Supporting Information

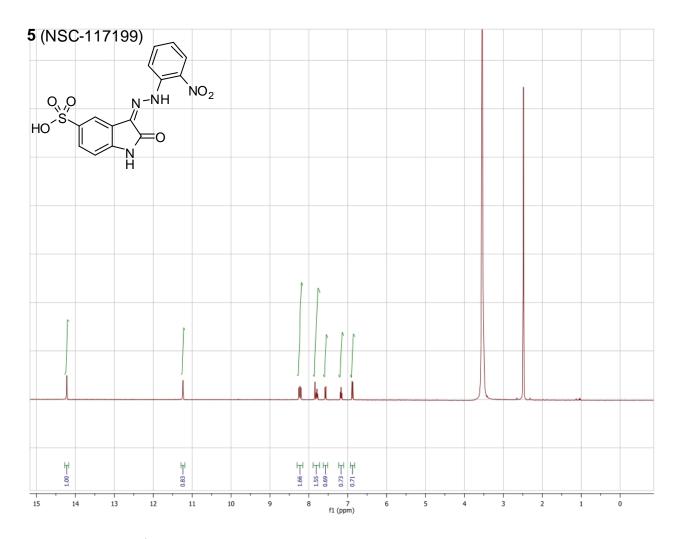
Inhibitors of Src Homology-2 Domain containing Protein Tyrosine Phosphatase-2 (Shp2) Based on Oxindole Scaffolds

Harshani R. Lawrence,* Roberta Pireddu, Liwei Chen, Yunting Luo, Shen-Shu Sung, Ann Marie Szymanski, Richard Yip, Wayne C. Guida, Saïd M. Sebti, Jie Wu and Nicholas J. Lawrence*

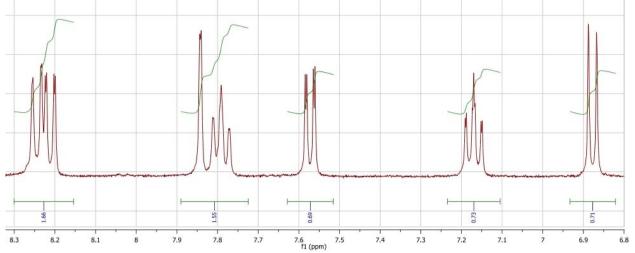
Moffitt Cancer Center, Tampa, FL

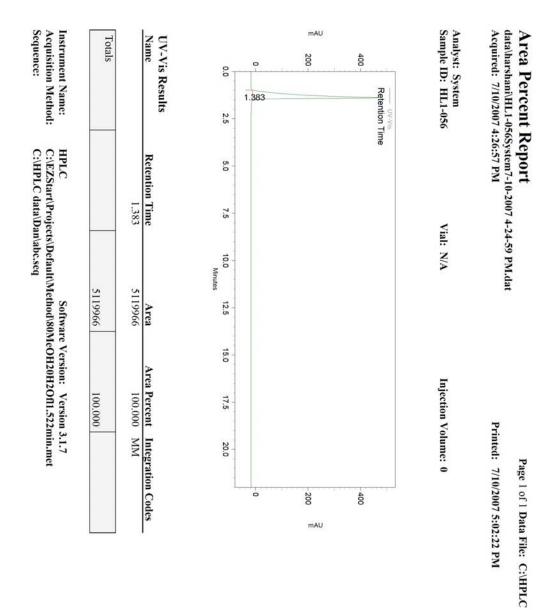
Contents.

Characterization data, mass and NMR spectra and HPLC traces of compounds **5** (NSC-117199), 10a-r, 14a-b, 17 and 18a-e, nOe and COSY data for **5** and 18c, and a description of the molecular modeling studies.

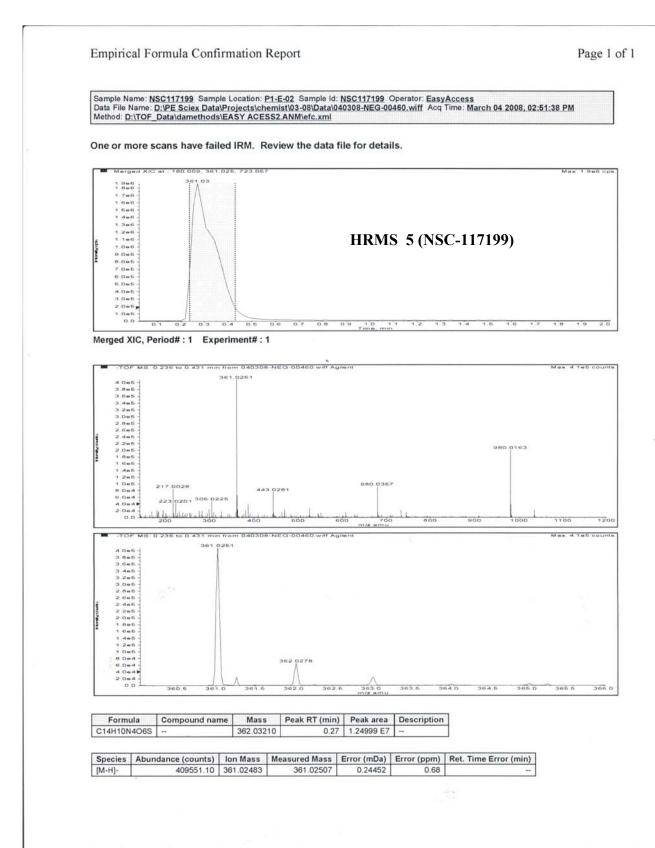


Expansion of the ¹H NMR (DMSO- d_6) spectrum of 5 (NSC-117199) (δ 6.8 – 8.3 ppm)



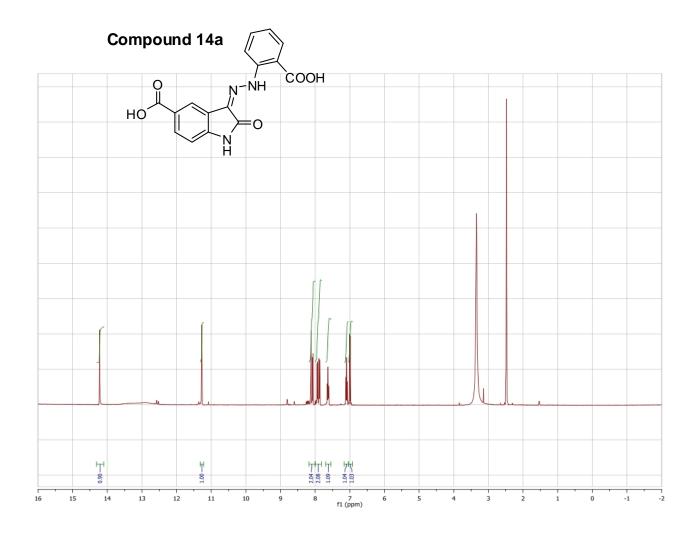


HPLC of 5 (NSC-117199)

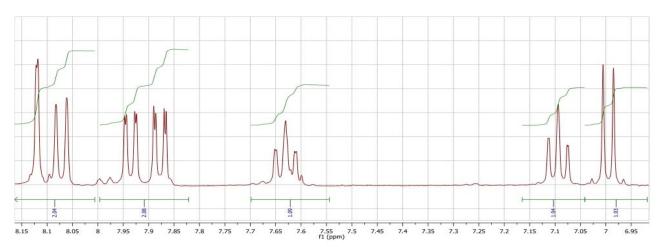


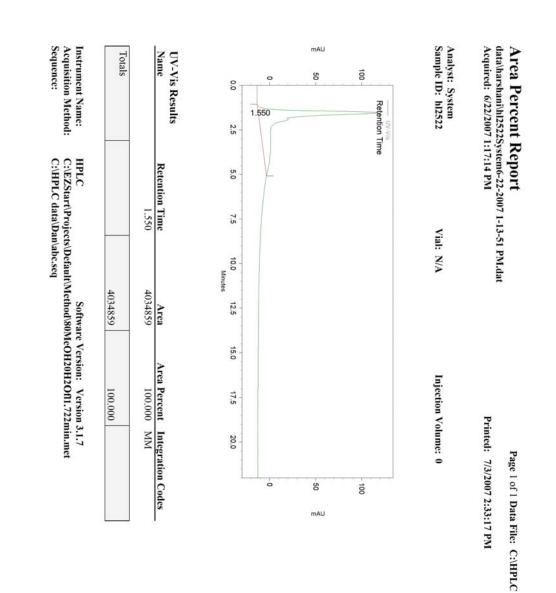
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14:53:49 PM



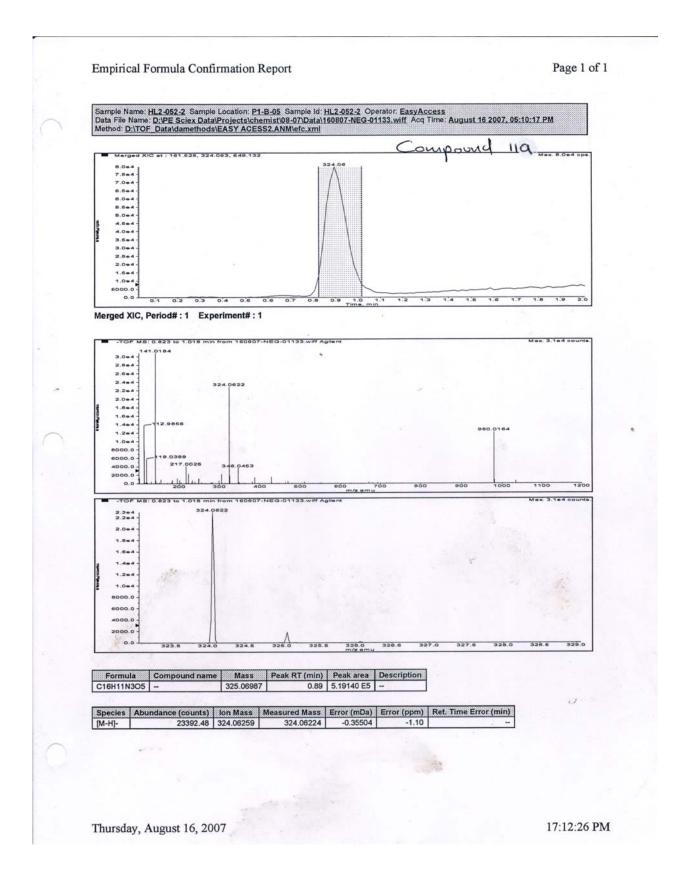
Expansion of the ¹H NMR (DMSO- d_6) spectrum of 14a (δ 6.9 – 8.2 ppm)

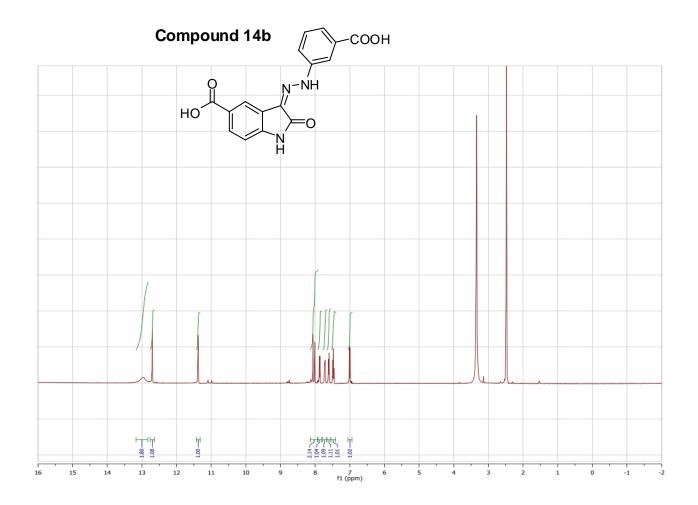




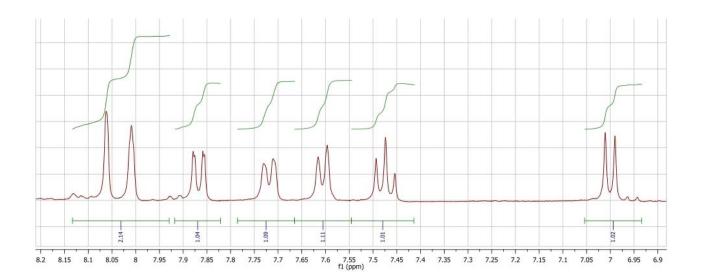
HPLC 14a

HRMS 14a



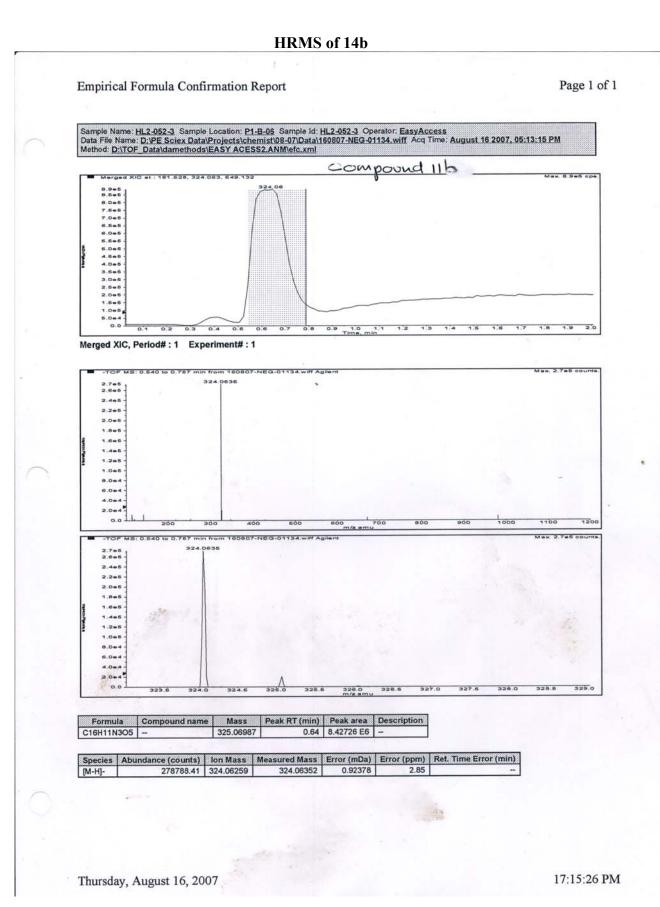


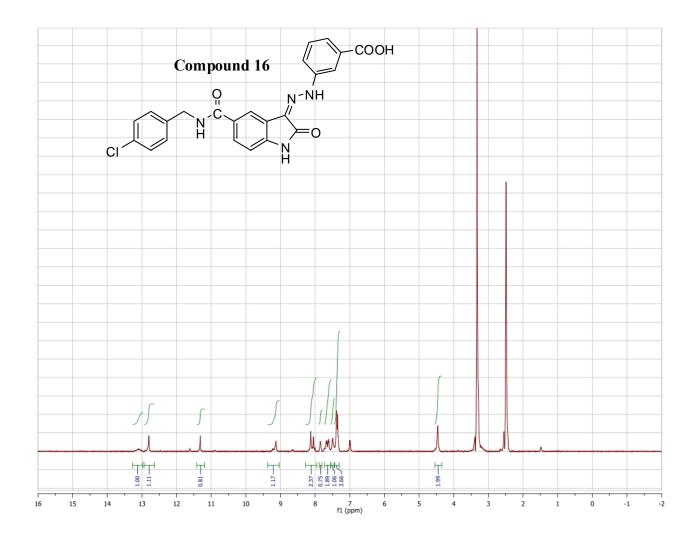
Expansion of the ¹H NMR (DMSO- d_6) spectrum of 14b (δ 6.9 – 8.2 ppm)



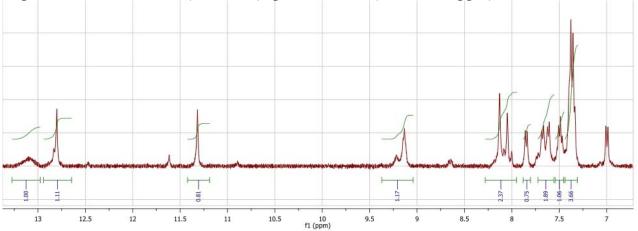
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Instrument Name: Acquisition Method:			sults	N _	1.600	- 1.350		Retention Time		tem 1 2522	data\harshani\h12522System6-27-2 Acquired: 6/27/2007 12:37:09 PM
HPLC Software Version: Version 3.1.7 C:\EZStart\Projects\Default\Method\80MeOH20H2Off1.722min.met C:\HPLC data\Dan\abc.seq			Retenti	5.0				Ø	COMPOUND	Via	Acquired: 6/27/2007 12:37:09 PM
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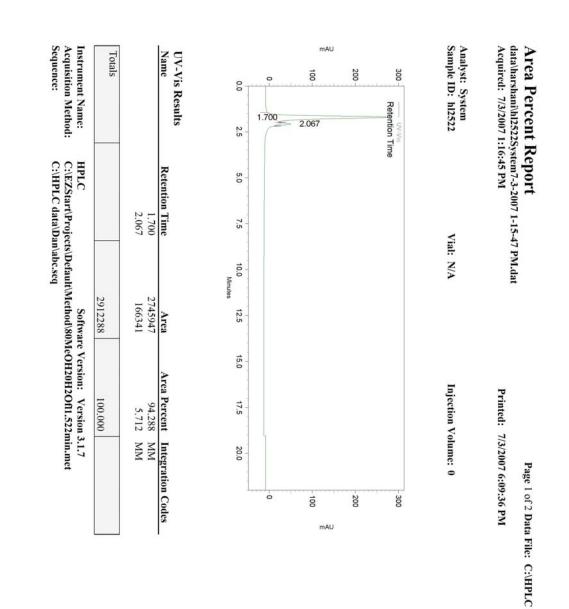
S9





Expansion of the ¹H NMR (DMSO- d_6) spectrum of 16 (δ 6.9 – 14.0 ppm)

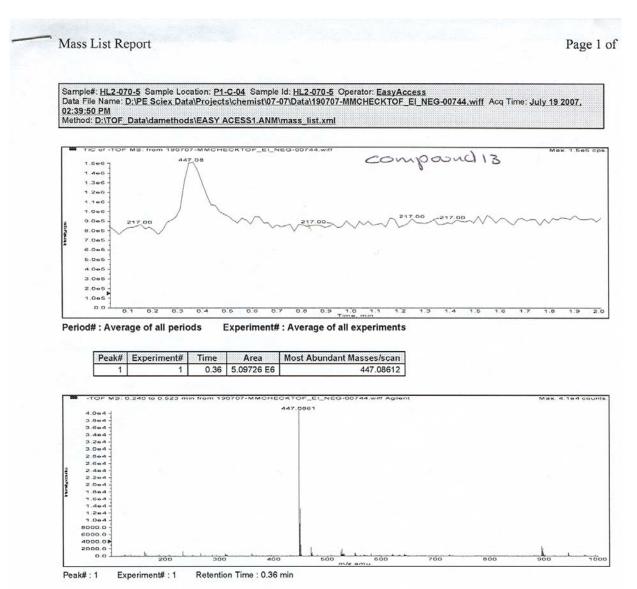


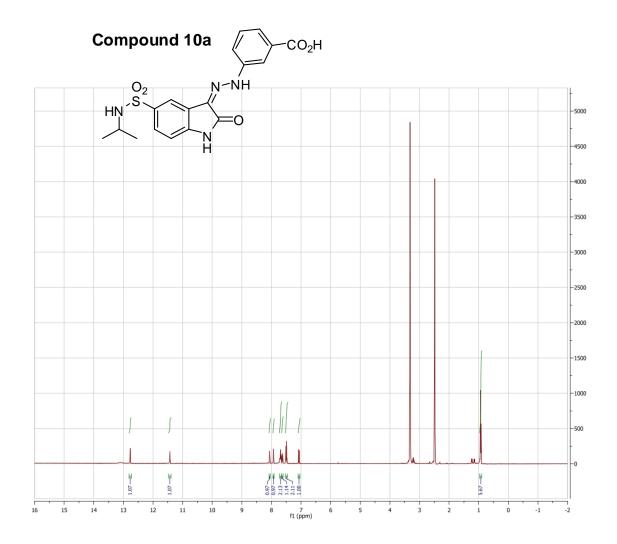


HPLC 16

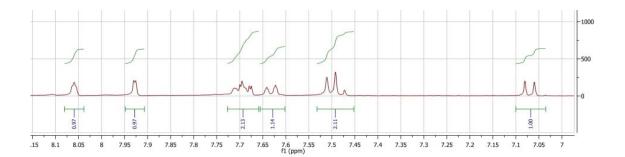
S12

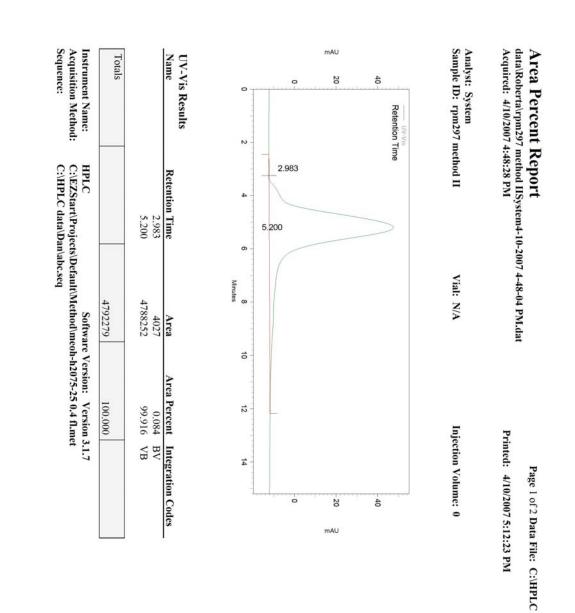
HRMS 16





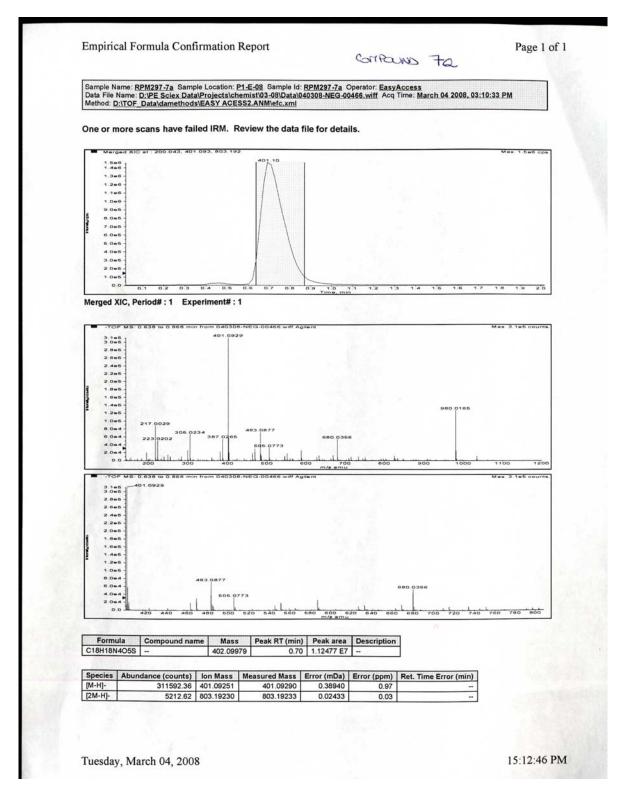
Expansion of the ¹H NMR (DMSO- d_6) spectrum of 10a (δ 7.0 – 8.2 ppm)

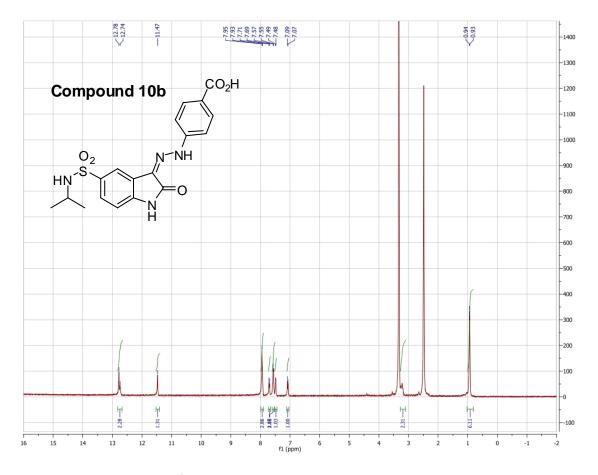




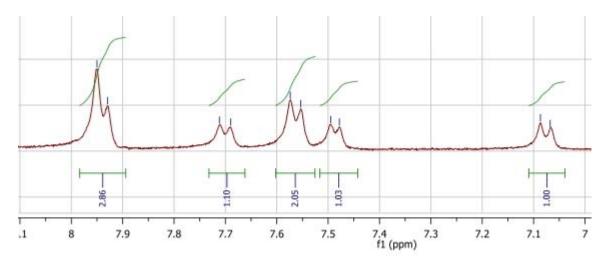
HPLC 10a

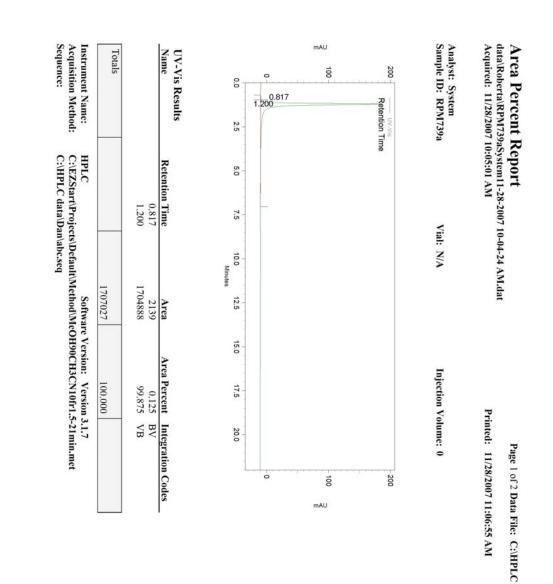
HRMS 10a





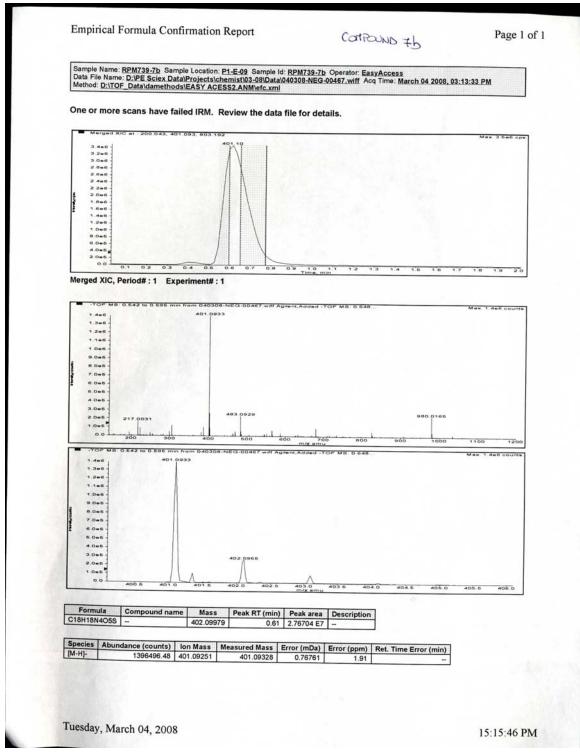
Expansion of the ¹H NMR (DMSO- d_6) spectrum of 10b (δ 7.0 – 8.1 ppm)



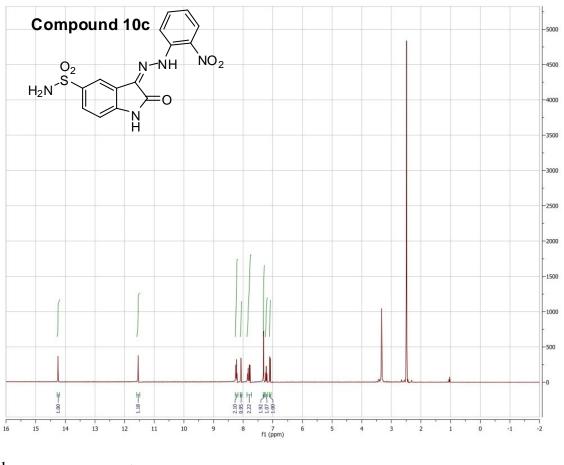


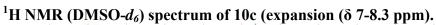
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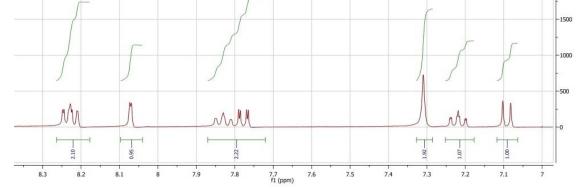
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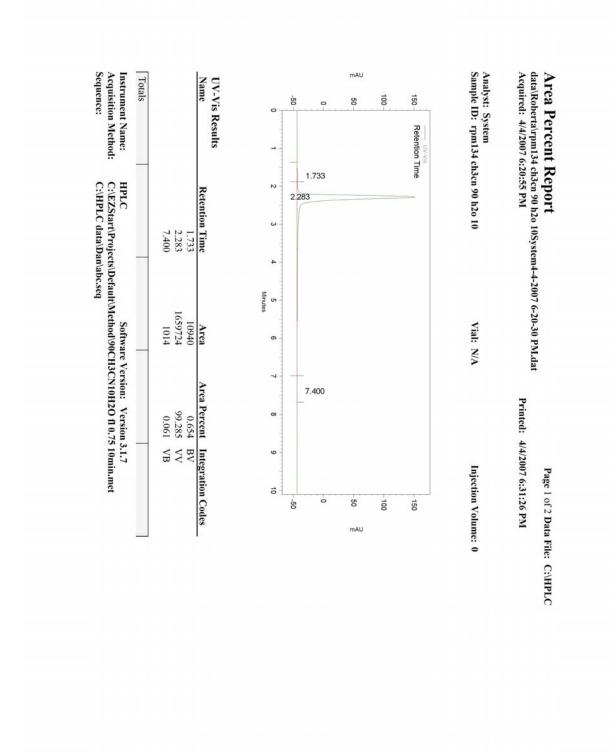


HRMS 10b

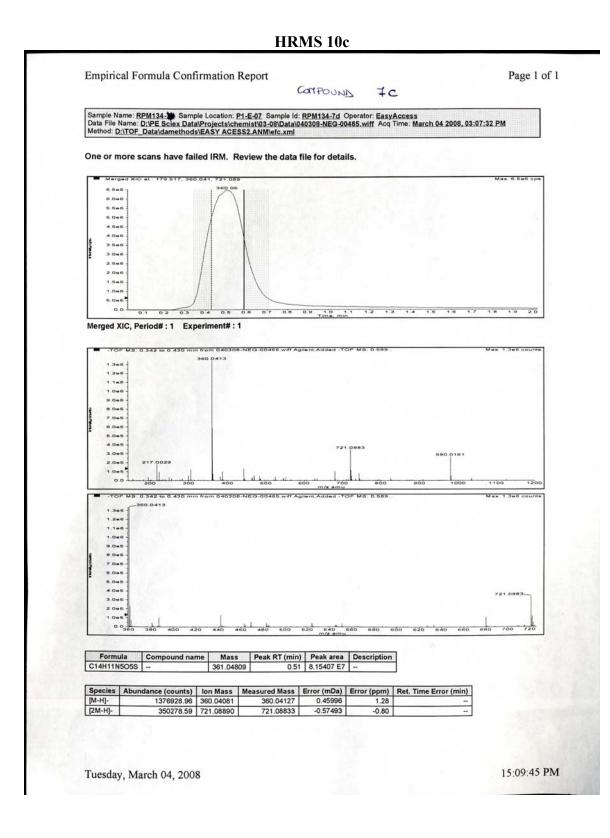


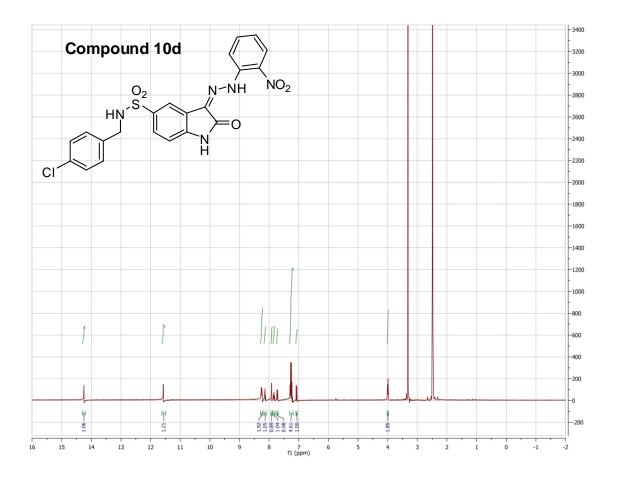


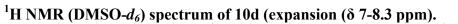


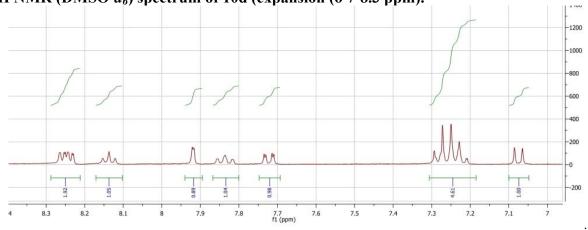


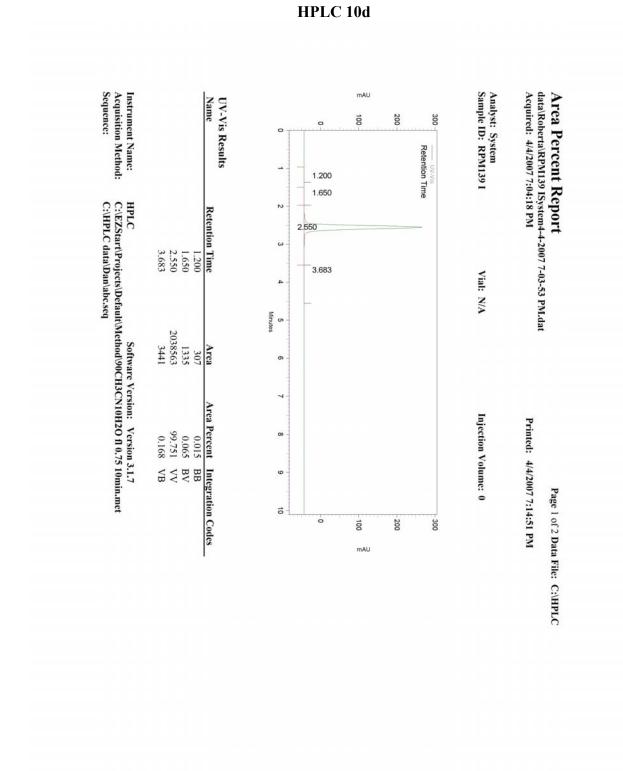
HPLC 10c

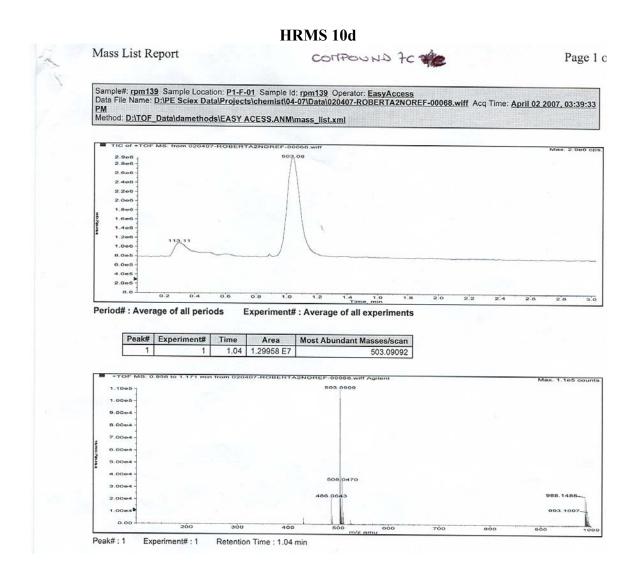


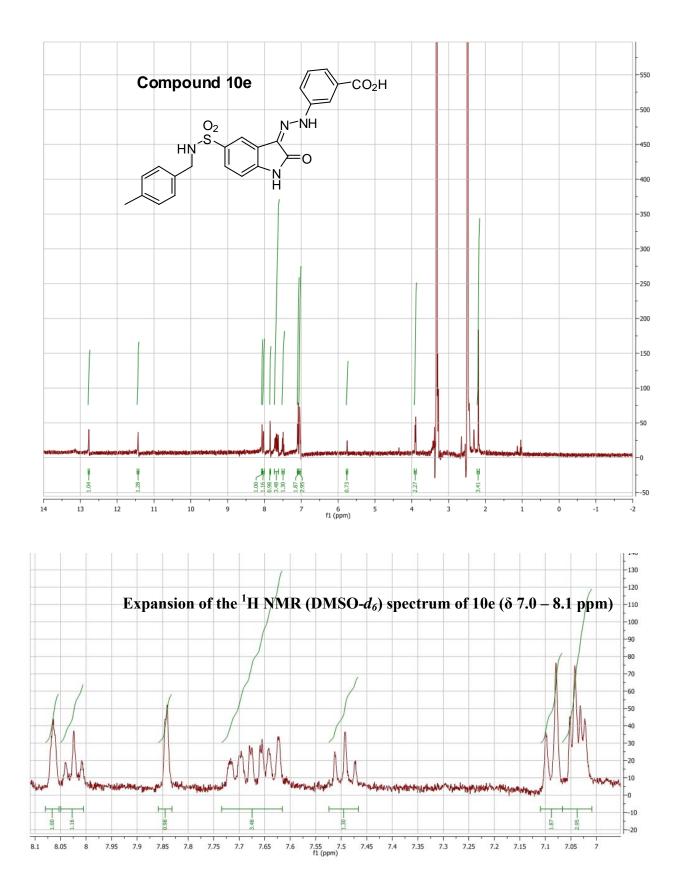


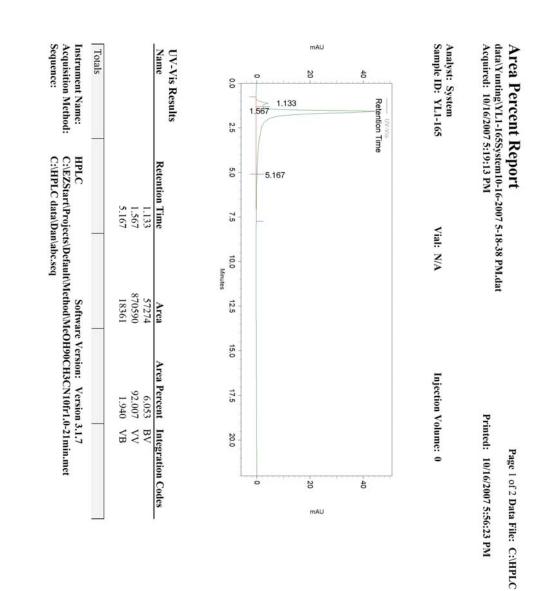






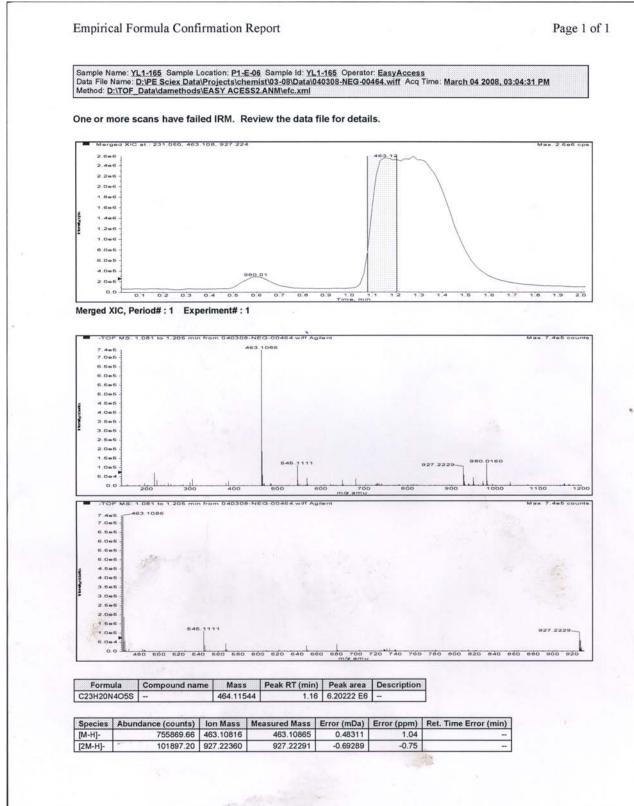






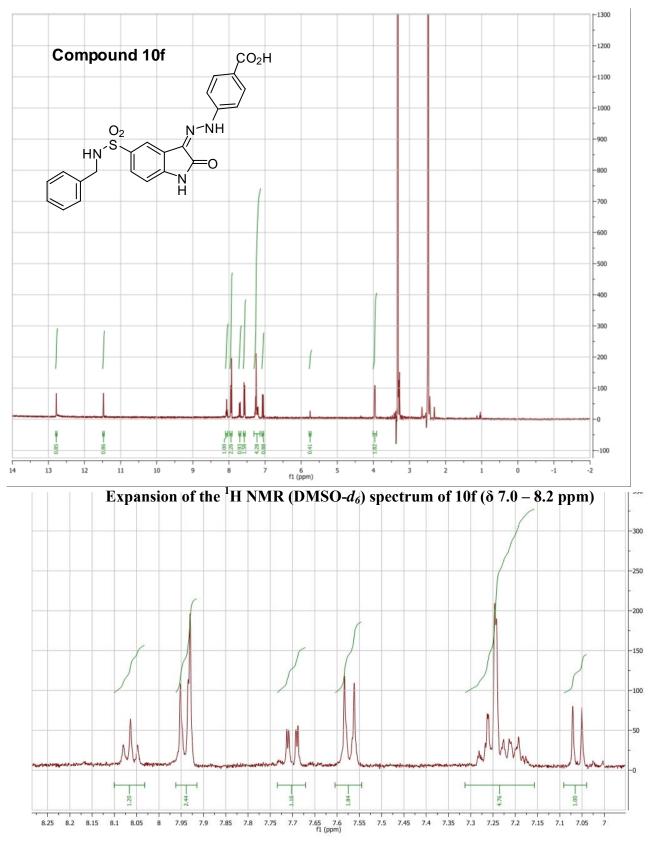
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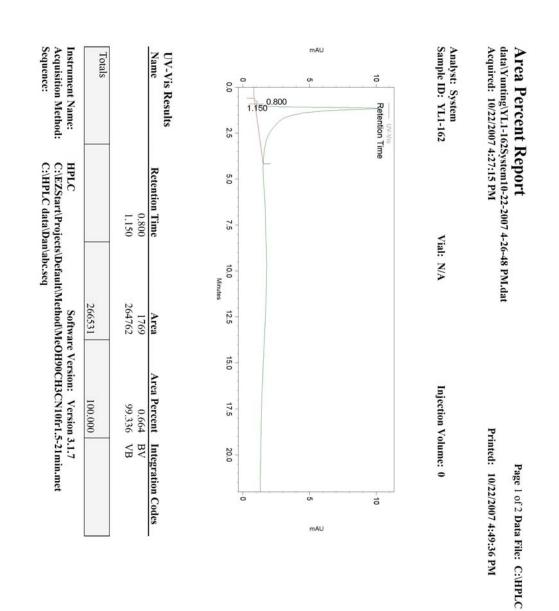
HRMS 10e



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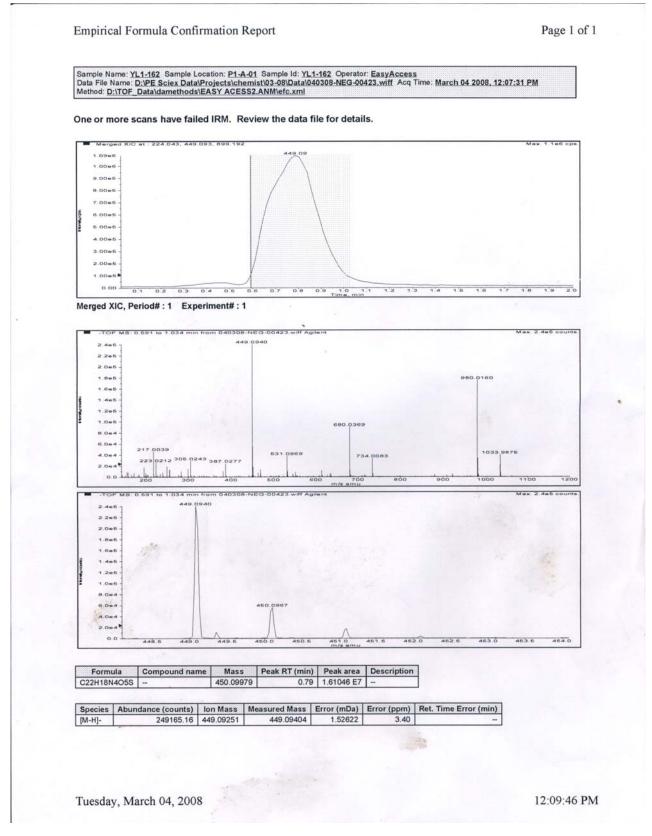


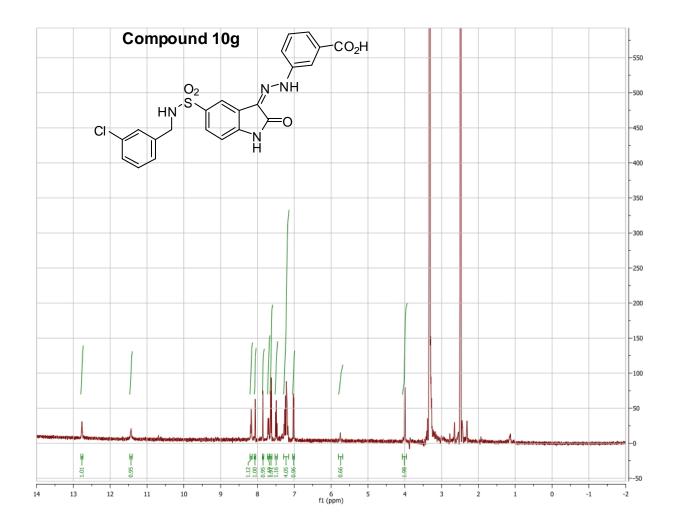


HPLC 10f

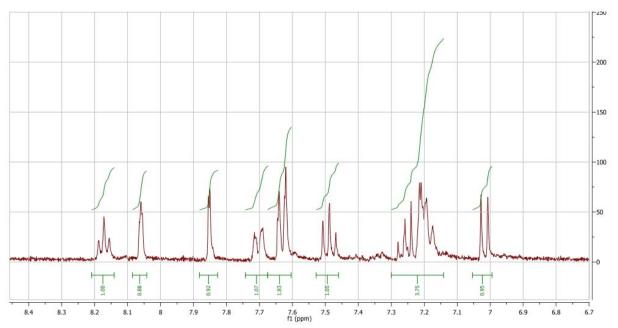
S30

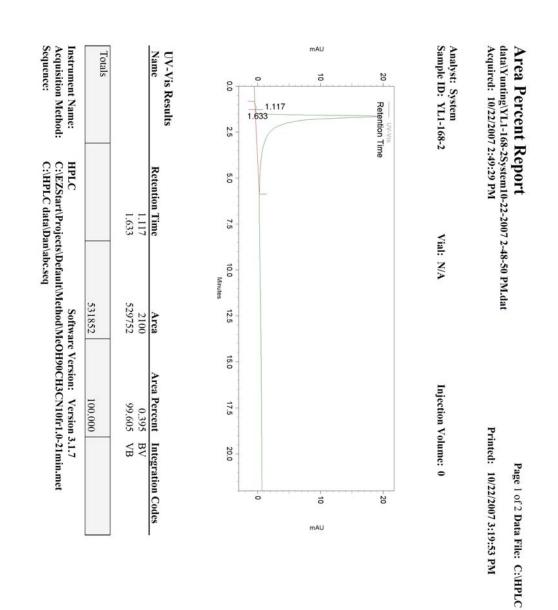
HRMS 10f





Expansion of the ¹H NMR (DMSO- d_6) spectrum of 10g (δ 6.7 – 8.4 ppm)

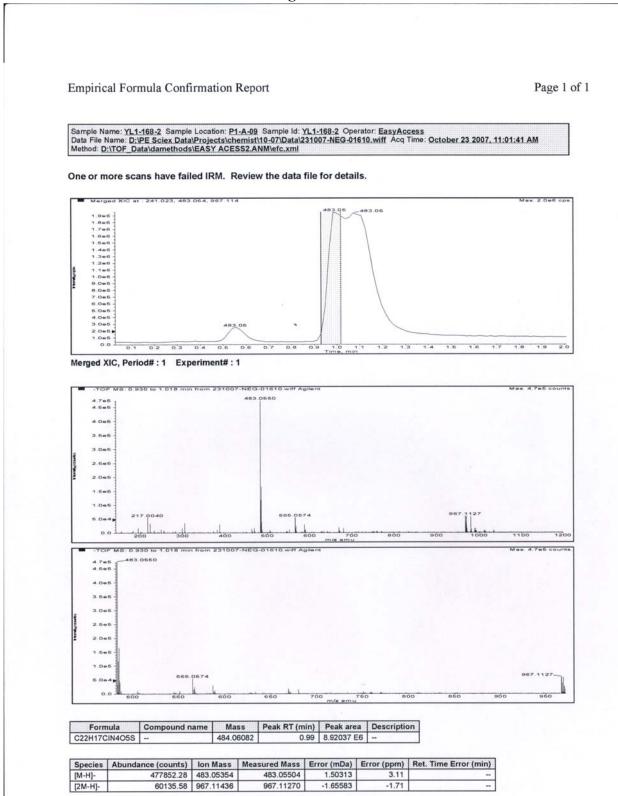


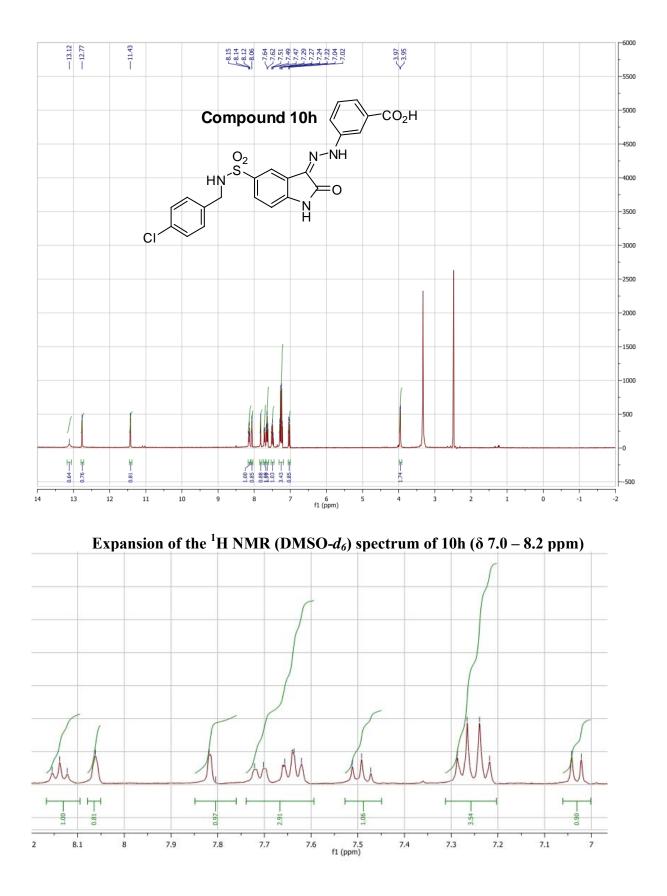


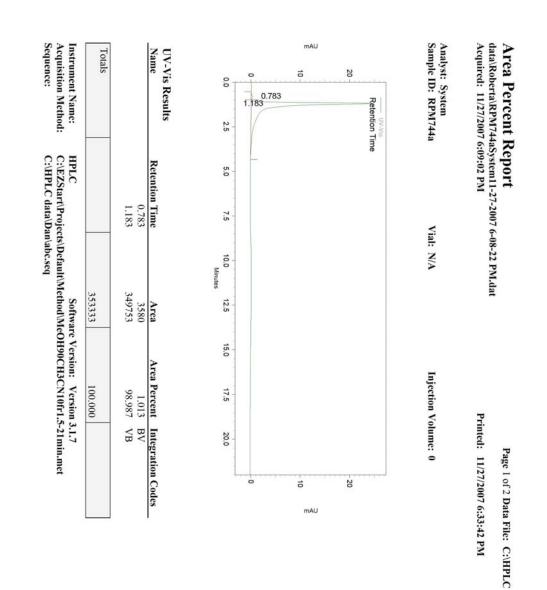
HPLC 10g

S33



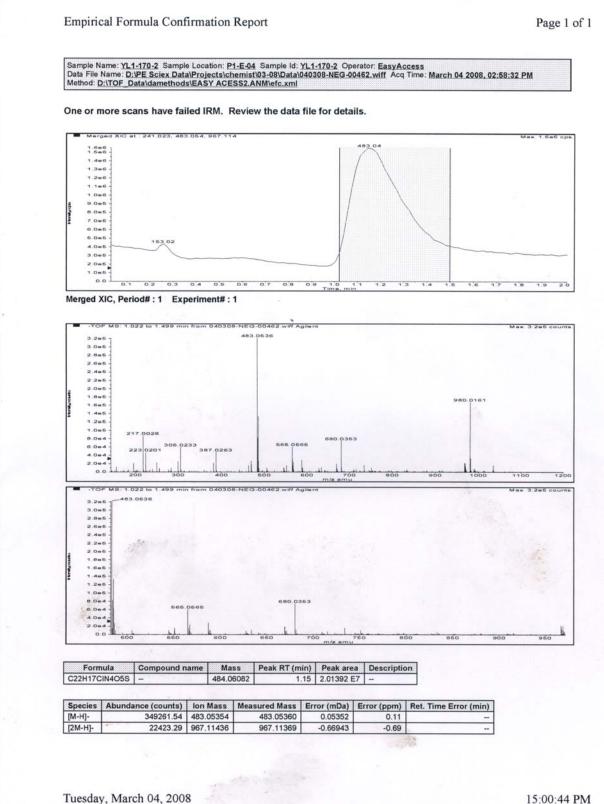


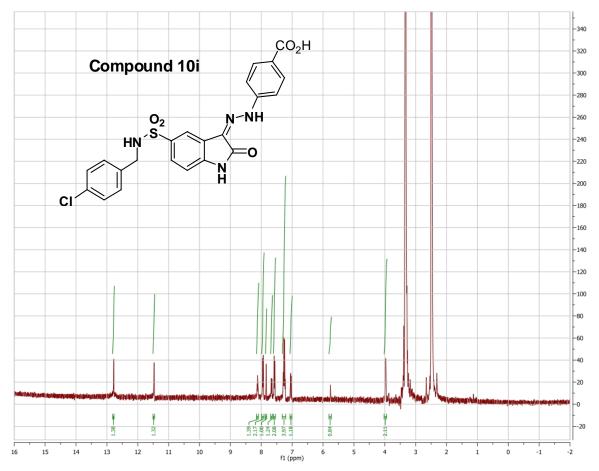




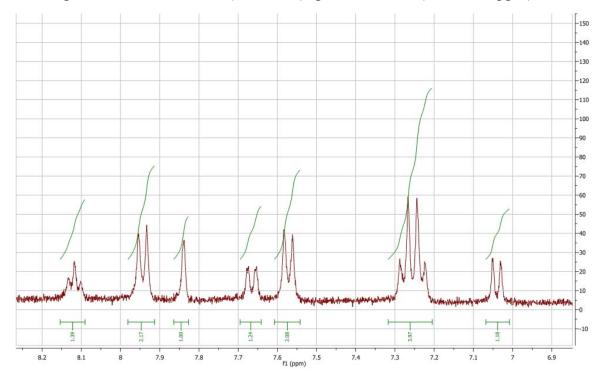
HPLC 10h

HRMS 10h

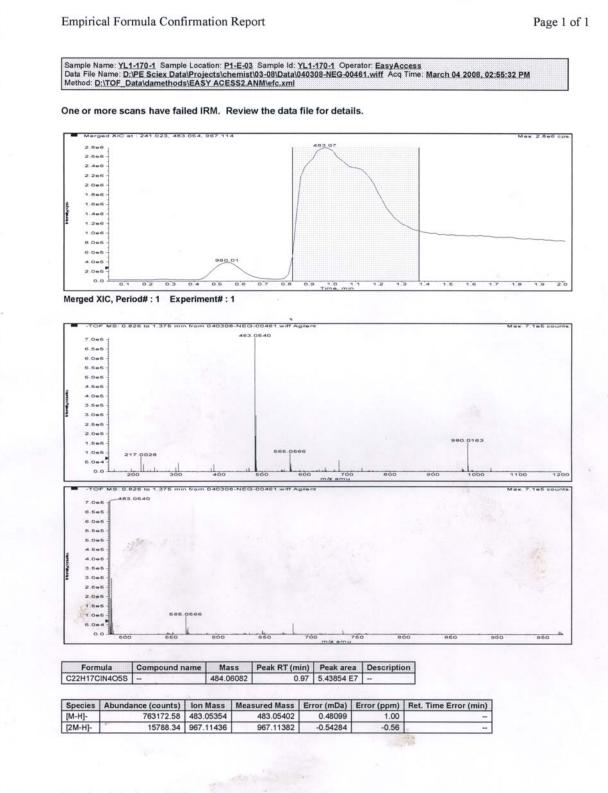




Expansion of the ¹H NMR (DMSO- d_6) spectrum of 10i (δ 6.9 – 8.2 ppm)

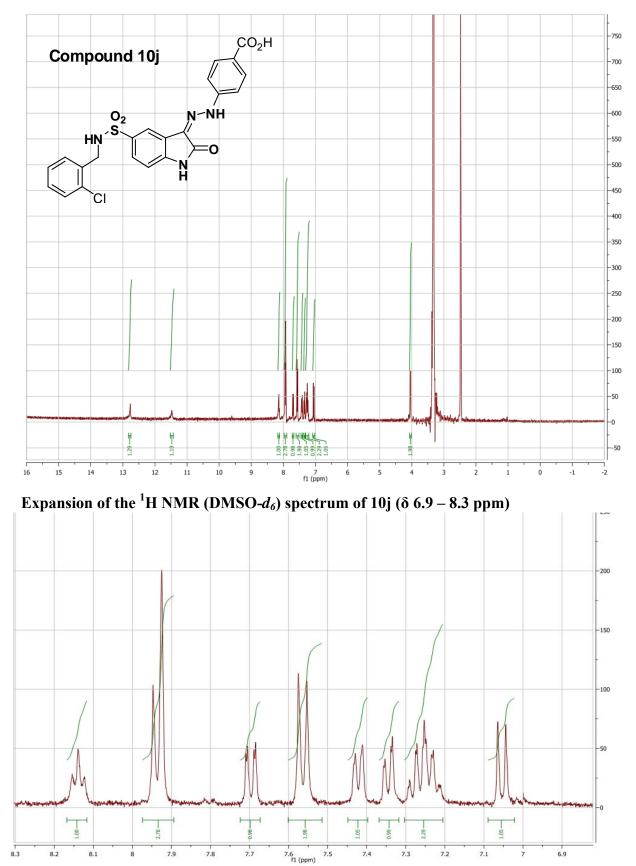


HRMS of 10i

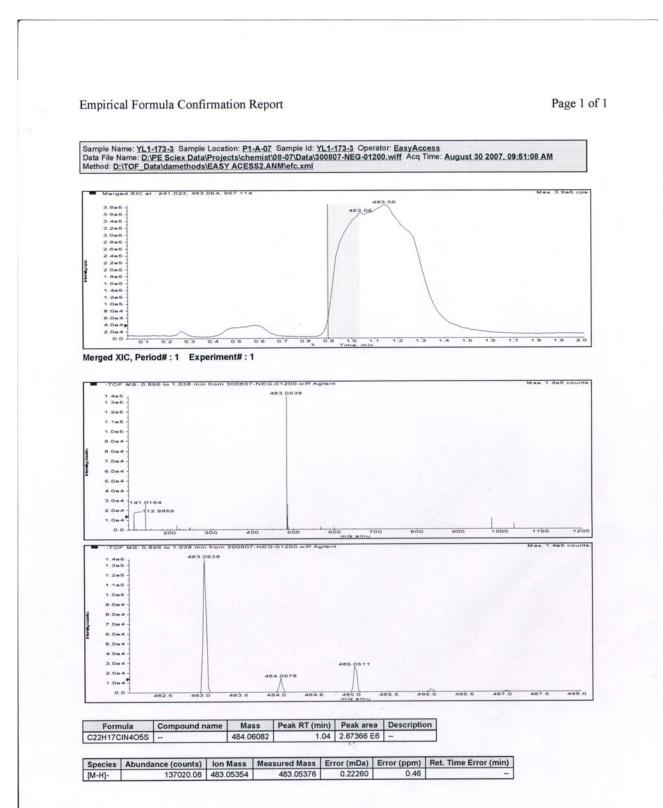


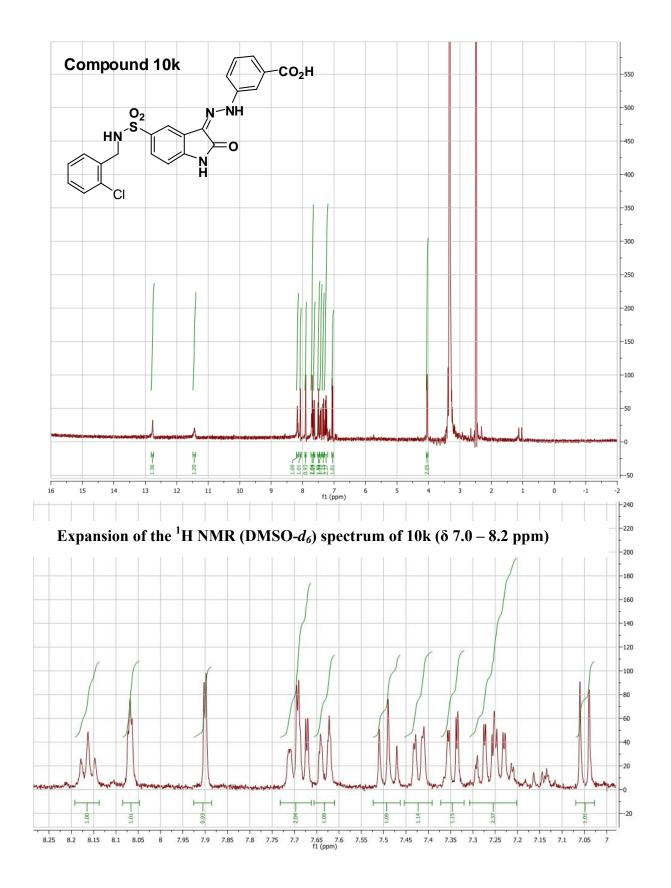
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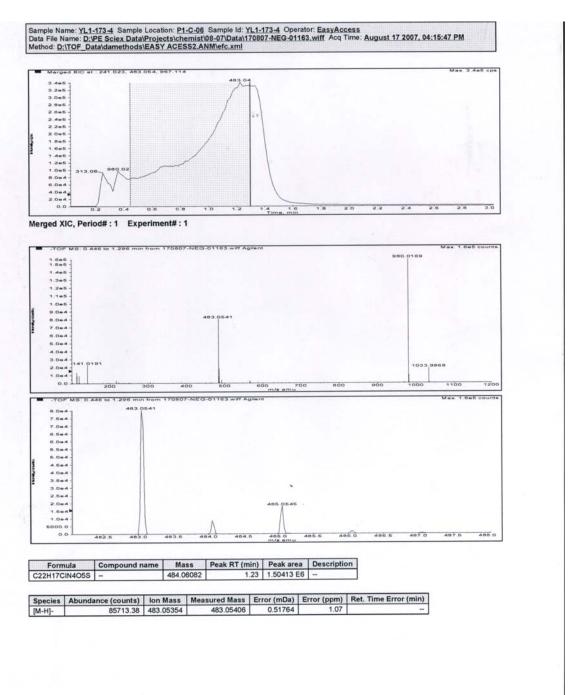
14:57:44 PM



HRMS 10j





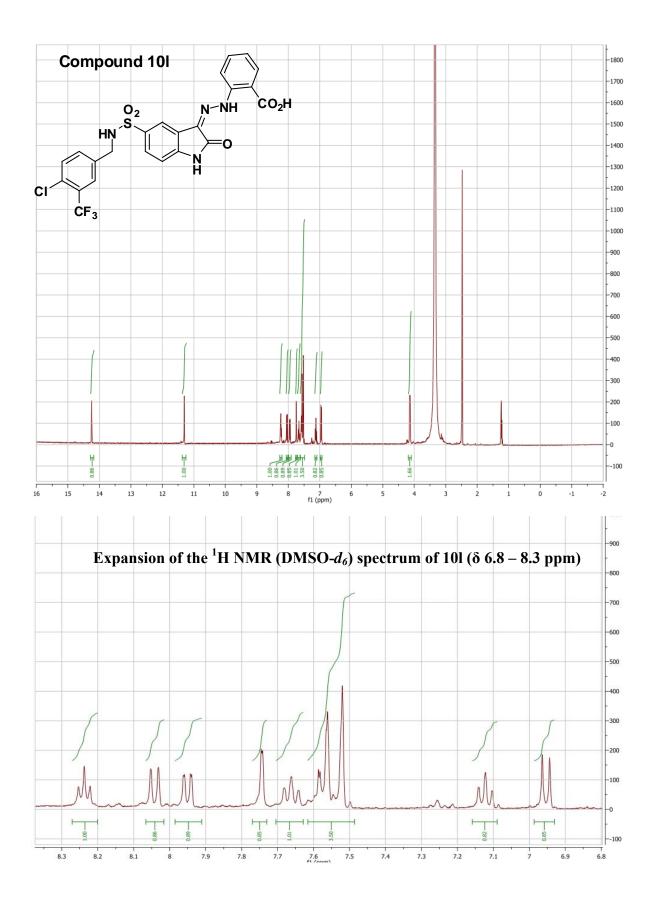


HRMS of 10k

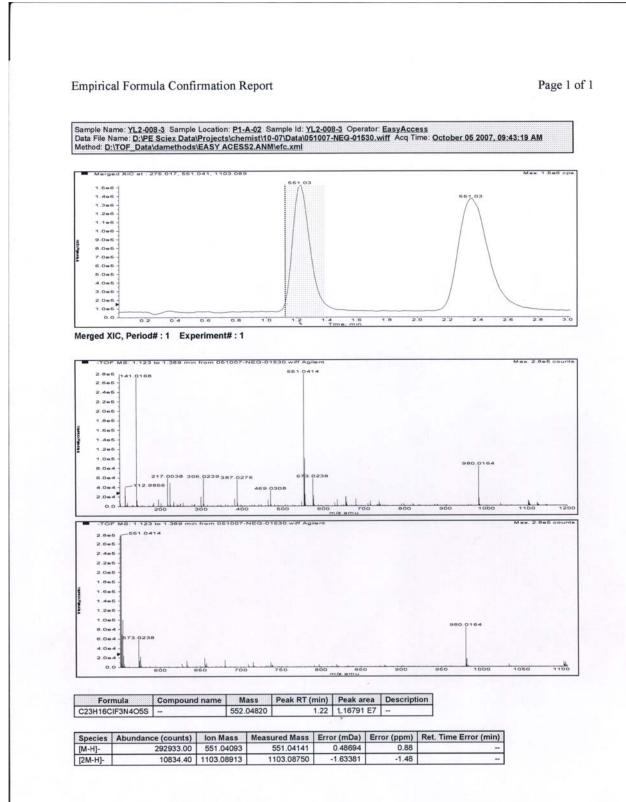
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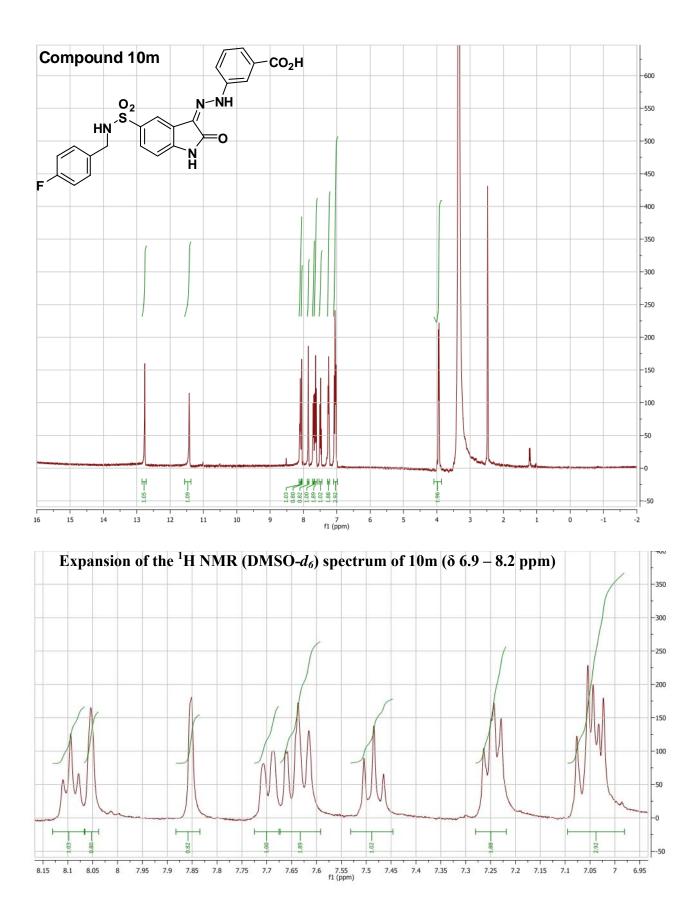
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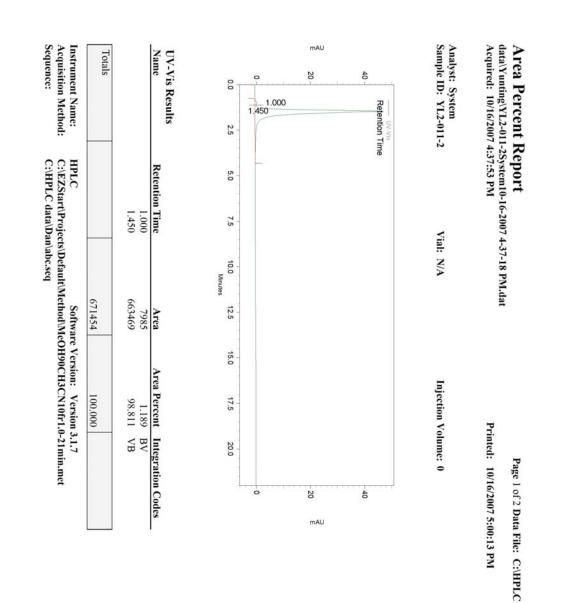
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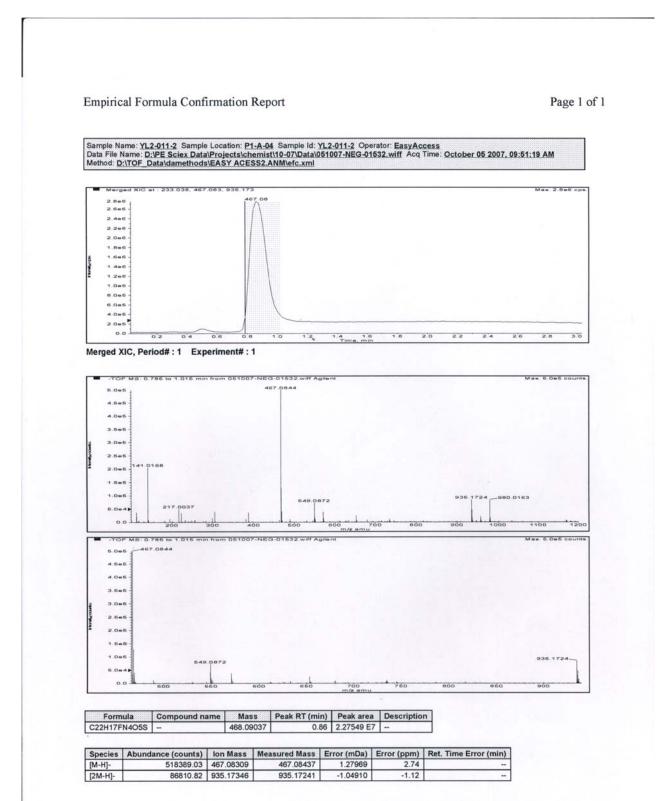


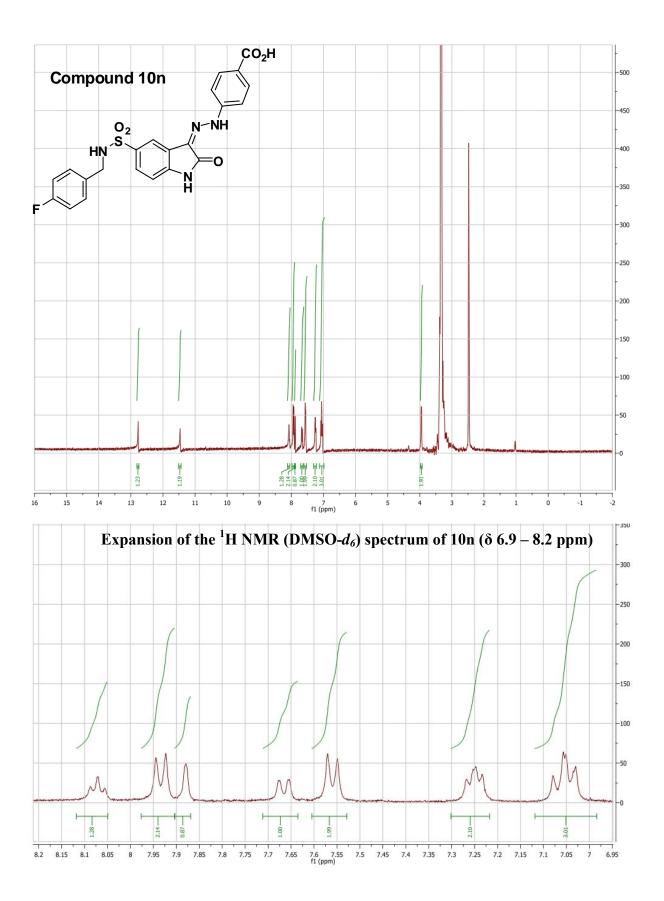


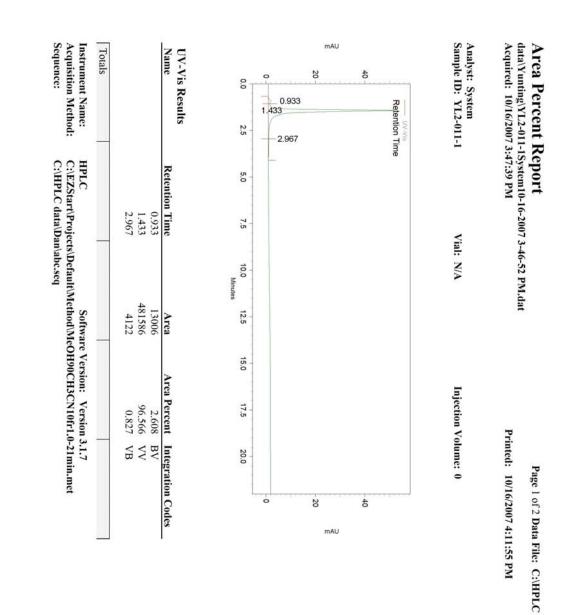


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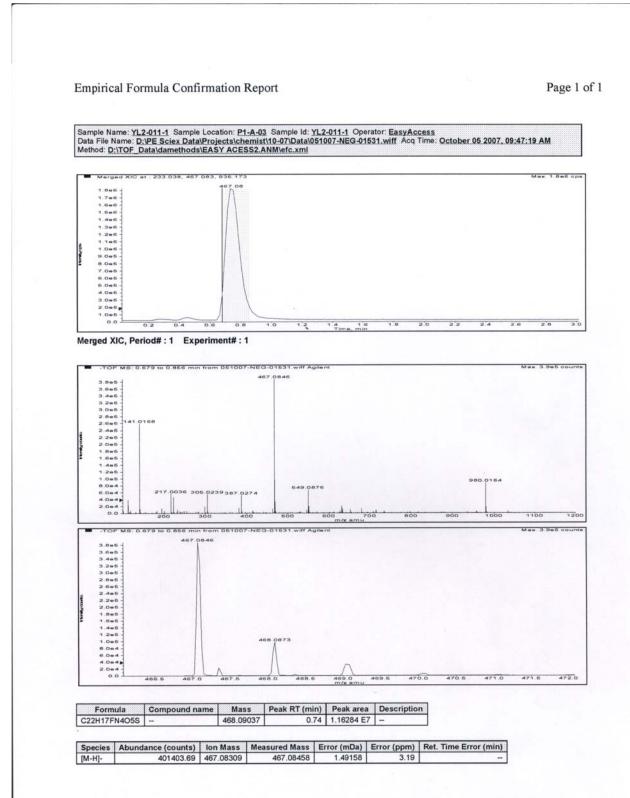


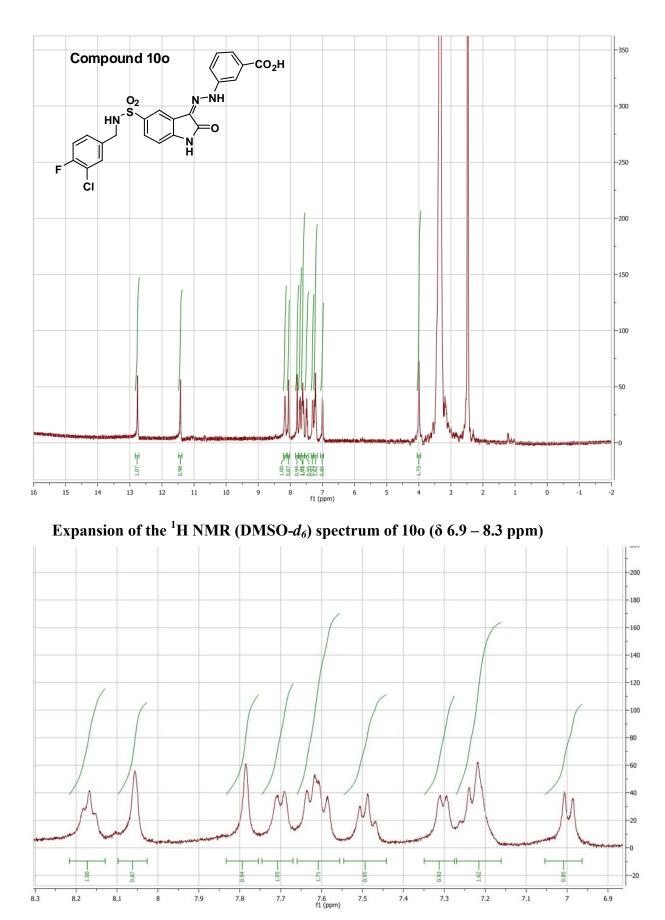




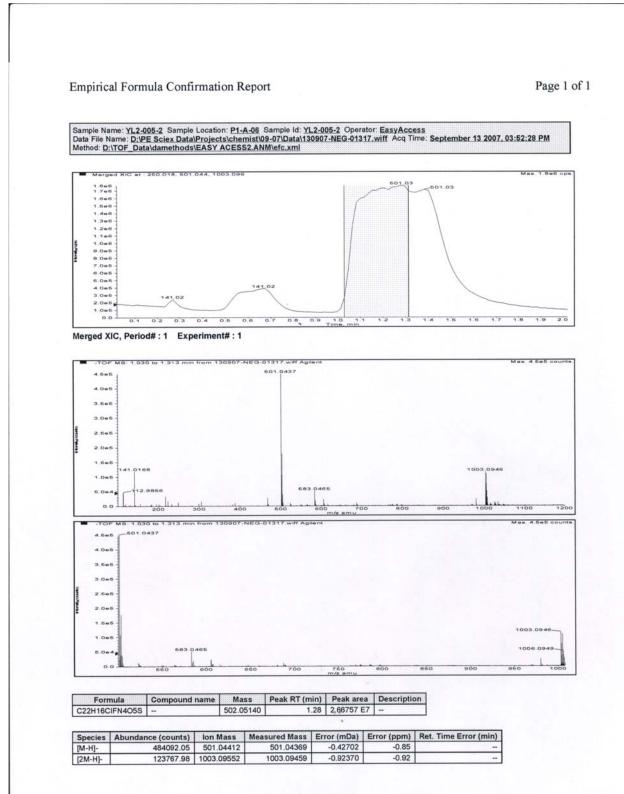
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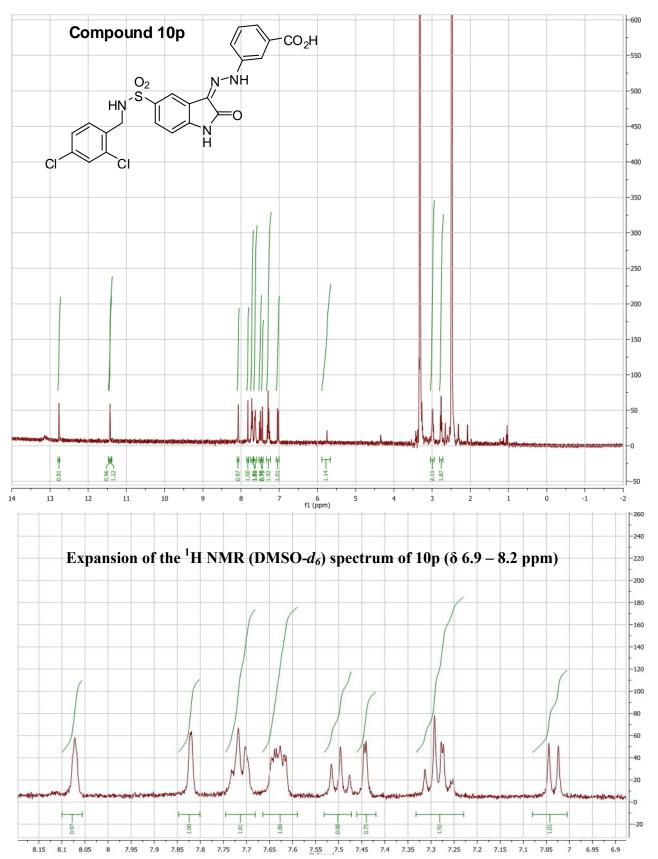
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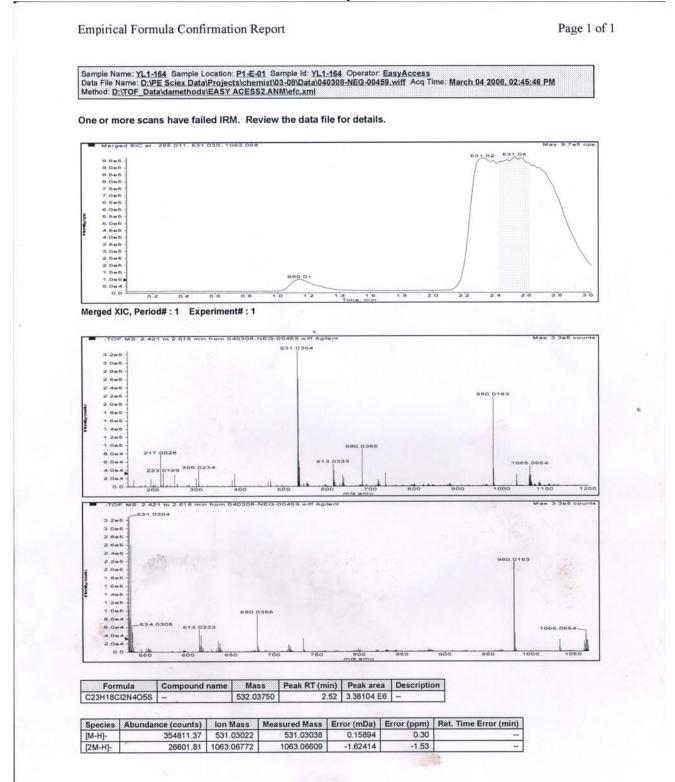






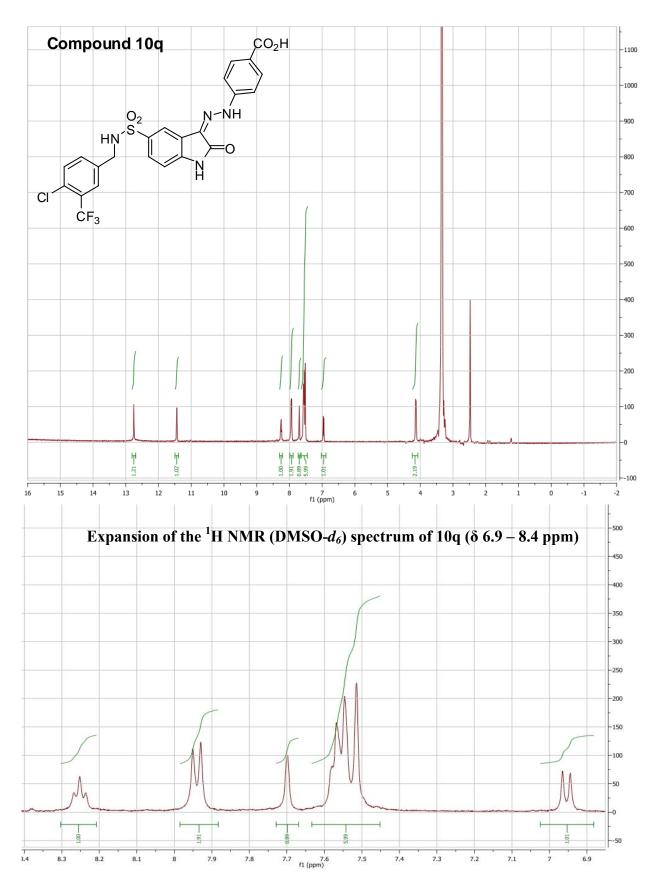


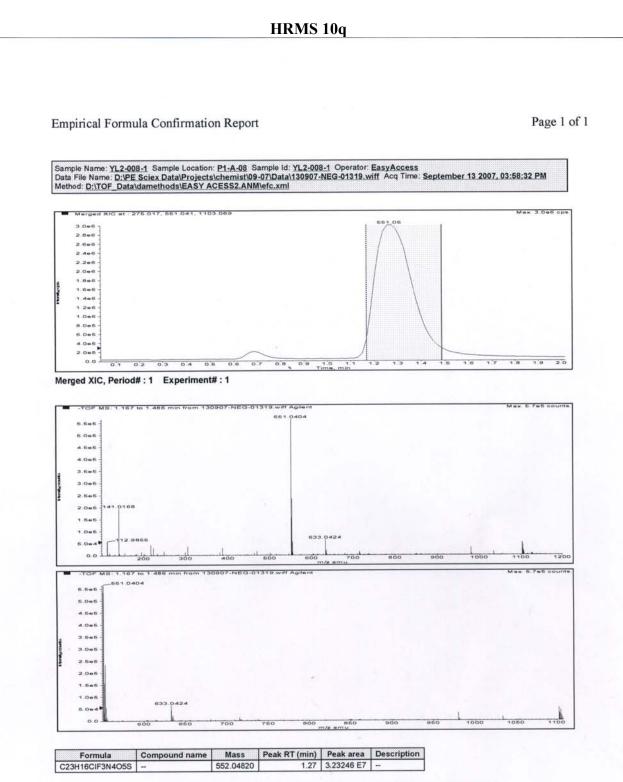
HRMS 10p



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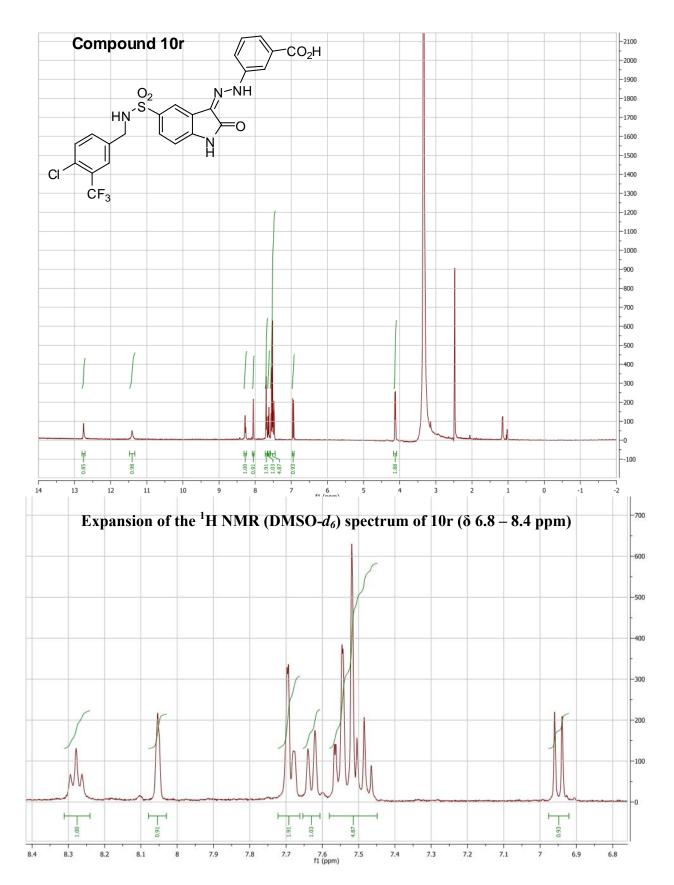
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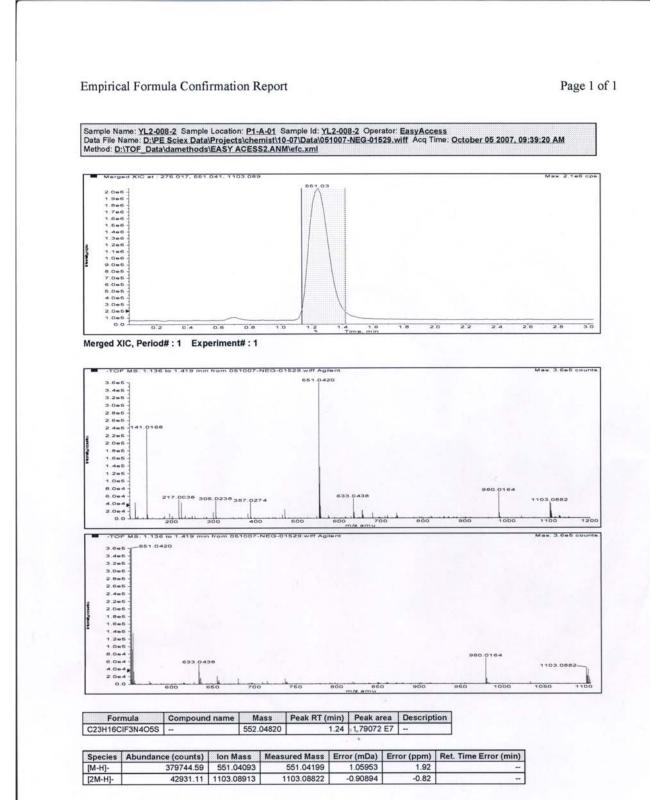


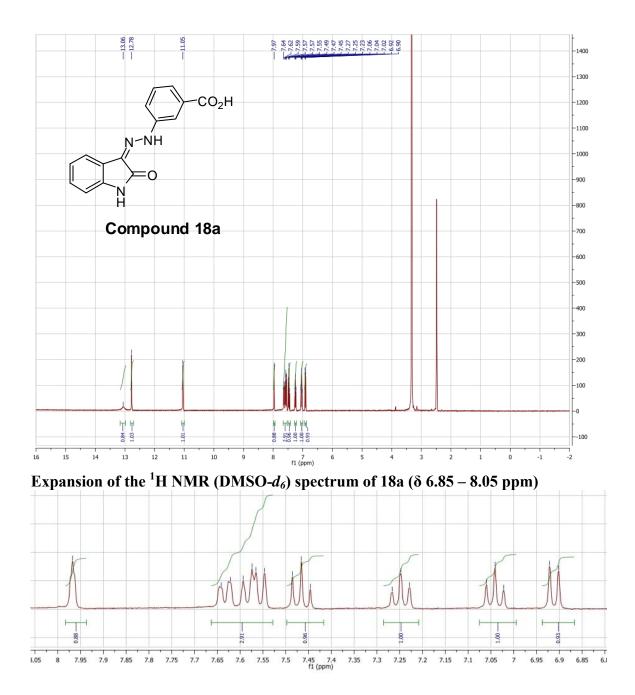
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[2M-H]-	53284.80	1103.08913	1103.08760	-1.52897	-1.39	-

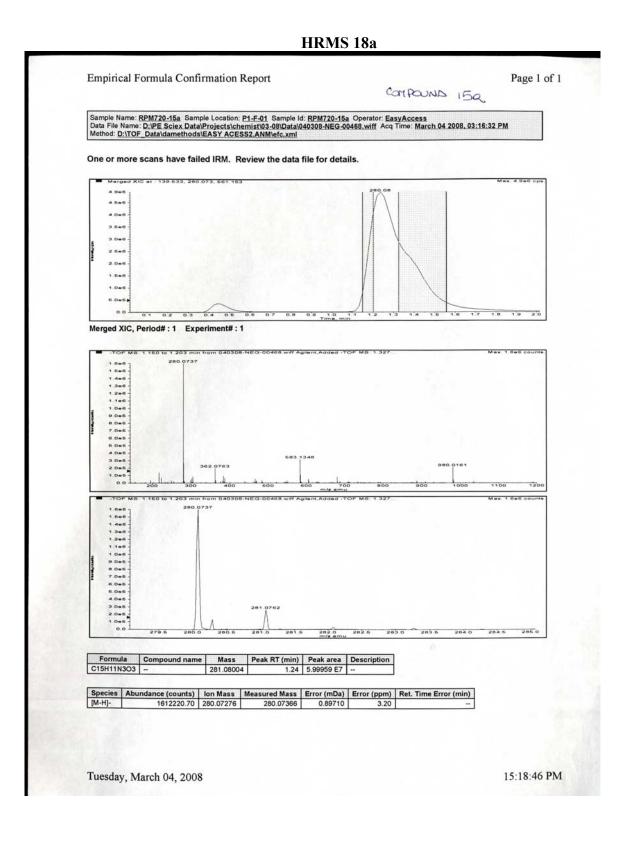
S57

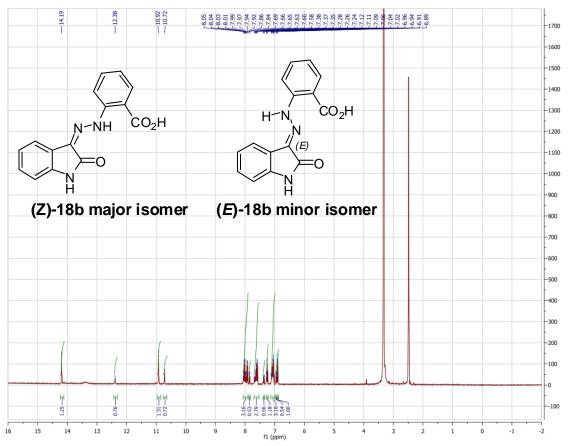




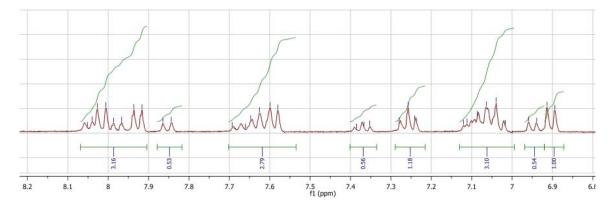




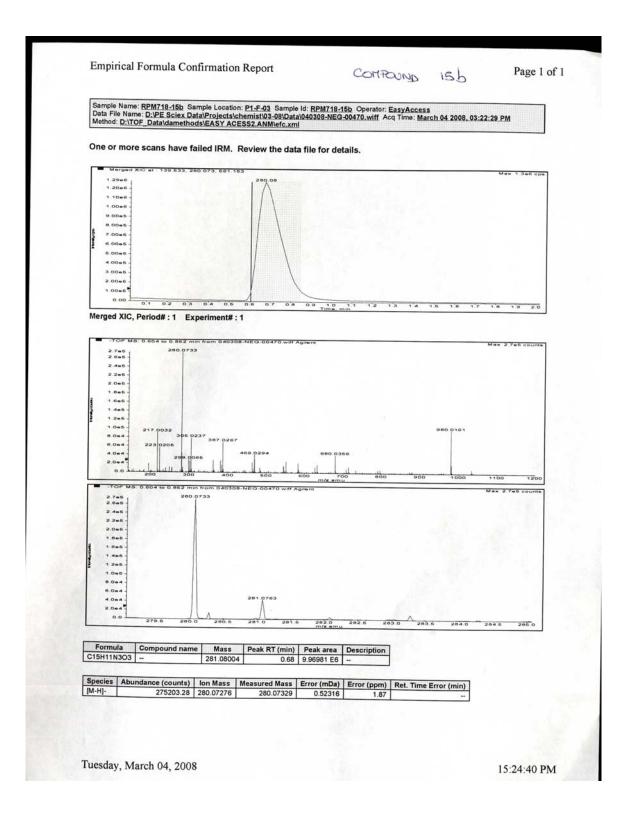




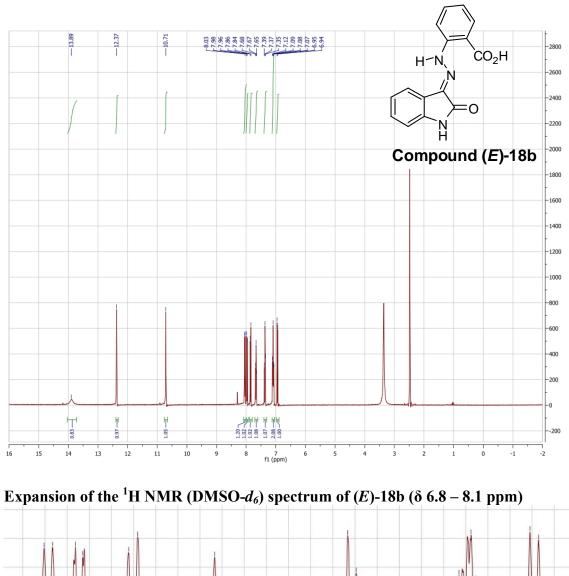
Expansion of the ¹H NMR (DMSO- d_6) spectrum of (E) and (Z)-18b (δ 6.80 – 8.2 ppm)

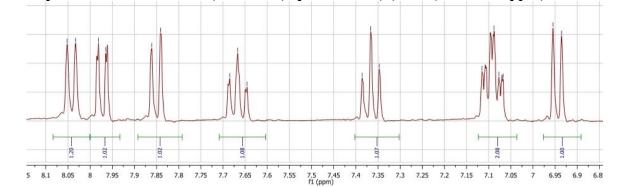


HRMS (E) and (Z)-18b



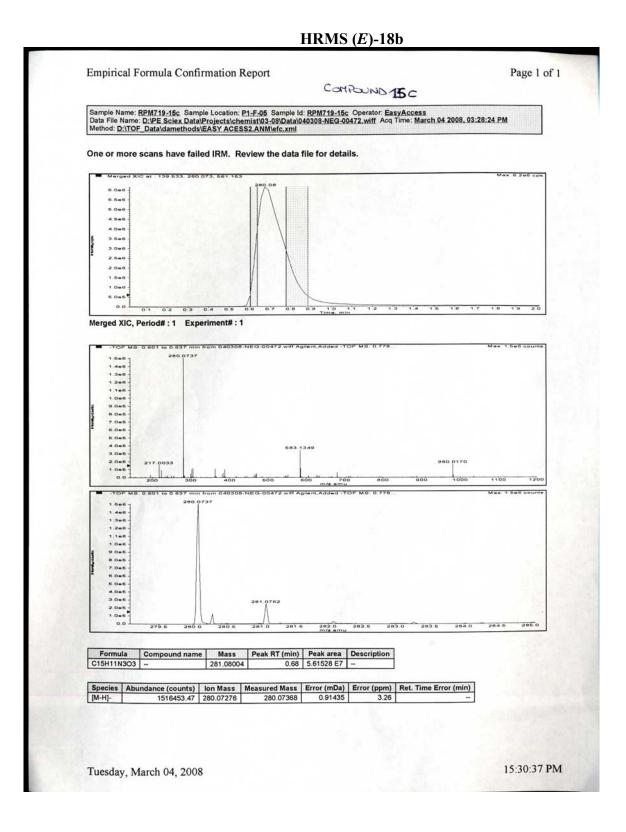
Supporting Information of Inhibitors of Shp2 Protein Tyrosine Phosphatase Based on Oxindole Scaffolds



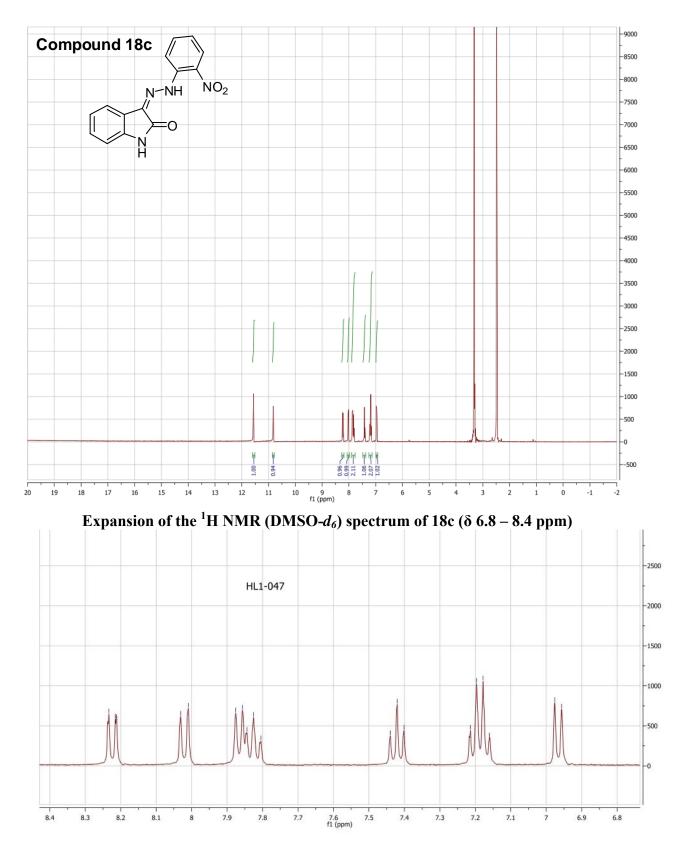


6.95 6.9 6.8

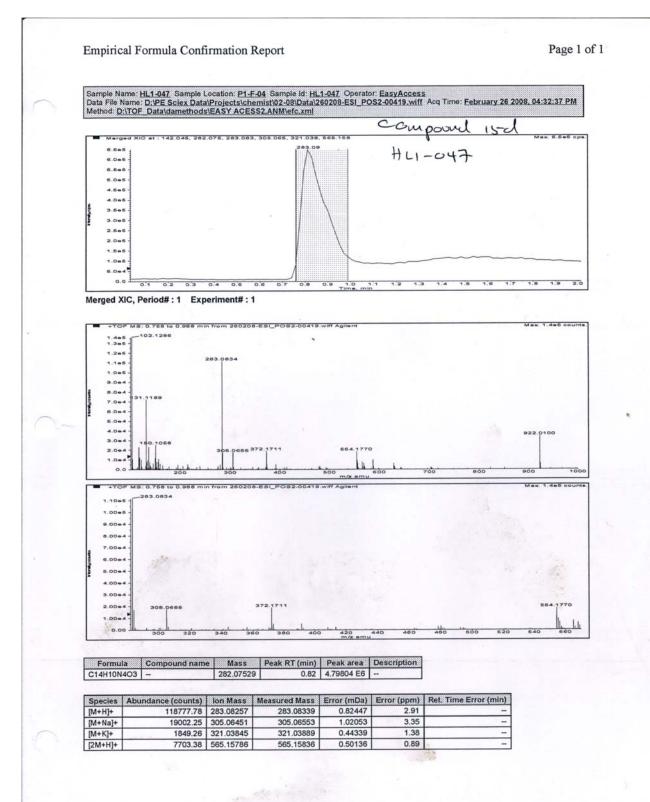
5 8.1 8.05



S65

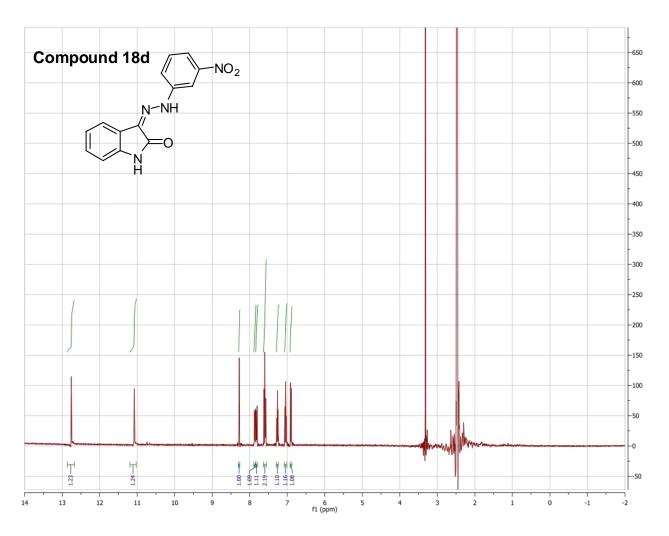


HRMS 18c

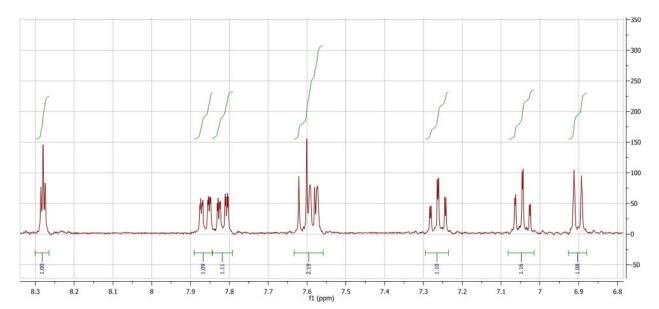


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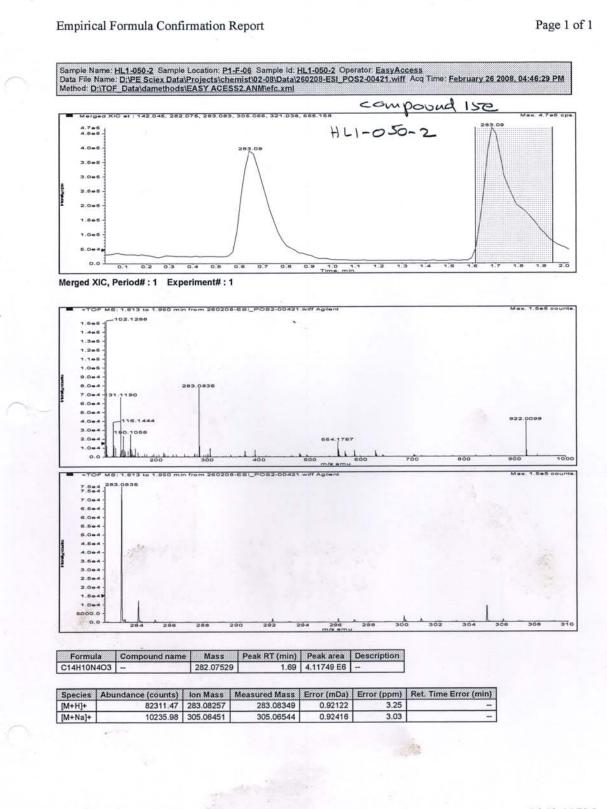
16:34:50 PM



Expansion of the ¹H NMR (DMSO- d_6) spectrum of 18d (δ 6.8 – 8.3 ppm)







Tuesday, February 26, 2008

Computer Docking. Computer docking was performed with the X-ray crystal structure of human Shp2 (PDB identification code: 2SHP)¹ and human Shp1 (PDB identification code: 1FPR)² using the GLIDE v4.0 (Grid-Based Ligand Docking with Energetics, from Schrödinger, L.L.C.) program.^{3,4} The N-SH2 domain of Shp2, which blocks the catalytic site, was removed from the 3D structure prior to the computer docking analysis. The optimal binding geometry for each model was obtained from the GLIDE docking which relies upon Monte Carlo sampling techniques coupled with energy minimization.

References

- Hof, P.; Pluskey, S.; Dhe-Paganon, S.; Eck, M. J.; Shoelson, S. E., Crystal structure of the tyrosine phosphatase SHP-2. *Cell* 1998, 92, 441-50.
- Yang, J.; Cheng, Z.; Niu, T.; Liang, X.; Zhao, Z. J.; Zhou, G. W., Structural basis for substrate specificity of protein-tyrosine phosphatase SHP-1. *J. Biol. Chem.* 2000, 275, 4066-4071.
- Friesner, R. A.; Banks, J. L.; Murphy, R. B.; Halgren, T. A.; Klicic, J. J.; Mainz, D. T.; Repasky, M. P.; Knoll, E. H.; Shelley, M.; Perry, J. K.; Shaw, D. E.; Francis, P.; Shenkin, P. S., Glide: A new approach for rapid, accurate docking and scoring. 1. Method and assessment of docking accuracy. *J. Med. Chem.* 2004, 47, 1739-1749.
- Halgren, T. A.; Murphy, R. B.; Friesner, R. A.; Beard, H. S.; Frye, L. L.; Pollard, W. T.; Banks, J. L., Glide: A new approach for rapid, accurate docking and scoring. 2. Enrichment factors in database screening. *J. Med. Chem.* 2004, 47, 1750-1759.