

ω -Alkynyl Lipid Surrogates for Polyunsaturated Fatty Acids: Free Radical and Enzymatic Oxidations

William N. Beavers^{1†}, Remigiusz Serwa,^{1,4†}, Yuki Shimozu², Keri A. Tallman¹, Melissa Vaught¹, Esha D. Dalvie^{3,5}, Lawrence J. Marnett^{1,2,3}, Ned A. Porter^{1,2}*

A.B. Hancock Memorial Laboratory for Cancer Research, Departments of Chemistry¹, Biochemistry², and Pharmacology³, Vanderbilt Institute for Chemical Biology, Vanderbilt Center in Molecular Toxicology, Vanderbilt Ingram Cancer Center, Vanderbilt University, Nashville, TN 37235

Author Notes

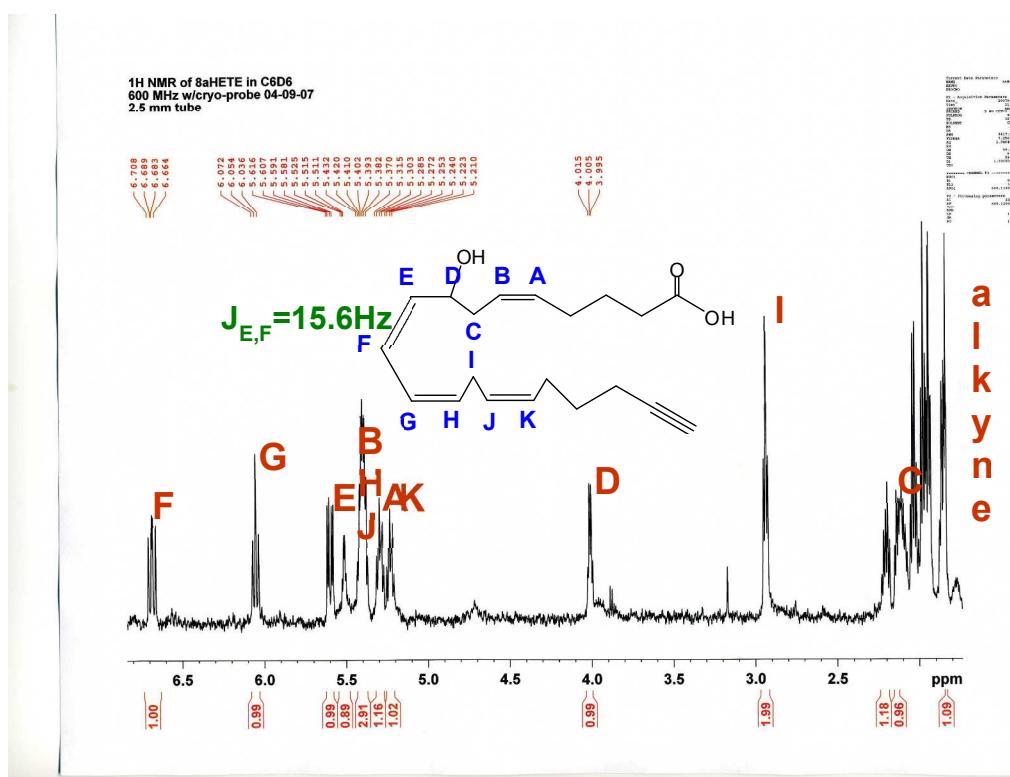
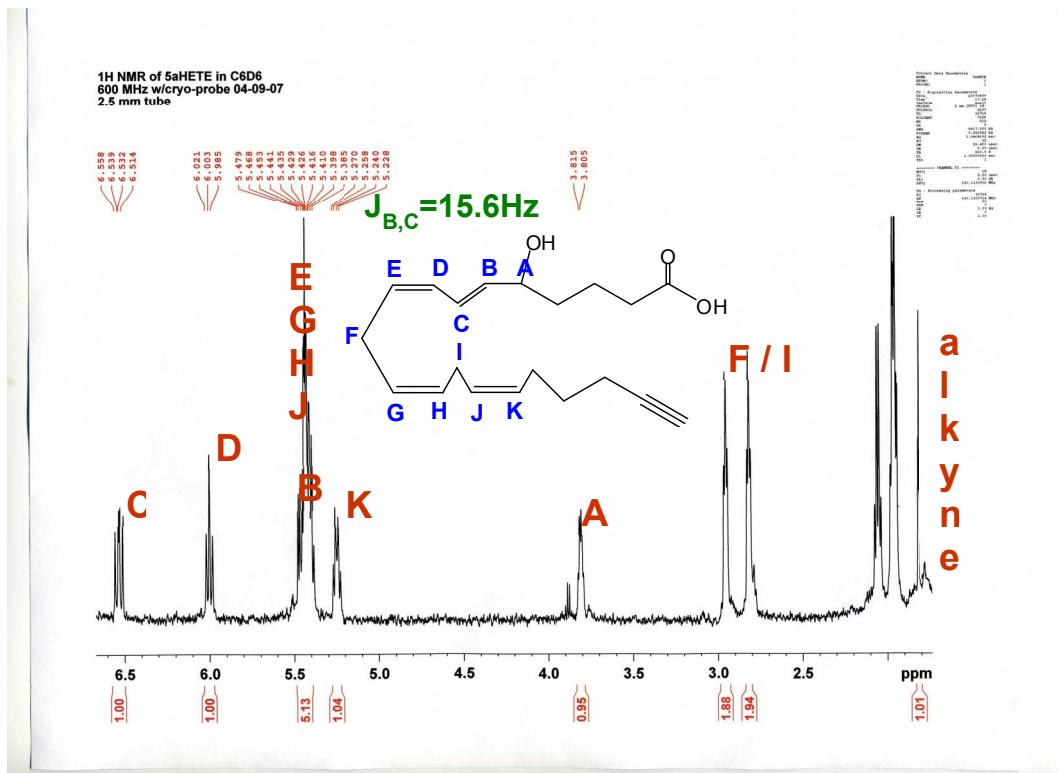
[†]These authors contributed equally to this research

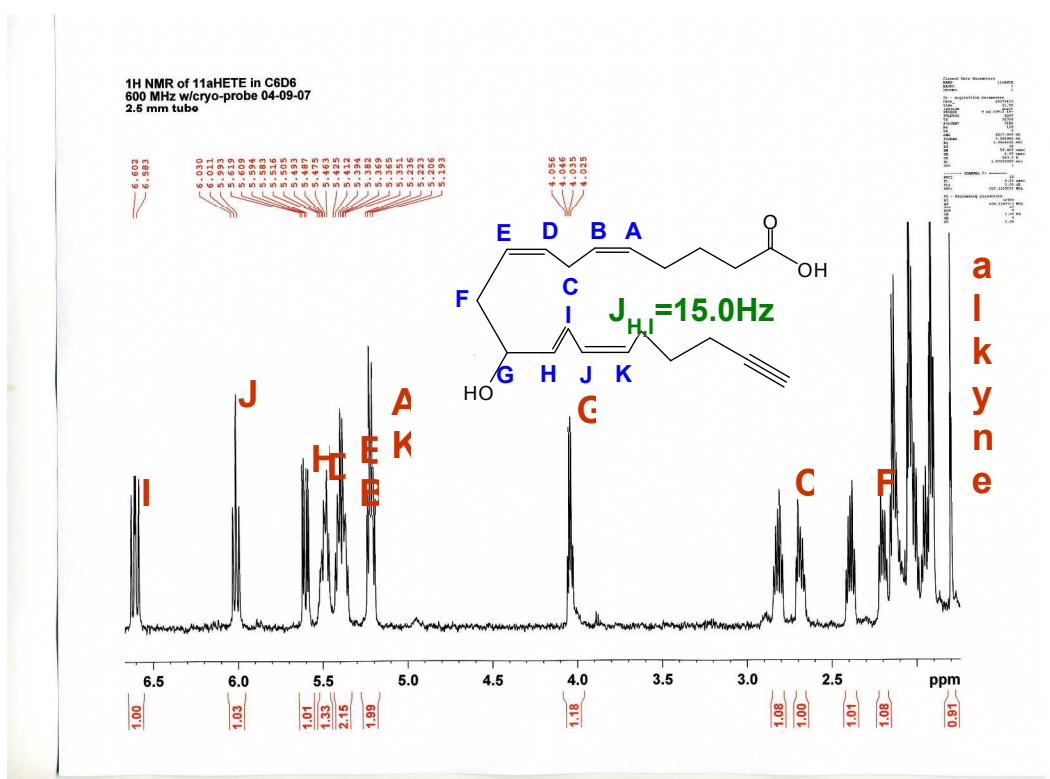
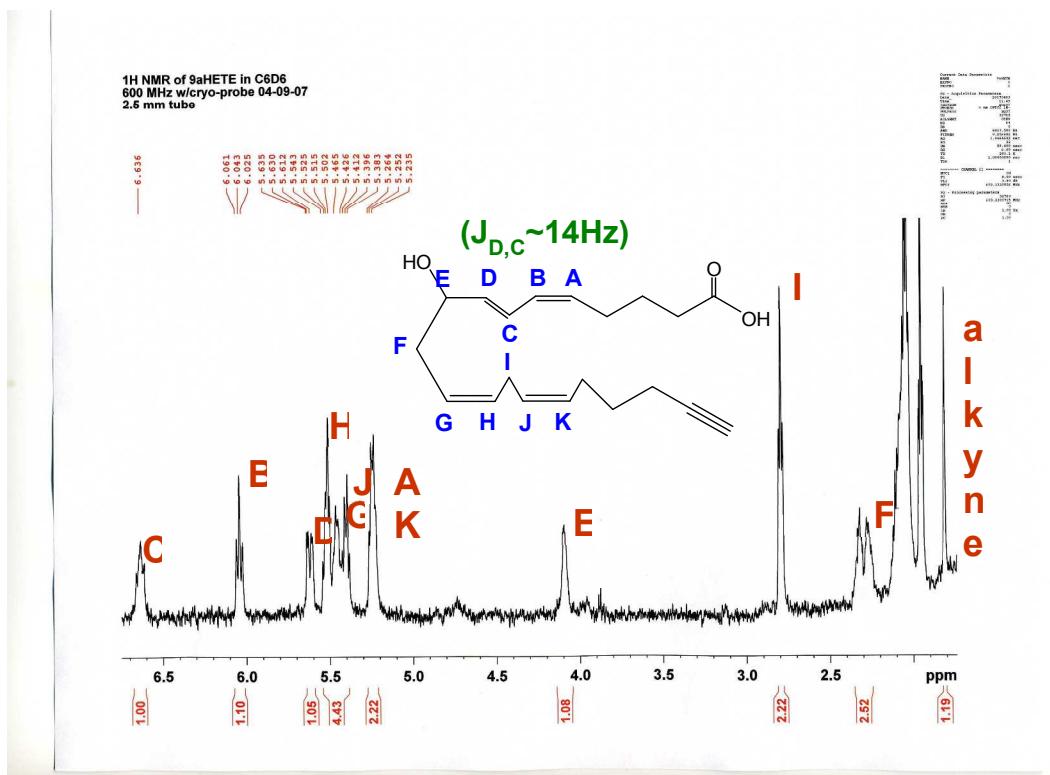
*To whom correspondence should be addressed.
n.porter@vanderbilt.edu

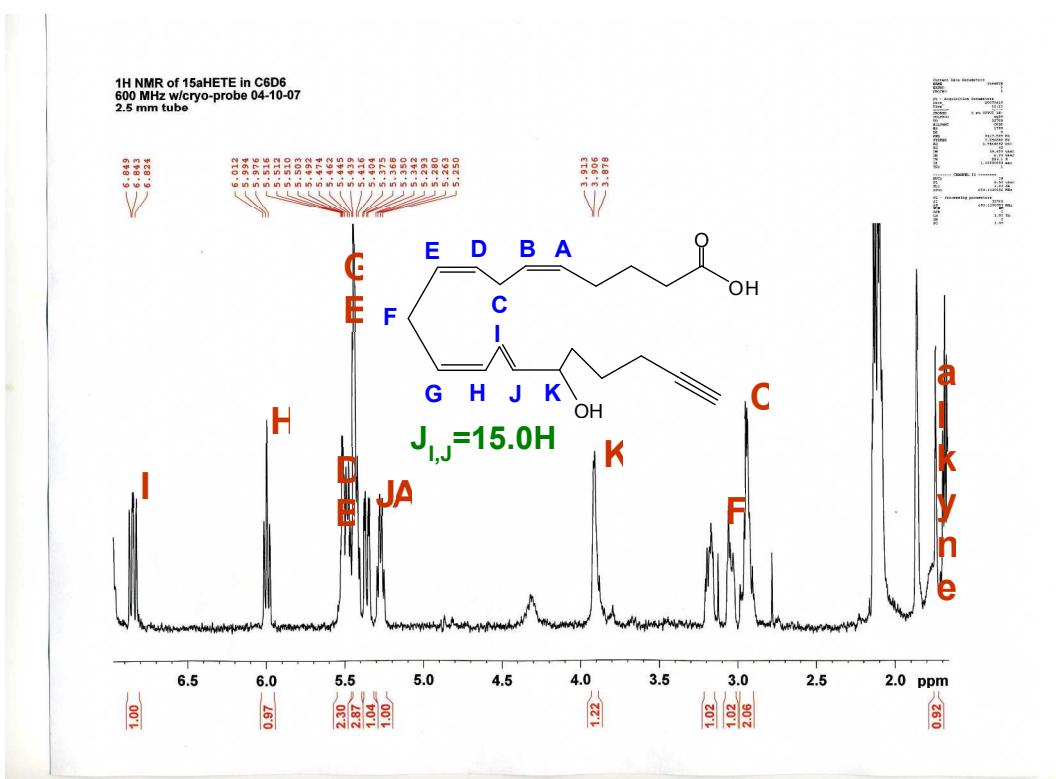
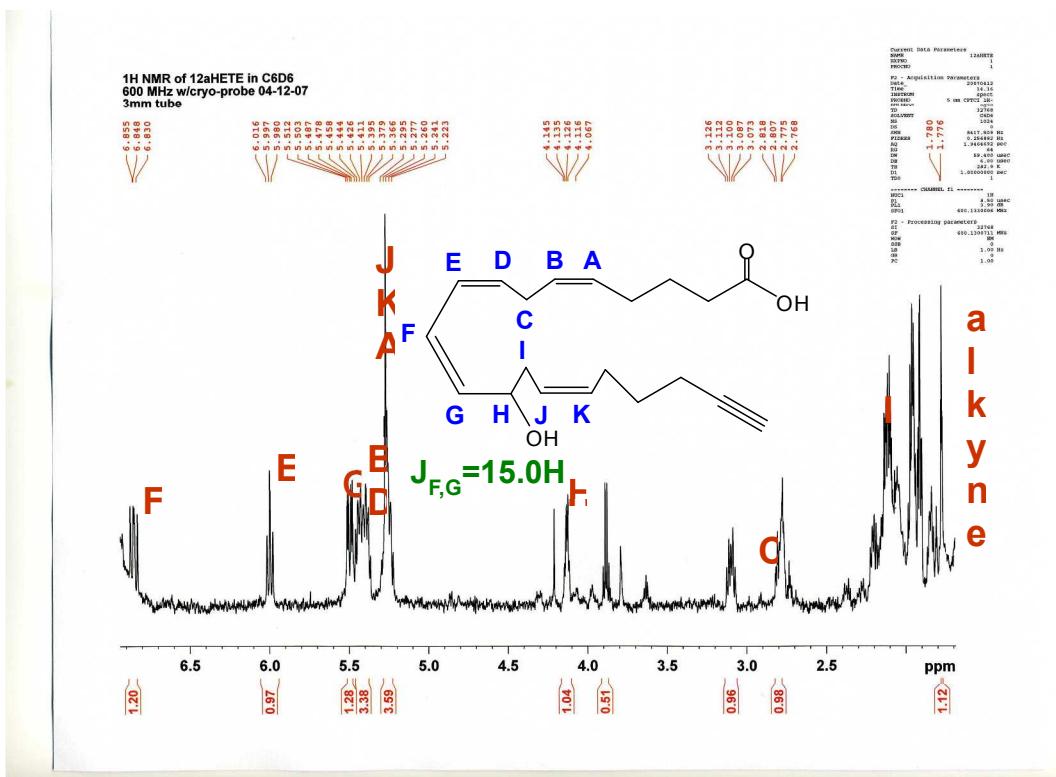
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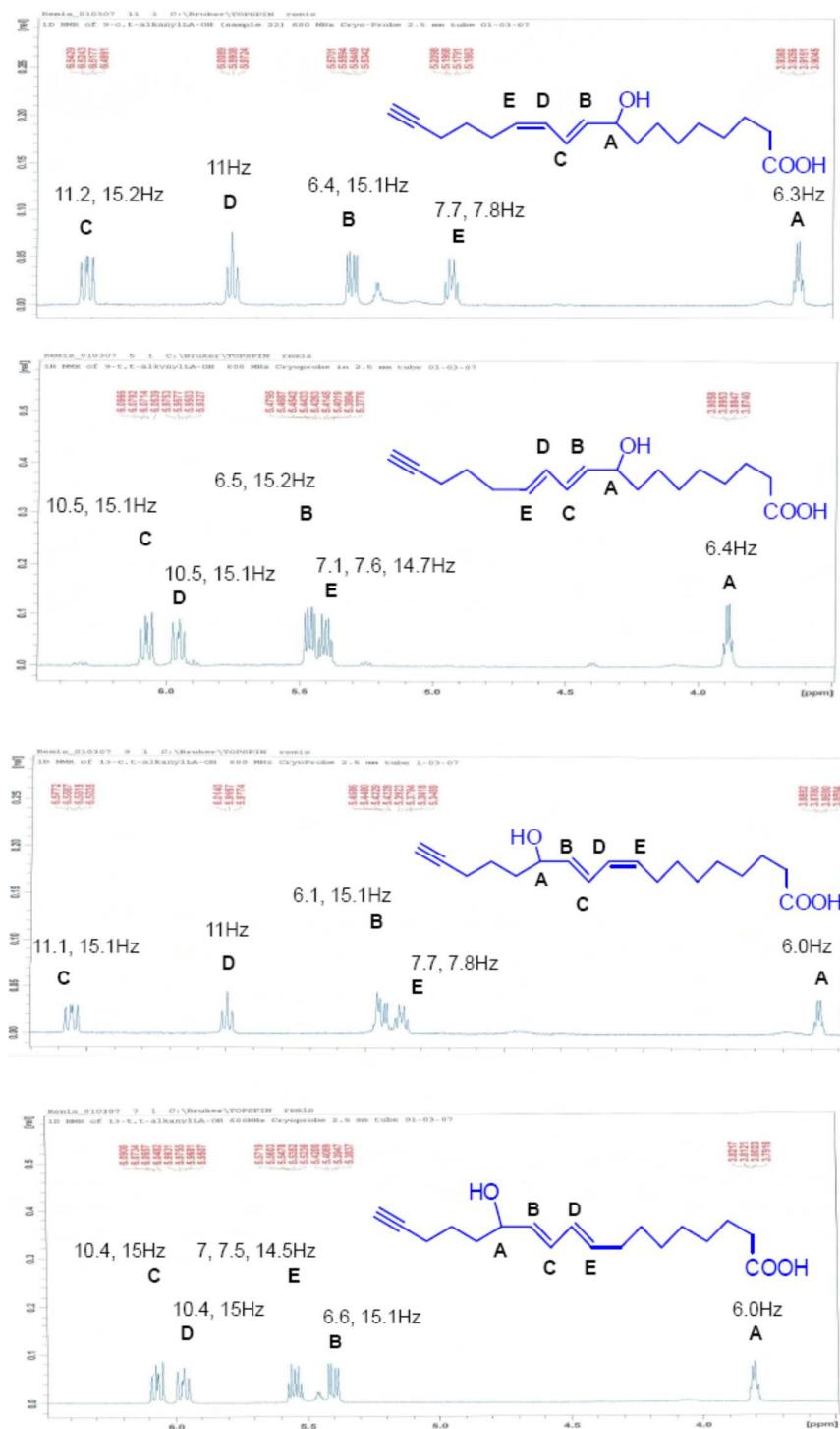
⁴*Department of Chemistry, Imperial College London, South Kensington Campus, Exhibition Road, London SW7 2AZ (UK)*

⁵*Department of Molecular Toxicology, University of California Berkeley, Berkeley, CA 94720*





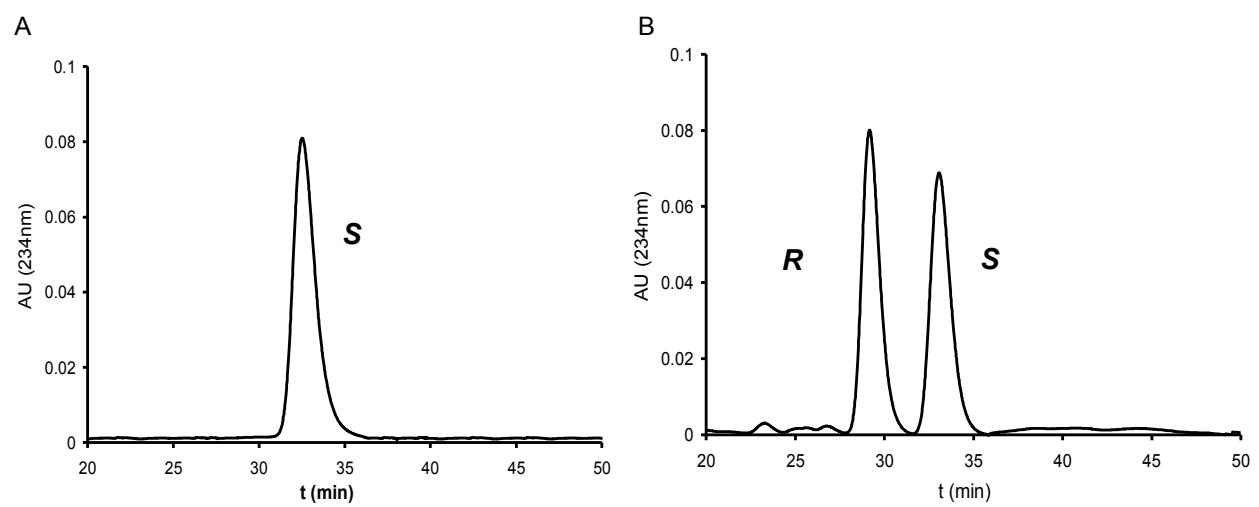




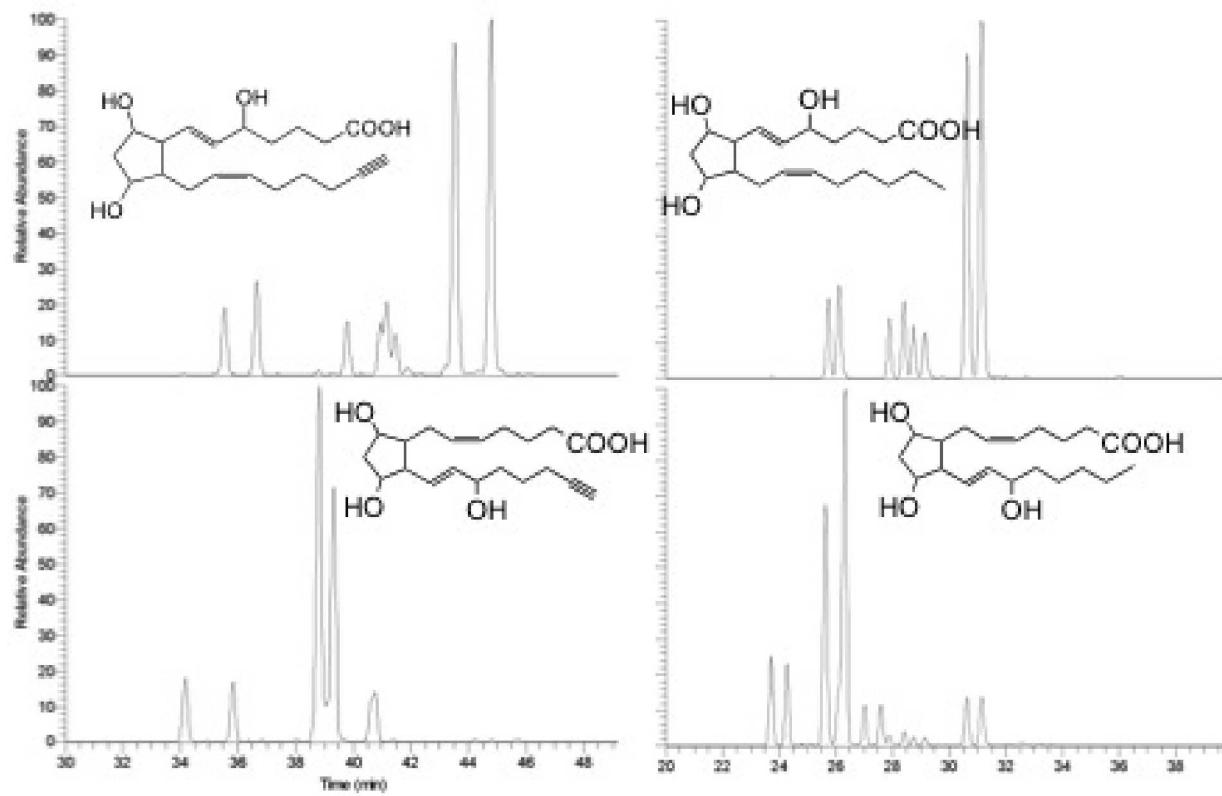
Supplemental Figure 1. ¹H NMR spectra of alkynyl HETE and HODE products, and coupling constants assigning the double bonds as either cis or trans.

	Parent ion (m/z)	Products of in source dehydration/decarboxylation (m/z)	Fragment ions (m/z)
5- <i>a</i> HETE	314.8	253.2, 297.2	115.2, 199.2
8- <i>a</i> HETE	315.3	253.4, 297.1	155.0, 159.1
9- <i>a</i> HETE	315.0	253.4, 296.9	123.1, 147.0, 166.9, 175.0
11- <i>a</i> HETE	315.1	297.3	166.9
12- <i>a</i> HETE	315.1	253.1, 297.2	179.2, 208.2
15- <i>a</i> HETE	315.2	253.2, 297.3	175.0 , 218.9

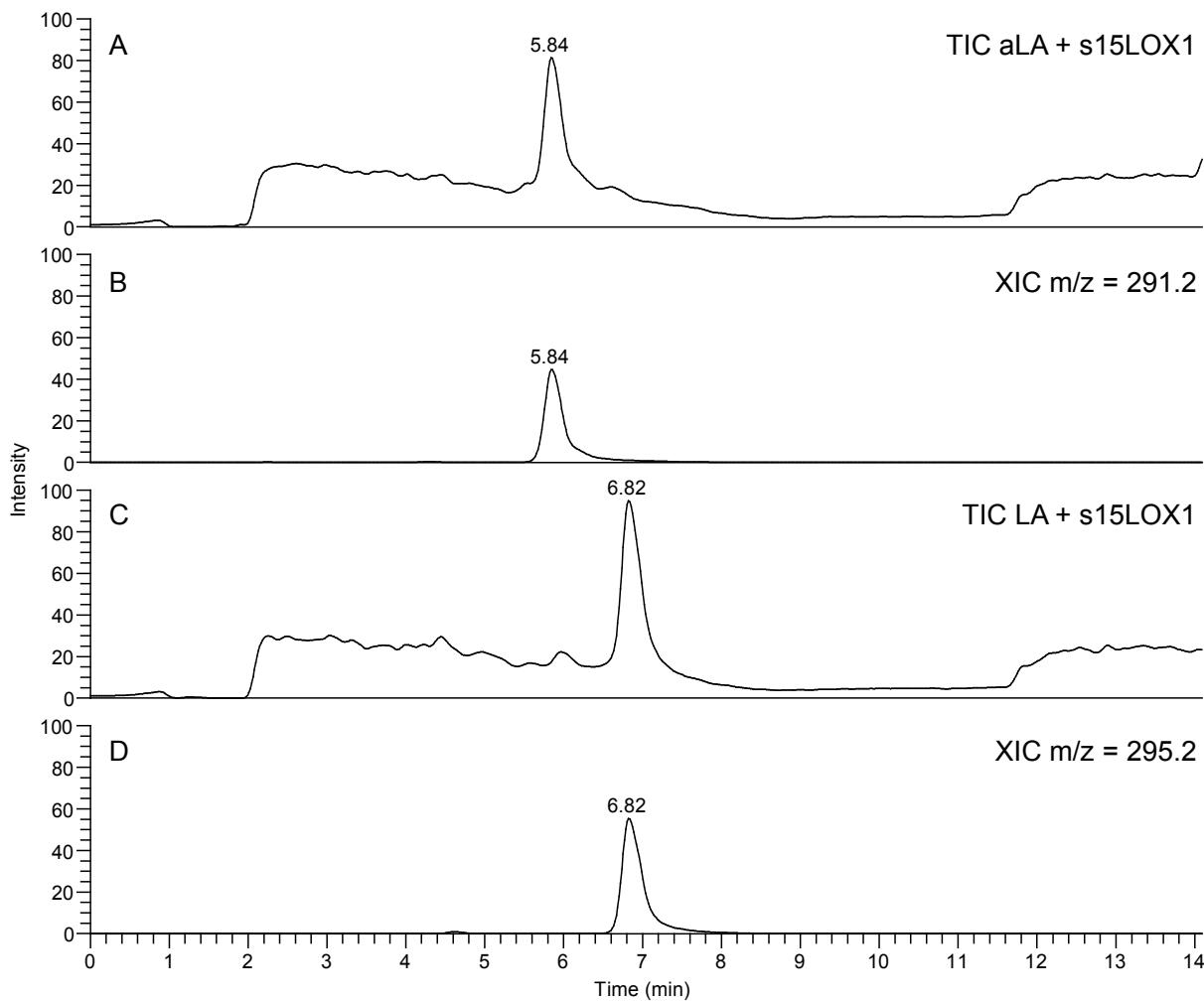
Supplemental Table 1. MS² fragmentation patterns for *a*HETE (MS signal optimized with 15-HETE). Red and blue numbers represent non-regiospecific fragments.



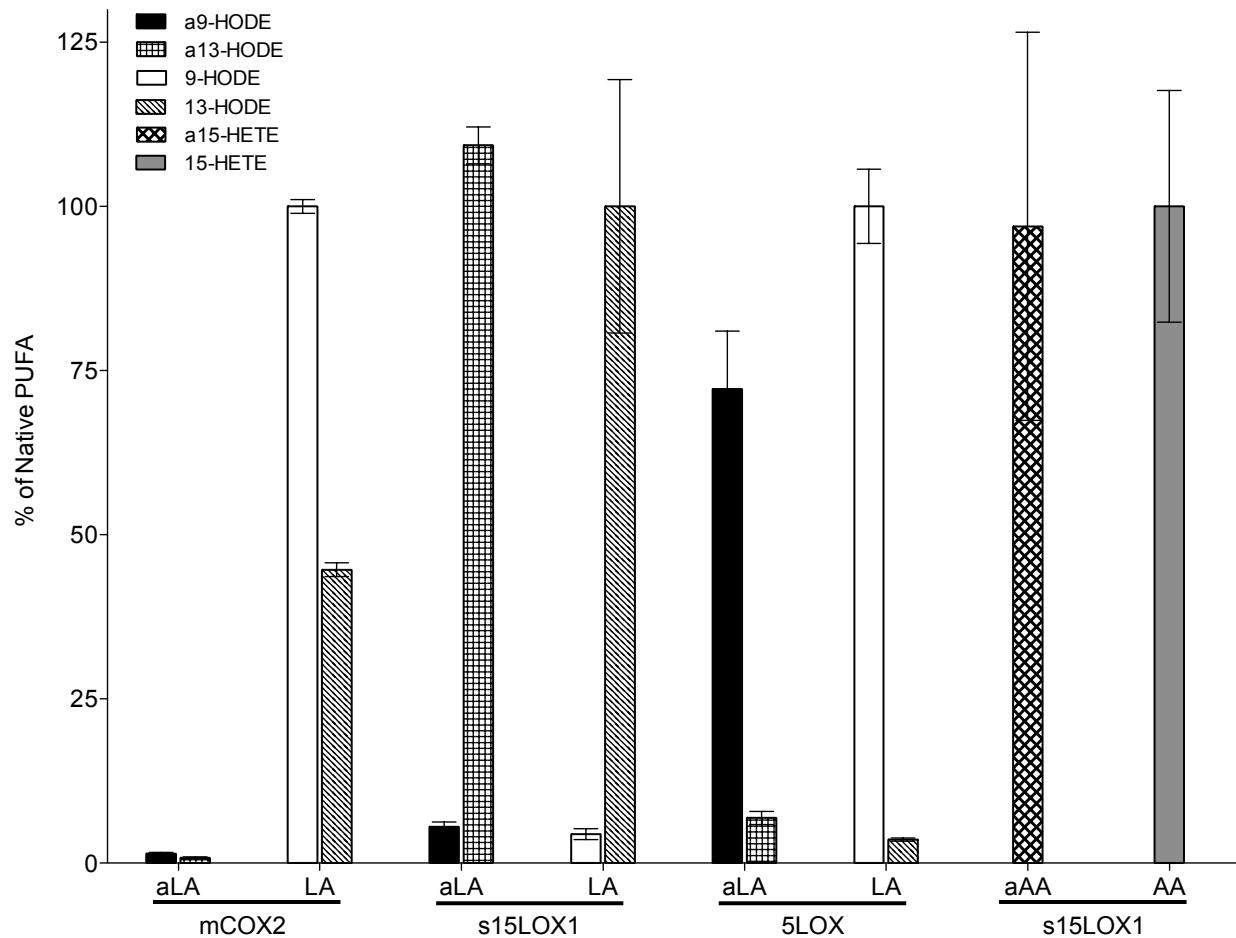
Supplemental Figure 2. Chiral analysis of alkynyl 13-c,t HODE methyl ester produced enzymatically by the reaction with s15LOX1 giving an optically pure product (A), and nonenzymatically giving mixture of optical enantiomers (B).



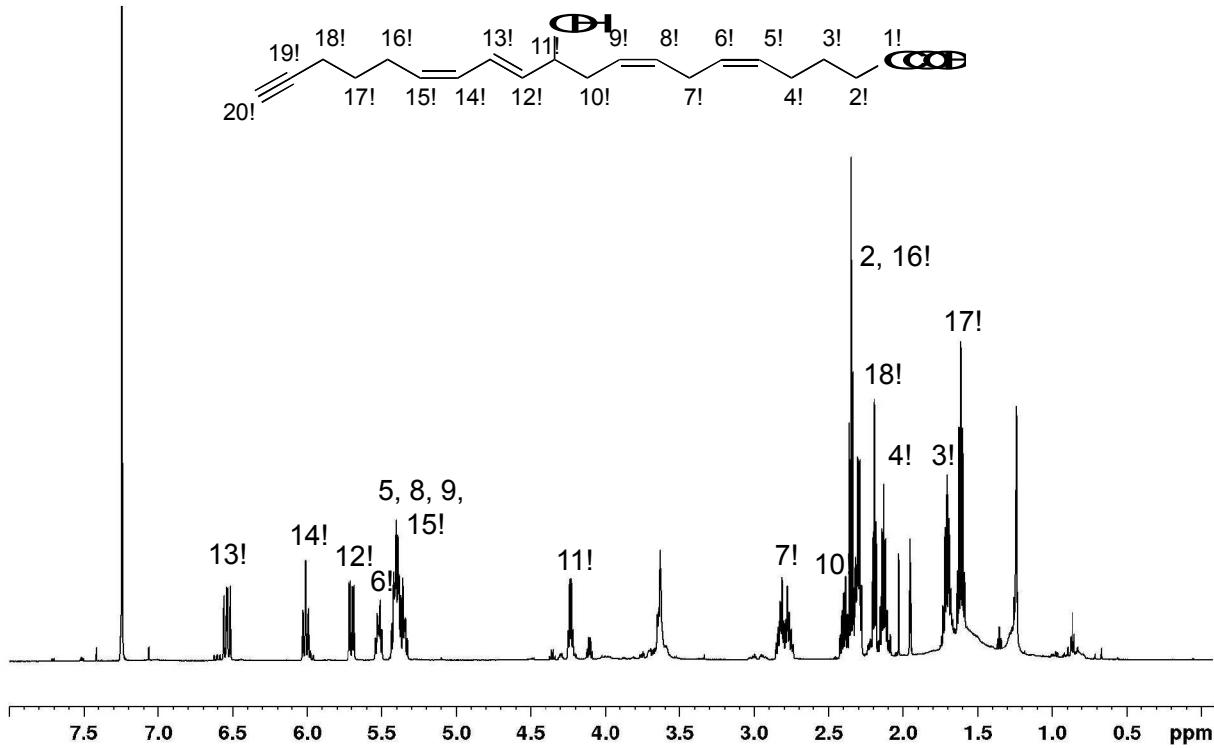
Supplemental Figure 3. RP-LC-MS (SRM) profiles of α F₂ α IsoPs generated upon MeOAMVN initiated oxidations of α AA compared to F₂-IsoPs formed from AA. Chromatography was with a MeCN/MeOH 2mM aq. NH₄OAc gradient as described in the Experimental Section.



Supplemental Figure 4. A comparison of the metabolite profiles of *a*LA (A) and LA (C) with s15LOX1. The metabolism of *a*LA by s15LOX1 shows a single product showing the addition of oxygen. The metabolism of LA by s15LOX1 also shows a single product showing the addition of oxygen.



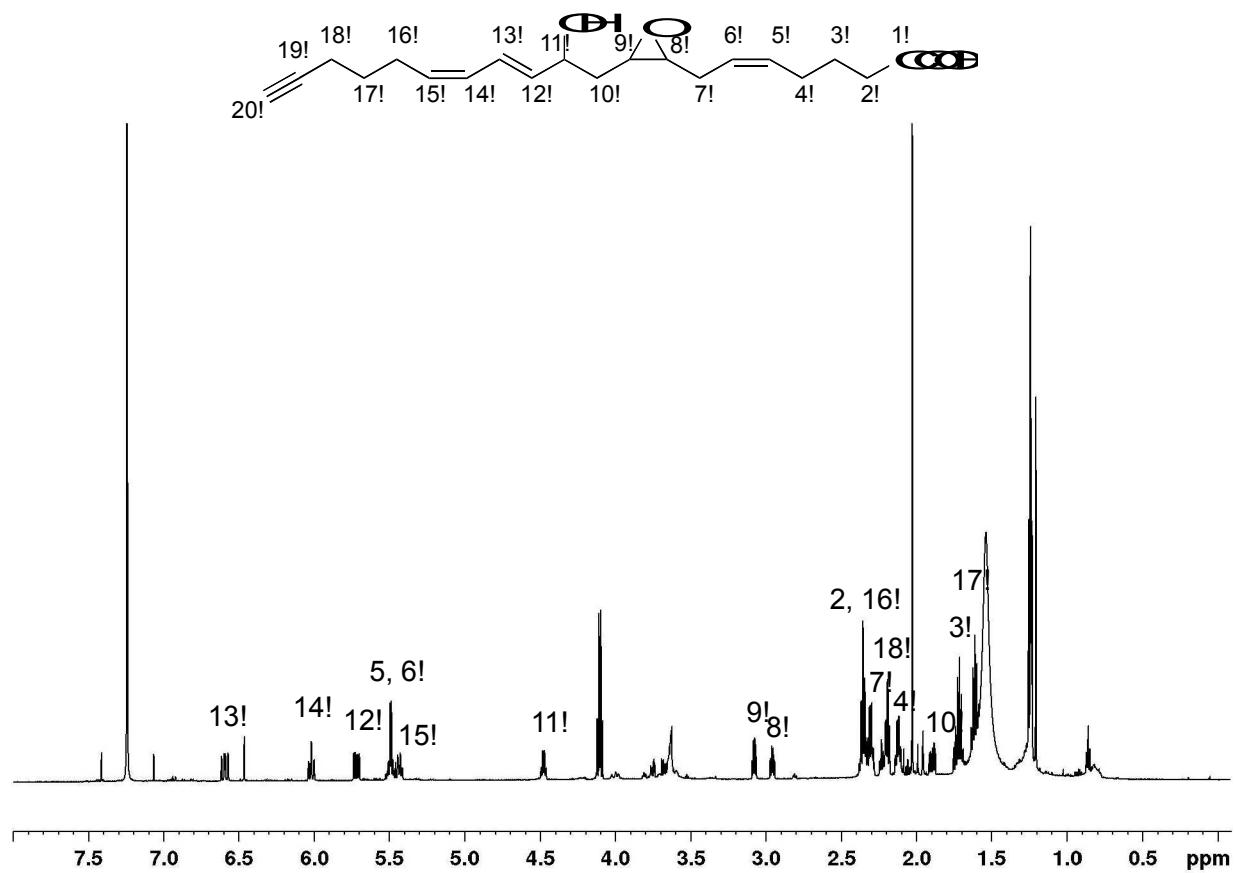
Supplemental Figure 5. Quantification of single oxygenation metabolites for the reaction between the PUFA pairs *a*LA/LA and *a*AA/AA with murine COX2, soybean 15LOX1, and potato 5LOX. Fatty acid pairs are normalized to the most abundant native (LA or AA) metabolite for each enzyme.



Supplemental Figure 6. ^1H NMR spectrum of $\alpha 11$ -HETE in CDCl_3

Chemical shift ppm	Multiplicity	Proton(s)	Coupling Constant Hz
		carbon no.	
6.54	dd	H13	$J_{12,13} = 15.1$
6.01	t	H14	$J_{14,15} = 11.0$
5.70	dd	H12	$J_{12,13} = 15.2$
5.51	m	H6	
5.39	m	H5, 8, 9, 15	
4.23	q	H11	
2.78	m	H7	
2.34	m	H2a, 10, 16	
2.19	m	H18	
2.12	quint	H4	
1.70	m	H3	
1.61	quint	H17	

Supplemental Table 2. ^1H -NMR chemical shifts and coupling constants of the collected LCMS peak with $m/z = 315.2$, which was identified to be $\alpha 11$ -HETE.



Supplemental Figure 7. ^1H NMR spectrum of *a*11-8,9-HEET in CDCl_3

Chemical shift ppm	Multiplicity	Proton(s)	Coupling Constant Hz
		carbon no.	
6.59	<i>dd</i>	H13	$J_{12,13} = 15.1$
6.02	<i>t</i>	H14	$J_{14,15} = 11.0$
5.72	<i>dd</i>	H12	$J_{12,13} = 15.2$
5.51	<i>m</i>	H5,6	
5.45	<i>dt</i>	H15	$J_{14,15} = 10.6$
4.48	<i>q</i>	H11	
3.08	<i>quint</i>	H9	$J_{8,9} = 4.2$
2.95	<i>dt</i>	H8	$J_{8,9} = 4.3$
2.24	<i>m</i>	H2,4,7,16,18	
1.90	<i>m</i>	H10a	
1.72	<i>m</i>	H10b	
1.61	<i>quint</i>	H17	

Supplemental Table 3. ^1H -NMR chemical shifts and coupling constants of the collected LCMS peak with $\text{m/z} = 331.2$, which was identified to be *a*11-8,9-HEET.