### **Supporting Information**

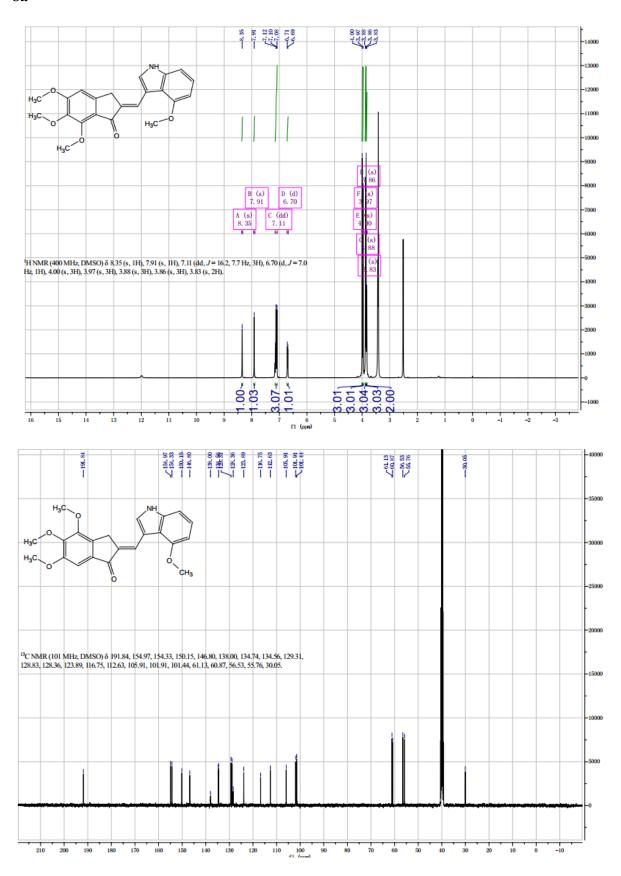
Synthesis, Biological Evaluation and Mechanism Study of Chalcone Analogues as Novel Anti-cancer Agents

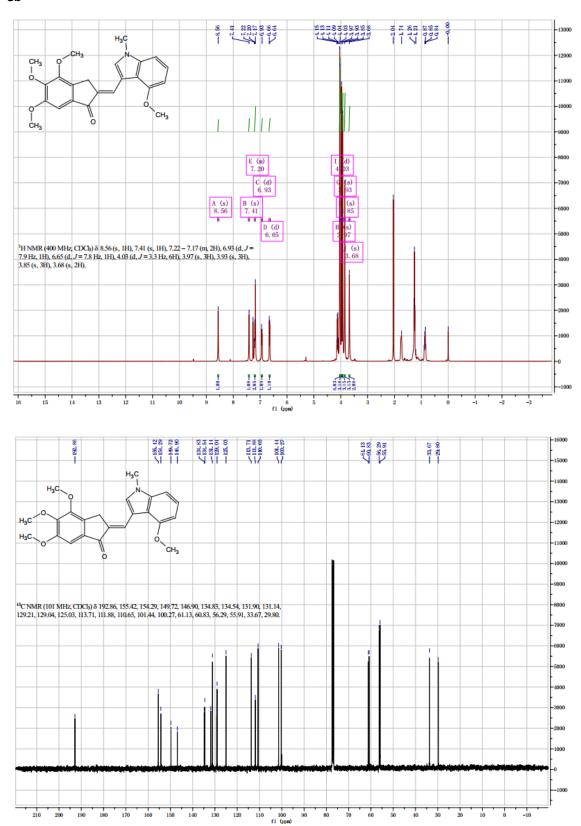
Jie Chena, Jun Yana, Jinhui Hua, Yanqing Panga, Ling Huanga\*, Xingshu Lia\*

<sup>a</sup>School of Pharmaceutical Sciences, Sun Yat-sen University, Guangzhou, 510006, China

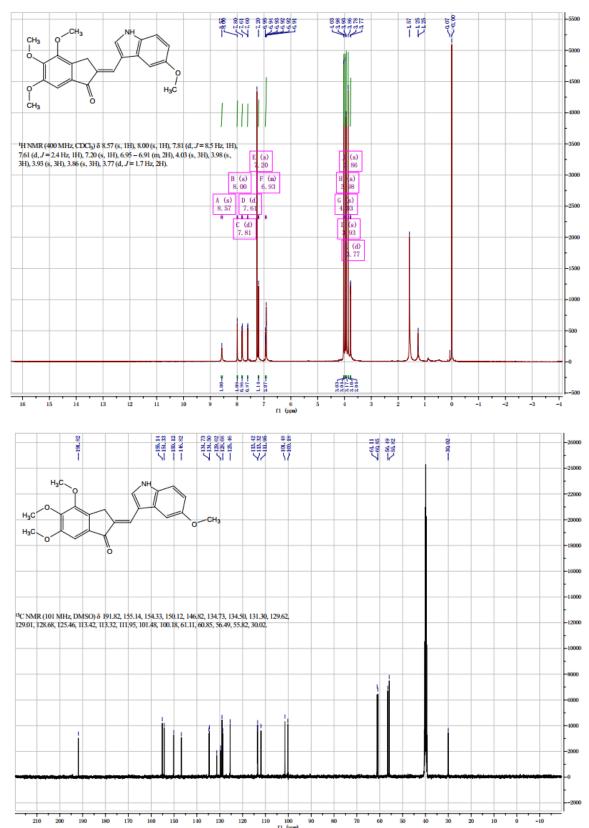
- S I. NMR spectrums of target compounds (S2-S15)
- S II. HPLC chromatograms of target compounds (S16 S20)
- S Ⅲ. High resolution mass spectra of target compounds (S21 S27)
- S IV. IR spectra of target compounds (S28 S32)

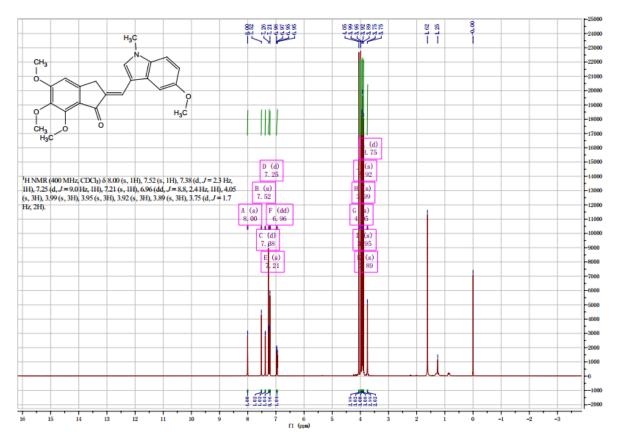
# SI. NMR spectra of target compounds 8a

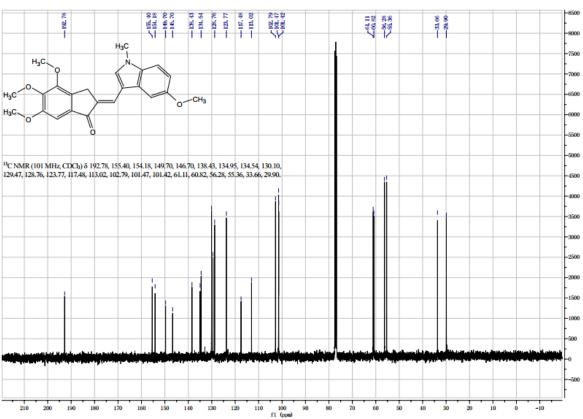


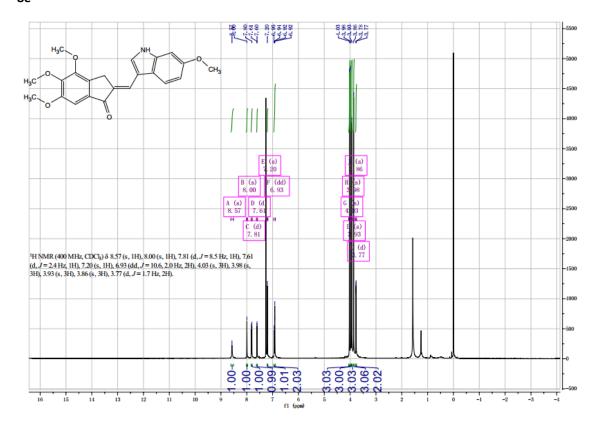


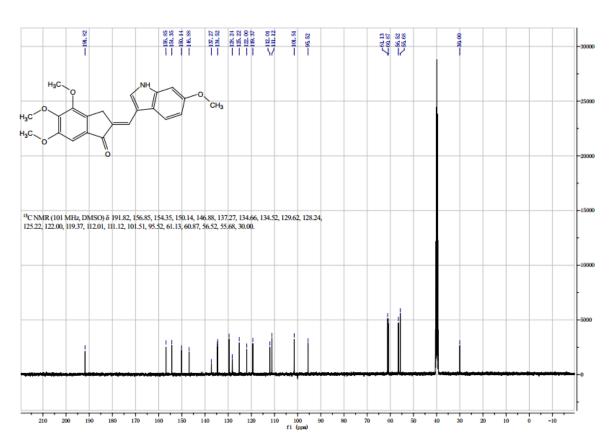


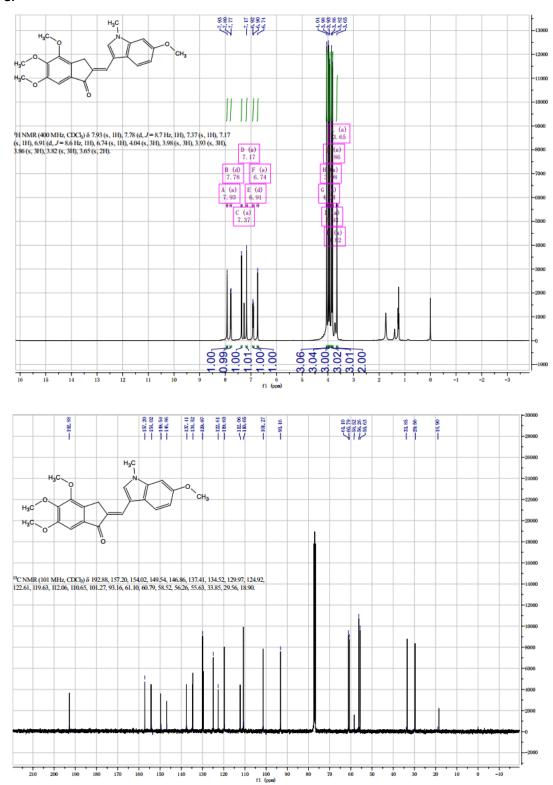


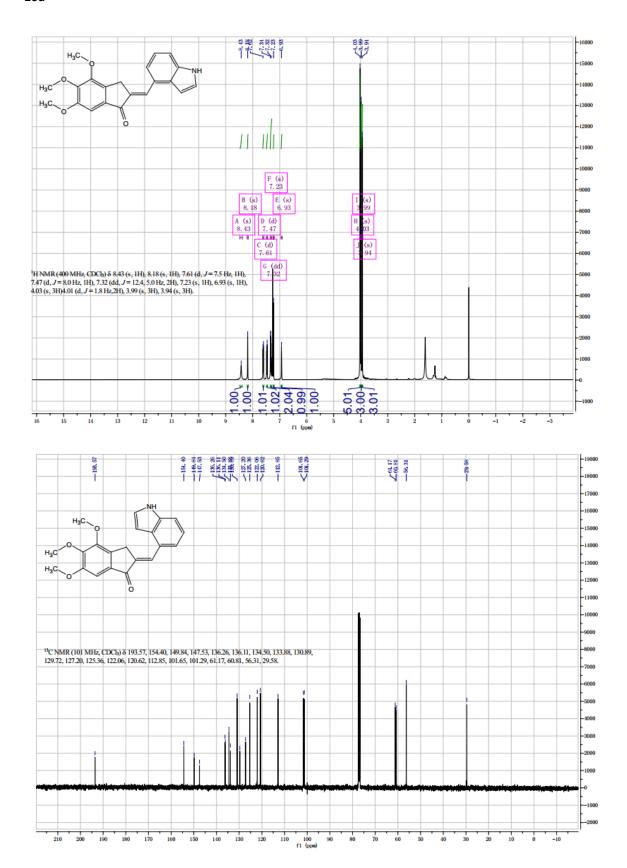


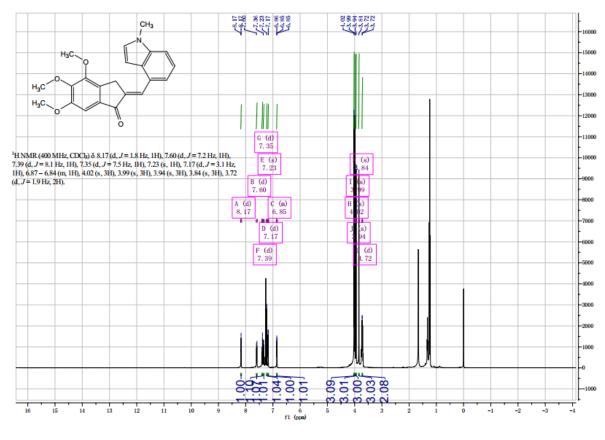


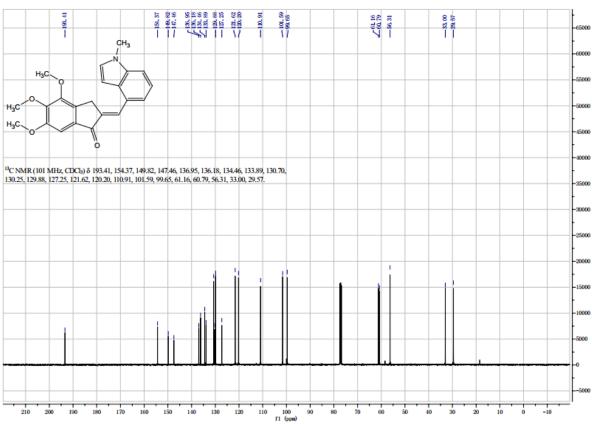


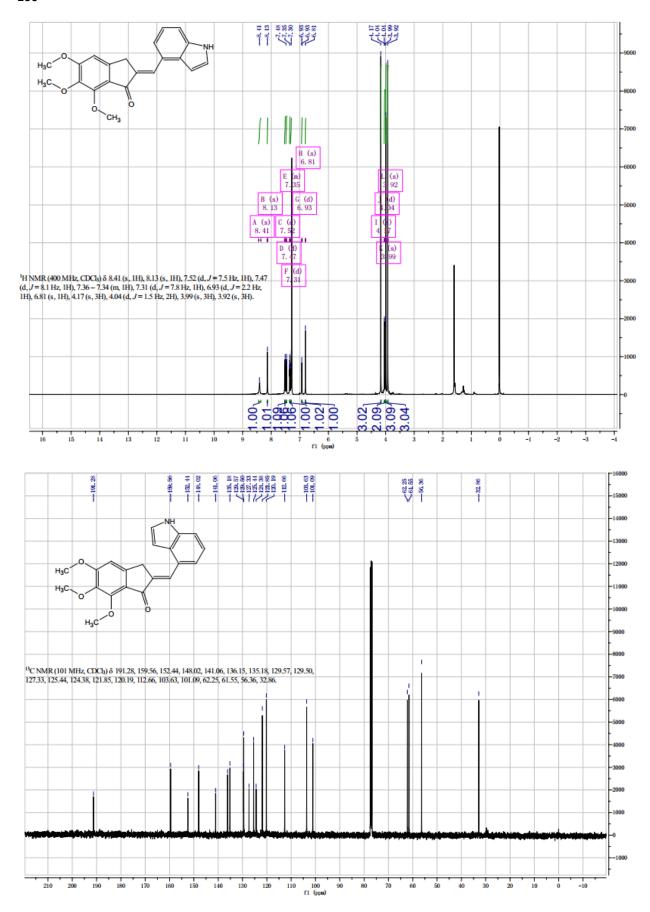


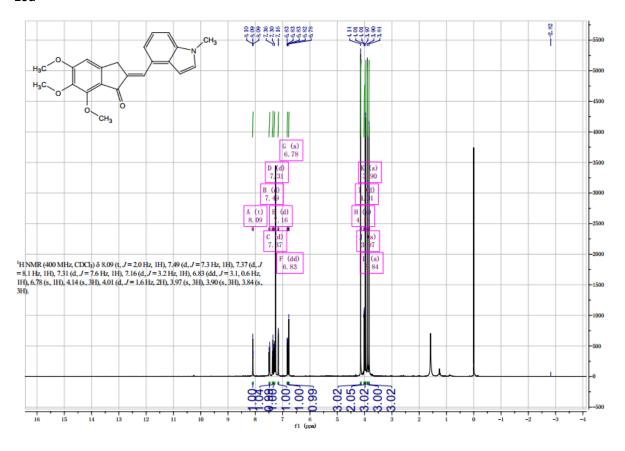


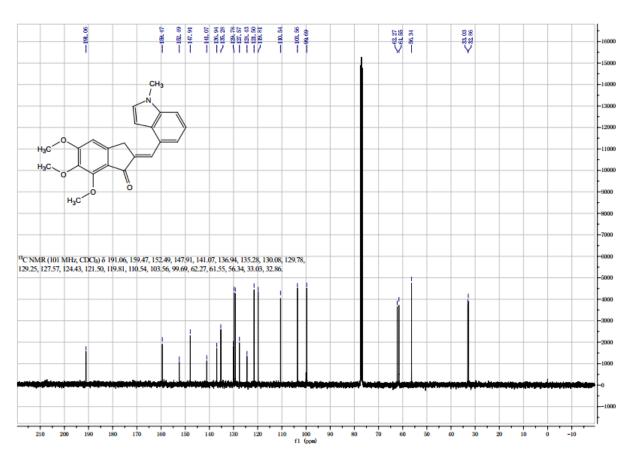


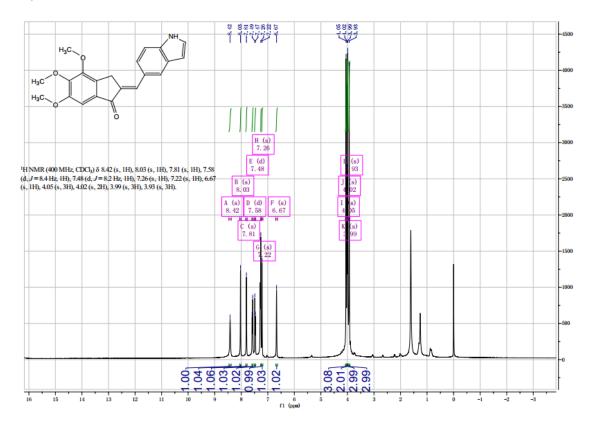


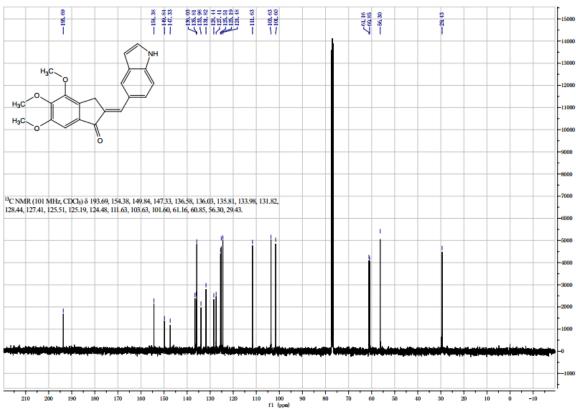


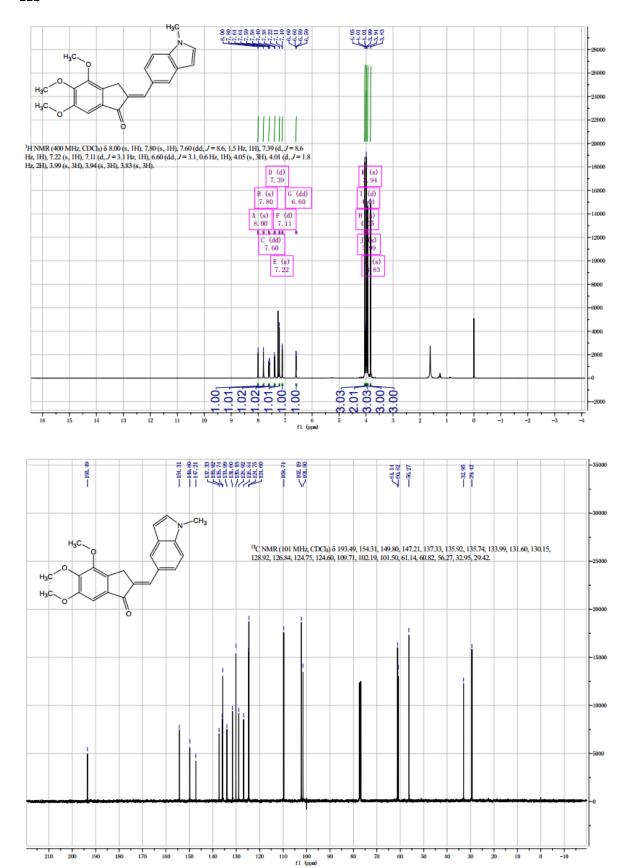


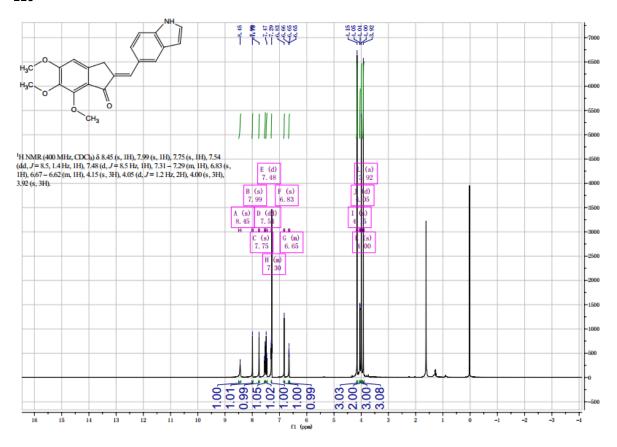


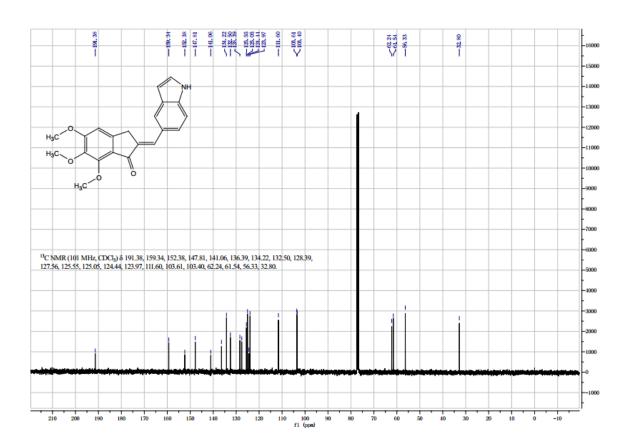


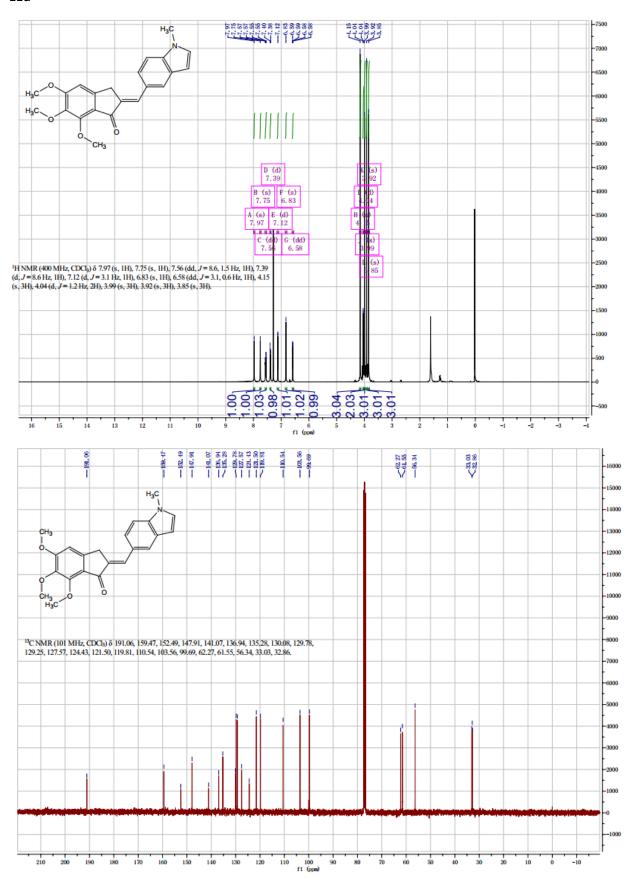






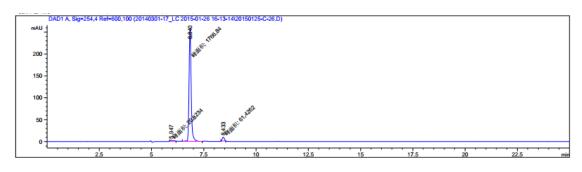






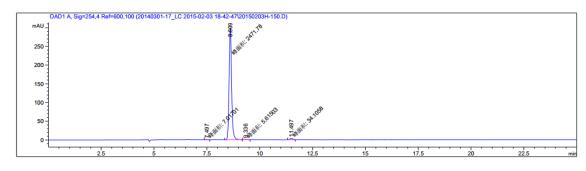
## $S\,I\!I$ . HPLC chromatograms of target compounds

#### 8a

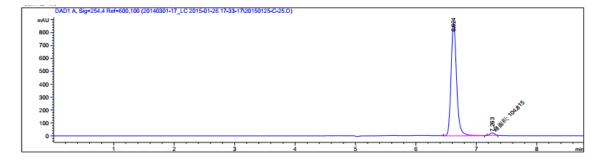


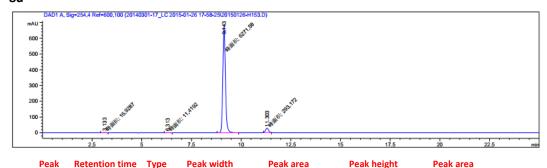
Реак	Retention time	туре	Peak width	Реак агеа	Peak neight	Реак агеа
#	[min]		[min]	[mAU*s]	[mAU]	%
1	5.947	MM	0.1528	20.82343	2.27158	1.1261
2	6.840	MM	0.1164	1766.83618	252.99455	95.5519
3	8.433	MM	0.1162	61.42618	8.81413	3.3220

#### 8b



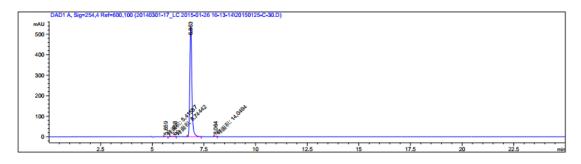
Peak	Retention time	Туре	Peak width	Peak area	Peak height	Peak area
#	[min]			[mAU*s]		용
1	7.497	MM	0.1580	7.01701	7.40000e-1	0.2786
2	8.609	MM	0.1382	2471.78442	298.17245	98.1442
3	9.336	MM	0.1755	5.61503	5.33199e-1	0.2229
4	11.497	MM	0.1659	34.10582	3.42686	1.3542





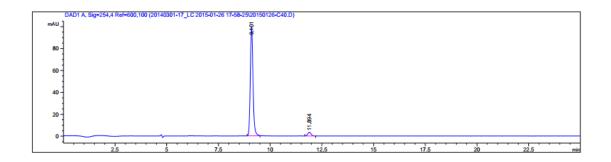
Peak	Retention time	туре	Peak width	reak area	Peak neight	Peak area	
#	[min]		[min]	[mAU*s]	[mAU]	8	
1	3.133	MM	0.2036	16.92868	1.38594	0.2568	
2	6.313	MM	0.2386	11.41923	7.97671e-1	0.1732	
3	9.143	MM	0.1546	6271.58398	676.11389	95.1234	
4	11.303	MM	0.1740	293.17224	28.08739	4.4466	

#### 8e



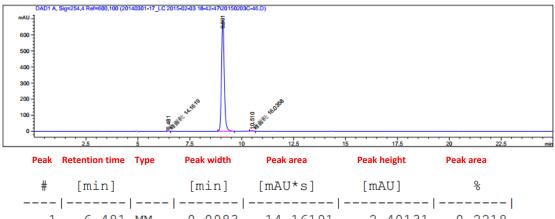
Peak	Retention time	Туре	Peak width	Peak area	Peak height	Peak area	
#	[min]		[min]	[mAU*s]	[mAU]	%	
1	5.659	MM	0.1147	5.41587	7.87158e-1	0.1435	
2	6.108	MM	0.1981	8.74442	7.35660e-1	0.2317	
3	6.863	BB	0.1076	3745.78003	535.80304	99.2525	
4	8.064	MM	0.1007	14.04943	2.32630	0.3723	

8f



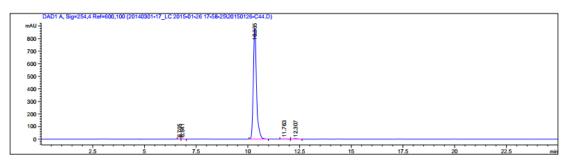
P	Peak	Retention time	Type	Peak width	Peak area	Peak height	Peak area
	#	[min]		[min]	[mAU*s]	[mAU]	8
-							
	1	9.101	BB	0.1383	908.48114	99.73994	95.9244
	2	11.894	BB	0.1785	38.59943	3.34932	4.0756

#### 10a

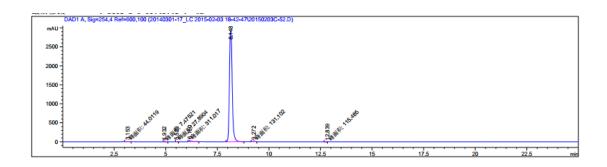


1 6.481 MM 0.0983 14.16191 2.40131 0.2218 2 9.091 BB 0.1414 6354.59326 690.33319 99.5270 3 10.510 MM 0.1360 16.03581 1.96487 0.2512

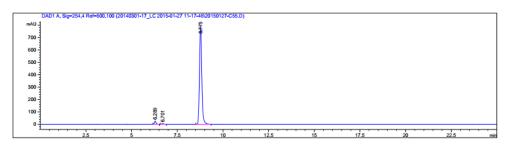
### **10b**



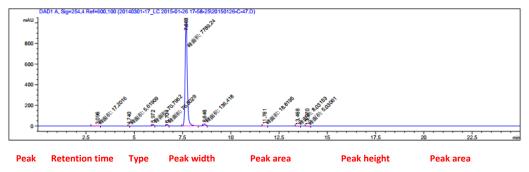
Peak	Retention time	Type	Peak width	Peak area	Peak height	Peak area	
#	[min]		[min]	[mAU*s]	[mAU]	%	
1	6.705	BV	0.0909	11.25573	1.90643	0.1171	
2	6.841	VB	0.1086	18.00187	2.42609	0.1873	
3	10.335	BB	0.1638	9511.89551	882.10077	98.9496	
4	11.763	BB	0.1880	23.20288	1.87931	0.2414	
5	12.307	BB	0.1955	48.50996	3.73635	0.5046	



Retention time	Туре	Peak width	Peak area	Peak height	Peak area
[min]		[min]	[mAU*s]	[mAU]	%
3.153	MM	0.1831	44.01191	4.00534	0.1558
4.932	MM	0.0996	7.47521	1.25040	0.0265
5.529	MM	0.0857	27.89041	5.42169	0.0987
6.160	MM	0.1805	311.01740	28.71350	1.1011
8.148	VB	0.1487	2.76086e4	2910.15405	97.7448
9.272	MM	0.1377	131.10223	15.86812	0.4642
12.839	MM	0.1186	115.48467	16.22391	0.4089
	[min]   3.153 4.932 5.529 6.160 8.148 9.272	3.153 MM 4.932 MM 5.529 MM 6.160 MM 8.148 VB 9.272 MM	[min] [min] 	[min] [min] [mAU*s]       3.153 MM	[min] [min] [mAU*s] [mAU]

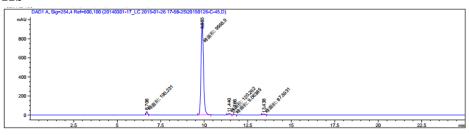


Peak	Retention time	Туре	Peak width	Peak area	Peak height	Peak area	
#	[min]		[min]	[mAU*s]	[mAU]	%	
1	6.289	BB	0.0961	158.81326	25.71469	2.2162	
2	6.701	BB	0.1063	37.10743	5.25904	0.5178	
3	8.775	VB	0.1348	6970.19092	791.03973	97.2660	

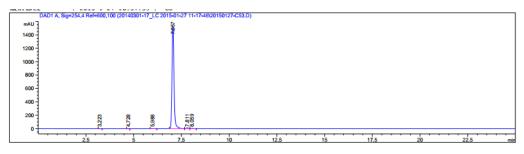


#	[min]		[min]	[mAU*s]	[mAU]	8
		-				
1	3.096	MM	0.2171	17.20162	1.32028	0.2116
2	4.740	MM	0.0632	5.61909	1.48231	0.0691
3	5.972	MM	0.0837	70.79625	14.10119	0.8710
4	6.704	MM	0.0915	76.80293	13.99040	0.9449
5	7.688	MM	0.1294	7789.24072	1002.89917	95.8327
6	8.646	MM	0.1229	136.41814	18.49550	1.6784
7	11.761	MM	0.1897	18.81947	1.65361	0.2315
8	13.468	MM	0.2662	8.03153	5.02806e-1	0.0988
9	13.970	MM	0.1882	5.03061	3.37868e-1	0.0619

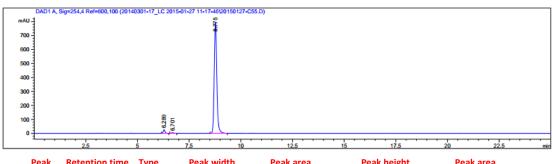
### 11b



Peak	Retention time	Туре	Peak width	Peak area	Peak height	Peak area
#	[min]		[min]	[mAU*s]	[mAU]	96
1	6.706	MM	0.0937	190.23053	33.82433	1.9069
2	9.885	MM	0.1632	9568.90137	977.41876	95.9187
3	11.440	MM	0.1527	120.26173	13.13027	1.2055
4	11.766	MM	0.1073	9.06385	1.40734	0.0909
5	13.438	MM	0.1858	87.59314	7.85670	0.8780



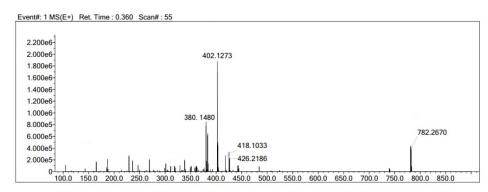
Peak	Retention time	Type	Peak width	Peak area	Peak height	Peak area
#	[min]		[min]	[mAU*s]	[mAU]	%
1	3.223	BB	0.0818	7.40275	1.31160	0.0655
2	4.728	BV	0.0906	16.64960	2.83334	0.1473
3	5.988	BV	0.1468	29.86816	2.74786	0.2642
4	7.057	BV	0.1130	1.11380e4	1529.22986	98.5142
5	7.811	VV	0.1245	75.73344	9.15919	0.6699
6	8.059	VB	0.1448	38.32880	4.03567	0.3390

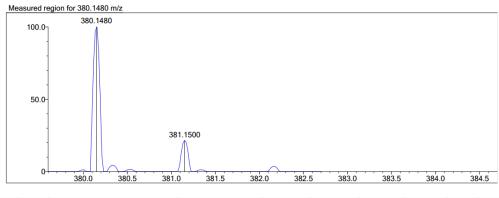


Peak	Retention time	Туре	Peak width	Peak area	Peak height	Peak area
#	[min]		[min]	[mAU*s]	[mAU]	8
1	6.289	BB	0.0961	158.81326	25.71469	2.2162
2	6.701	BB	0.1063	37.10743	5.25904	0.5178
3	8.775	VB	0.1348	6970.19092	791.03973	97.2660

### SIII. High resolution mass spectra of target compounds

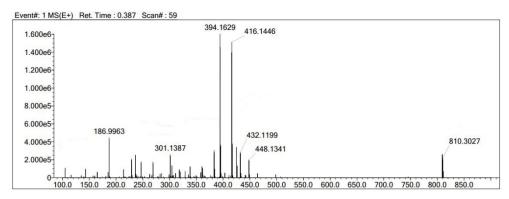
#### 8a

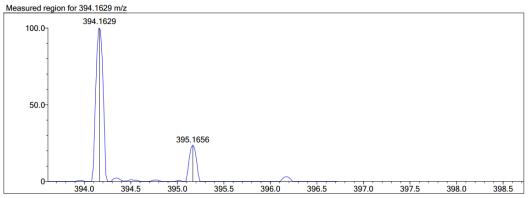




 Rank
 Score
 Formula (M)
 Ion
 Meas. m/z
 Pred. m/z
 Df. (mDa)
 Df. (ppm)
 Iso
 DBE

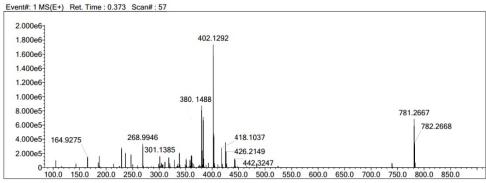
 2
 85.07
 C22 H21 N O5
 IM+HI+
 380.1480
 380.1492
 -1.2
 -3.16
 89.92
 13.0

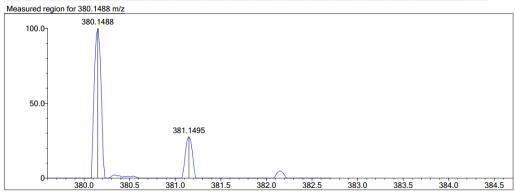




Rank	Score Formula (M)	Ion	Meas. m/z	Pred. m/z	Df. (mDa)	Df. (ppm)	Iso	DBE
1	84.53 C23 H23 N O5	[M+H]+	394.1629	394.1649	-2.0	-5.07	94.66	13.0

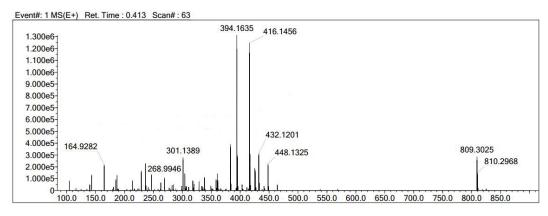
#### 8c

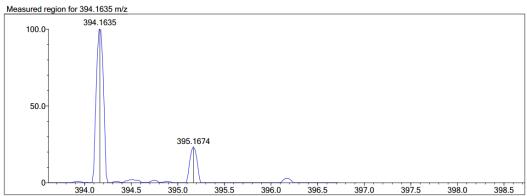




Rank	Score Formula (M)	lon	Meas. m/z	Pred. m/z	Df. (mDa)	Df. (ppm)	Iso	DBE
1	87.39 C22 H21 N O5	[M+H]+	380.1488	380.1492	-0.4	-1.05	87.50	13.0

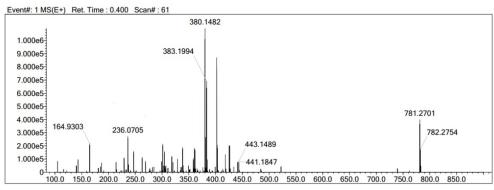
8d

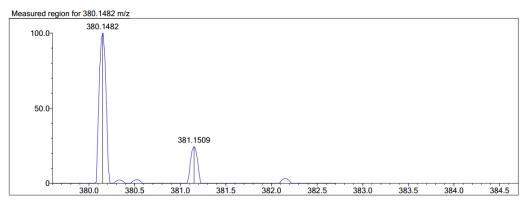




Rank	Score Formula (M)	Ion	Meas. m/z	Pred. m/z	Df. (mDa)	Df. (ppm)	Iso	DBE
1	89.78 C23 H23 N O5	[M+H]+	394.1635	394.1649	-1.4	-3.55	95.89	13.0

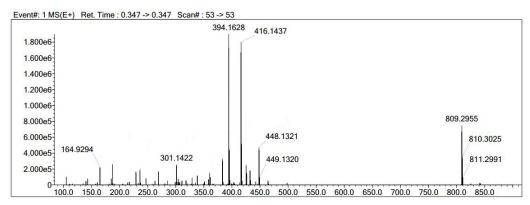
#### 8e

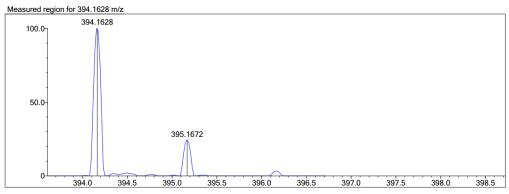




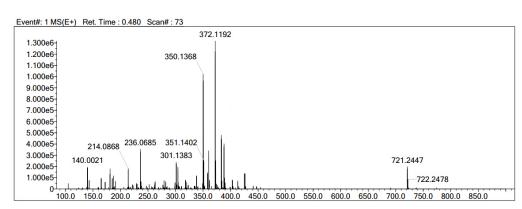
Rank	Score Formula (M)	Ion	Meas. m/z	Pred. m/z	Df. (mDa)	Df. (ppm)	Iso	DBE
2	85.98 C22 H21 N O5	[M+H]+	380.1482	380.1492	-1.0	-2.63	89.63	13.0

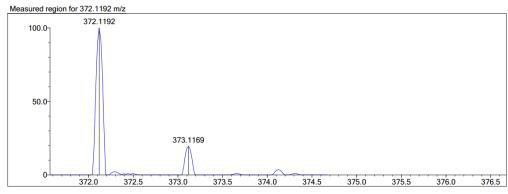
#### 8f





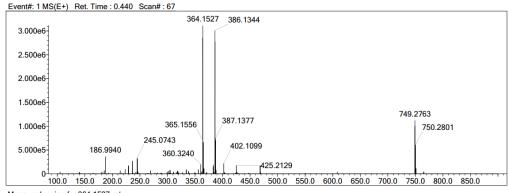
Rank	Score Formula (M)	Ion	Meas. m/z	Pred. m/z	Df. (mDa)	Df. (ppm)	Iso	DBE
3	76.43 C23 H23 N O5	[M+H]+	394.1628	394.1649	-2.1	-5.33	88.16	13.0

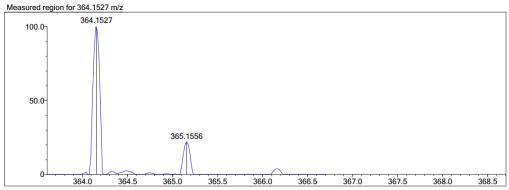




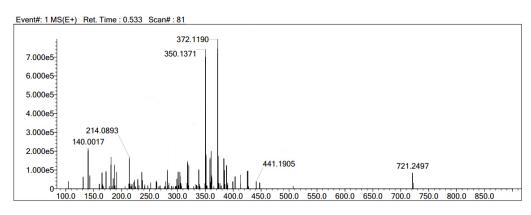
Rank	Score	Formula (M)	Ion	Meas. m/z	Pred. m/z	Df. (mDa)	Df. (ppm)	Iso	DBE
2	69.02	C21 H19 N O4	[M+Na]+	372.1192	372.1206	-1.4	-3.76	74.14	13.0

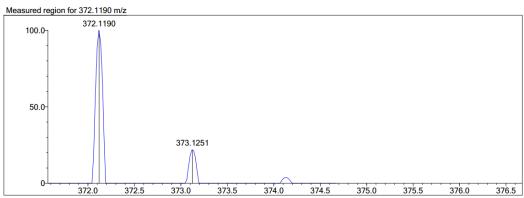
#### 10b



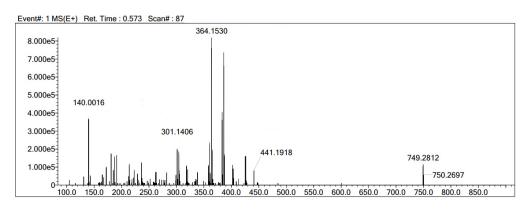


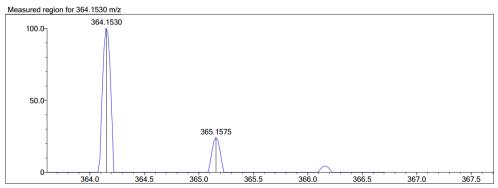
Rank	Score Formula (M)	lon	Meas. m/z	Pred. m/z	Df. (mDa)	Df. (ppm)	Iso	DBE
1	83.95 C22 H21 N O4	[M+H]+	364.1527	364.1543	-1.6	-4.39	91.73	13.0



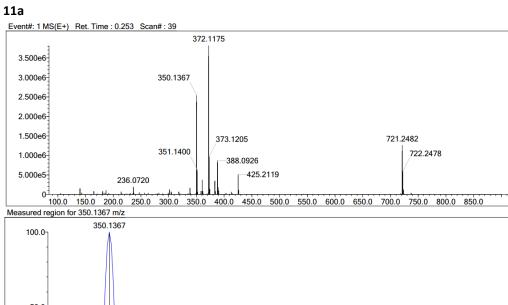


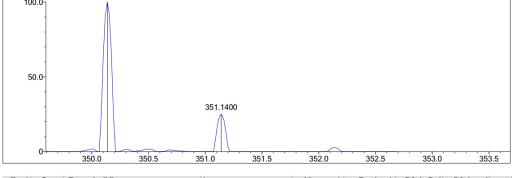
Rank	Score	Formula (M)	Ion	Meas. m/z	Pred. m/z	Df. (mDa)	Df. (ppm)	Iso	DBE
2	76.86	C21 H19 N O4	[M+Na]+	372.1190	372.1206	-1.6	-4.30	83.77	13.0





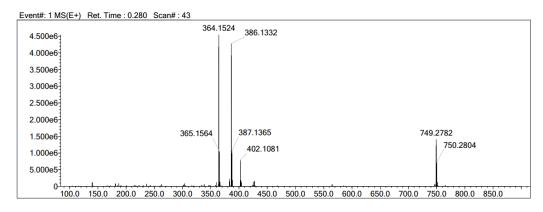
Rank	Score For	mula (M)	lon	Meas. m/z	Pred. m/z	Df. (mDa)	Df. (ppm)	Iso	DBE
1	85.43 C22	2 H21 N O4	[M+H]+	364.1530	364.1543	-1.3	-3.57	91.30	13.0

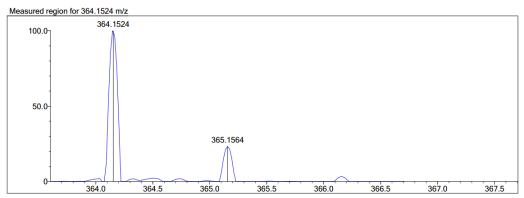




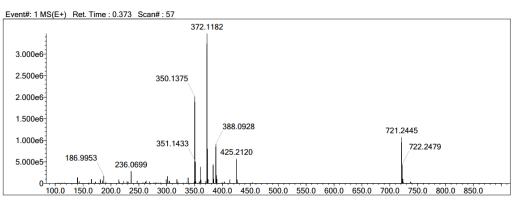
Rank	Score	Formula (M)	Ion	Meas. m/z	Pred. m/z	Df. (mDa)	Df. (ppm)	Iso	DBE
1	62.51	C21 H19 N O4	[M+H]+	350.1367	350.1387	-2.0	-5.71	75.40	13.0

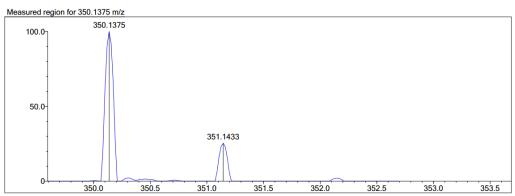
11b



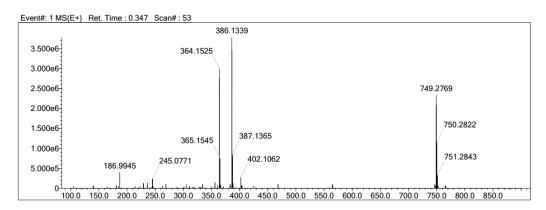


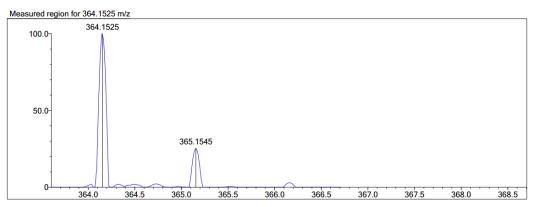
Rank	Score	Formula (M)	Ion	Meas. m/z	Pred. m/z	Df. (mDa)	Df. (ppm)	Iso	DBE
2	78.66	C22 H21 N O4	[M+H]+	364.1524	364.1543	-1.9	-5.22	89.59	13.0





Rank	Score Formula (M)	Ion	Meas. m/z	Pred. m/z	Df. (mDa)	Df. (ppm)	Iso	DBE
1	73.38 C21 H19 N O4	[M+H]+	350.1375	350.1387	-1.2	-3.43	78.13	13.0

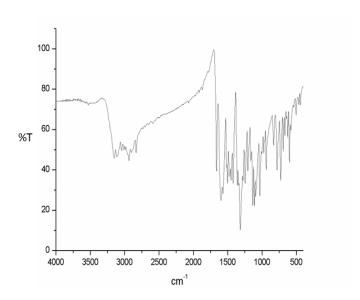




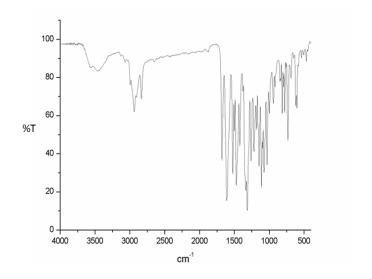
Rank	Score	Formula (M)	Ion	Meas. m/z	Pred. m/z	Df. (mDa)	Df. (ppm)	Iso	DBE
1	80.53	C22 H21 N O4	[M+H]+	364.1525	364.1543	-1.8	-4.94	89.33	13.0

## SIV.IR spectra of target compounds

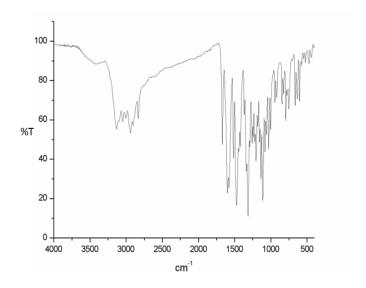
### 8a



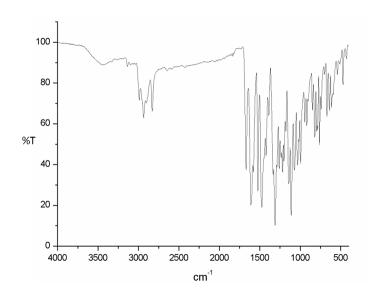
8b



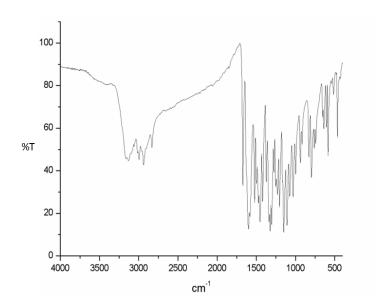
8c



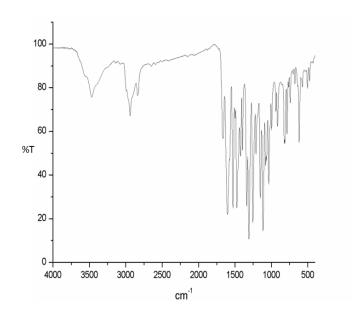
8d

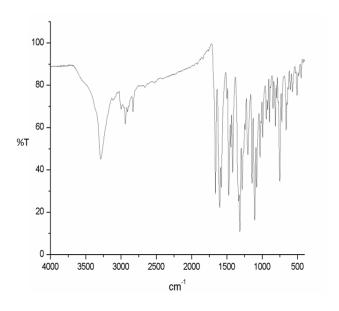


8e

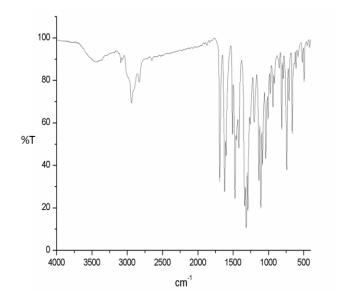


8f

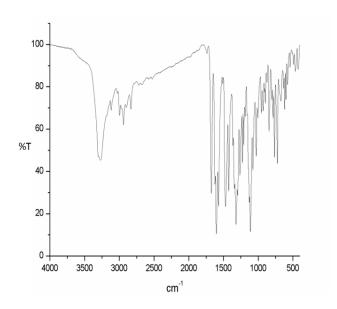




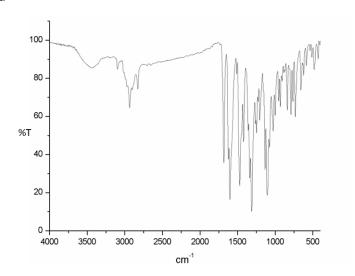
10b



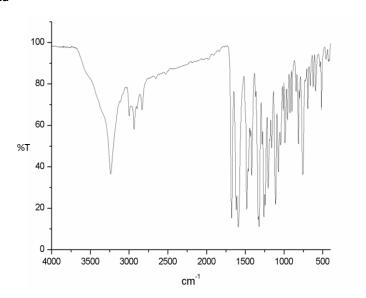
**10**c



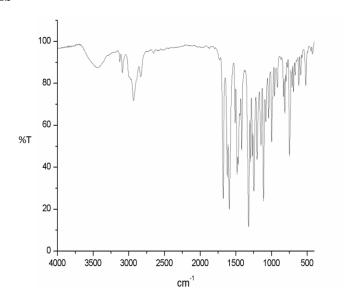
10d

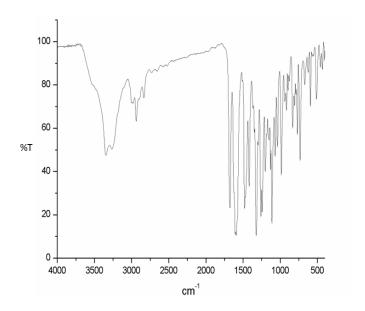


### **11**a



## 11b





11d

