

Supplementary Information

A study on the chiral inversion of mandelic acid in humans

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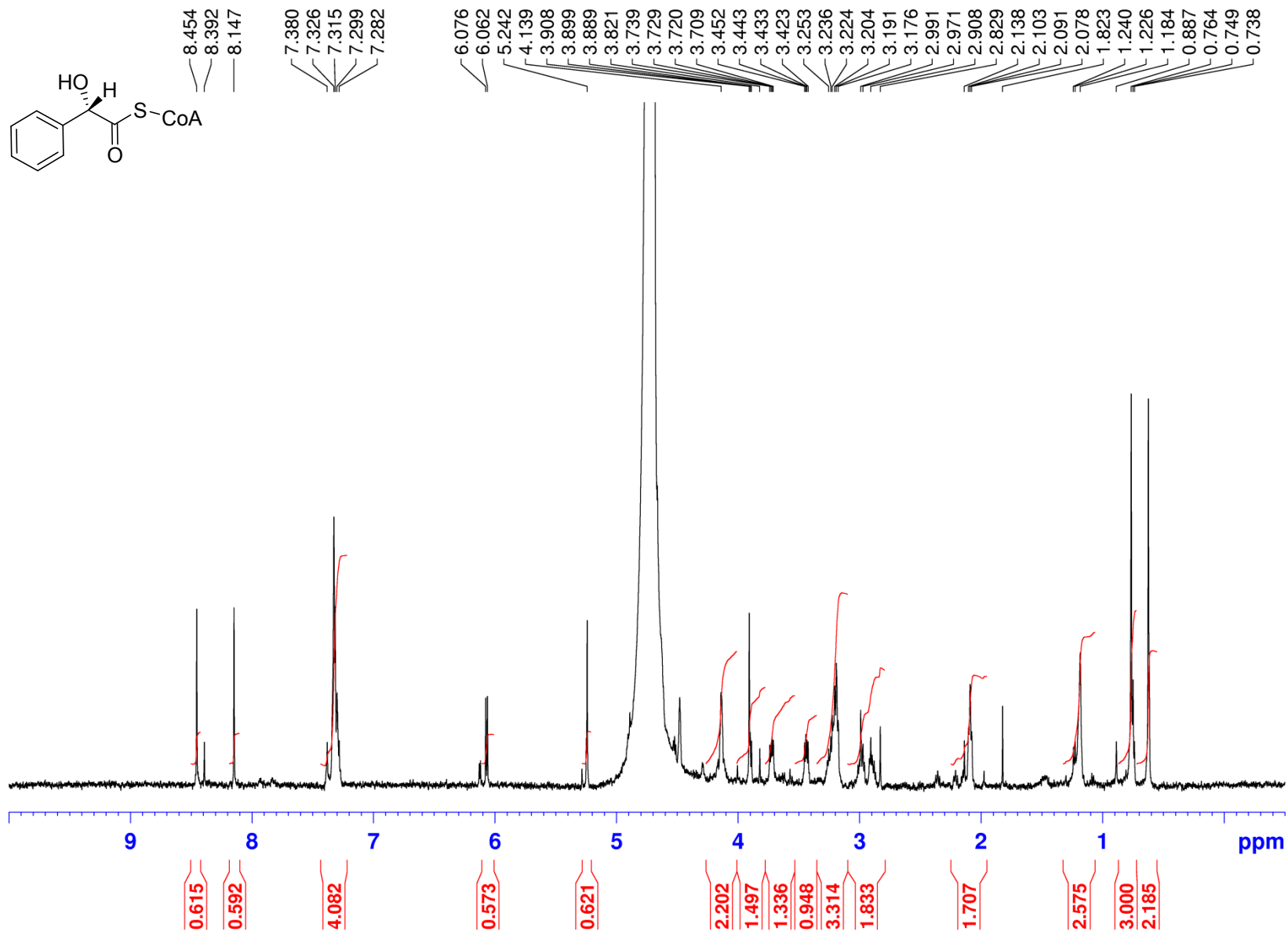
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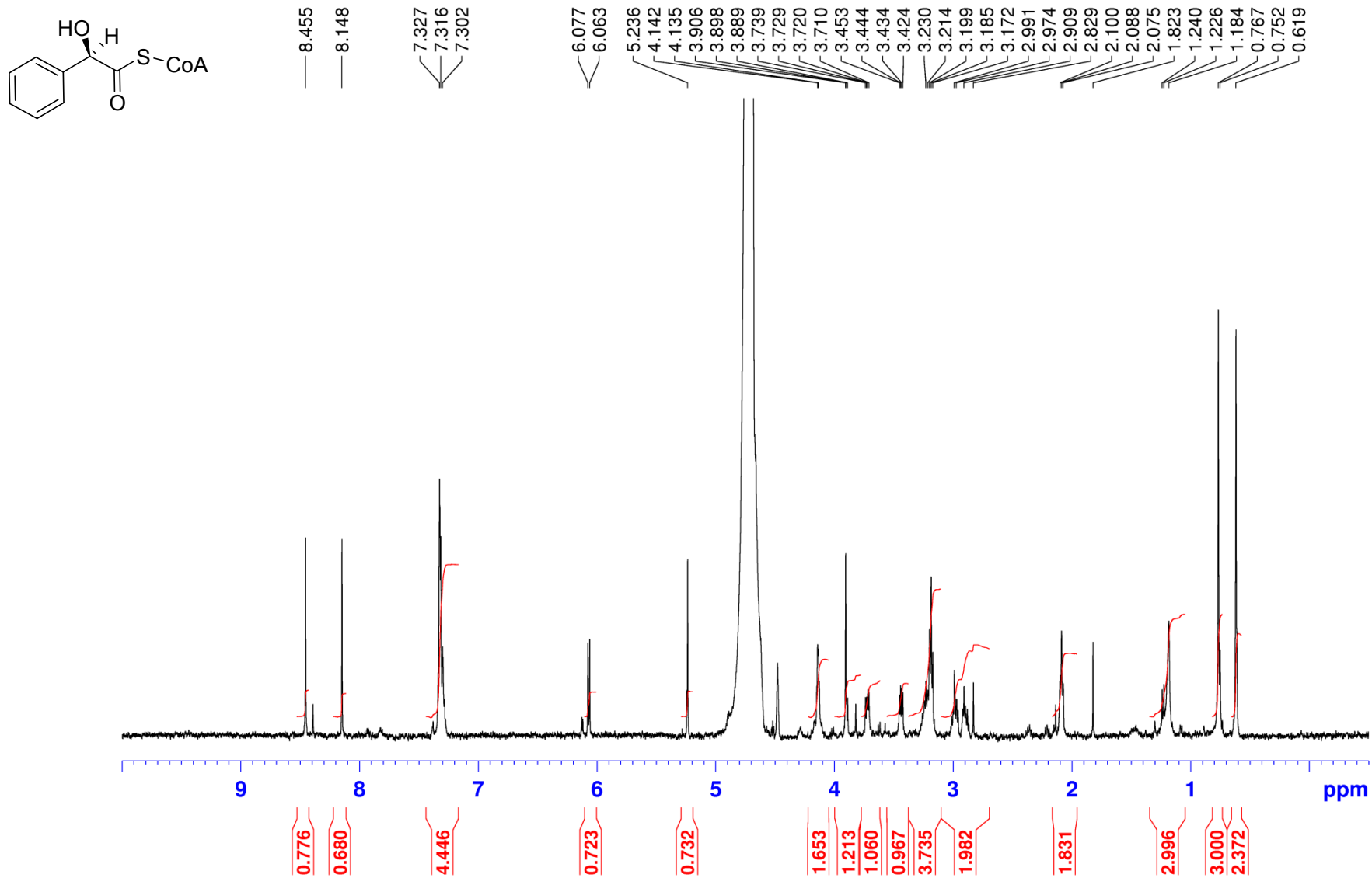
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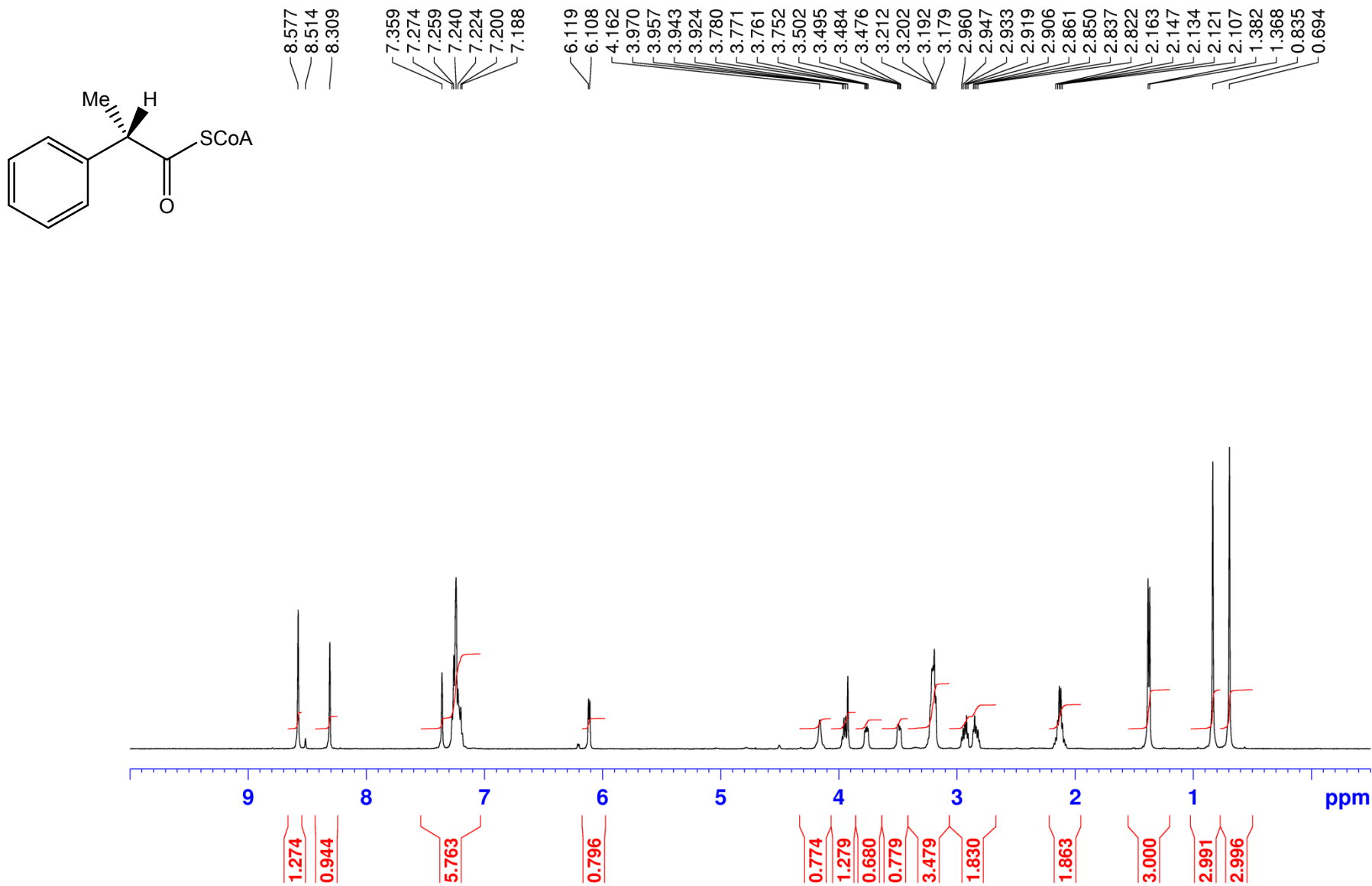
S-2-Hydroxyphenylacetyl-CoA **2S** (¹H NMR, 500.13 MHz)



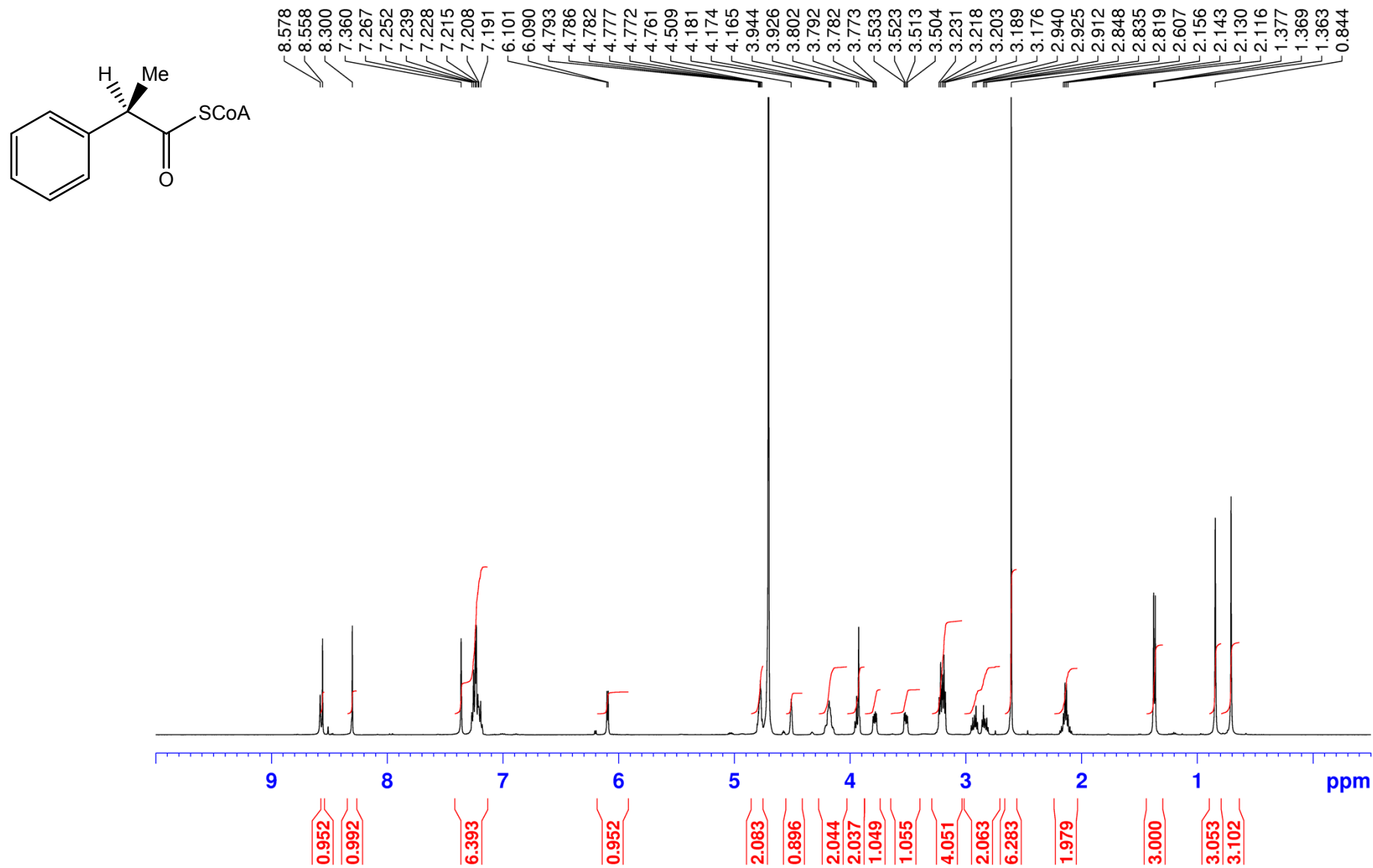
R-2-Hydroxy-2-phenylacetyl-CoA **2R** (¹H NMR, 500.13 MHz)



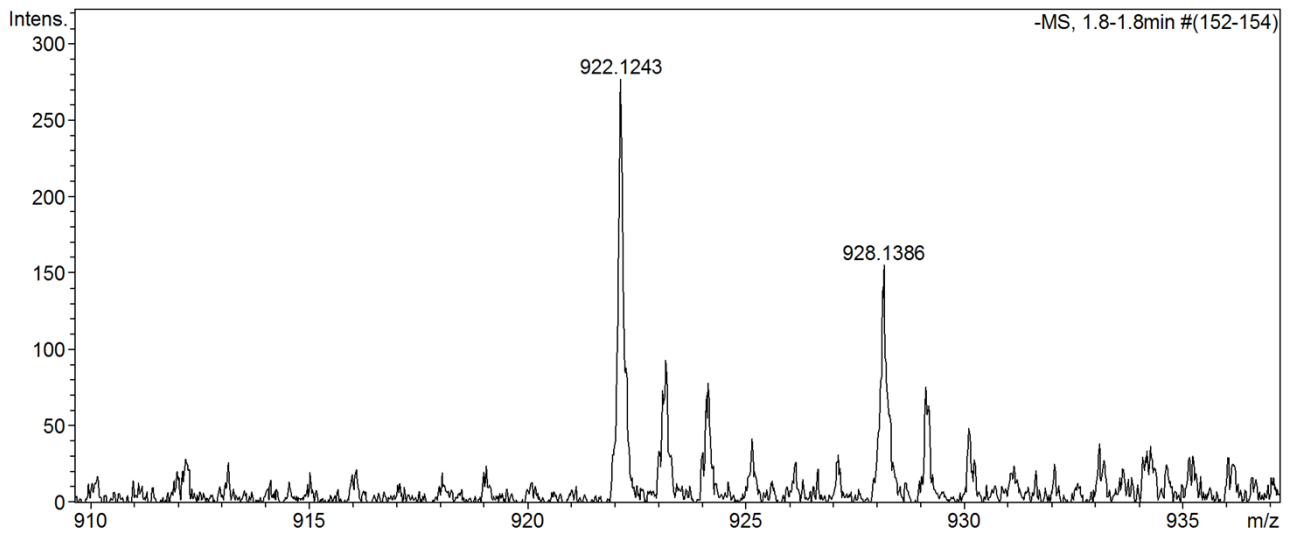
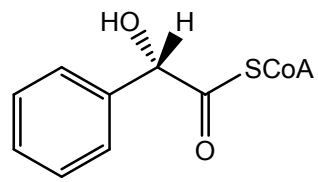
S-2-Methyl-2-phenylacetyl-CoA **8S** (^1H NMR, 500.13 MHz)



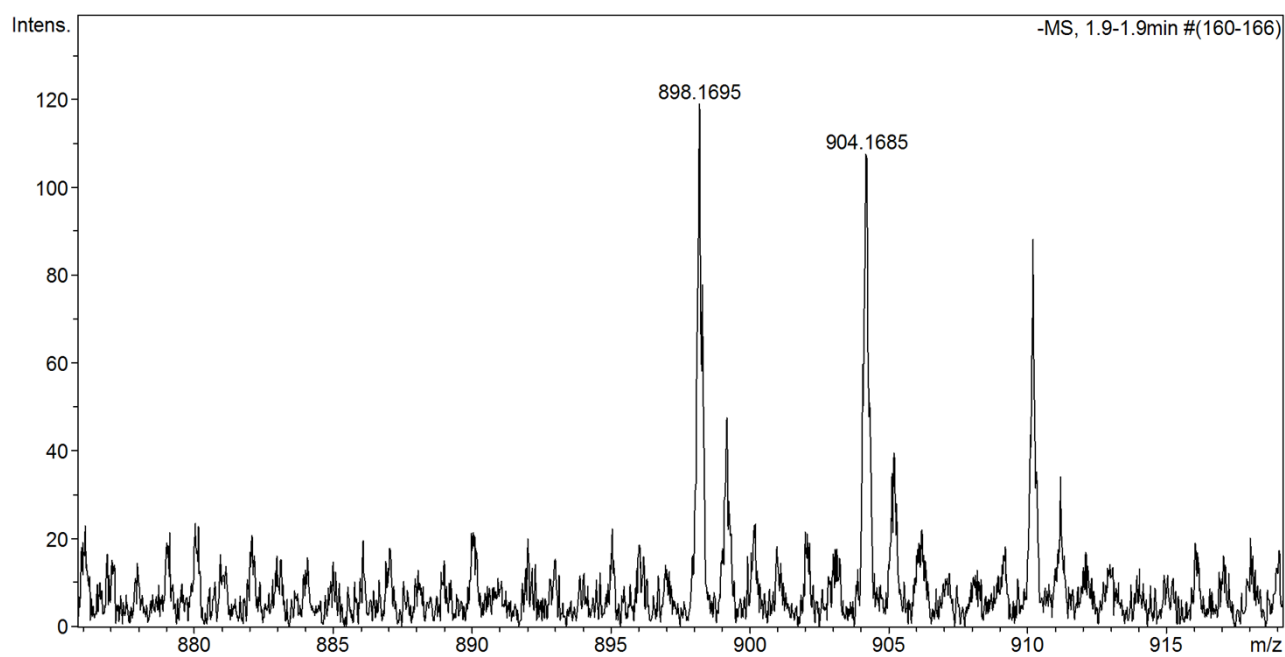
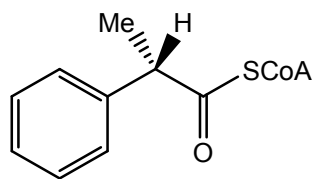
R-2-Methyl-2-phenylacetyl-CoA **8R** (^1H NMR, 500.13 MHz)



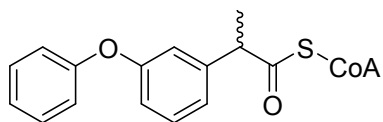
S-2-Hydroxy-2-phenylacetyl-CoA 2*S* (as Na adduct)



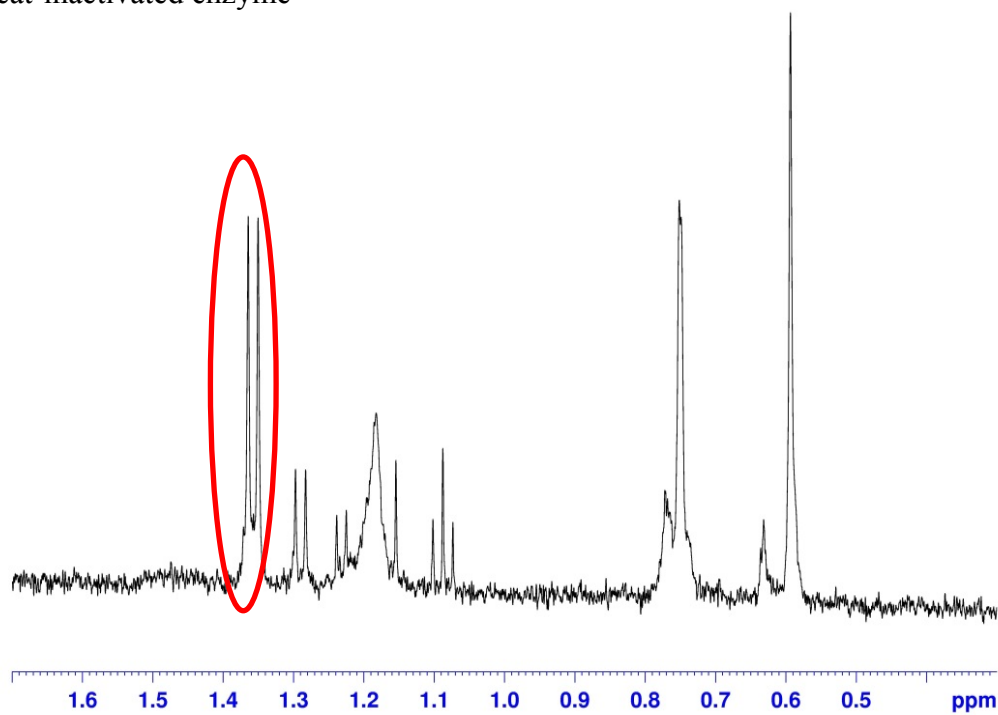
S-2-Phenylpropanoyl-CoA **8S**



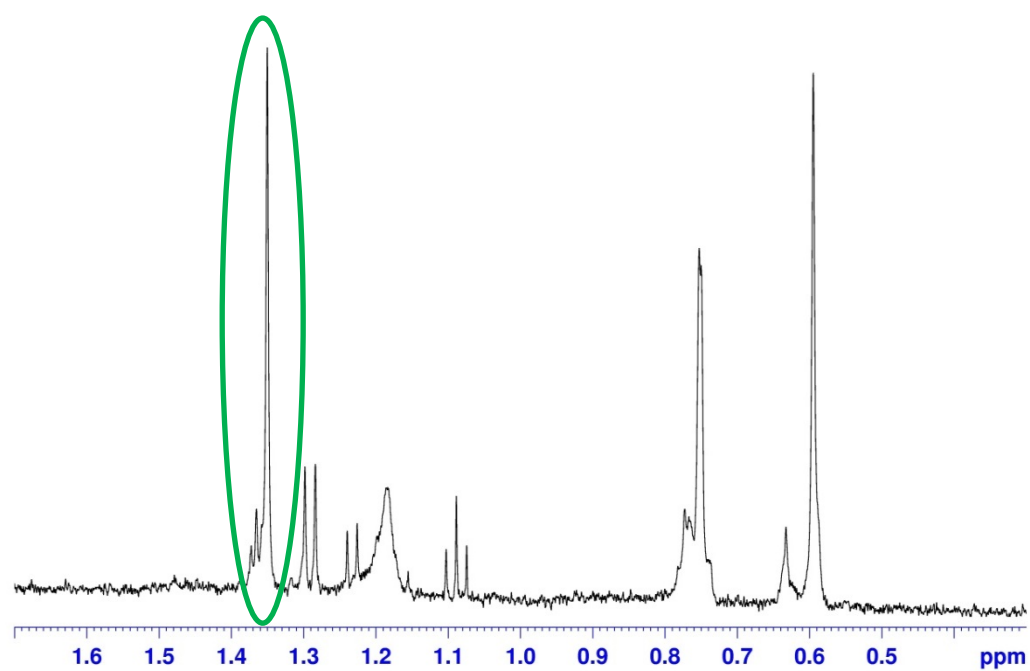
Incubation of \pm -Fenoprofenoyl-CoA with human recombinant AMACR 1A



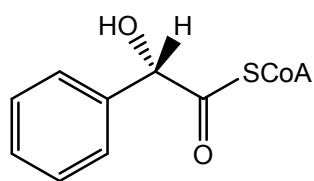
Heat-inactivated enzyme



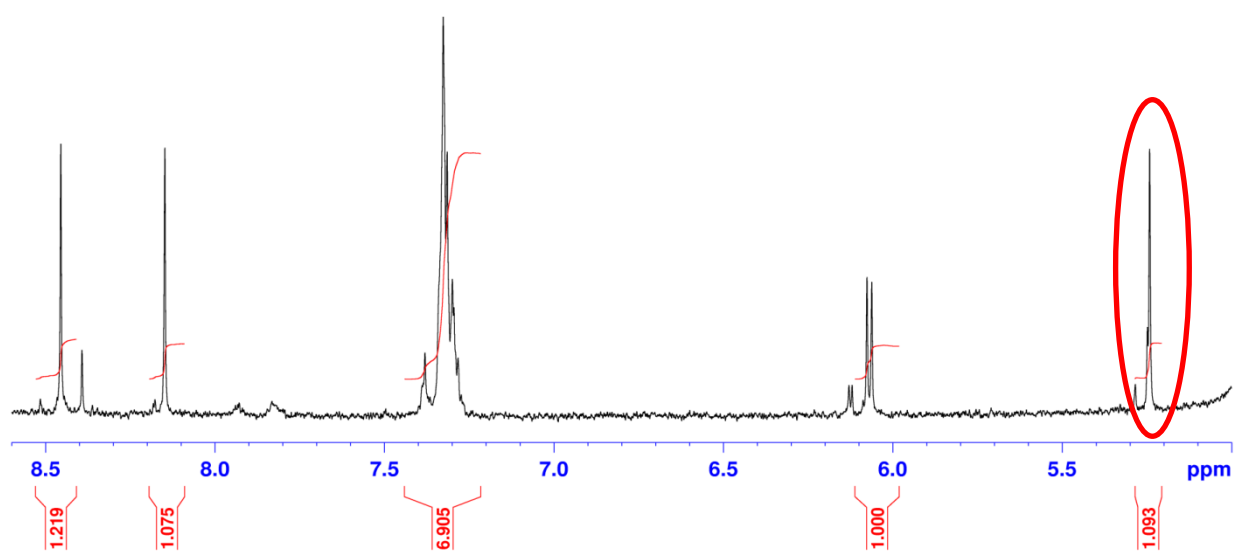
Live enzyme



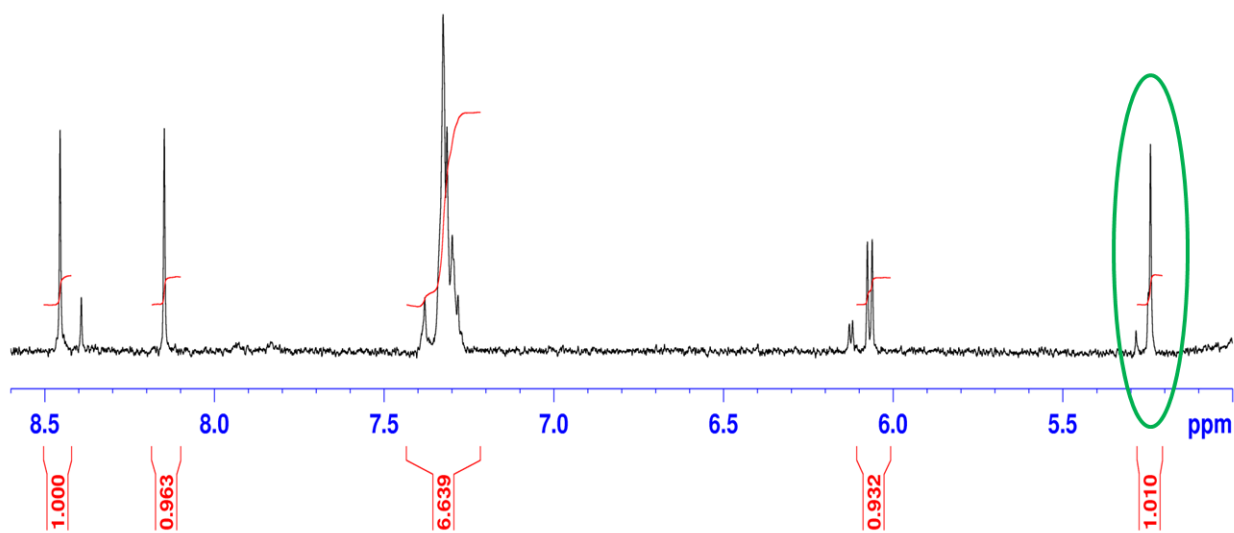
Incubation of *S*-2-hydroxy-2-phenylacetyl-CoA **2S** with human recombinant AMACR 1A



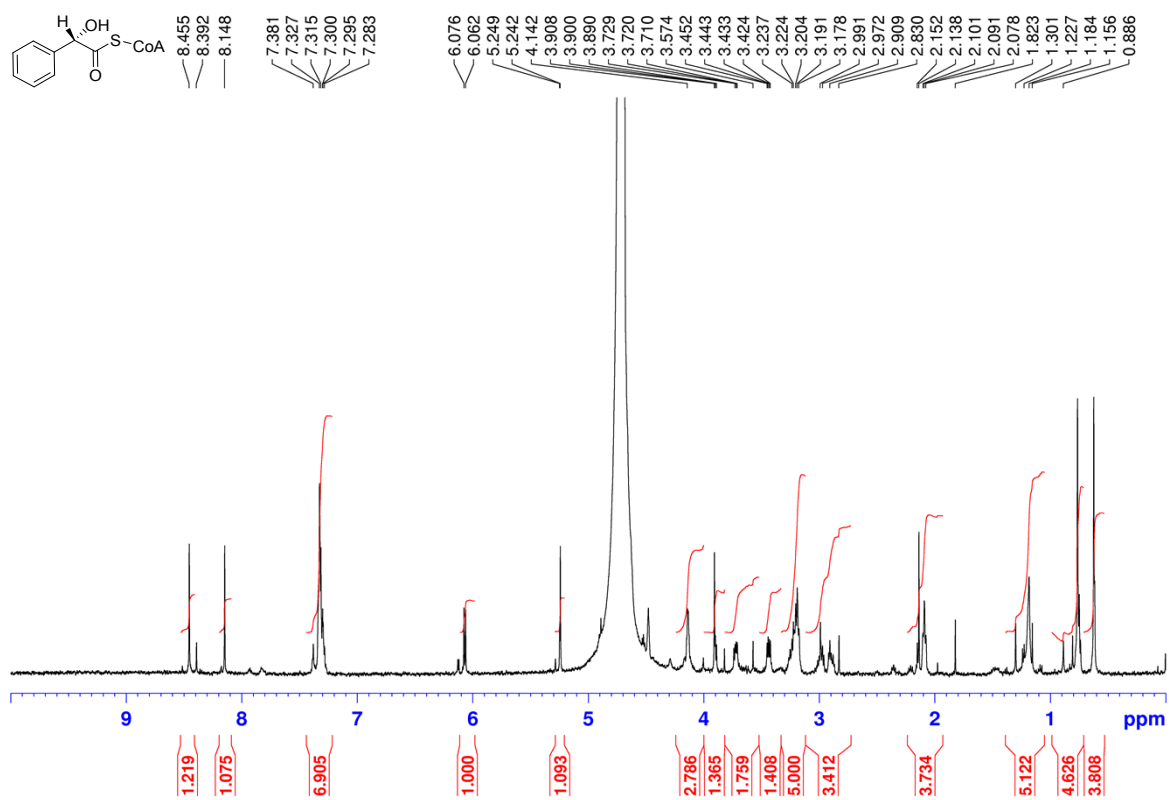
Heat-inactivated enzyme



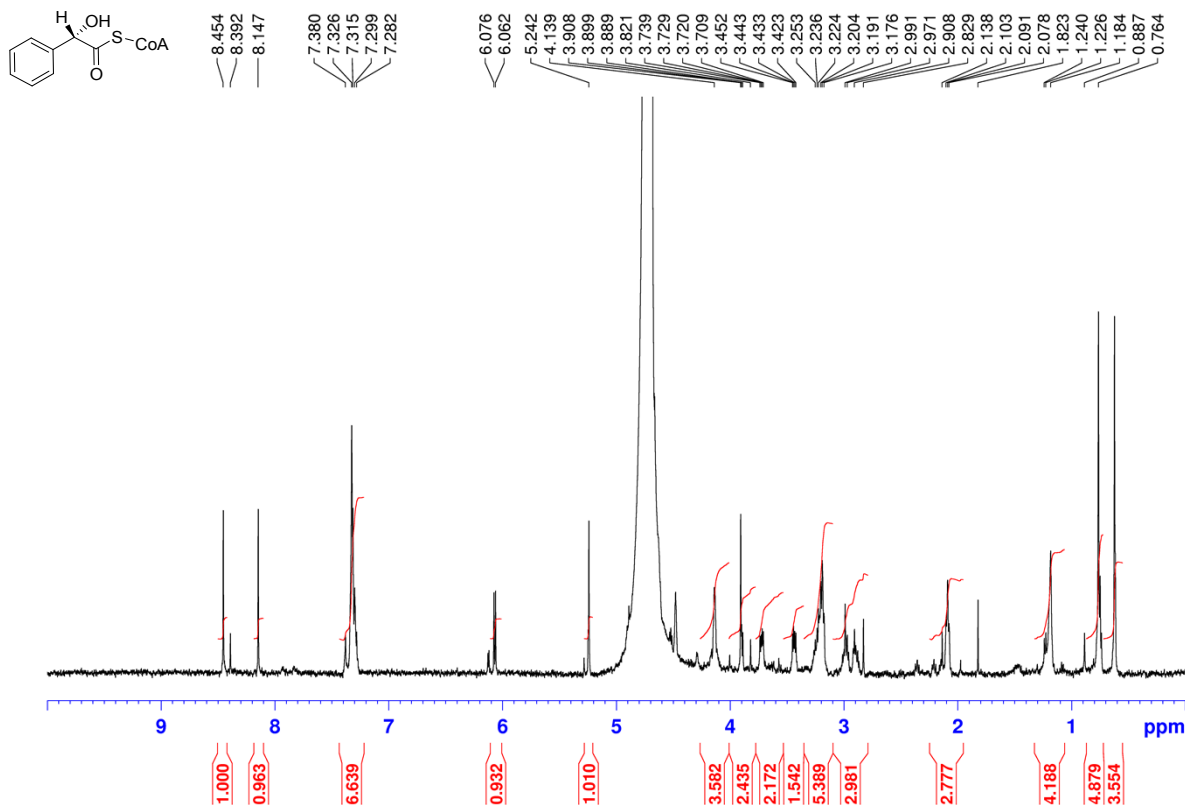
Live enzyme



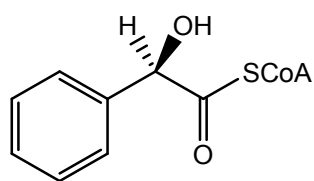
S-2-Hydroxy-2-phenylacetyl-CoA **2S** incubated with heat inactivated AMACR (full spectrum)



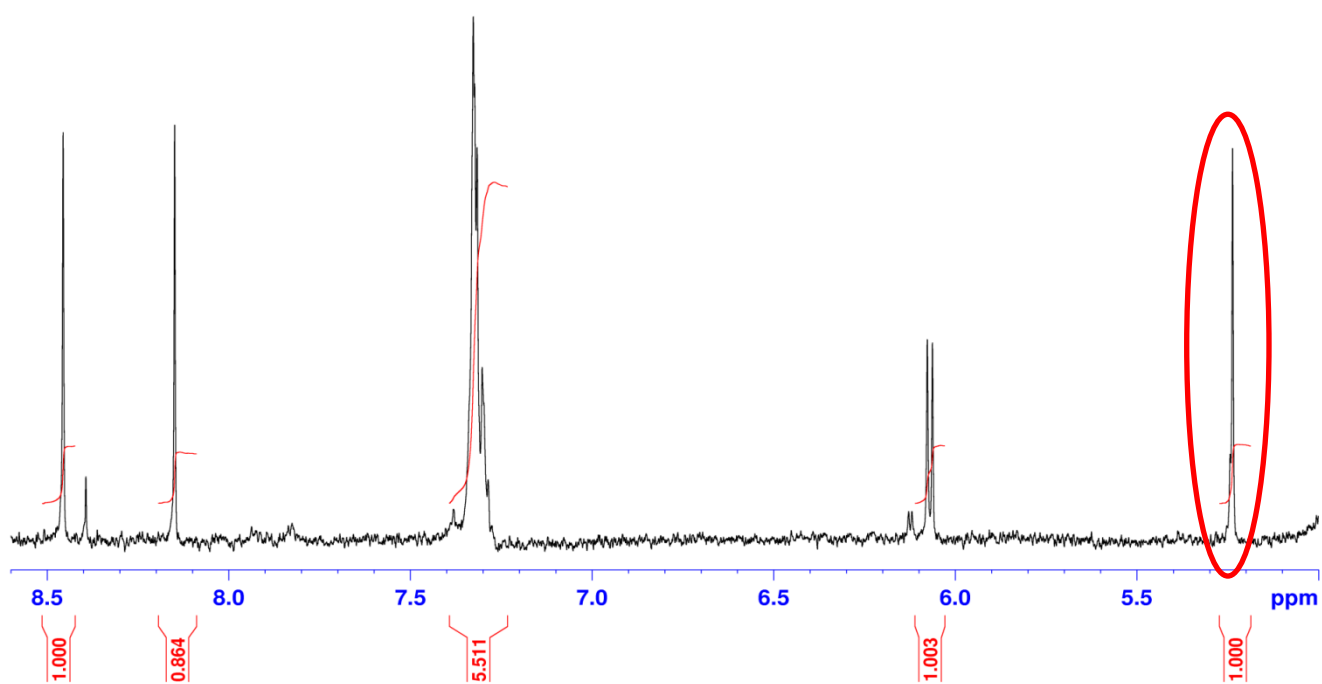
S-2-Hydroxy-2-phenylacetyl-CoA **2S** incubated with active AMACR (full spectrum)



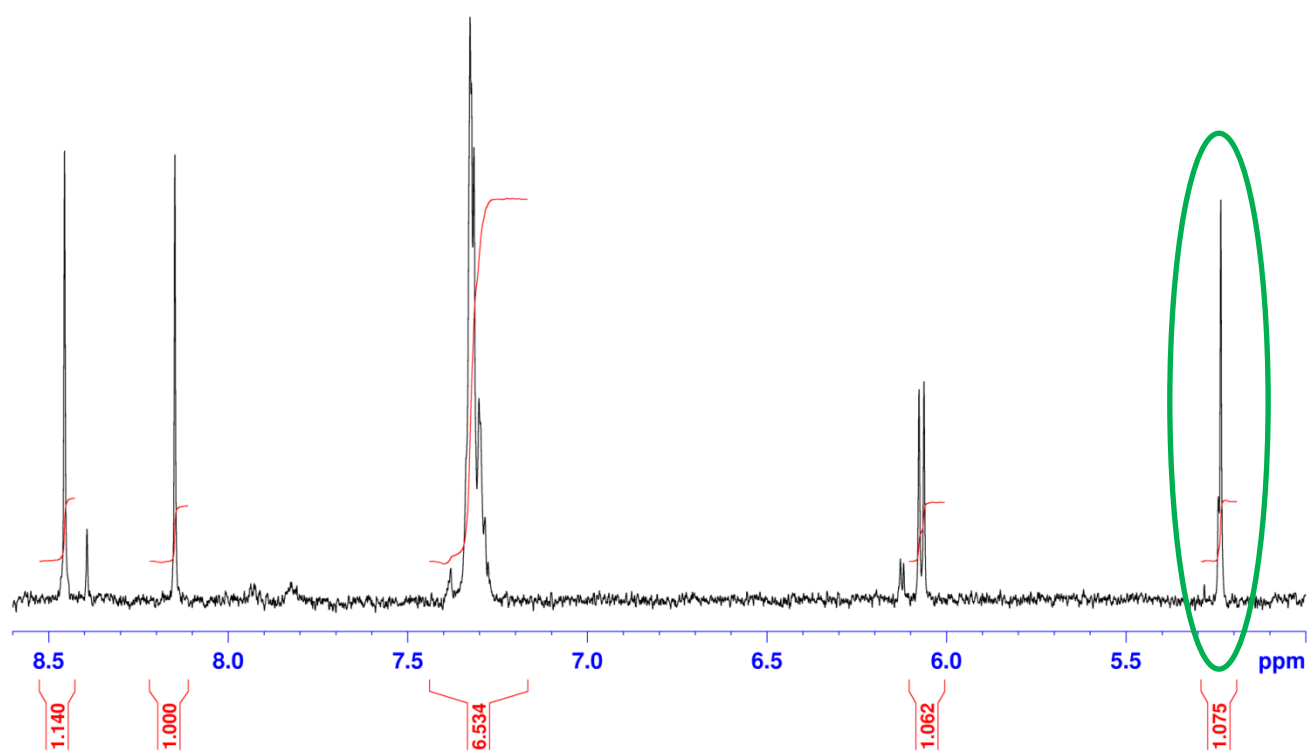
Incubation of *R*-2-hydroxy-2-phenylacetyl-CoA **2R** with human recombinant AMACR 1A



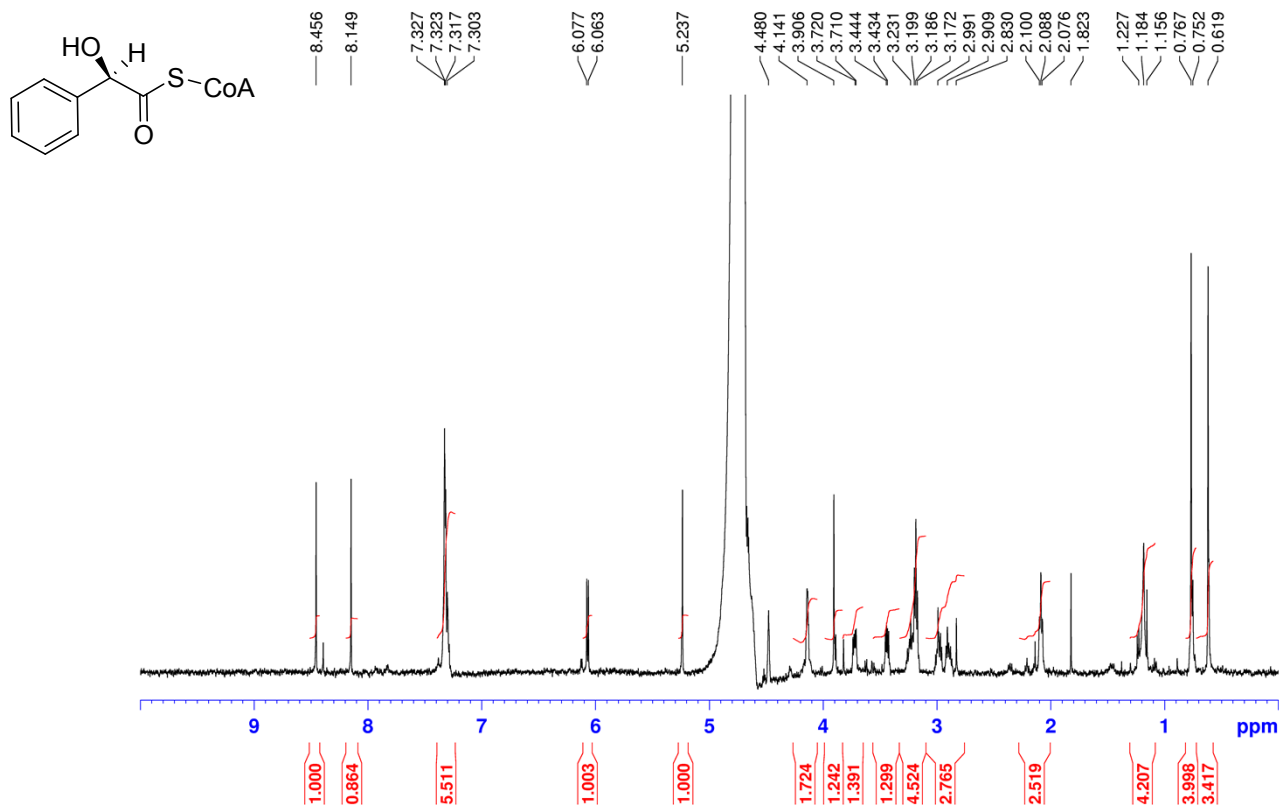
Heat-inactivated enzyme



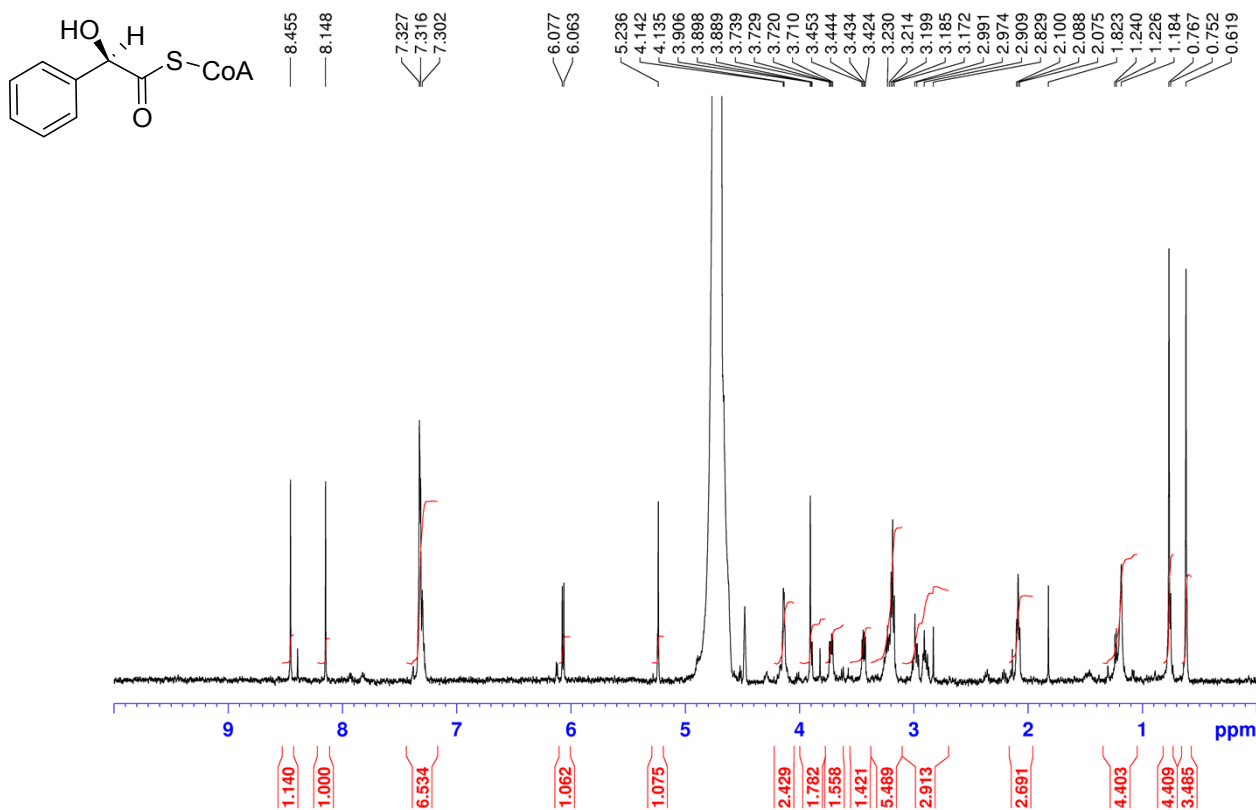
Live enzyme



R-2-Hydroxy-2-phenylacetyl-CoA **2R** incubated with heat inactivated AMACR (full spectrum)

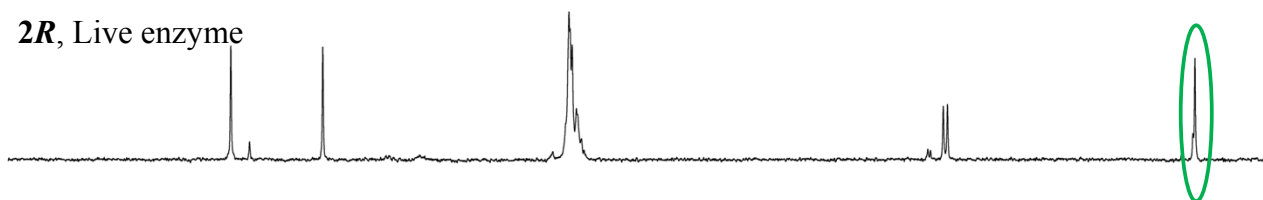


R-2-Hydroxy-2-phenylacetyl-CoA **2R** incubated with active AMACR (full spectrum)

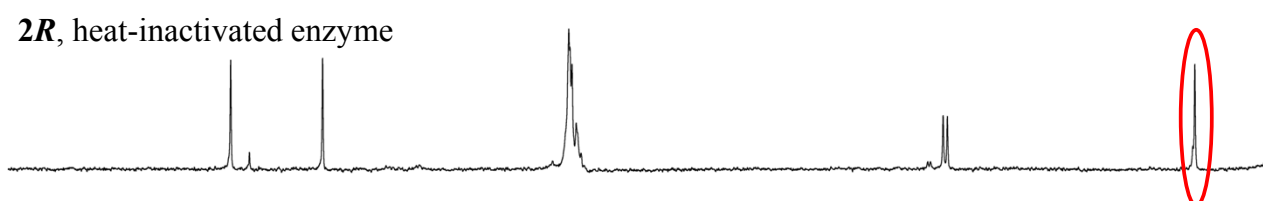


Stack plot showing incubation of **2R** and **2S** with live and heat-inactivated AMACR

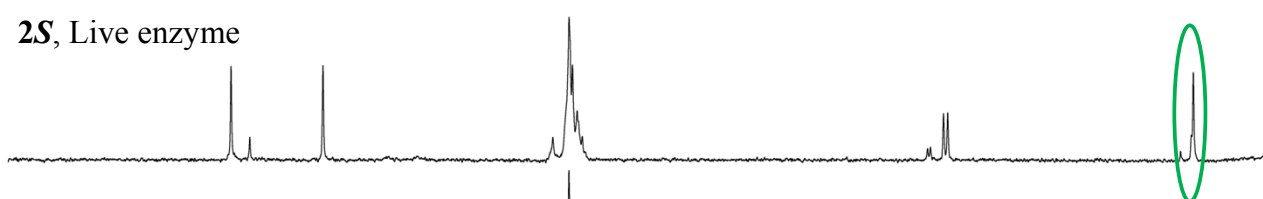
2R, Live enzyme



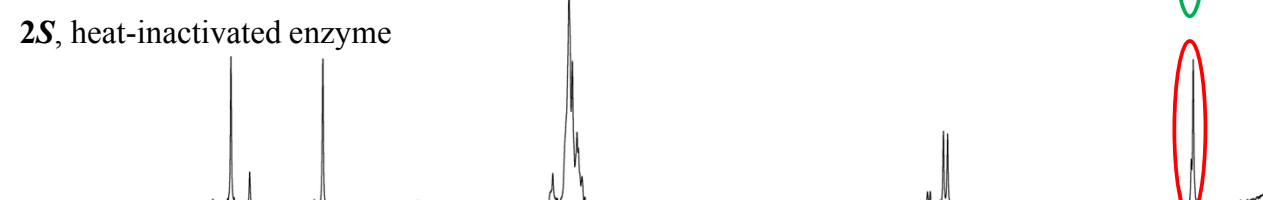
2R, heat-inactivated enzyme



2S, Live enzyme

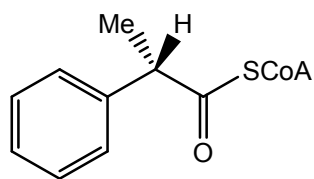


2S, heat-inactivated enzyme

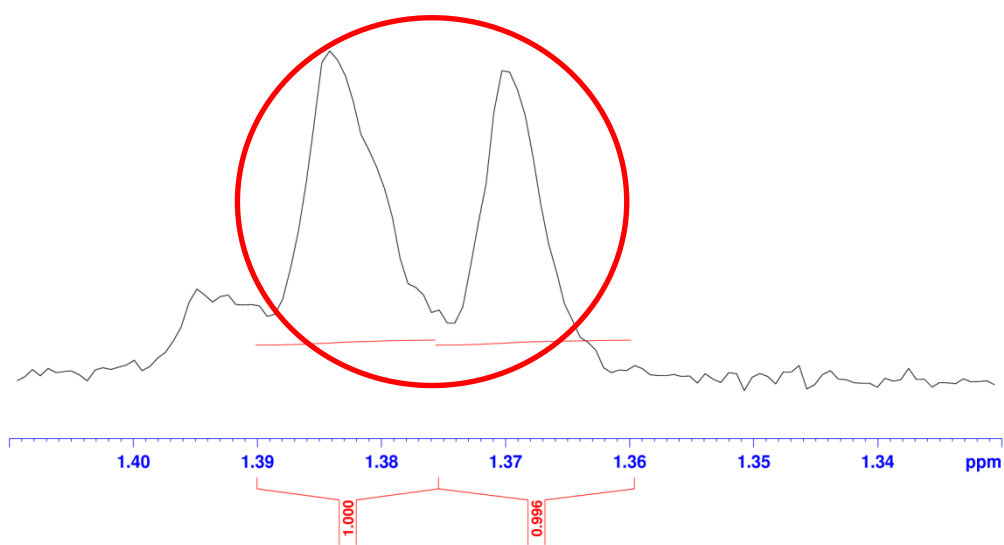


9.0 8.5 8.0 7.5 7.0 6.5 6.0 5.5 ppm

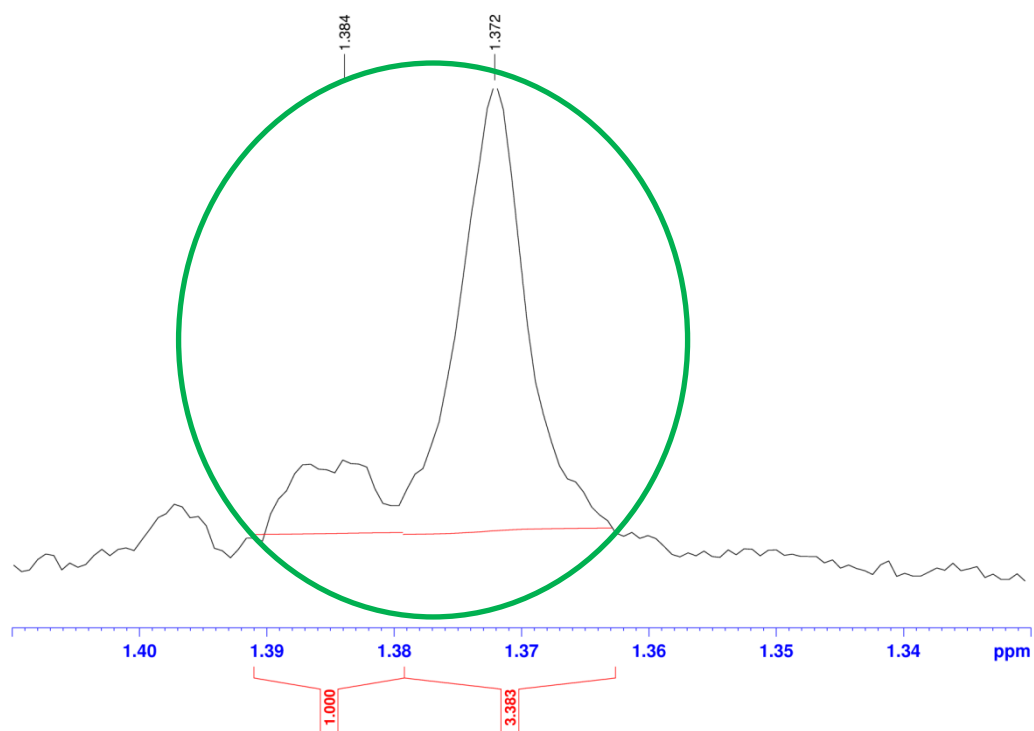
Incubation of *S*-2-phenylpropanoyl-CoA **8S** with human recombinant AMACR 1A



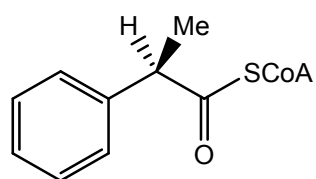
Heat-inactivated enzyme



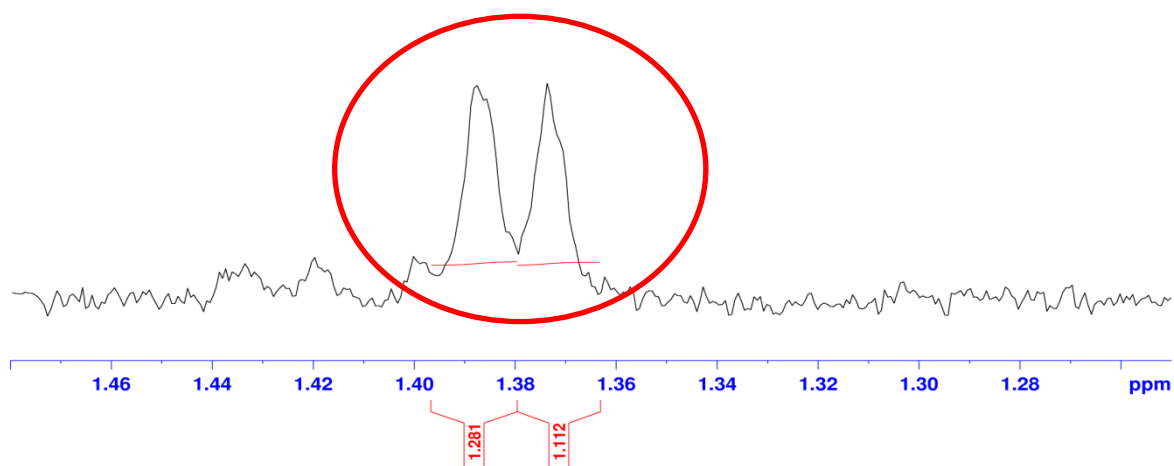
Live enzyme



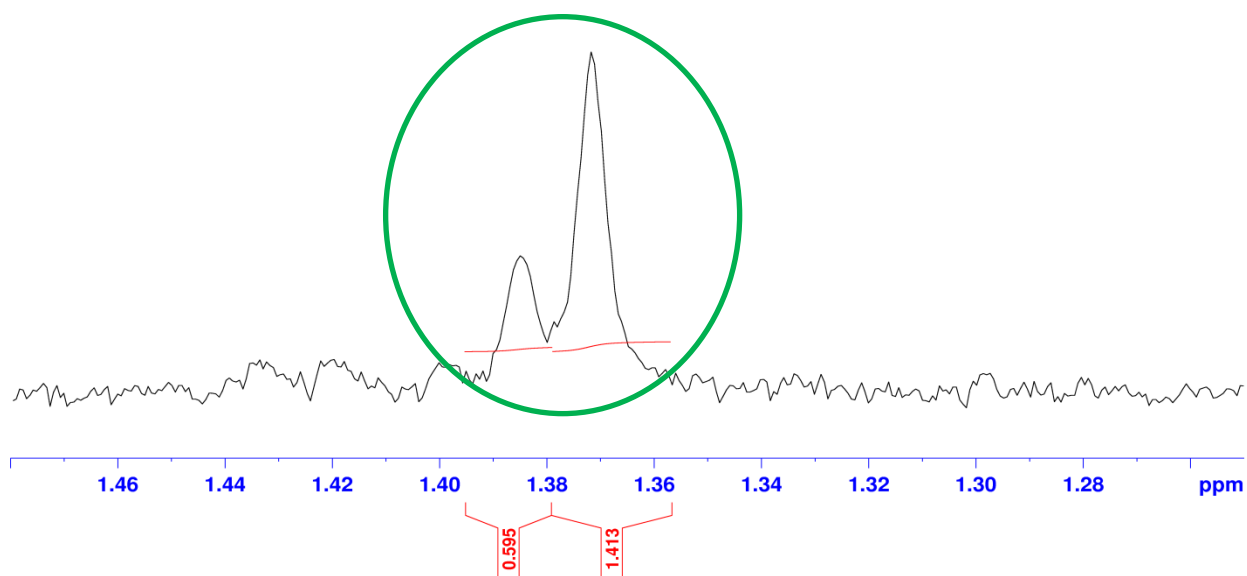
Incubation of *R*-2-phenylpropanoyl-CoA **8R** with human recombinant AMACR 1A



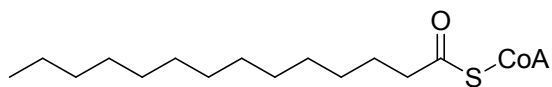
Heat-inactivate enzyme



Live enzyme



ACOT1, Myristoyl-CoA 11



Parameters

	Value	\pm Std. Error	95% Conf. Interval	
Vmax	68.1711	118.7410	-178.7692	to 315.1114
Km	84.3676	170.3888	-269.9825	to 438.7178
Ki	28.1262	69.3833	-116.1673	to 172.4196

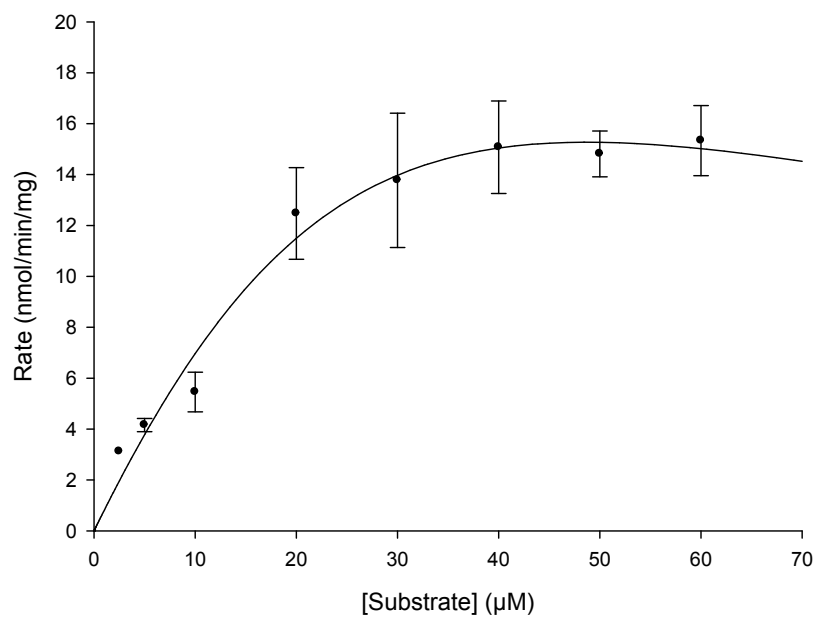
Goodness of Fit

Degrees of Freedom	21
AICc	48.022
R ²	0.832
Sum of Squares	116.501
Sy.x	2.355
Runs Test p Value	0.501

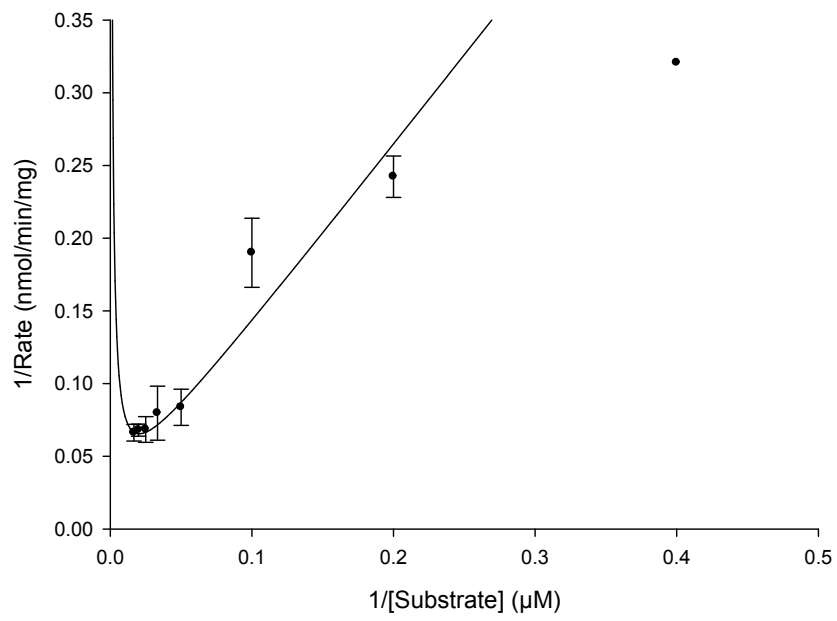
Data

Number of x values	8
Number of replicates	3
Total number of values	24
Number of missing values	0

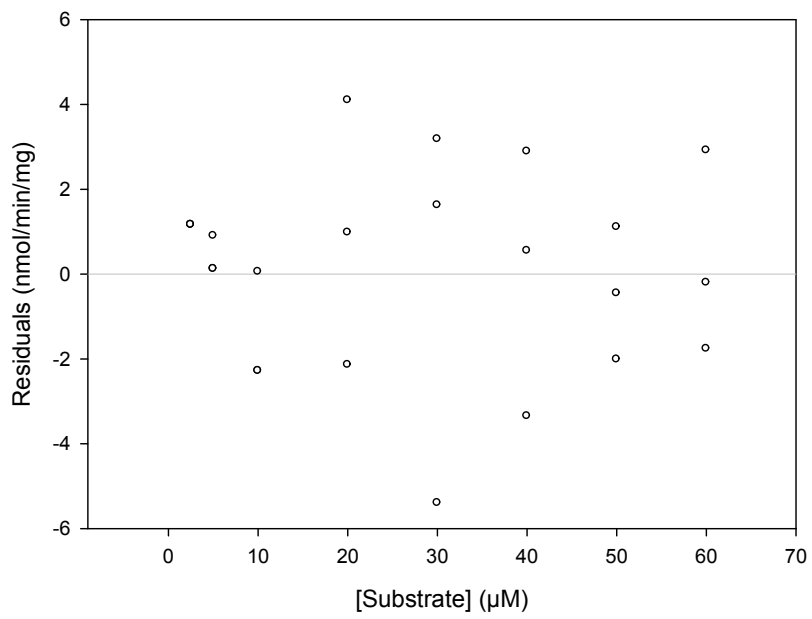
Michaelis-Menten



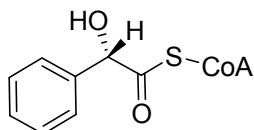
Lineweaver-Burk



Residuals



ACOT-1, S-2-hydroxy-2-phenylacetyl-CoA 2S



Parameters

	Value	\pm Std. Error	95% Conf. Interval	
Vmax	75.4081	56.1754	-41.4173	to 192.2335
Km	156.4288	138.3438	-131.2787	to 444.1362
Ki	40.4438	38.0679	-38.7243	to 119.6120

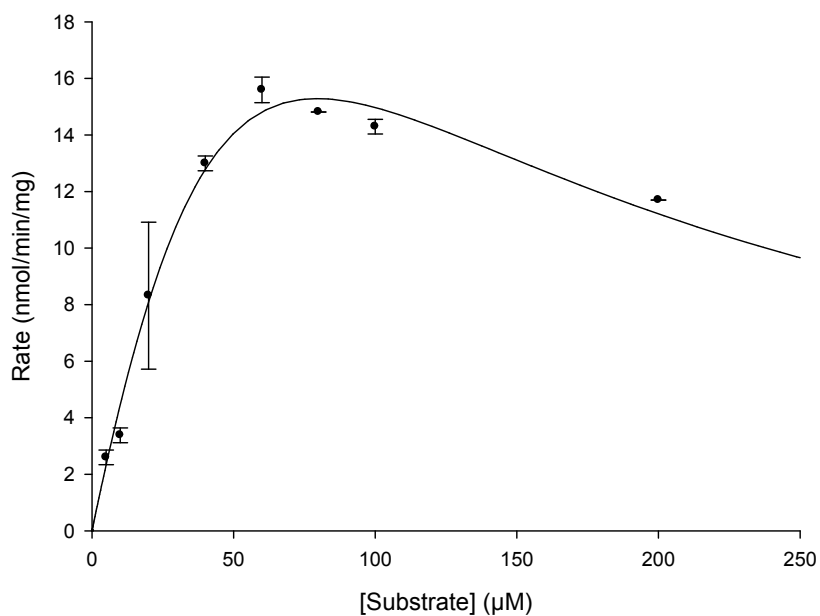
Goodness of Fit

Degrees of Freedom	21
AICc	28.657
R ²	0.913
Sum of Squares	51.989
Sy.x	1.573
Runs Test p Value	0.486

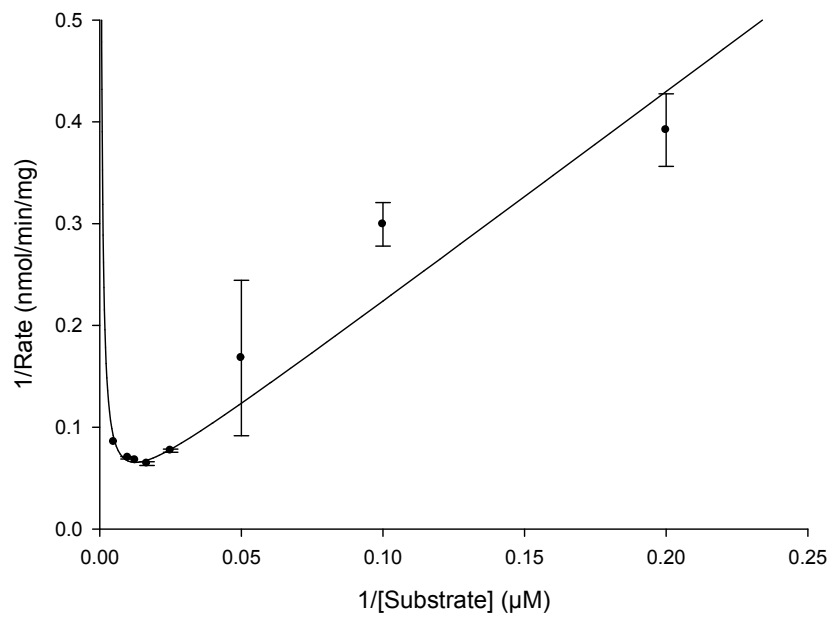
Data

Number of x values	8
Number of replicates	3
Total number of values	24
Number of missing values	0

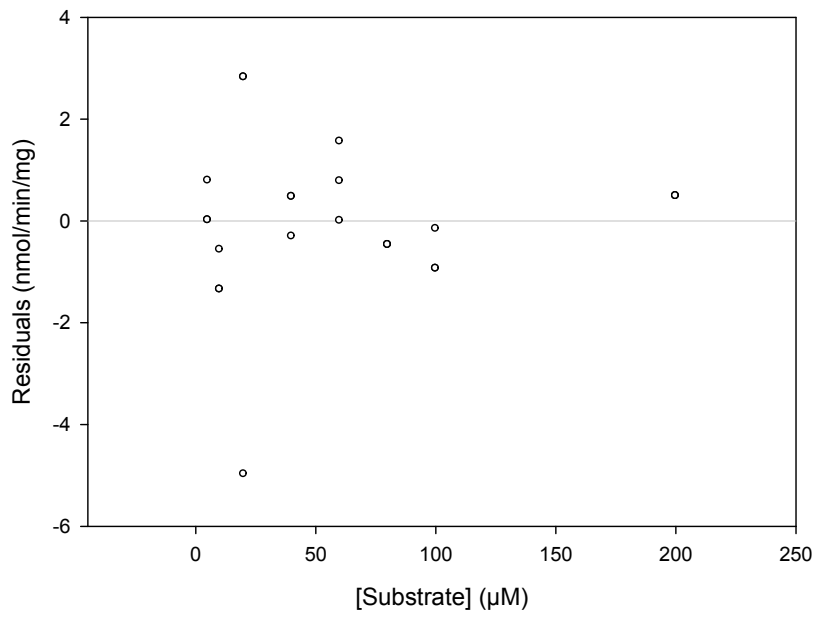
Michaelis-Menten



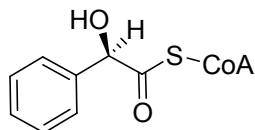
Lineweaver-Burk



Residuals



ACOT-1, *R*-2-hydroxy-2-phenylacetyl-CoA **2R**



Parameters

	Value	\pm Std. Error	95% Conf. Interval	
Vmax	12.2541	1.5178	9.0975	to 15.4106
Km	61.6170	18.1924	23.7830	to 99.4509

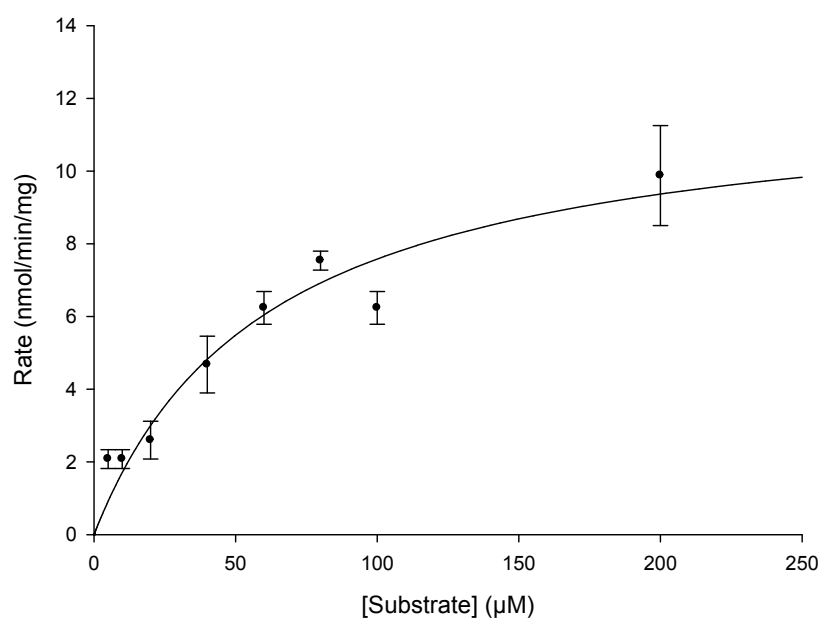
Goodness of Fit

Degrees of Freedom	21
AICc	13.563
R ²	0.837
Sum of Squares	30.247
Sy.x	1.200
Runs Test p Value	0.334

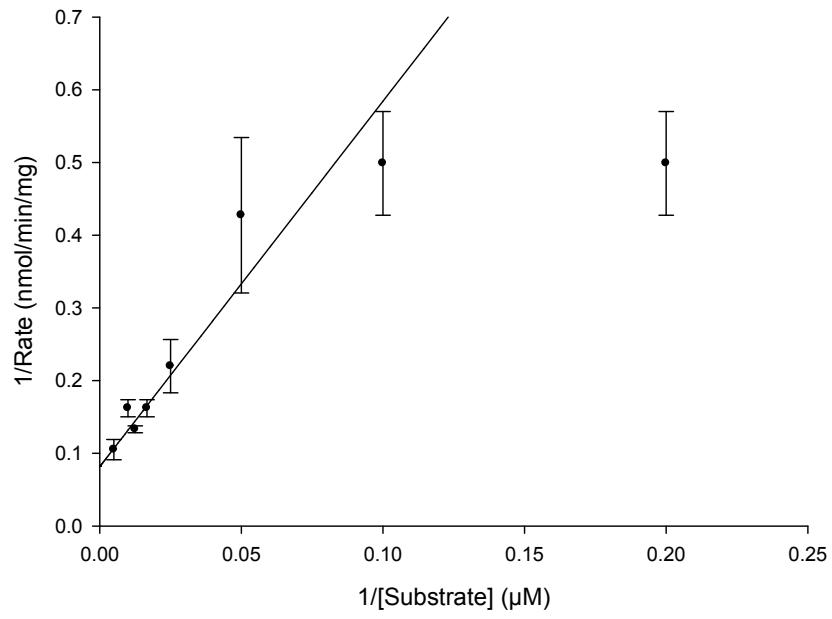
Data

Number of x values	8
Number of replicates	3
Total number of values	23
Number of missing values	1

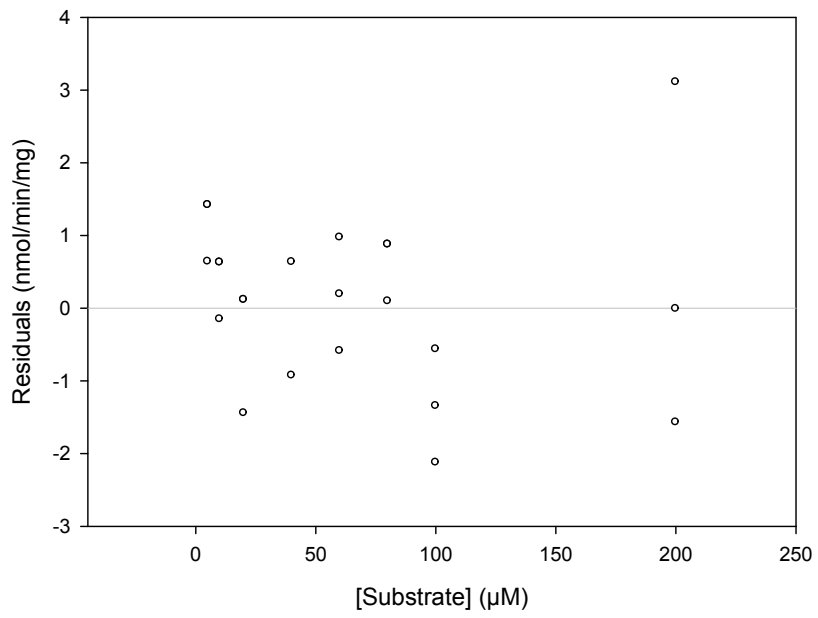
Michaelis-Menten



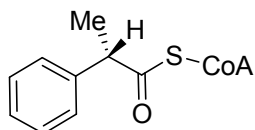
Lineweaver-Burk



Residuals



ACOT-1, S-2-Phenylpropanoyl-CoA **8S**



Parameters

	Value	\pm Std. Error	95% Conf. Interval	
Vmax	26,802.5216	6.645e+6	-1.379e+7	to 1.385e+7
Km	35,967.0081	8.924e+6	-1.852e+7	to 1.859e+7
Ki	0.1140	28.2948	-58.7294	to 58.9574

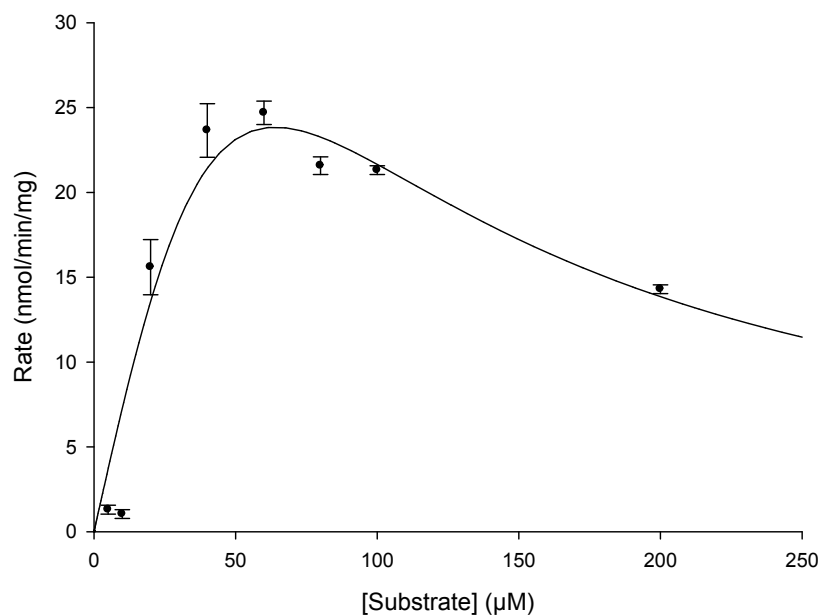
Goodness of Fit

Degrees of Freedom	21
AICc	62.143
R ²	0.892
Sum of Squares	209.830
Sy.x	3.161
Runs Test p Value	0.126

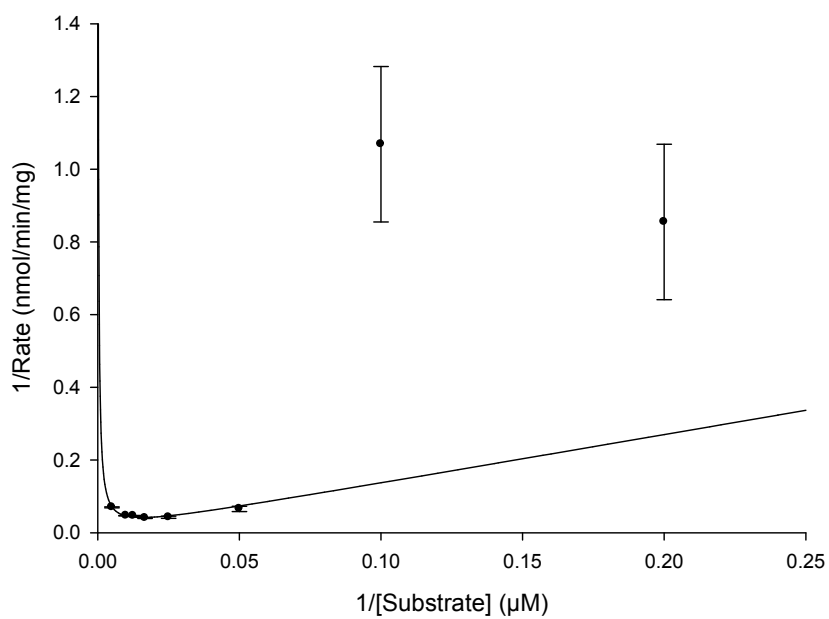
Data

Number of x values	8
Number of replicates	3
Total number of values	24
Number of missing values	0

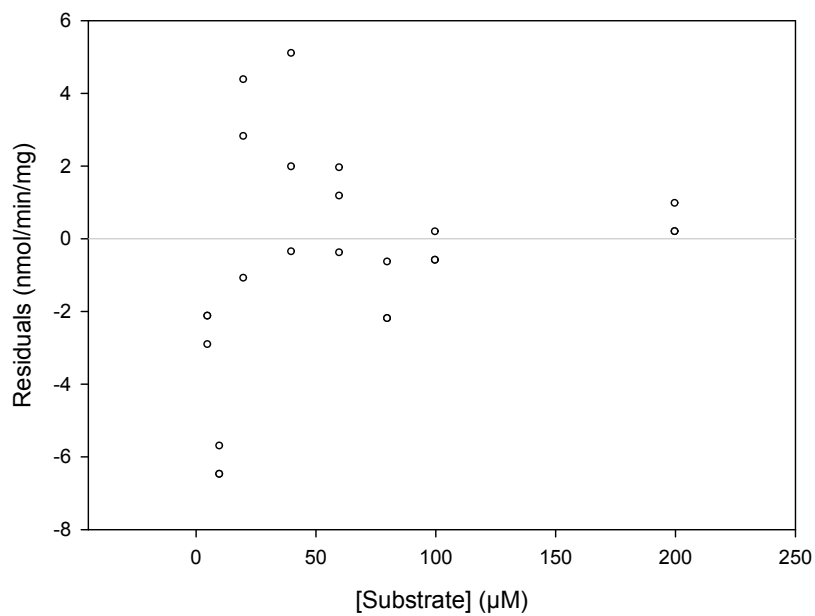
Michaelis-Menten



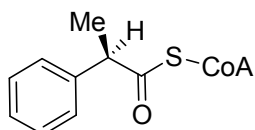
Lineweaver-Burk



Residuals



ACOT-1, *R*-2-phenylpropanoyl-CoA **8R**



Parameters

	<u>Value</u>	<u>±Std. Error</u>	<u>95% Conf. Interval</u>	
Vmax	4.9646	0.3707	4.1959	to 5.7334
Km	22.1012	5.7426	10.1914	to 34.0109

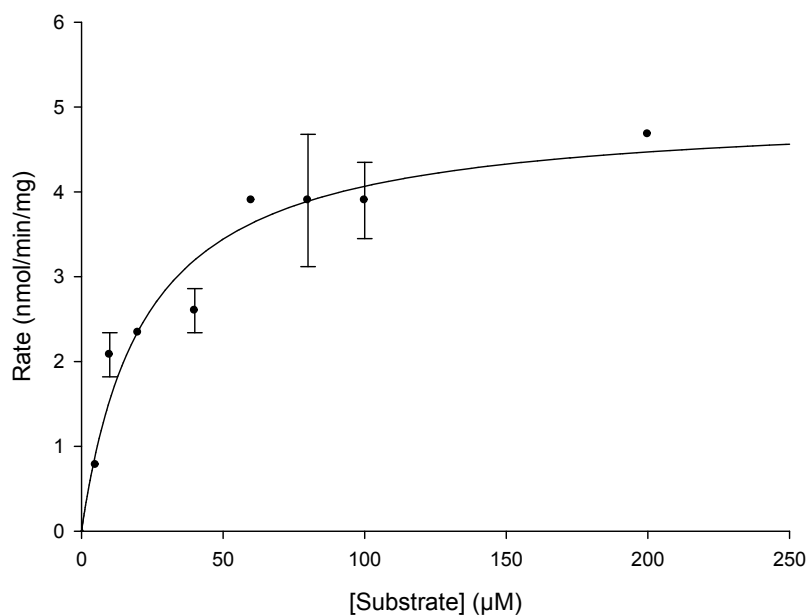
Goodness of Fit

Degrees of Freedom	22
AICc	-18.897
R ²	0.800
Sum of Squares	8.090
Sy.x	0.606
Runs Test p Value	0.501

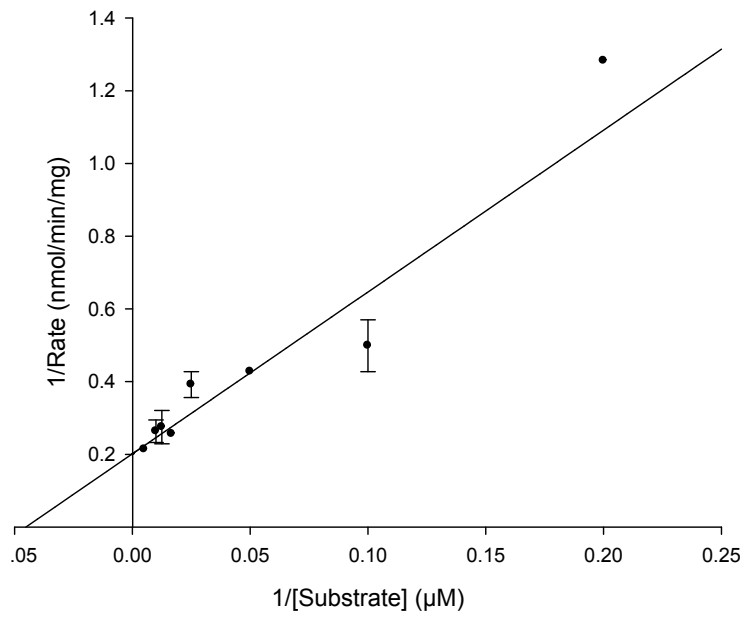
Data

Number of x values	8
Number of replicates	3
Total number of values	24
Number of missing values	0

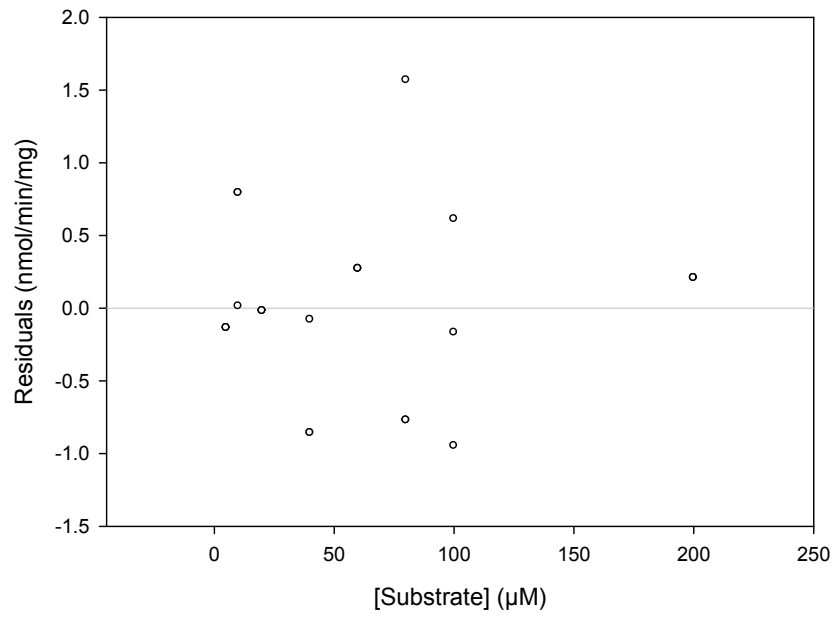
Michaelis-Menten



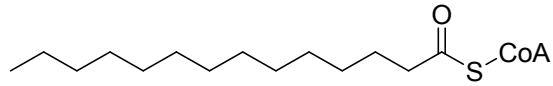
Lineweaver-Burk



Residuals



ACOT-2, Myristoyl-CoA 11



Parameters

	Value	\pm Std. Error	95% Conf. Interval	
Vmax	29.3472	11.0834	6.2271	to 52.4672
Km	15.7935	9.9807	-5.0262	to 36.6132
Ki	152.5699	205.6633	-276.4448	to 581.5847

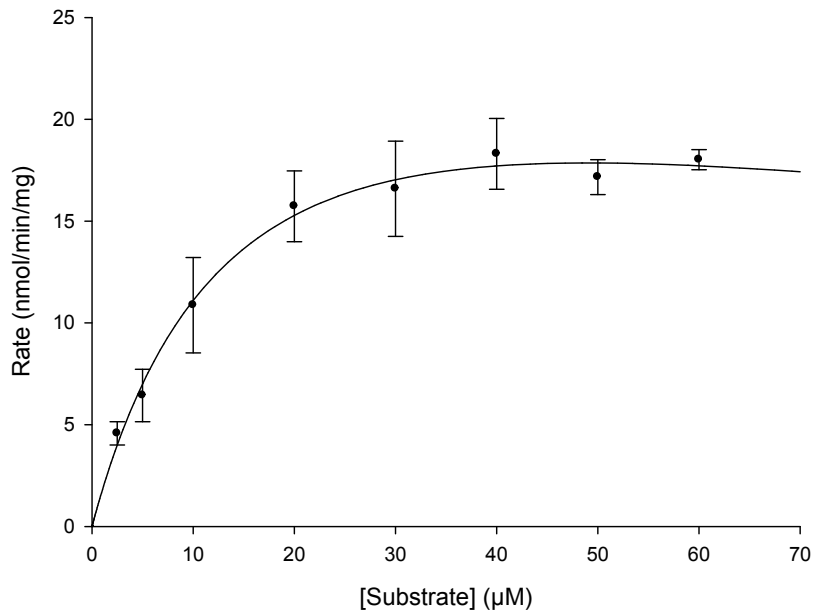
Goodness of Fit

Degrees of Freedom	20
AICc	48.032
R ²	0.826
Sum of Squares	119.032
Sy.x	2.440
Runs Test p Value	0.500

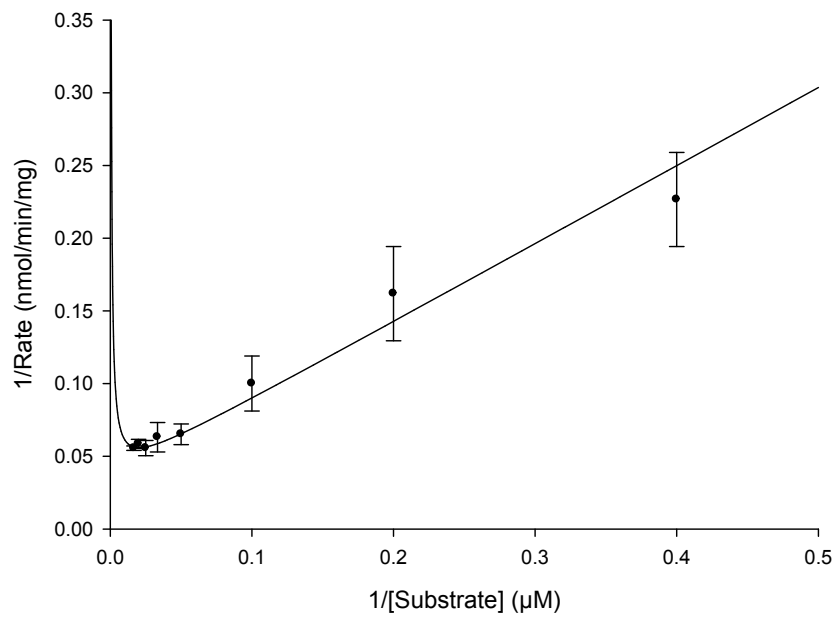
Data

Number of x values	8
Number of replicates	3
Total number of values	23
Number of missing values	1

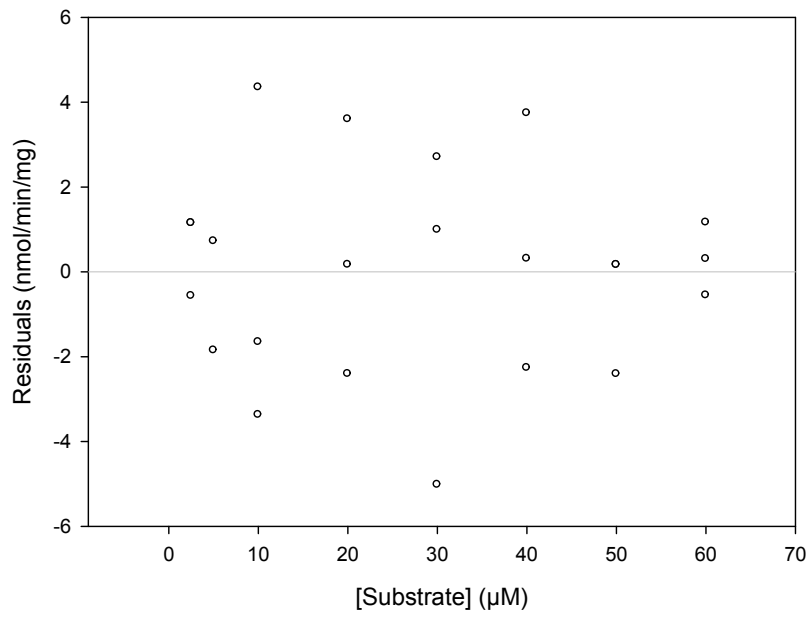
Michaelis-Menten



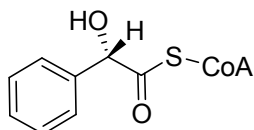
Lineweaver-Burk



Residuals



ACOT-2, S-2-hydroxy-2-phenylacetyl-CoA 2S



Parameters

	Value	\pm Std. Error	95% Conf. Interval	
Vmax	102.8182	103.7608	-112.9686	to 318.6050
Km	171.6409	198.9373	-242.0801	to 585.3619
Ki	26.8023	32.3655	-40.5068	to 94.1115

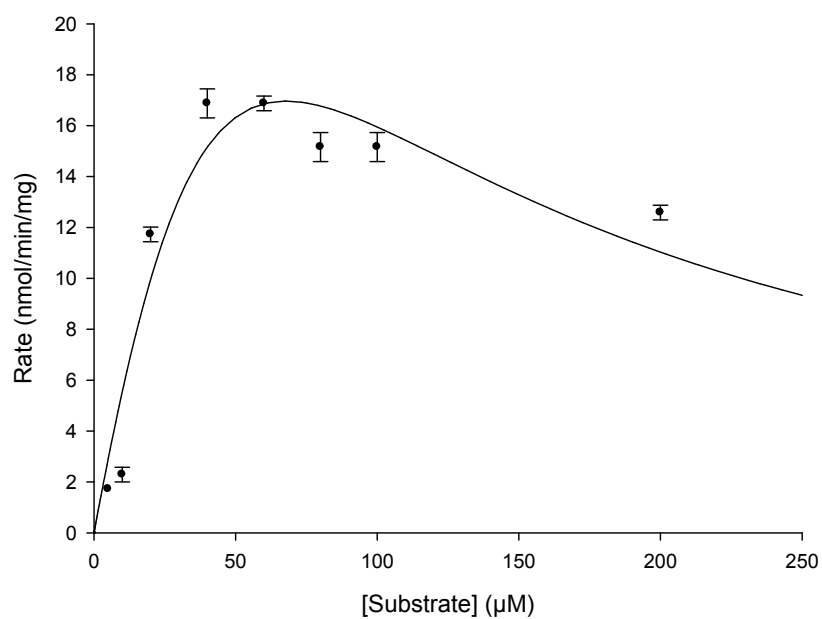
Goodness of Fit

Degrees of Freedom	21
AICc	38.715
R ²	0.902
Sum of Squares	79.053
Sy.x	1.940
Runs Test p Value	0.338

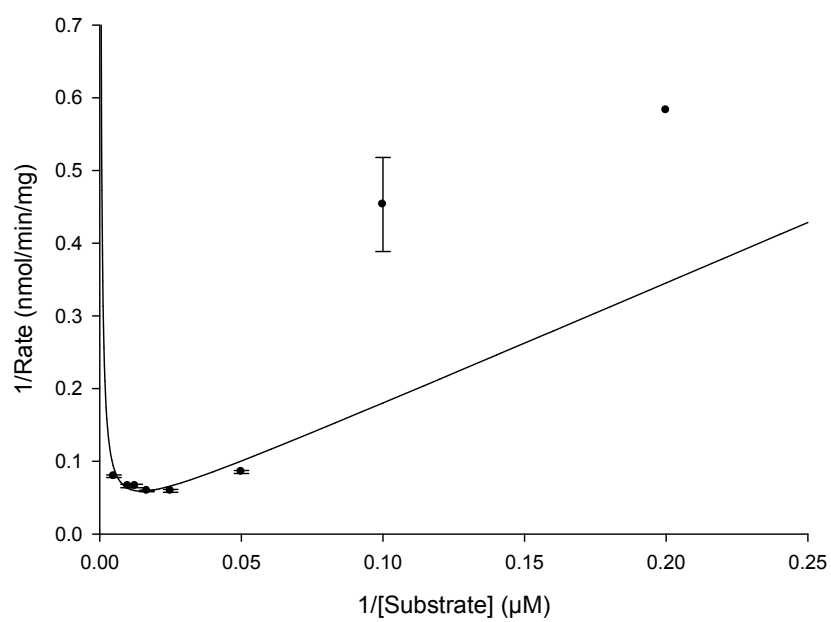
Data

Number of x values	8
Number of replicates	3
Total number of values	24
Number of missing values	0

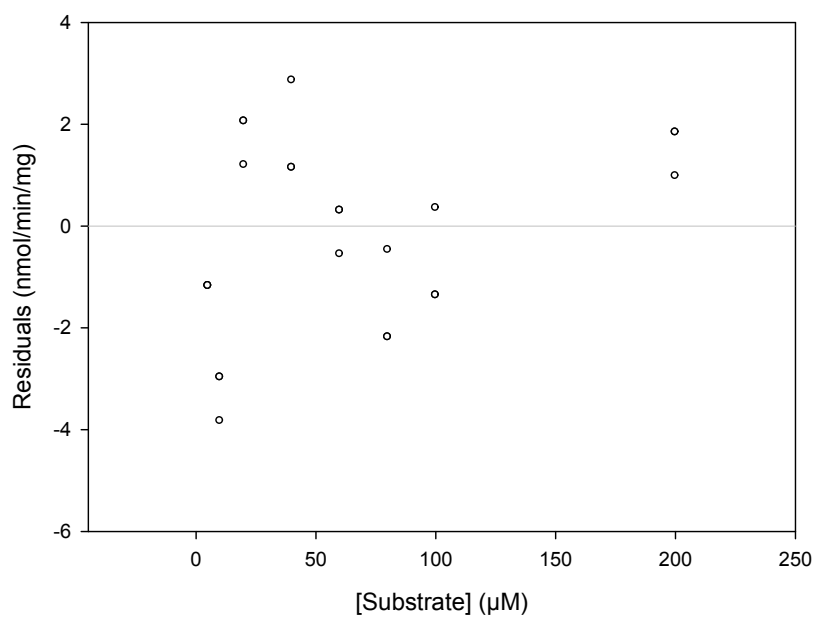
Michaelis-Menten



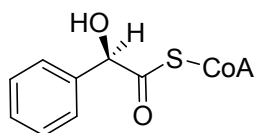
Lineweaver-Burk



Residuals



ACOT-2, *R*-2-hydroxy-2-phenylacetyl-CoA **2R**



Parameters

	<u>Value</u>	<u>±Std. Error</u>	<u>95% Conf. Interval</u>	
Vmax	20.3377	3.1959	13.6231	to 27.0522
Km	130.7584	37.3894	52.2047	to 209.3122

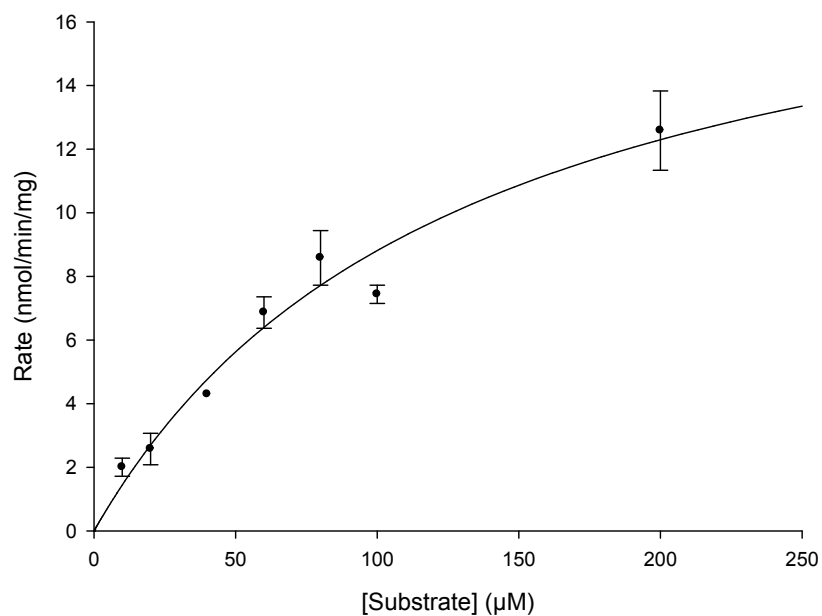
Goodness of Fit

Degrees of Freedom	18
AICc	14.166
R ²	0.893
Sum of Squares	27.911
Sy.x	1.245
Runs Test p Value	0.179

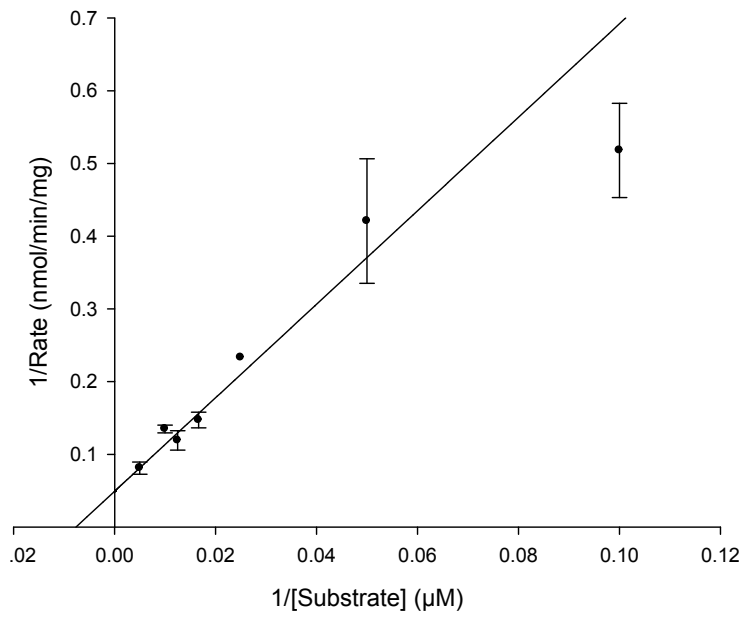
Data

Number of x values	7
Number of replicates	3
Total number of values	20
Number of missing values	1

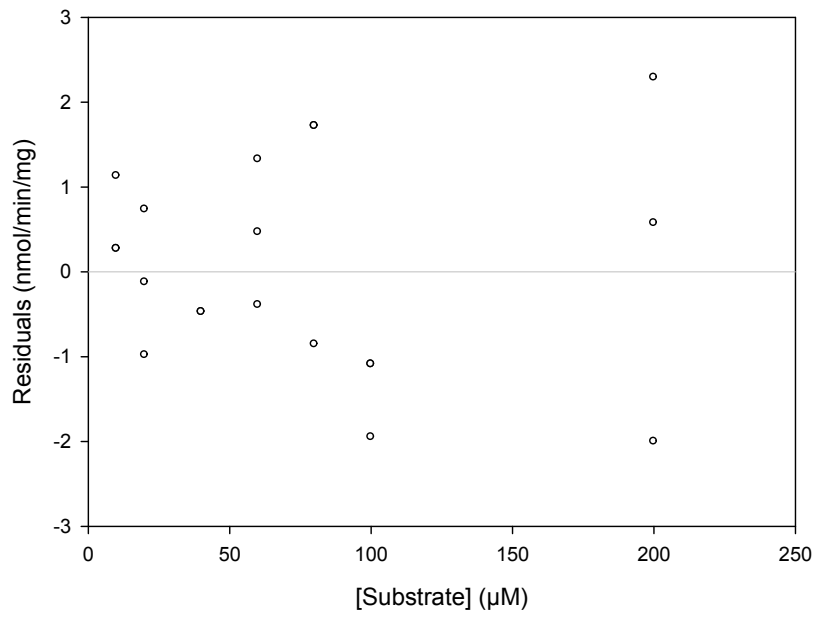
Michaelis-Menten



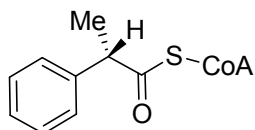
Lineweaver-Burk



Residuals



ACOT-2, *S*-2-Phenylpropanoyl-CoA **8S**



Parameters

	Value	\pm Std. Error	95% Conf. Interval	
Vmax	33,339.3892	7.917e+6	-1.643e+7	to 1.650e+7
Km	46,916.6408	1.115e+7	-2.314e+7	to 2.323e+7
Ki	0.1081	25.6837	-53.3051	to 53.5212

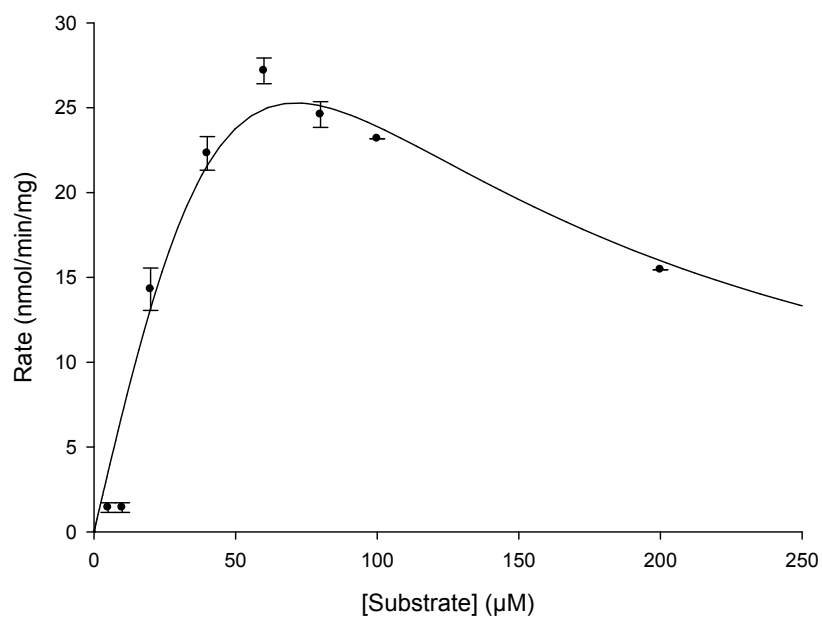
Goodness of Fit

Degrees of Freedom	21
AICc	54.443
R ²	0.930
Sum of Squares	152.241
Sy.x	2.693
Runs Test p Value	0.501

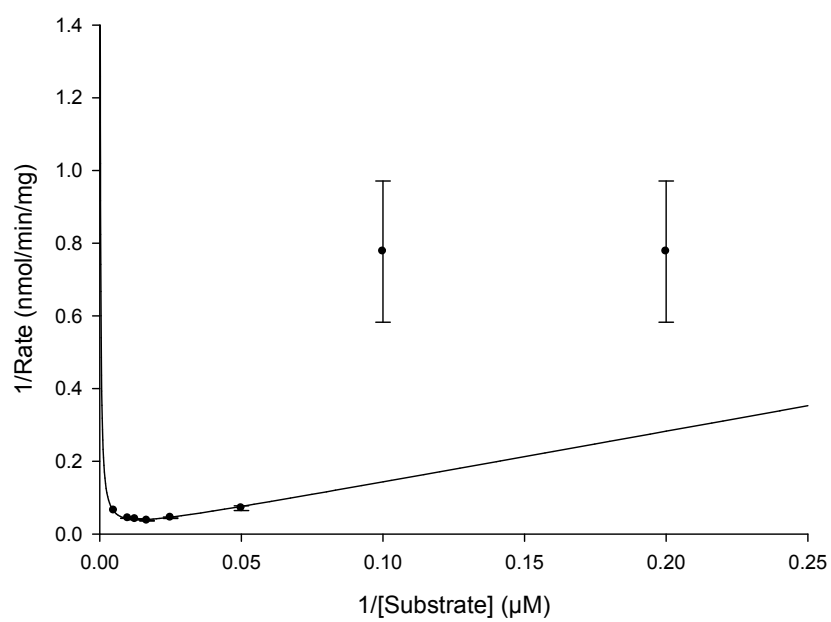
Data

Number of x values	8
Number of replicates	3
Total number of values	24
Number of missing values	0

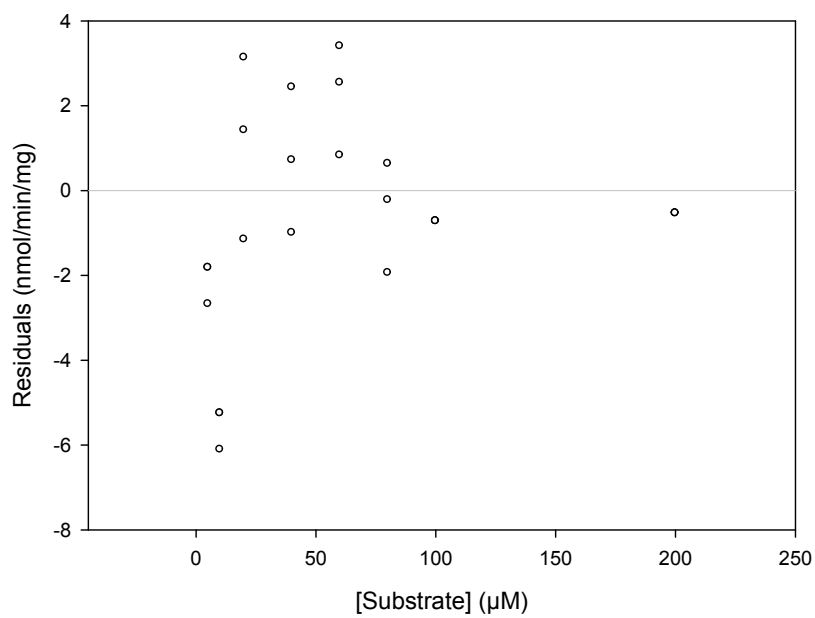
Michaelis-Menten



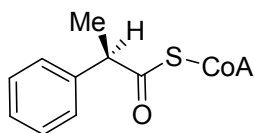
Lineweaver-Burk



Residuals



ACOT-2, *R*-2-Phenylpropanoyl-CoA **8R**



Parameters

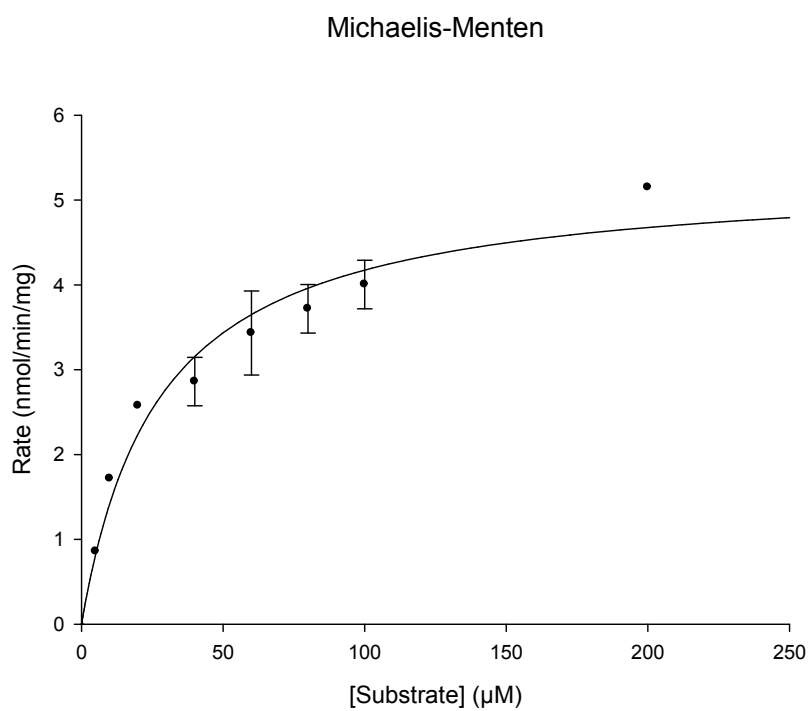
	<u>Value</u>	<u>±Std. Error</u>	<u>95% Conf. Interval</u>	
Vmax	5.3167	0.3275	4.6375	to 5.9960
Km	27.3880	5.4159	16.1558	to 38.6202

Goodness of Fit

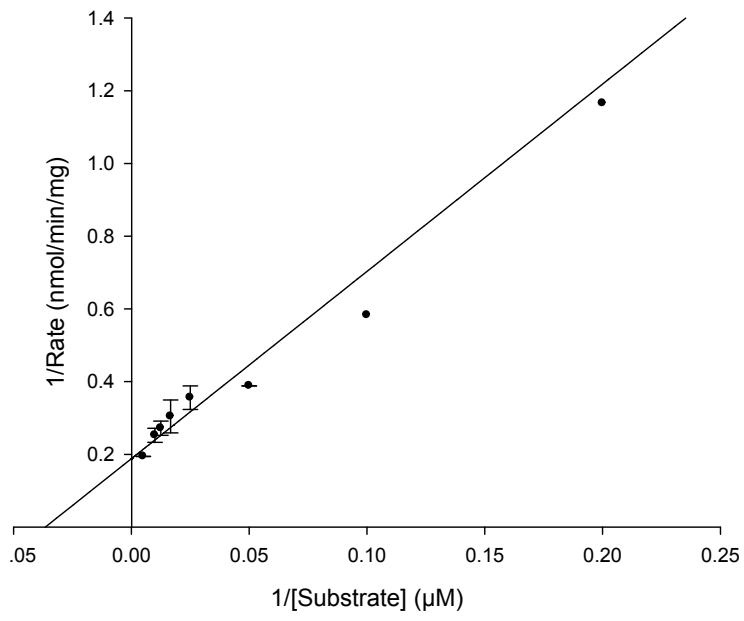
Degrees of Freedom	22
AICc	-31.069
R ²	0.882
Sum of Squares	4.872
Sy.x	0.471
Runs Test p Value	0.023

Data

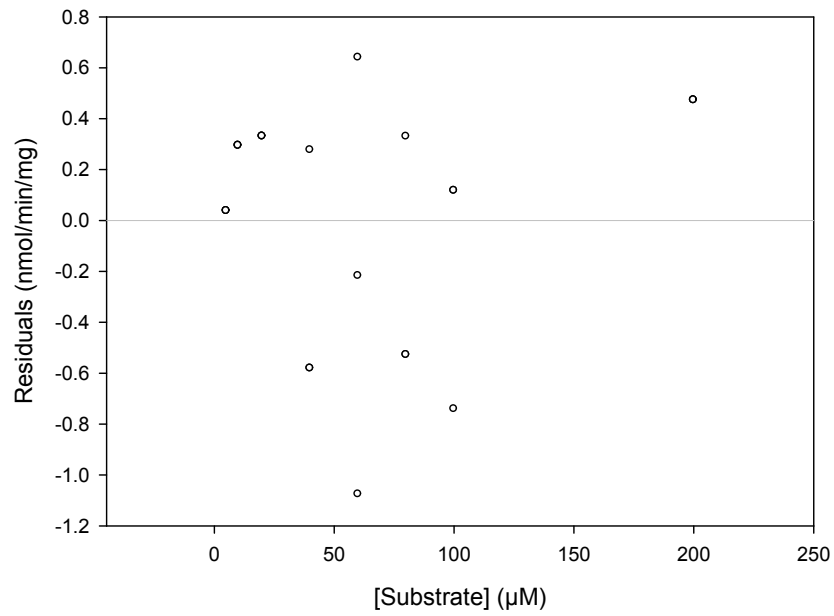
Number of x values	8
Number of replicates	3
Total number of values	24
Number of missing values	0



Lineweaver-Burk



Residuals



MCR	MAGPLSGLRVVELAGIGPGPHAAMILGDLGADVVRIDRPSSVDGISRDAMLRNRRIVTAD
AMACR	--MALQGIVVELSGLAPGPFCAVLADFGARVVRVDRPGSRVDVSR--LGRGKRSLVLD
MCR	LKSDQGLELALKLIAKADVLIIEGYRPGVTERLGLGPEECAKVNDRLIYARMTGWGQTGPR
AMACR	LKQPRGAAVLRRLCKRSDVLEPFRRGVMEKQLGPEILQRENPRLIYARLSGFGQSGSF
MCR	SQQAG HD INYISLNGILHAIGRGDERVPVPL N LVG D FGGGSMFLLVGILAAALWERQSSGK
AMACR	CRLAG HD INYLALSGVLSKIGRSGENPYAPL N LL D FAGGGLMCALGIIMALFDRTRTGK
MCR	GQVVDAAAMVDGSSVLIQMMWAMRATGMWTDTRGAN M LDGGAPY Y DTYECADGRYVAVG A I
AMACR	GQVIDANMVEGTAYLSSFLWKTQKSSLWEAPRGQN M LDGGAP F YTTYRTADGEFMAVG A I
MCR	EPQFYAAMLAGLGLDAAELPPQNDRARWPELRALLTEAFASHDRDHGAVFANSDACVTP
AMACR	EPQFYELLIKGLGLKSDLEPNQMSMDDWPEMKKKFADVFAKKTAEWCQIFDGTDACVTP
MCR	VLAFGVHNEPHIIERNTFYANG---GWQMPAPRFSRTASSQPRPPAATIDIEAVLTD
AMACR	VLTFFEEVVHHDHDKERGSFITSEEQDVSPRPAPLLLNTPAIPSFKRDPFIGEHTEEILEE
MCR	WDG-----
AMACR	FGFSREEIYQLNSDKIIIESNKVKASL

Figure S1: Sequence alignment of MCR from *M. tuberculosis* (O06543) and human AMACR 1A (Q9UHK6), showing residues involved in methyl group binding pocket (Bold).