Supporting Information

Undecaprenyl Diphosphate Synthase Inhibitors: Antibacterial Drug Leads

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Figure S1: Correlation of pIC_{50} with docking scores

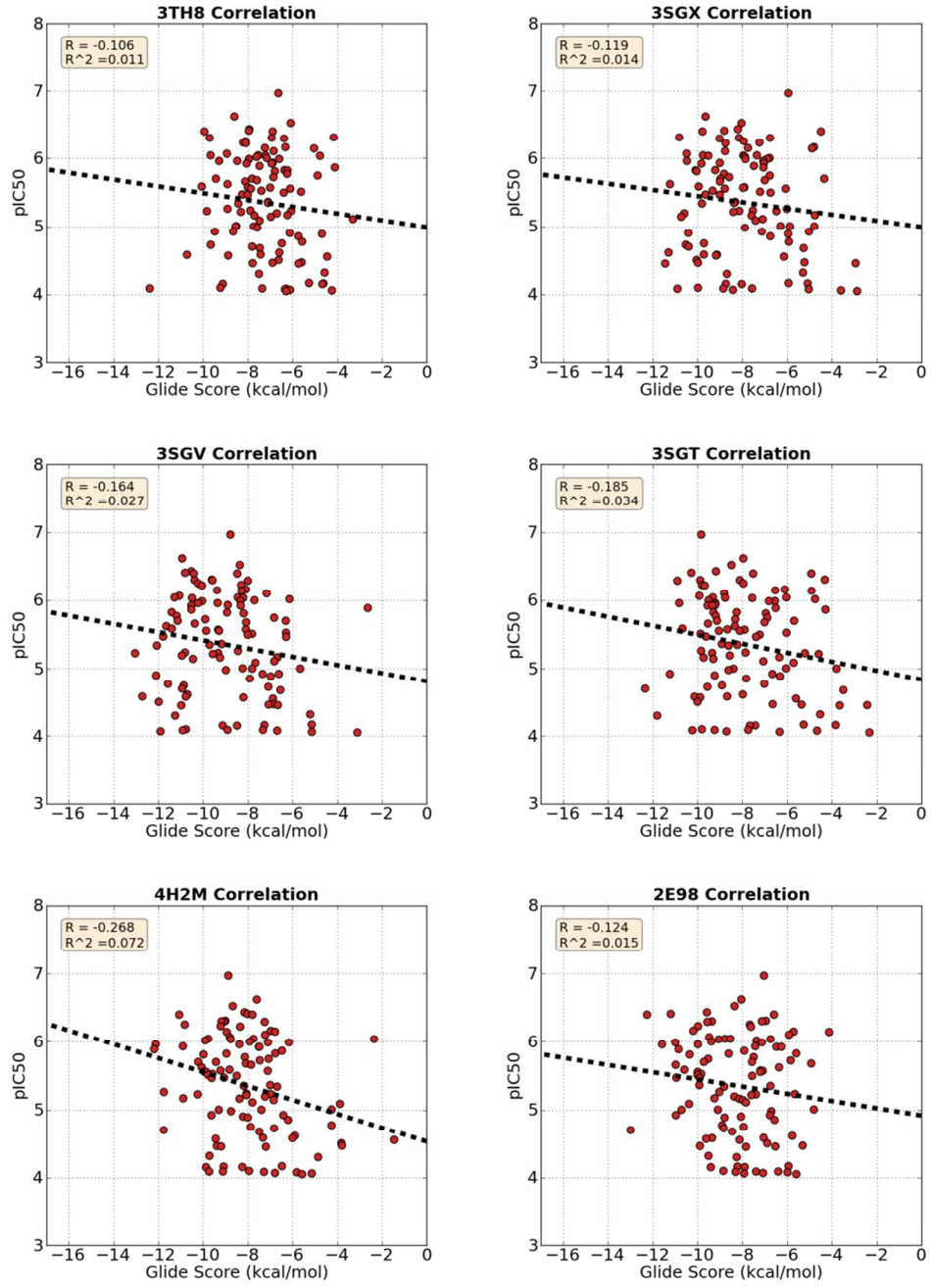


Figure S1(continued): Correlation of pIC_{50} with docking scores

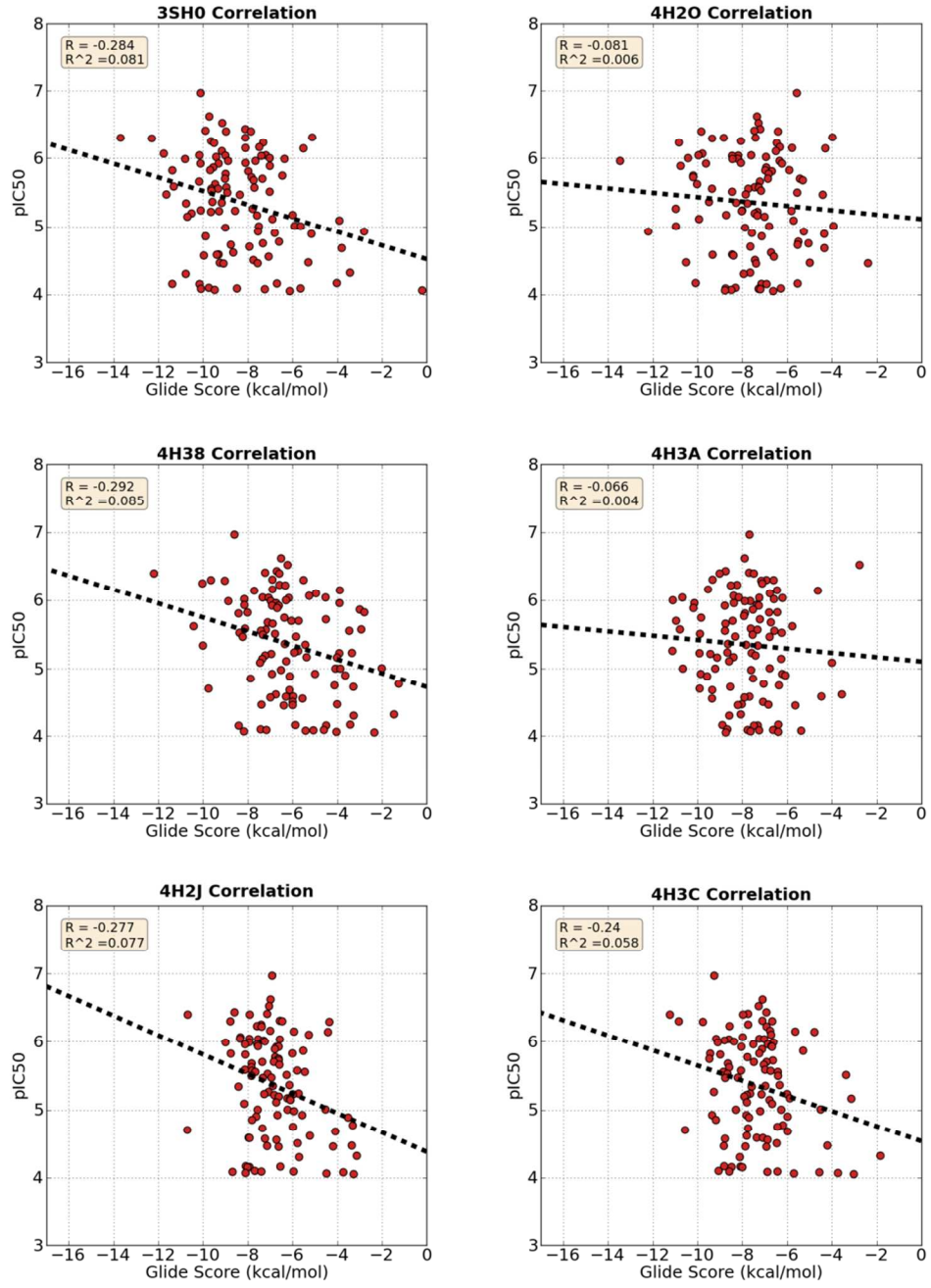
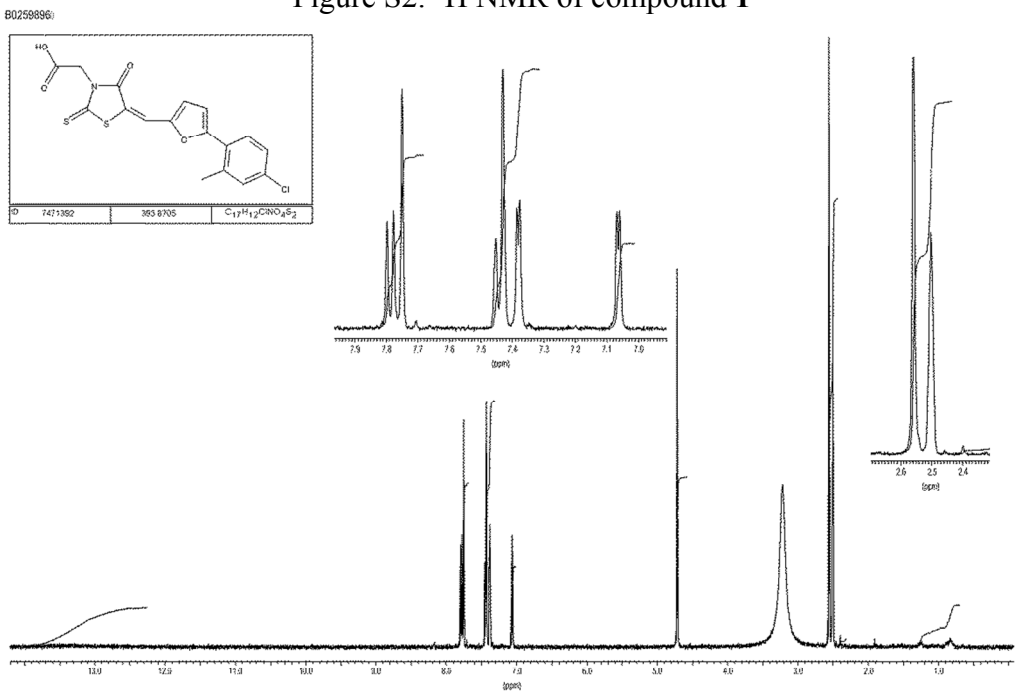


Figure S2. ^{1}H NMR of compound **1**



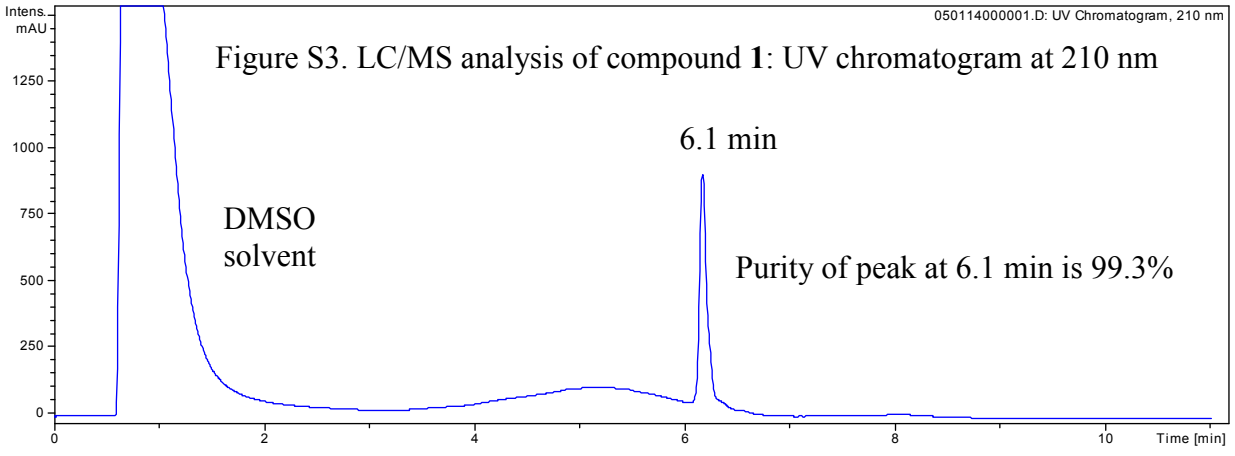


Figure S3. LC/MS analysis of compound **1**: UV chromatogram at 210 nm

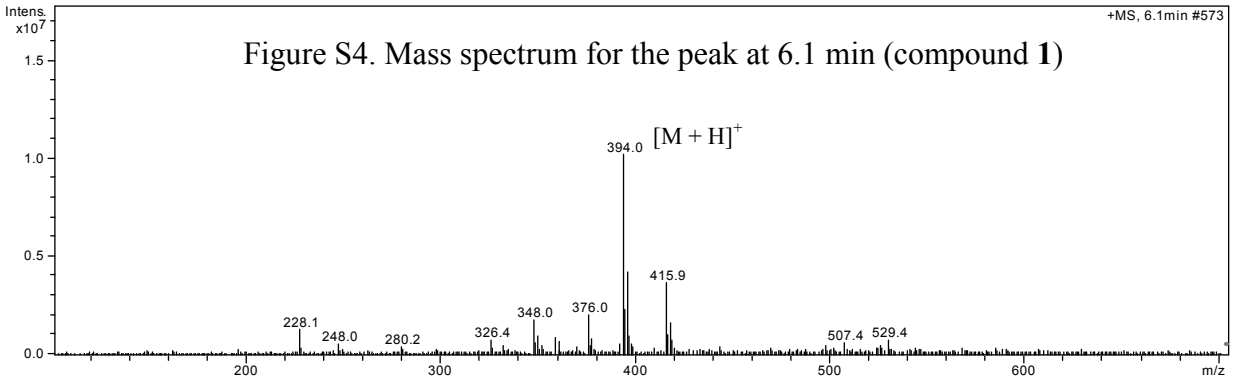
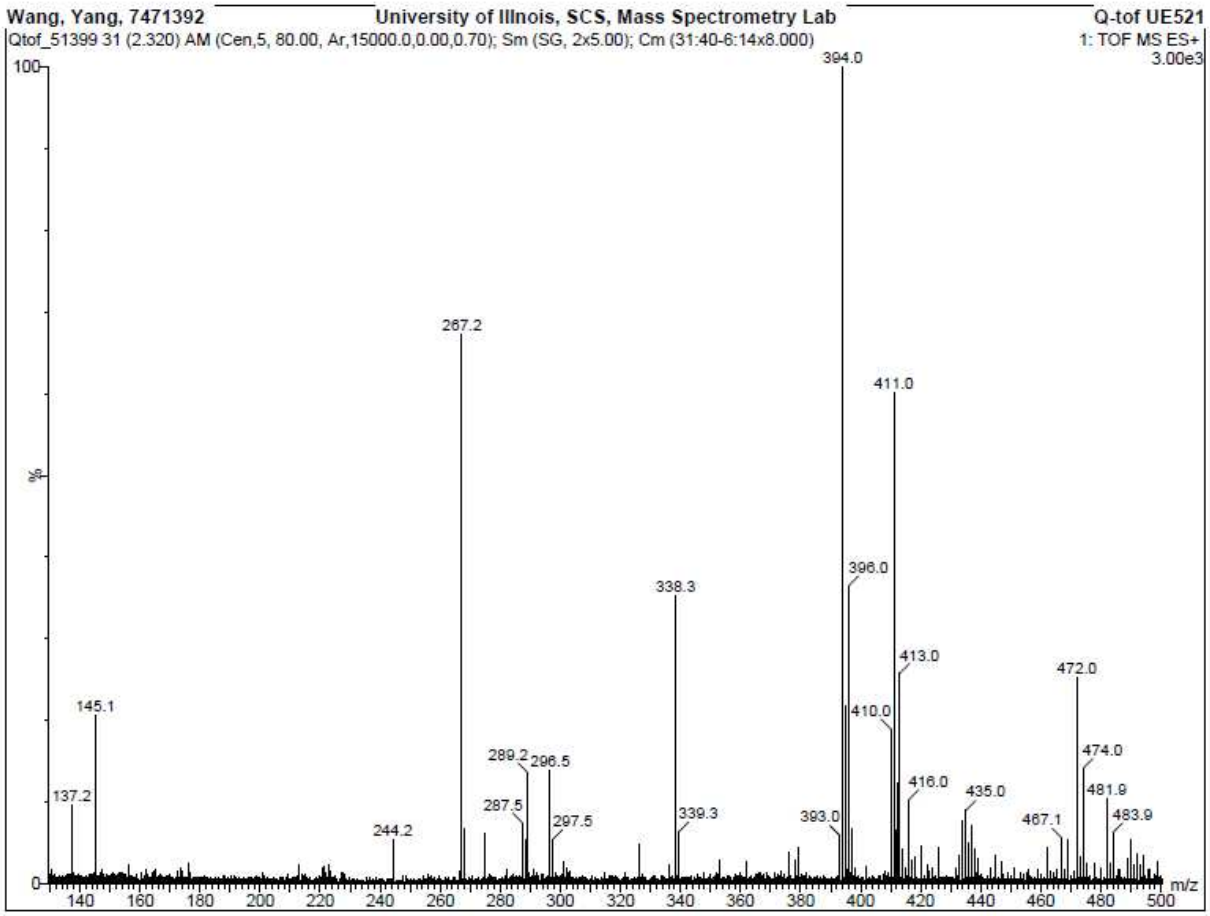


Figure S4. Mass spectrum for the peak at 6.1 min (compound **1**)

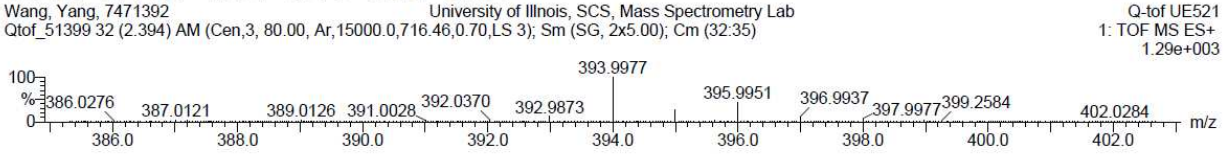
Figure S5. High-resolution mass spectrum of compound **1**



Elemental Composition Report

Single Mass Analysis
Tolerance = 10.0 PPM / DBE: min = -1.5, max = 600.0
Element prediction: Off
Number of isotope peaks used for i-FIT = 3

Monoisotopic Mass, Even Electron Ions
23 formula(e) evaluated with 1 results within limits (all results (up to 1000) for each mass)
Elements Used:
C: 0-125 H: 0-250 N: 0-1 O: 3-5 S: 2-2 Cl: 1-1



Minimum:				-1.5		
Maximum:		5.0	10.0	600.0		
Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	Formula
393.9977	393.9975	0.2	0.5	11.5	6.2	C17 H13 N O4 S2 Cl

Figure S6. ^{1}H NMR of compound **4**

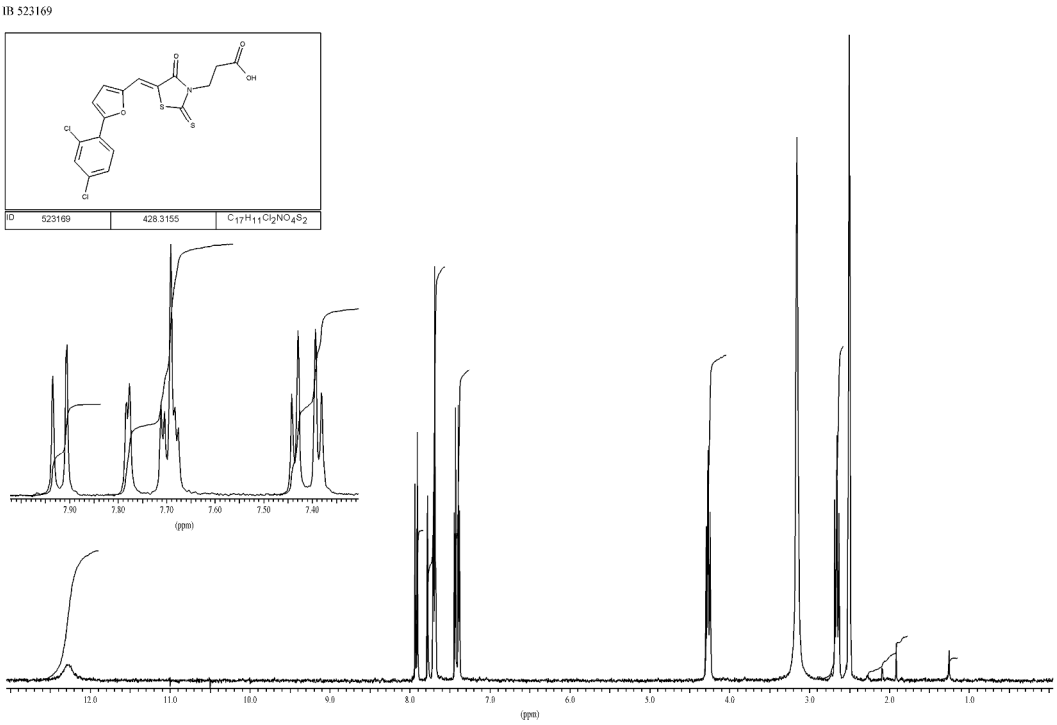


Figure S7. LC/MS analysis of compound **4**: UV chromatogram at 210 nm

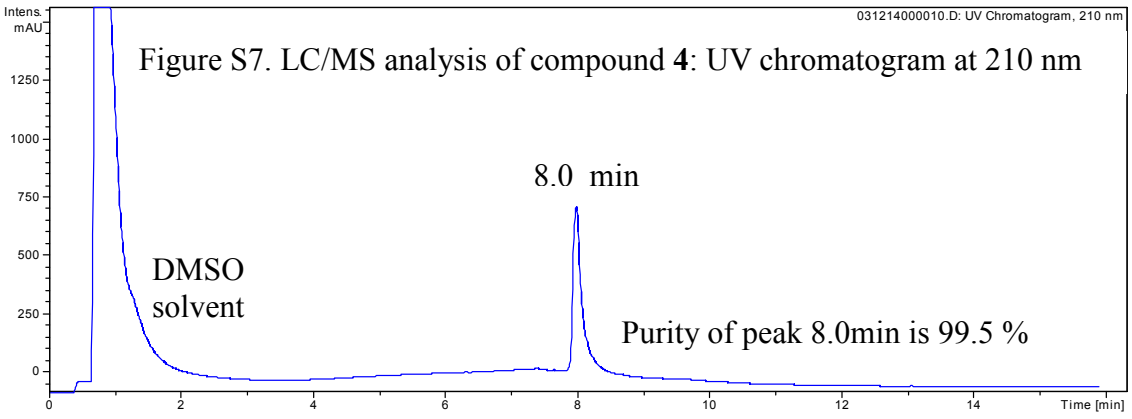


Figure S8. Mass spectrum for the peak at 8.0 min (compound **4**)

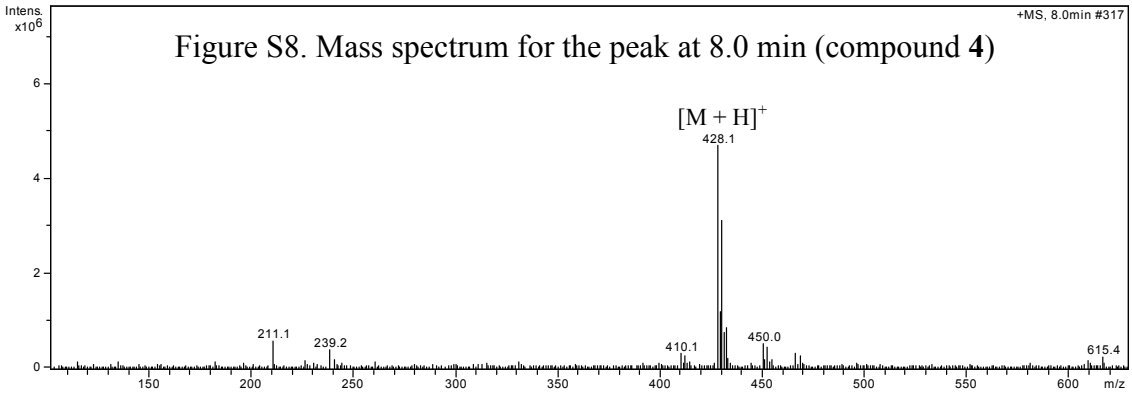
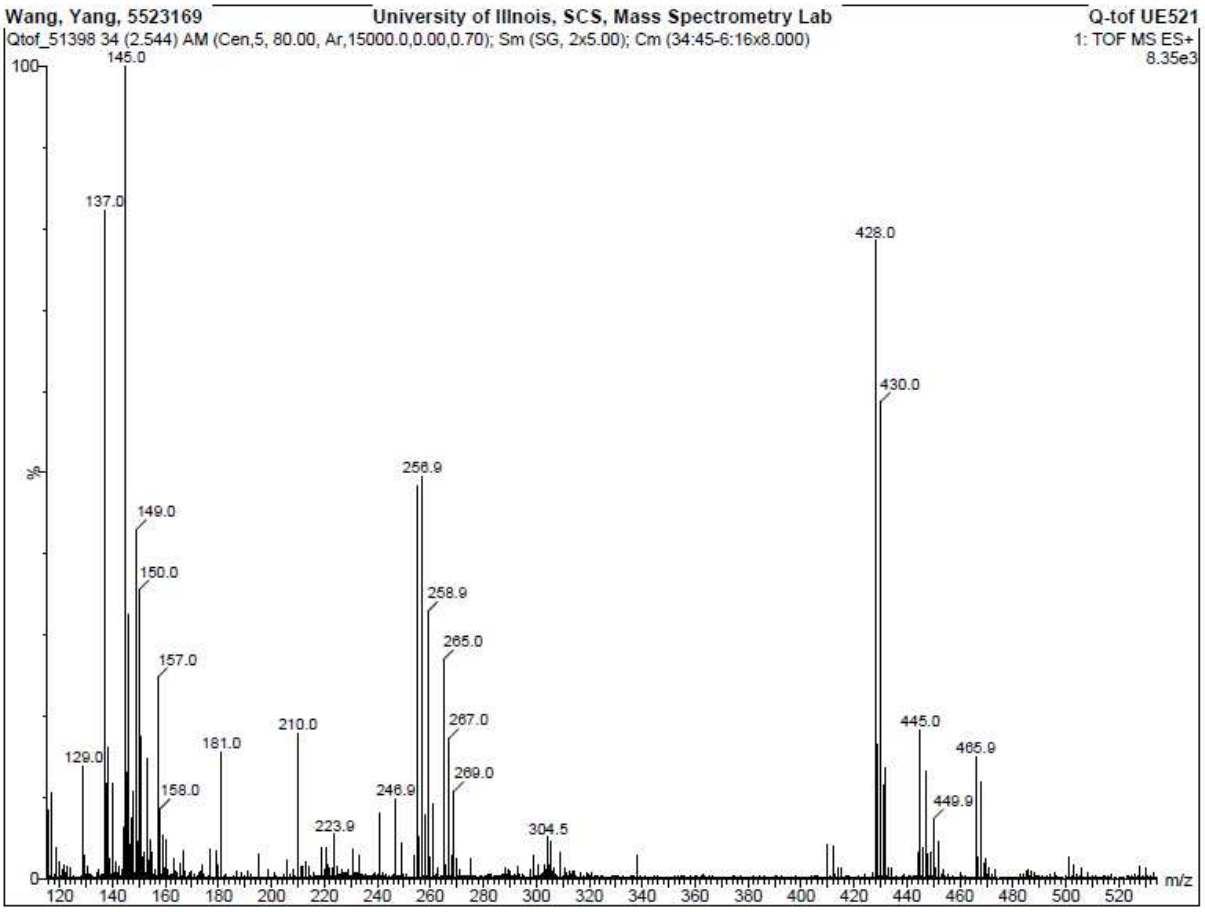


Figure S9. High-resolution mass spectrum of compound **4**



Elemental Composition Report

Single Mass Analysis
Tolerance = 10.0 PPM / DBE: min = -1.5, max = 600.0
Element prediction: Off
Number of isotope peaks used for i-FIT = 3

Monoisotopic Mass, Even Electron Ions
22 formula(e) evaluated with 1 results within limits (all results (up to 1000) for each mass)
Elements Used:
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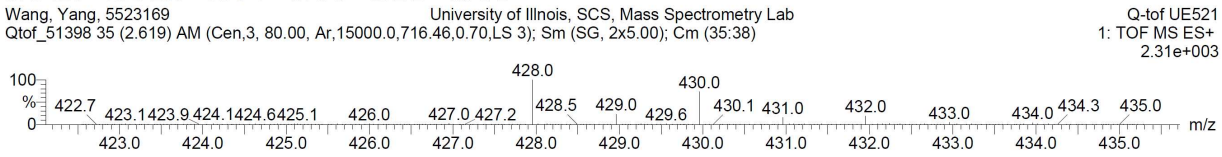

Minimum:				-1.5		
Maximum:		5.0	10.0	600.0		
Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	Formula
427.9586	427.9585	0.1	0.2	11.5	2.2	C17 H12 N O4 S2 Cl2