtained from asymmetric reduction of symmetrical benzil derivatives with *T. flavus* at pH 7.0^a

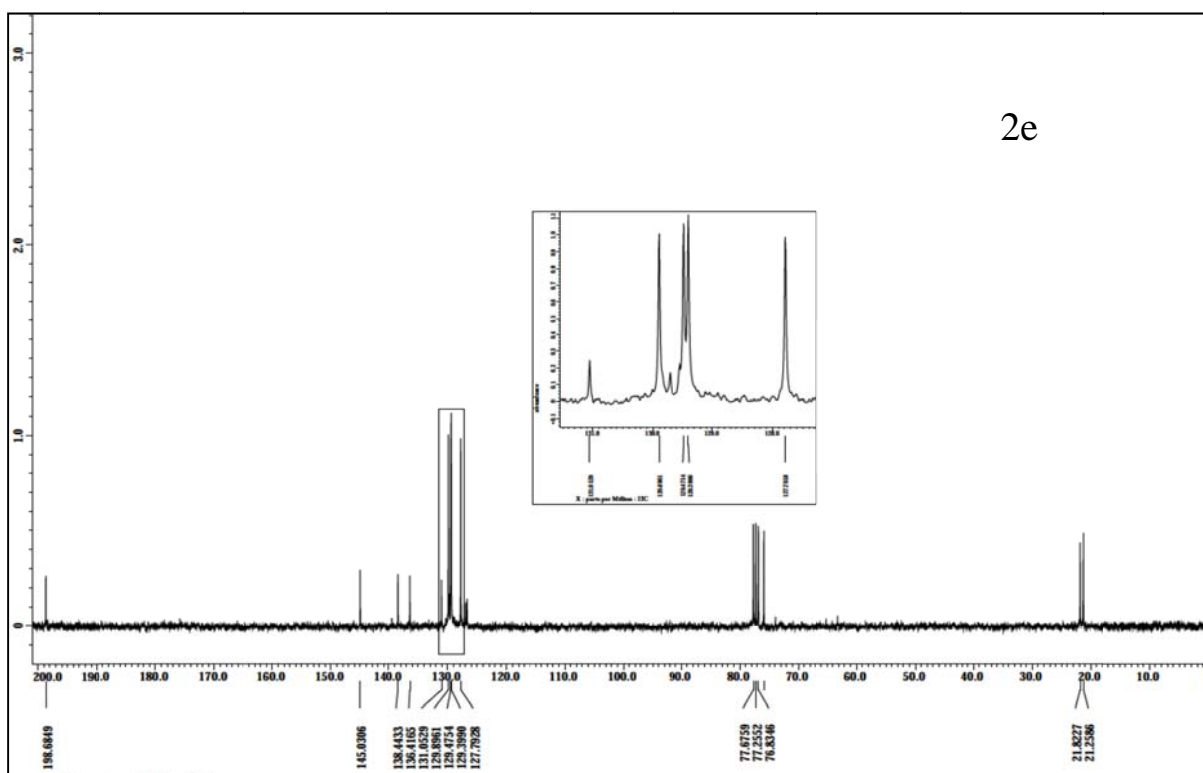
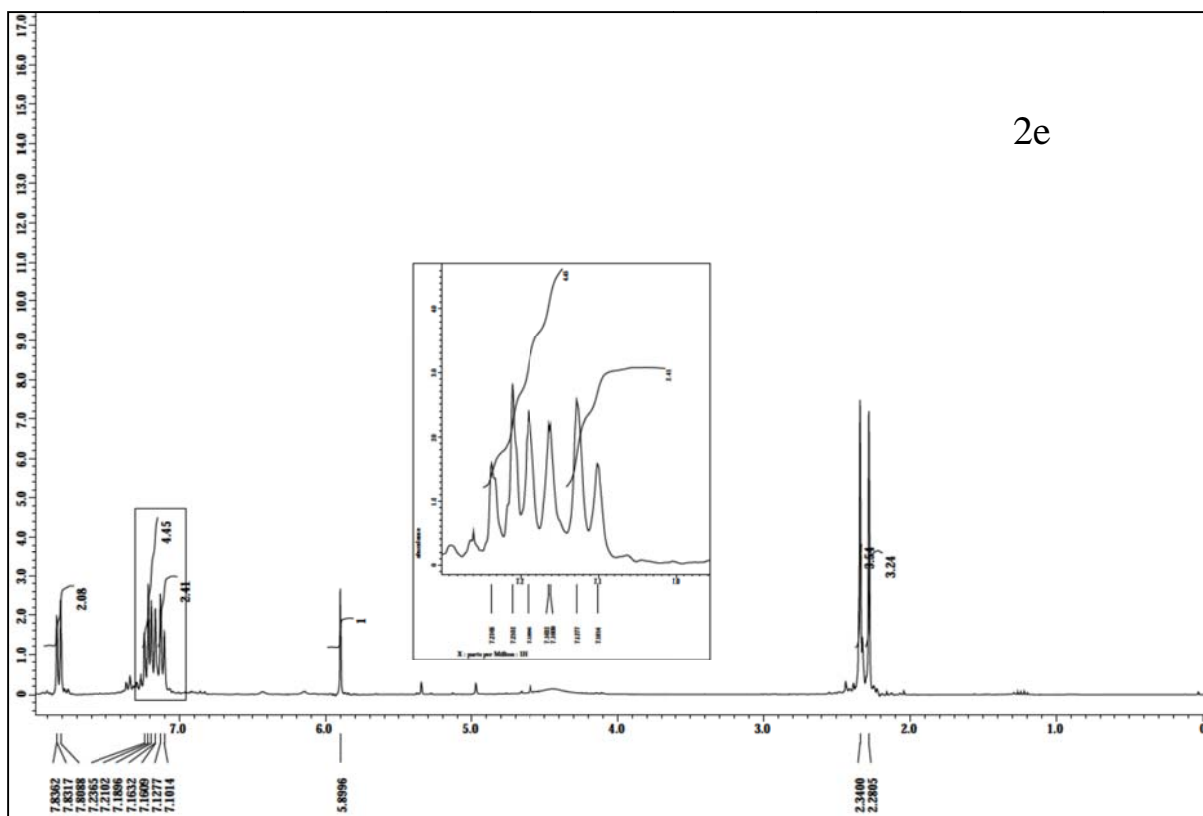
Entry	Biocatalyzed product	<i>rac.</i> benzoin	biocatalyzed benzoin
1	 <p>(S,S)-3a + meso-3a</p>		
2	 <p>(S,S)-3e + meso-3e</p>		
3	 <p>(S,S)-3g + meso-3g</p>		
4	 <p>(S,S)-3i + meso-3i</p>		

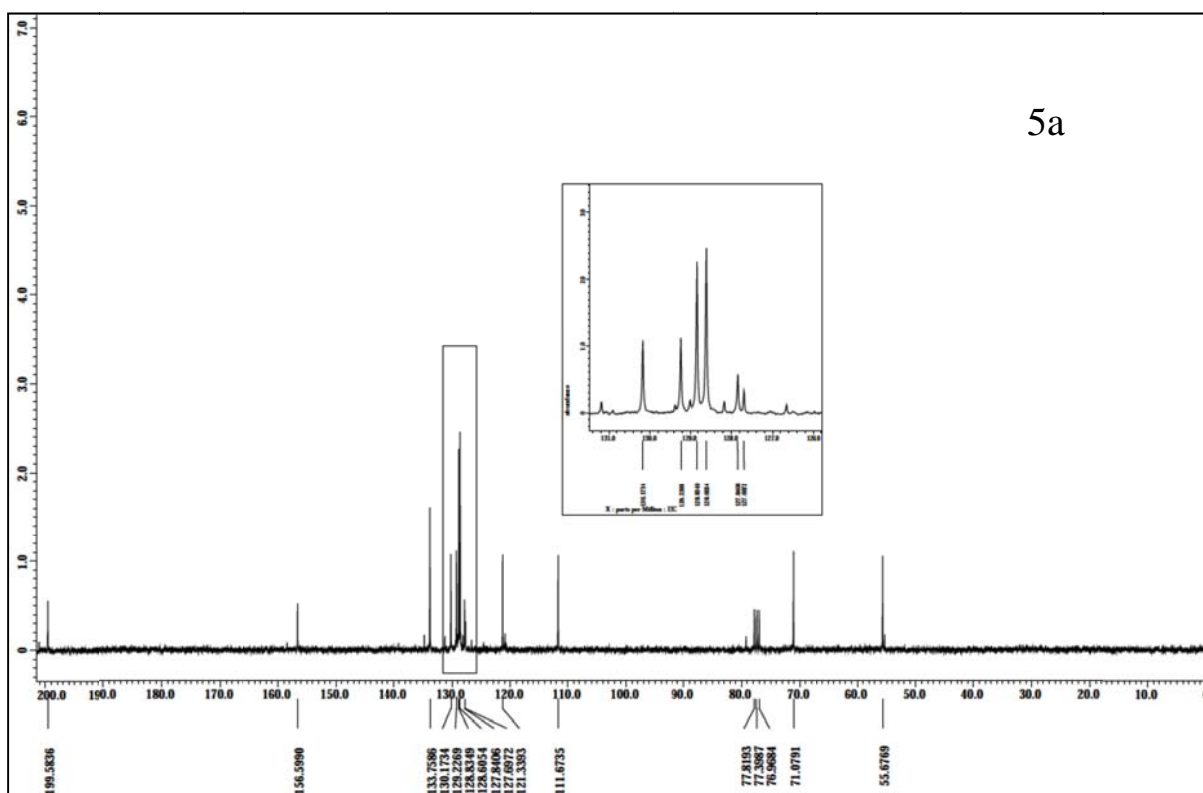
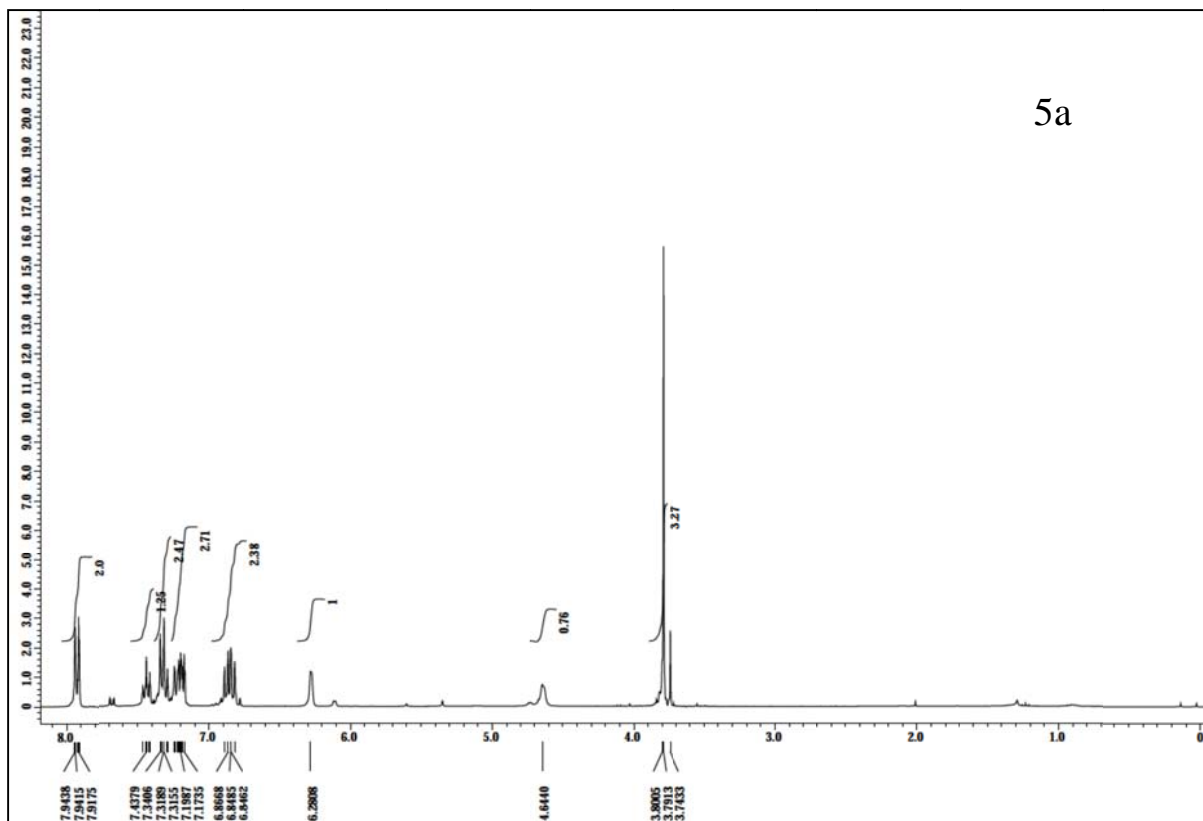
^ae.e. was determined by chiral HPLC on Chiralcel OJ-H (Daicel, Japan) column

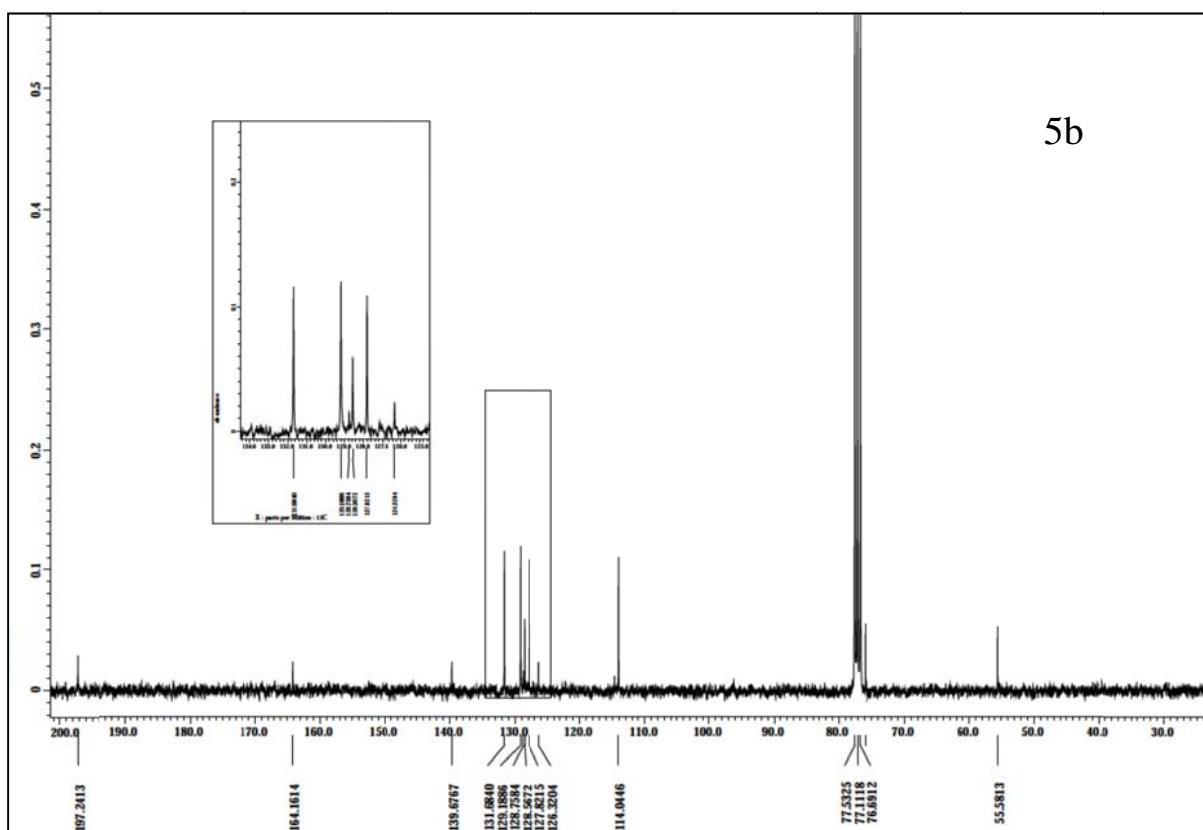
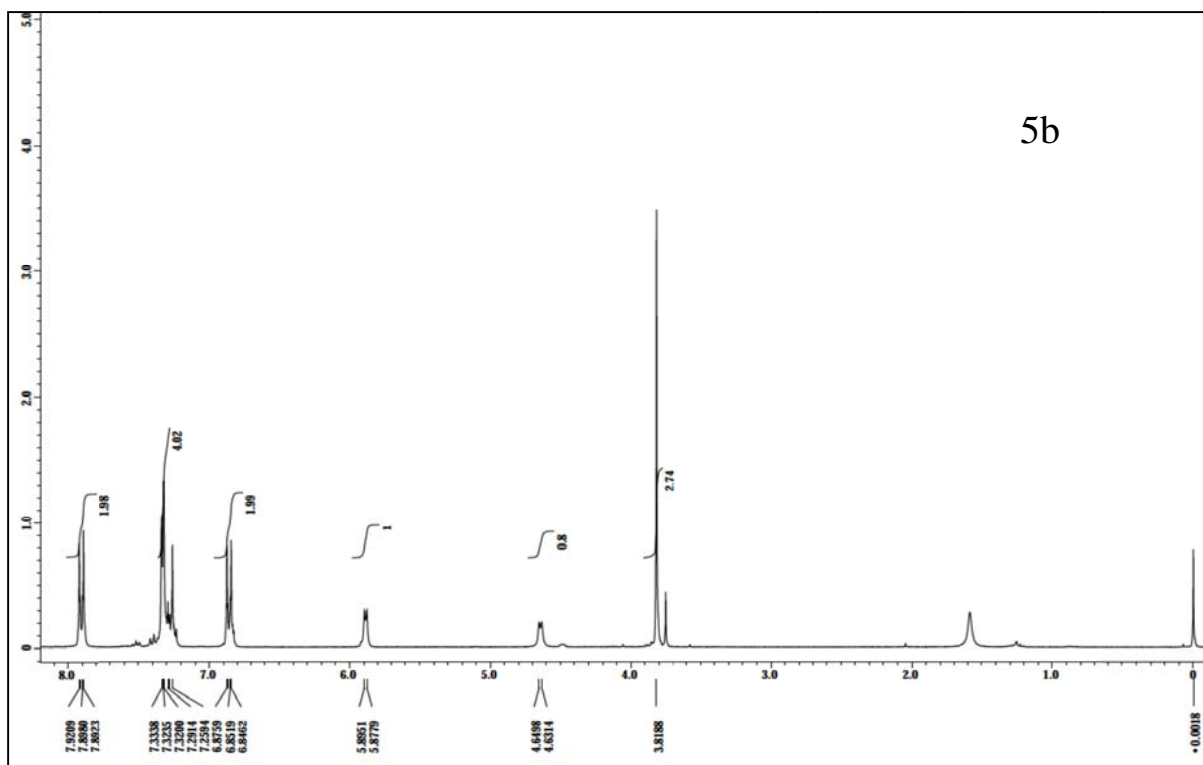


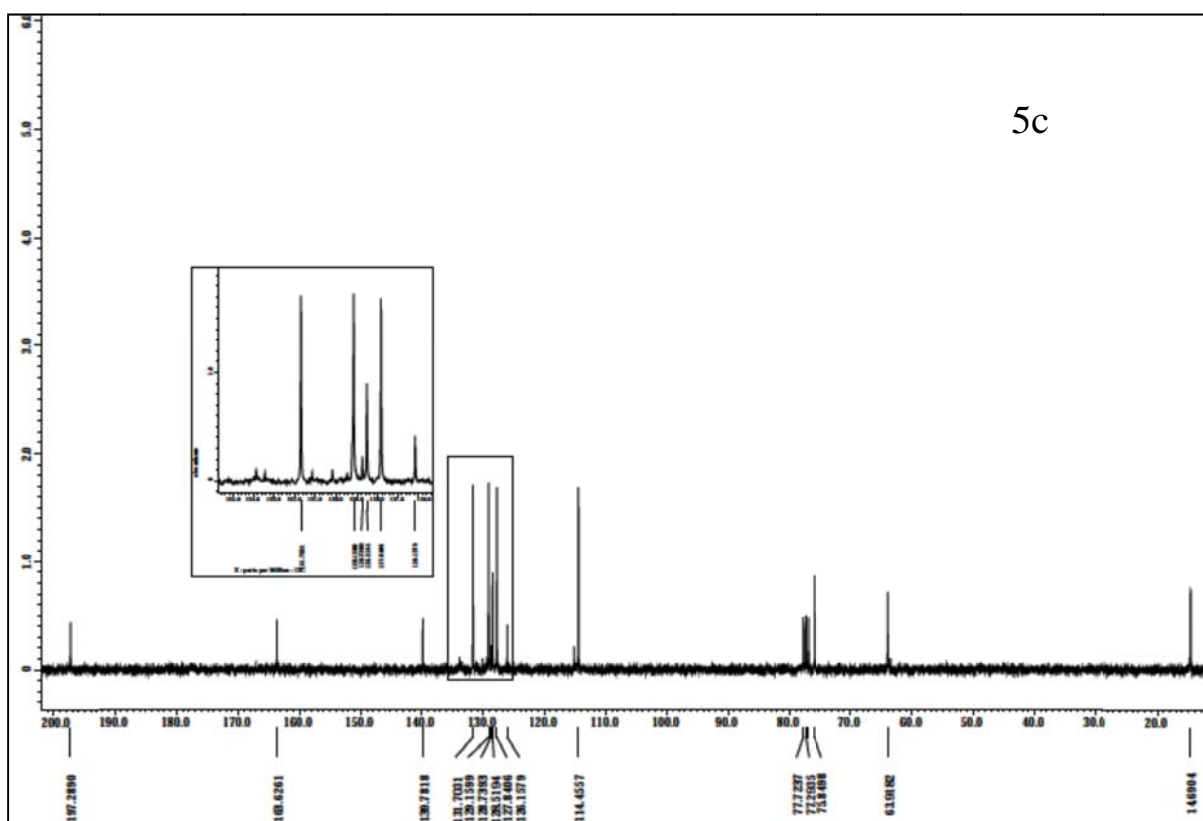
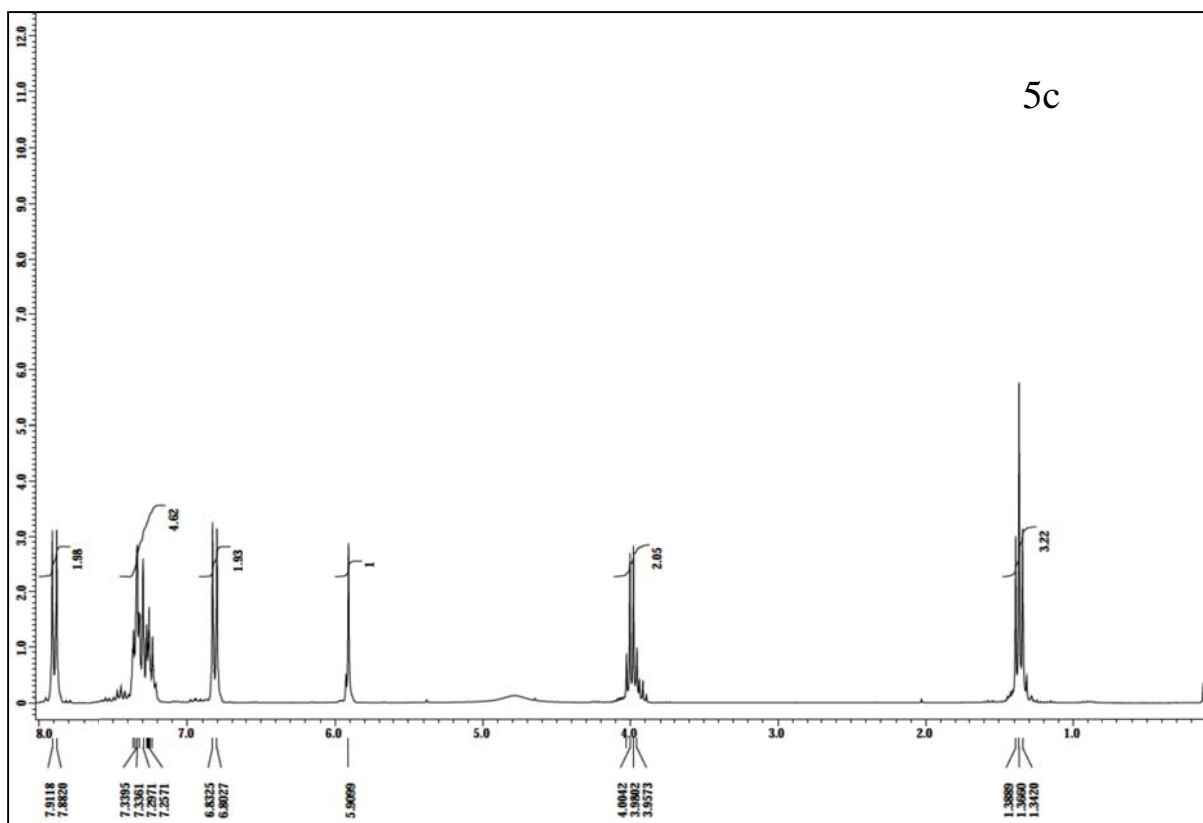


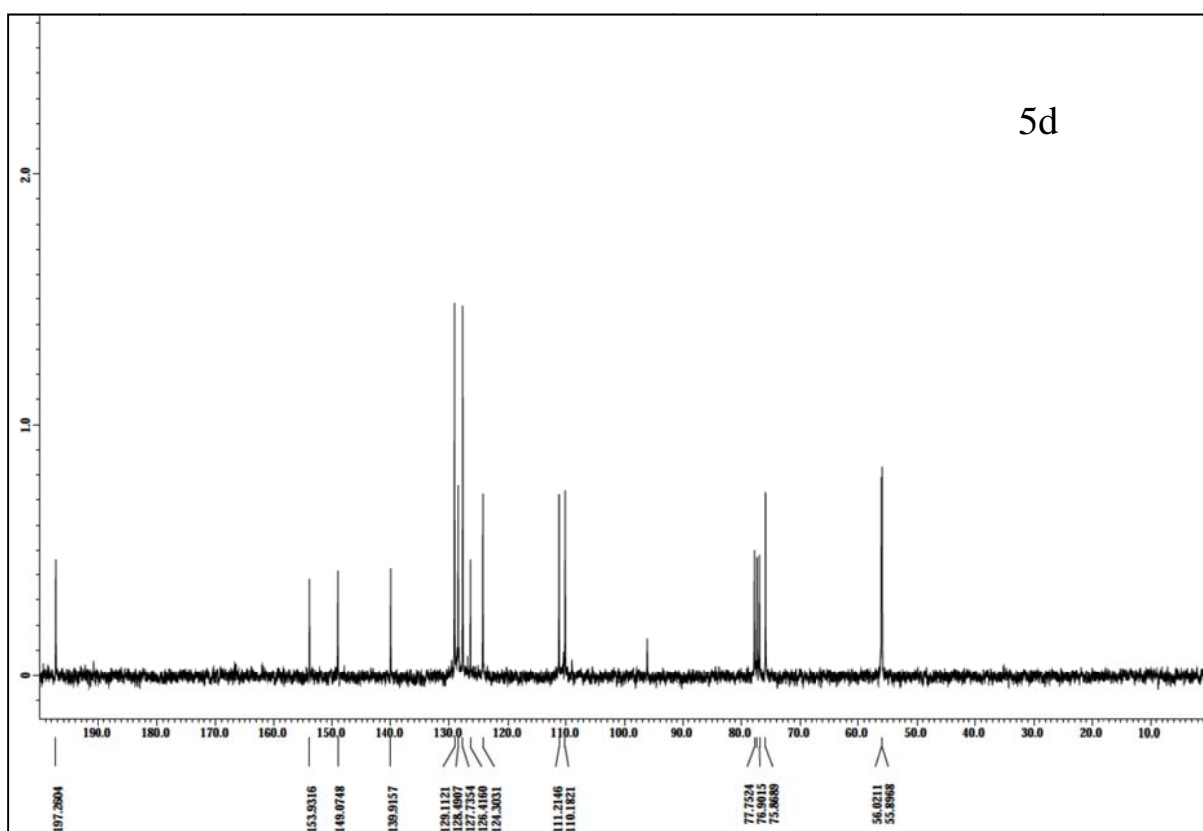
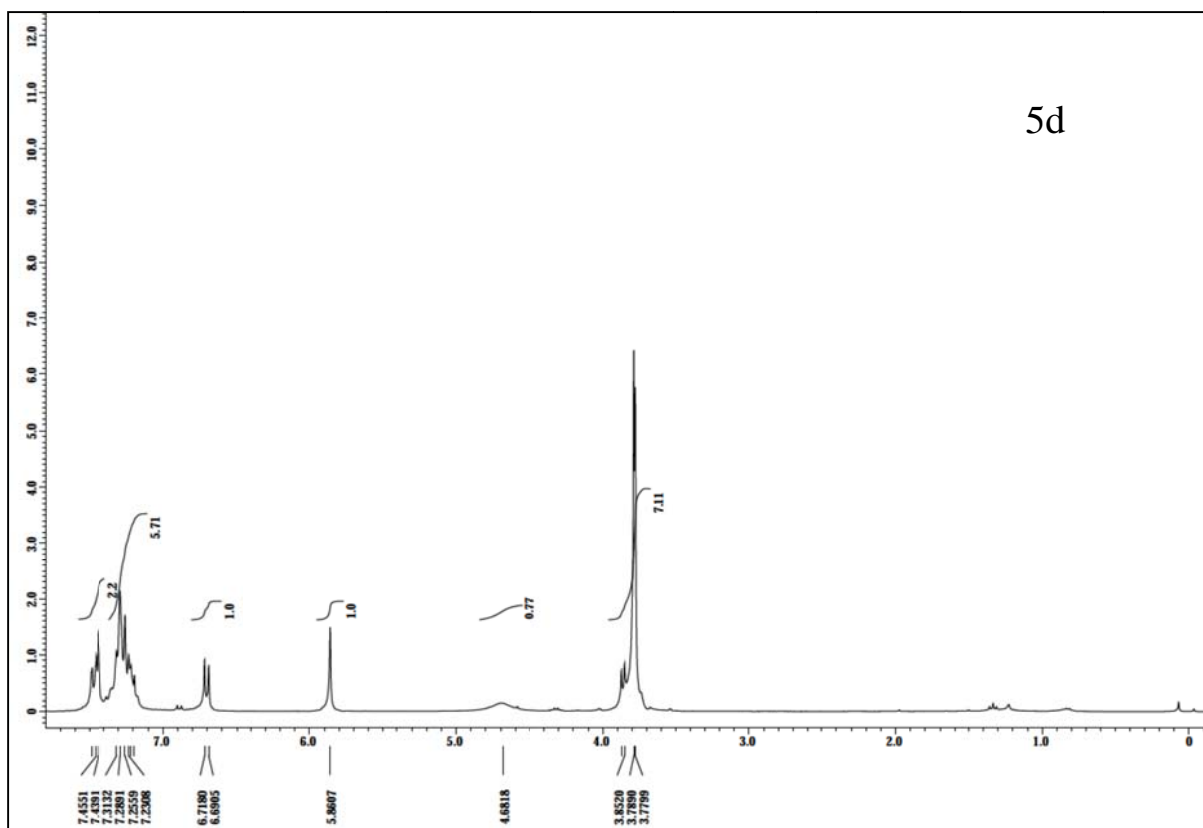


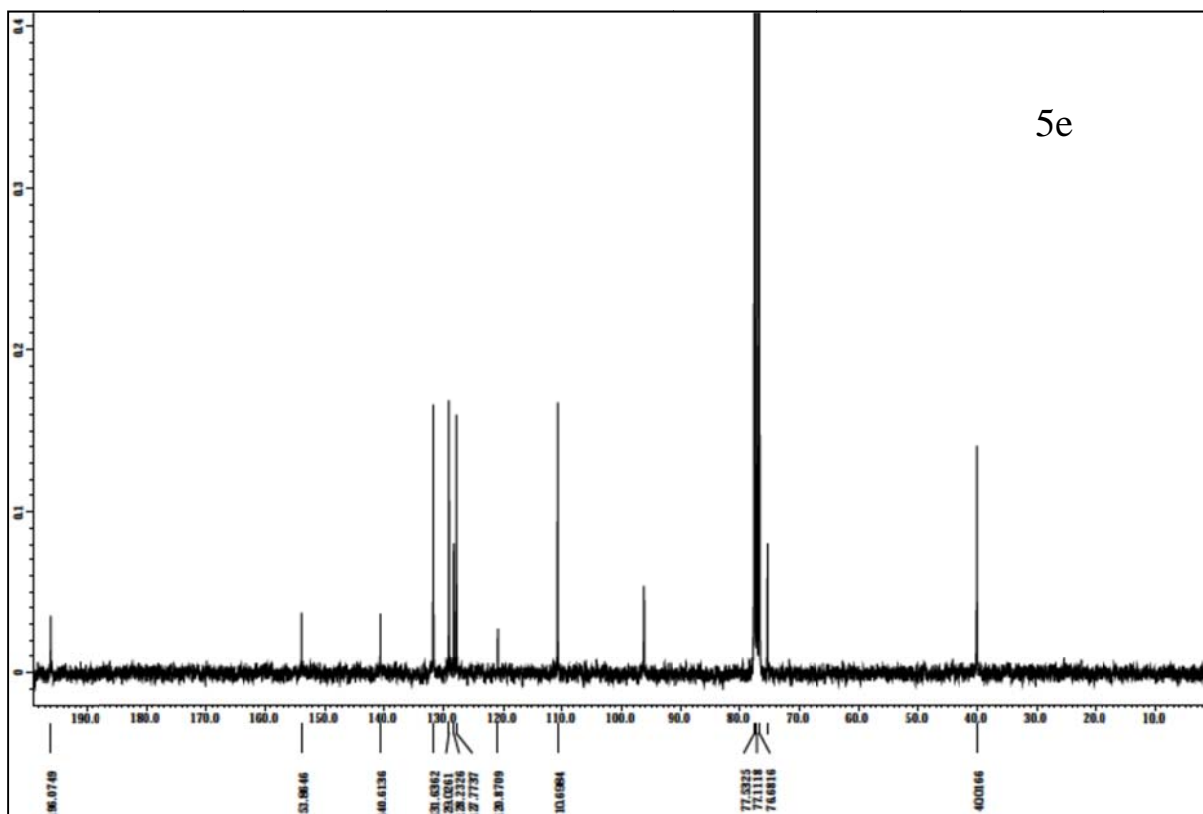
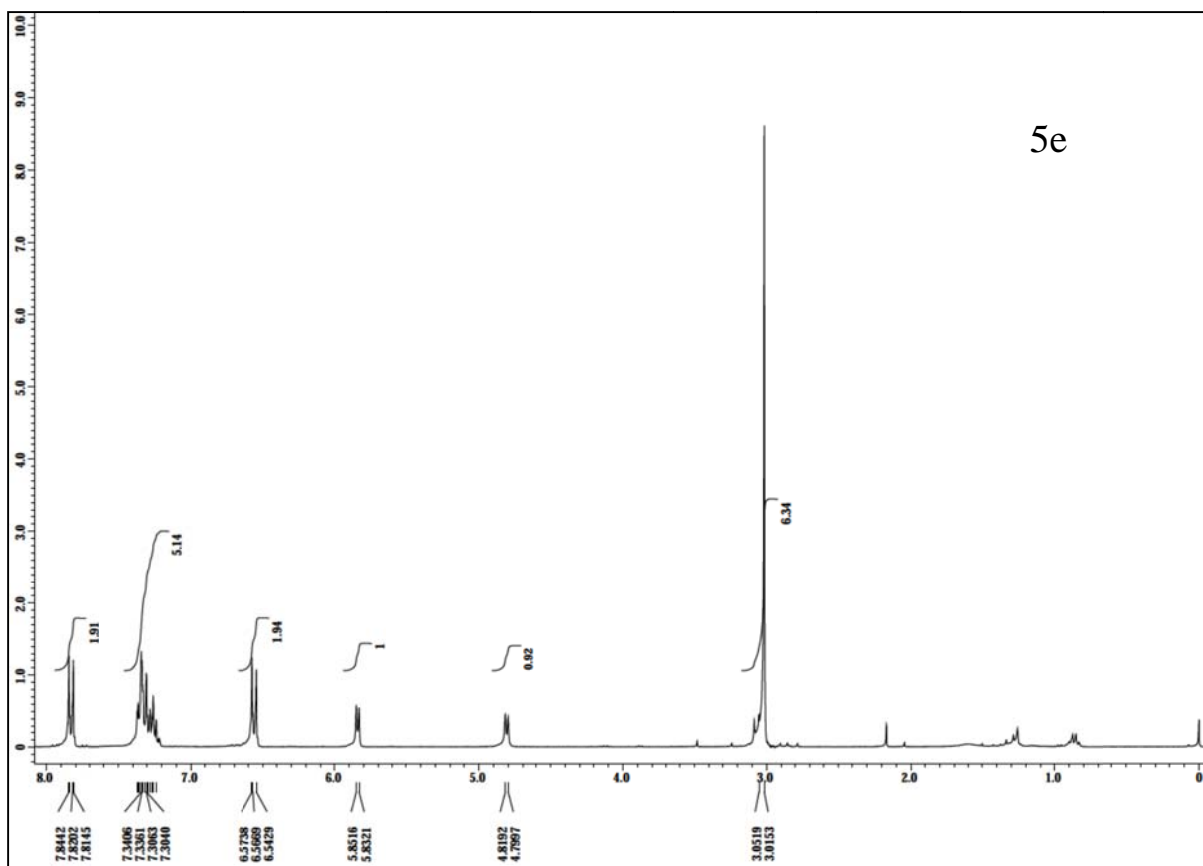


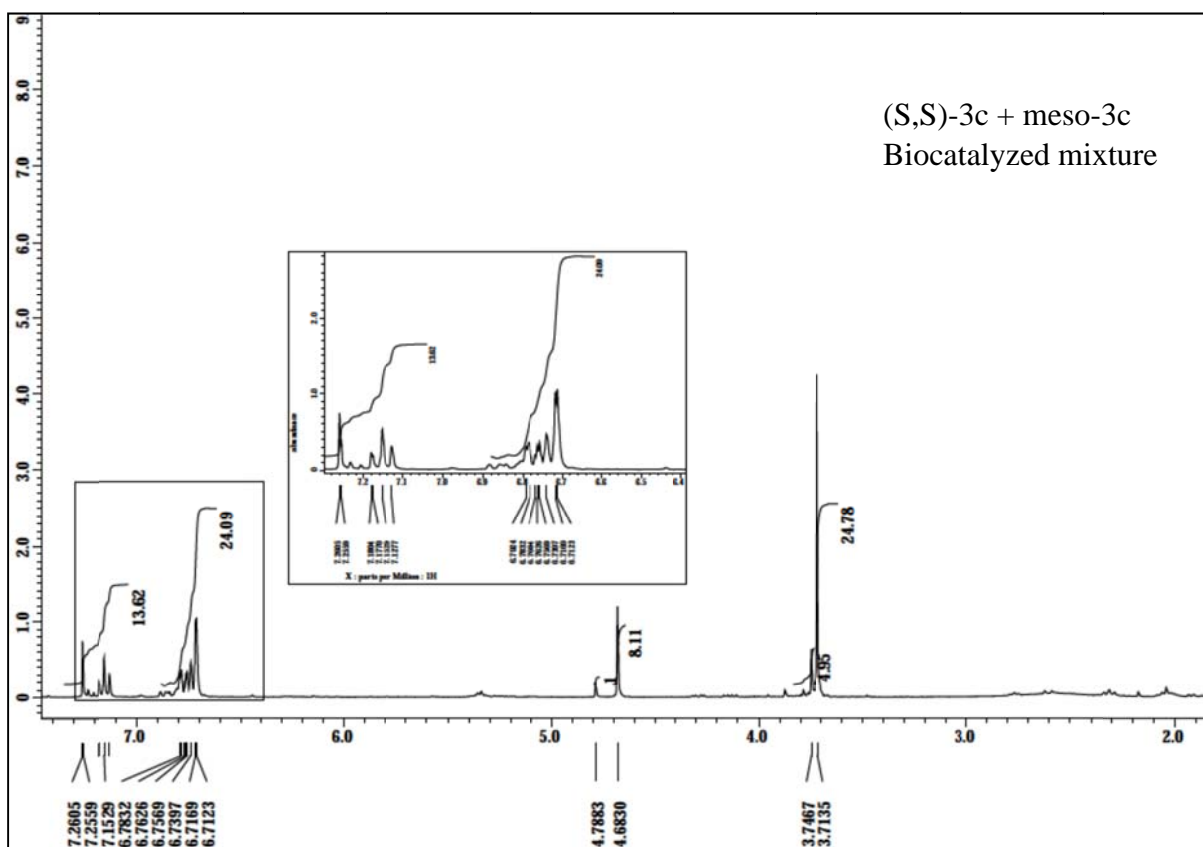
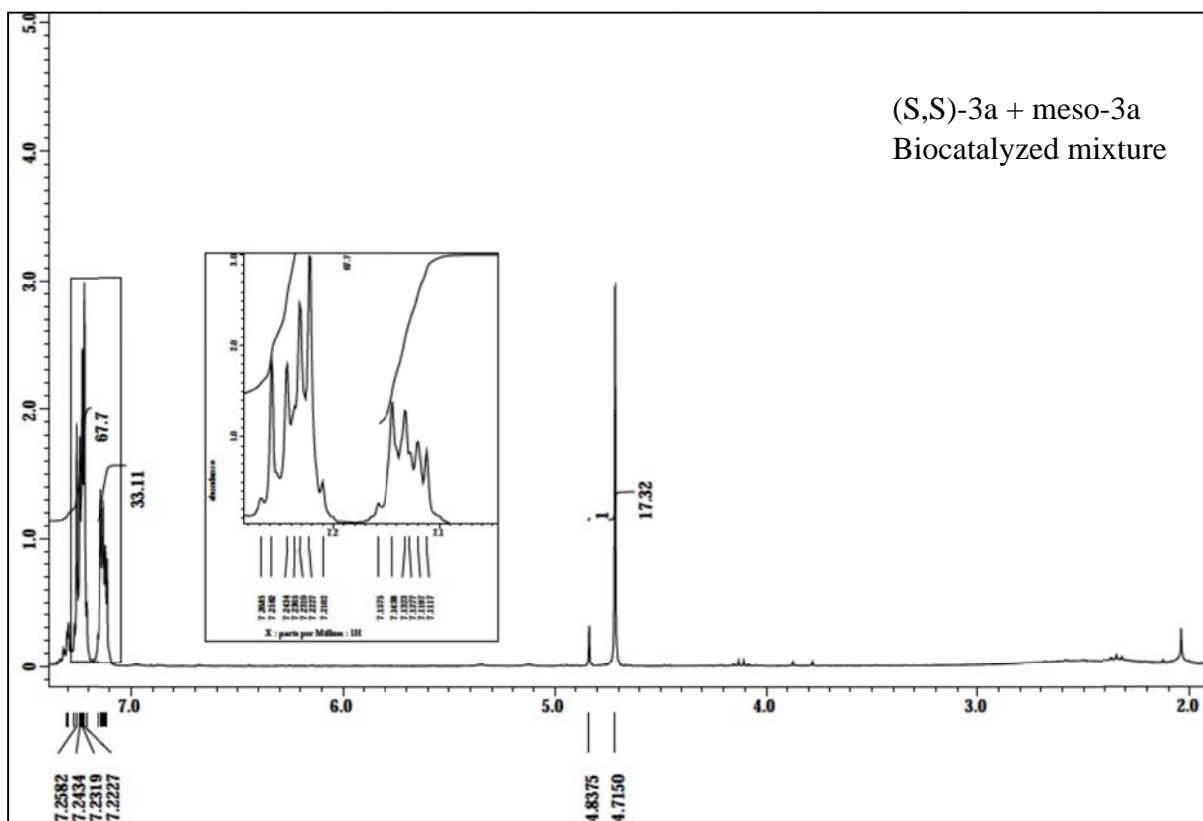


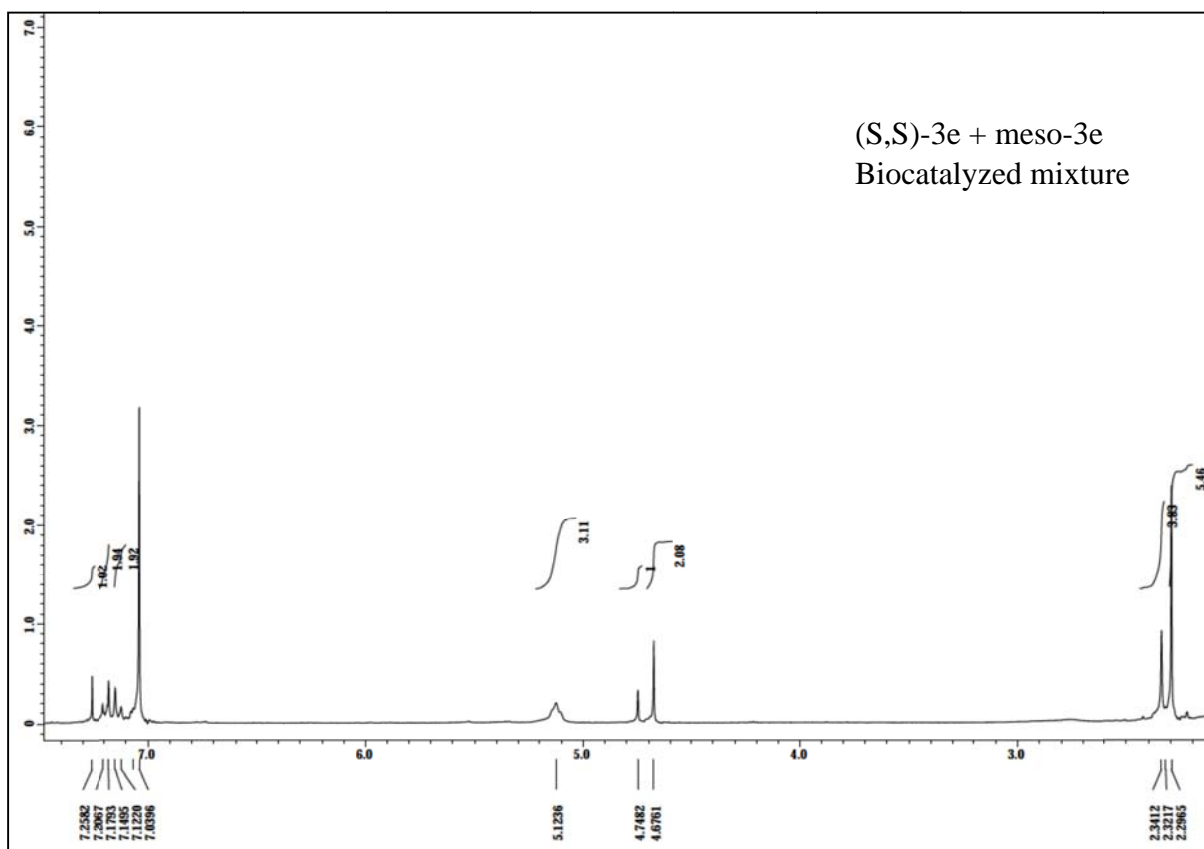
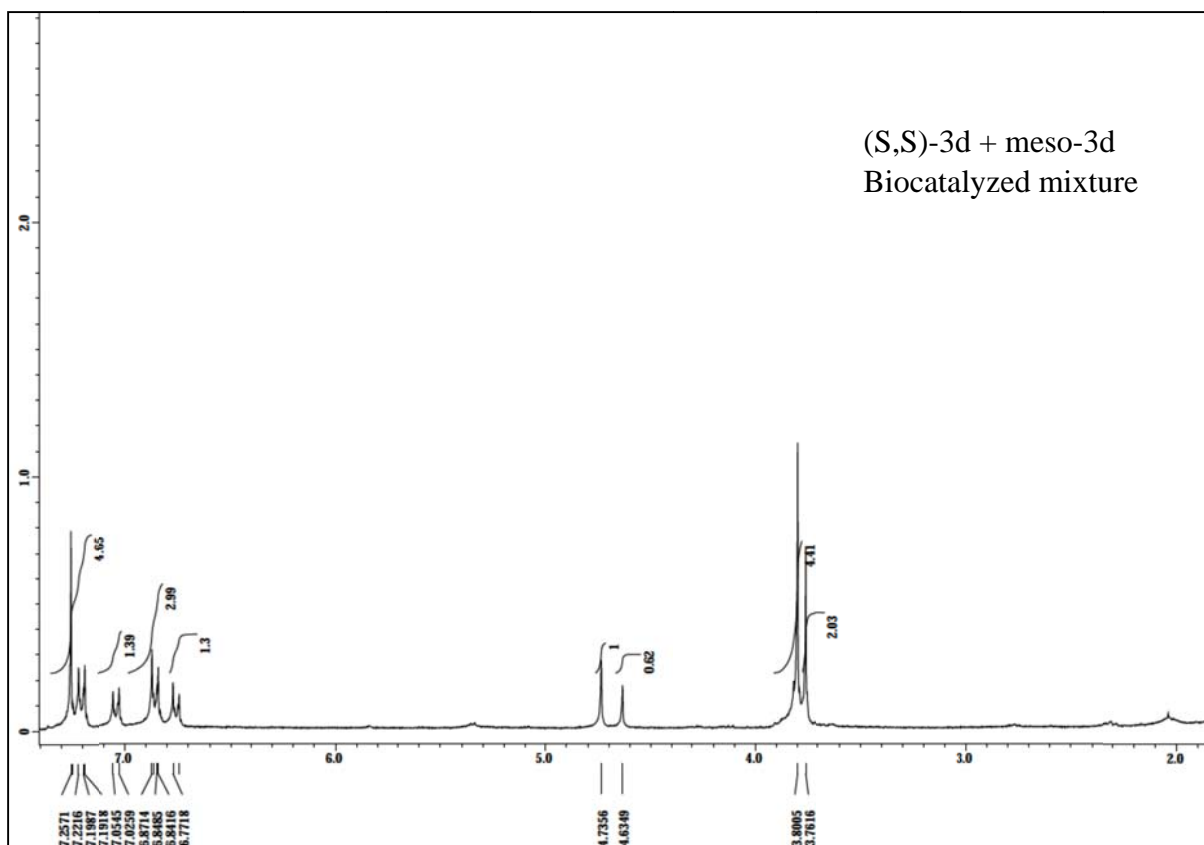


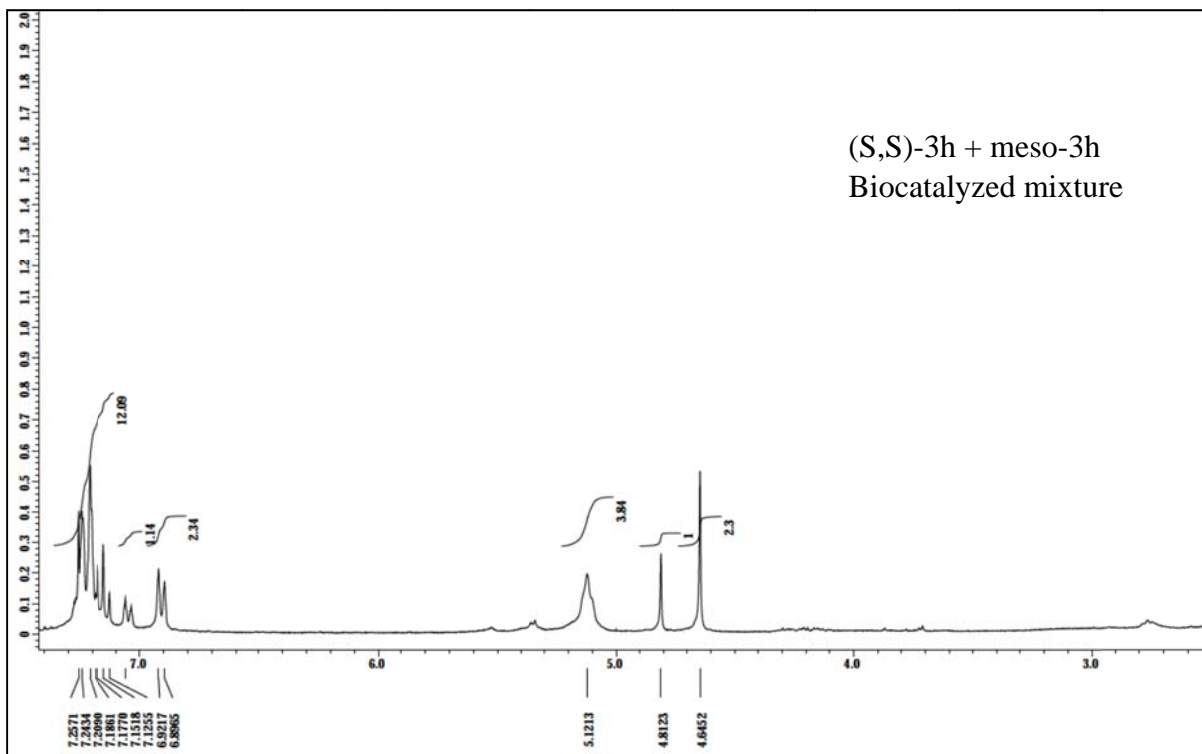
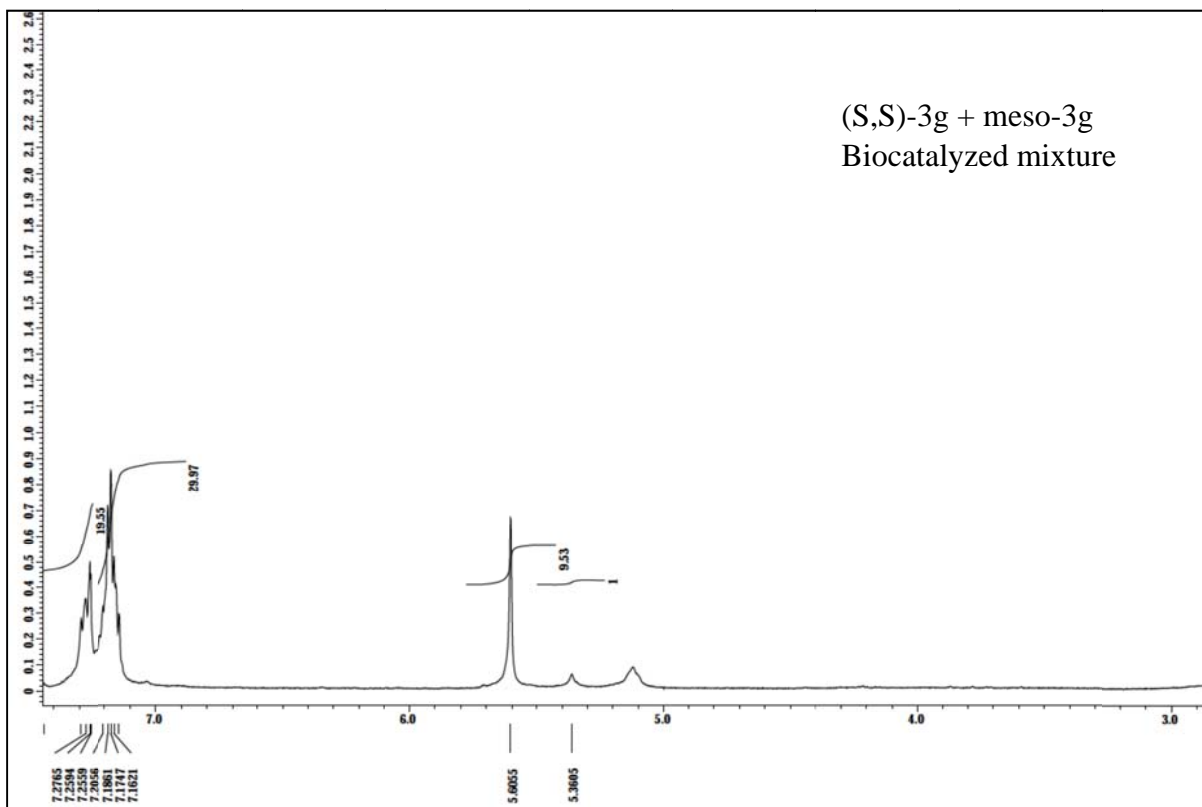












(S,S)-3i + meso-3i
Biocatalyzed mixture

