Supplemental Data for:

Propofol Inhibits SIRT2 Deacetylase Through a Conformation-Specific, Allosteric Site*

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*Running title: *Inhibition of SIRT2 by propofol*

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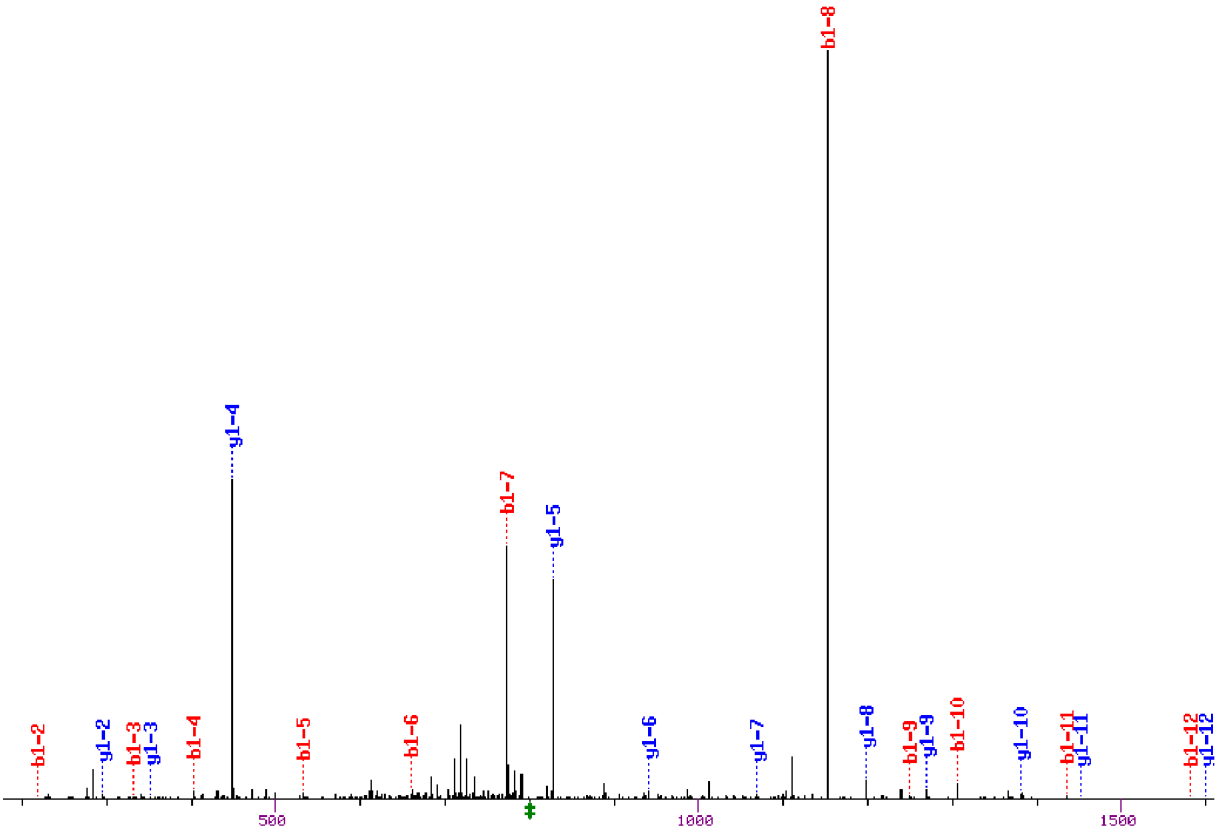
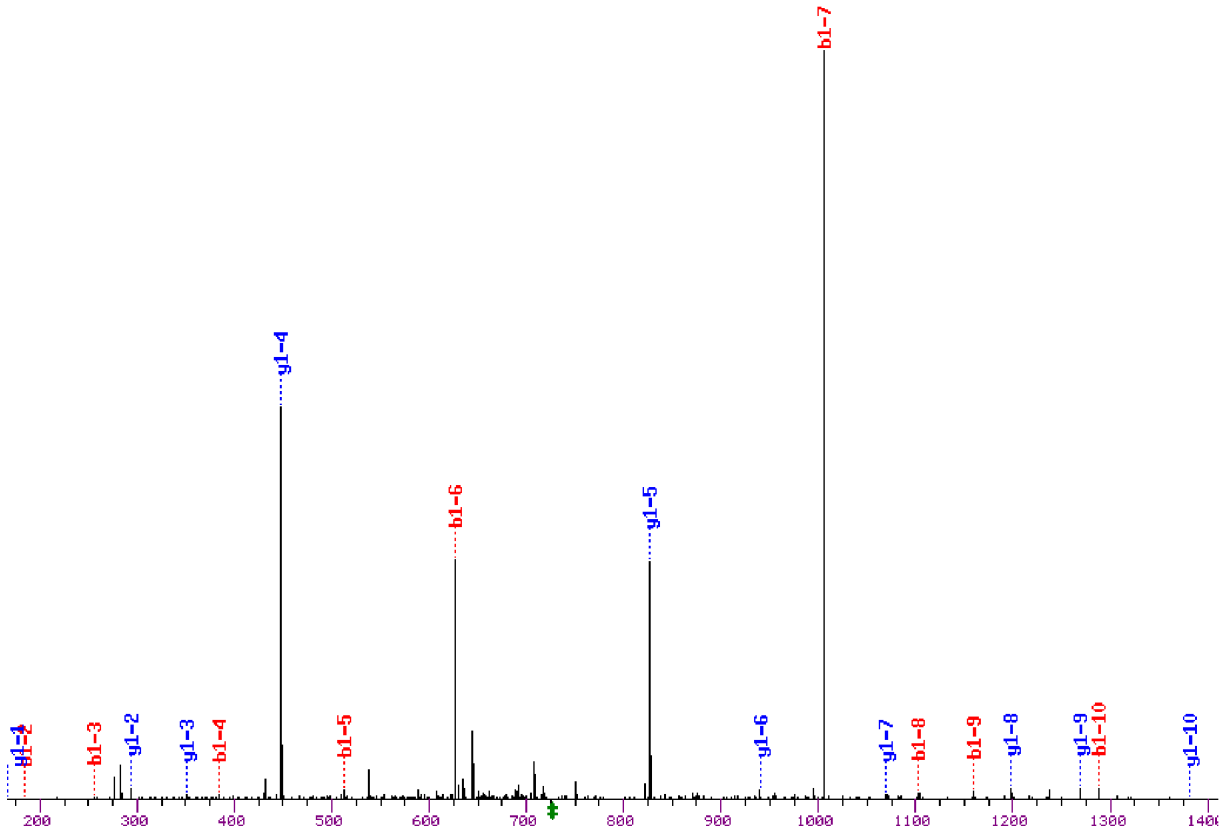
Fig. S1. Mass spectra of SIRT2 peptides photolabeled by AziP*m*. For all spectra, hypothetical fragment ions are listed in the tables, and their predicted positions are indicated on the spectra. Fragment ions that were identified on the spectra are colored in the ion tables. Only +1 fragment ions are shown. #Indicates a 216.0762 Da modification was detected; amino acid numbering is according to full-length rat SIRT2.

Peptide: ^{131}F.FALAKELY$^{\#}$PGQF.K^{144}



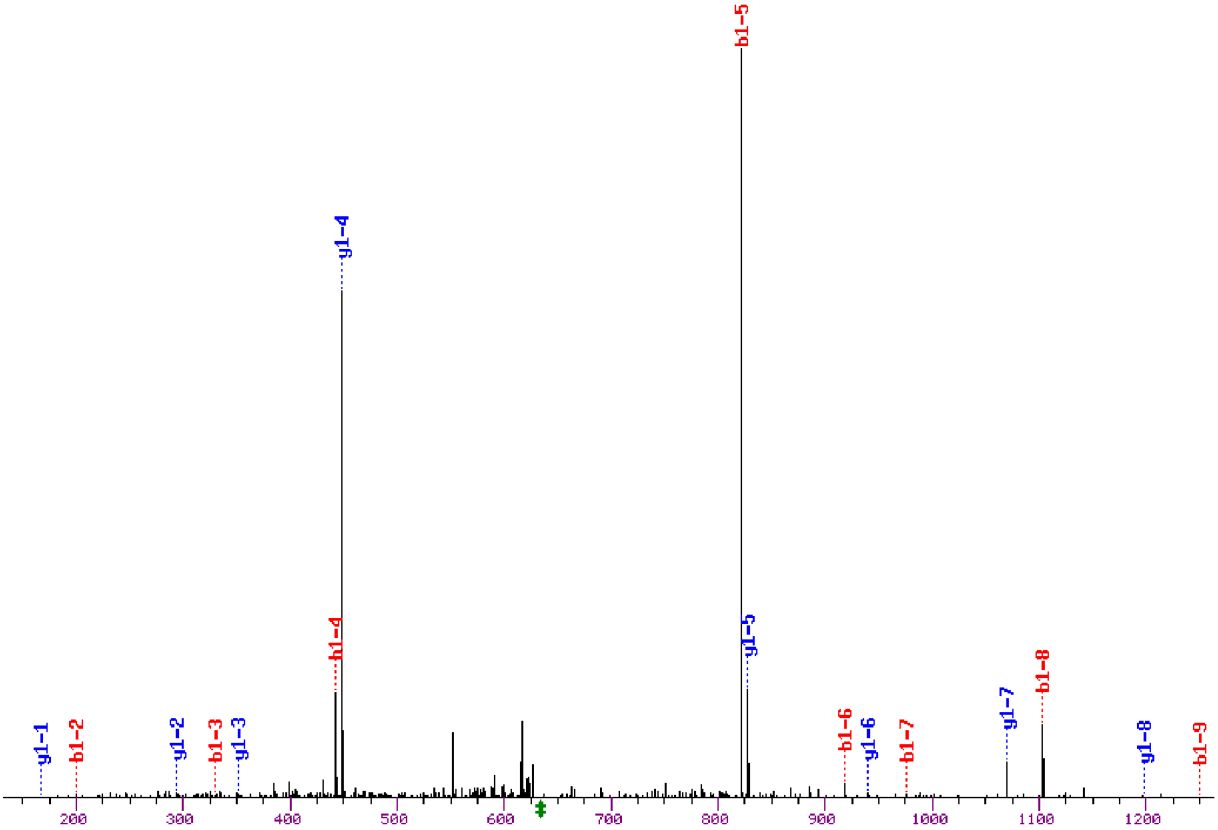
Sequence	#	b	y	#
F	1	148.1	1599.8	12
A	2	219.1	1452.7	11
L	3	332.2	1381.7	10
A	4	403.2	1268.6	9
K	5	531.3	1197.6	8
E	6	660.4	1069.5	7
L	7	773.5	940.4	6
Y#	8	1152.6	827.4	5
P	9	1249.6	448.2	4
G	10	1306.7	351.2	3
Q	11	1434.7	294.1	2
F	12	1581.8	166.1	1

Peptide: ^{132}F.ALAKELY$^{\#}$PGQF.K^{144}



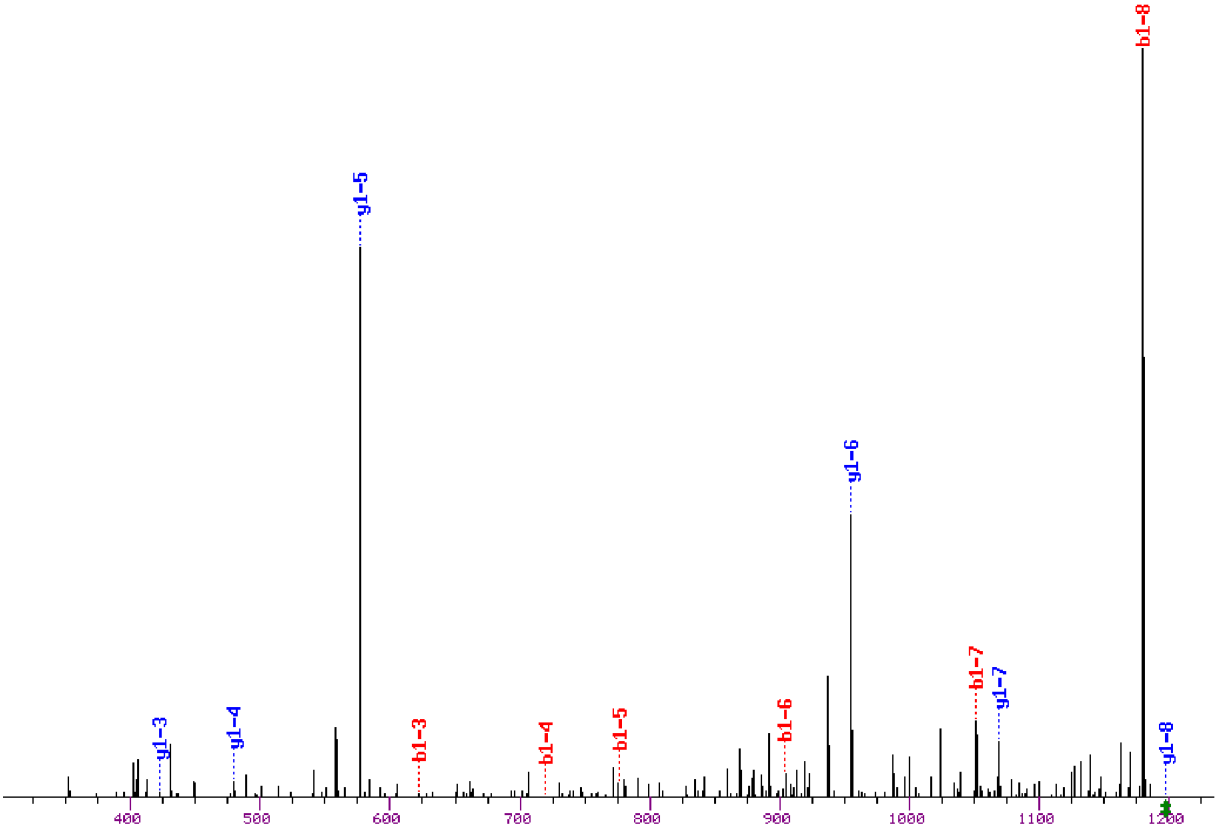
Sequence	#	b	y	#
A	1	72.0	1452.7	11
L	2	185.1	1381.7	10
A	3	256.2	1268.6	9
K	4	384.3	1197.6	8
E	5	513.3	1069.5	7
L	6	626.4	940.4	6
Y#	7	1005.5	827.4	5
P	8	1102.6	448.2	4
G	9	1159.6	351.2	3
Q	10	1287.7	294.1	2
F	11	1434.7	166.1	1

Peptide: ^{134}L.AKELY$^{\#}$PGQF.K^{144}



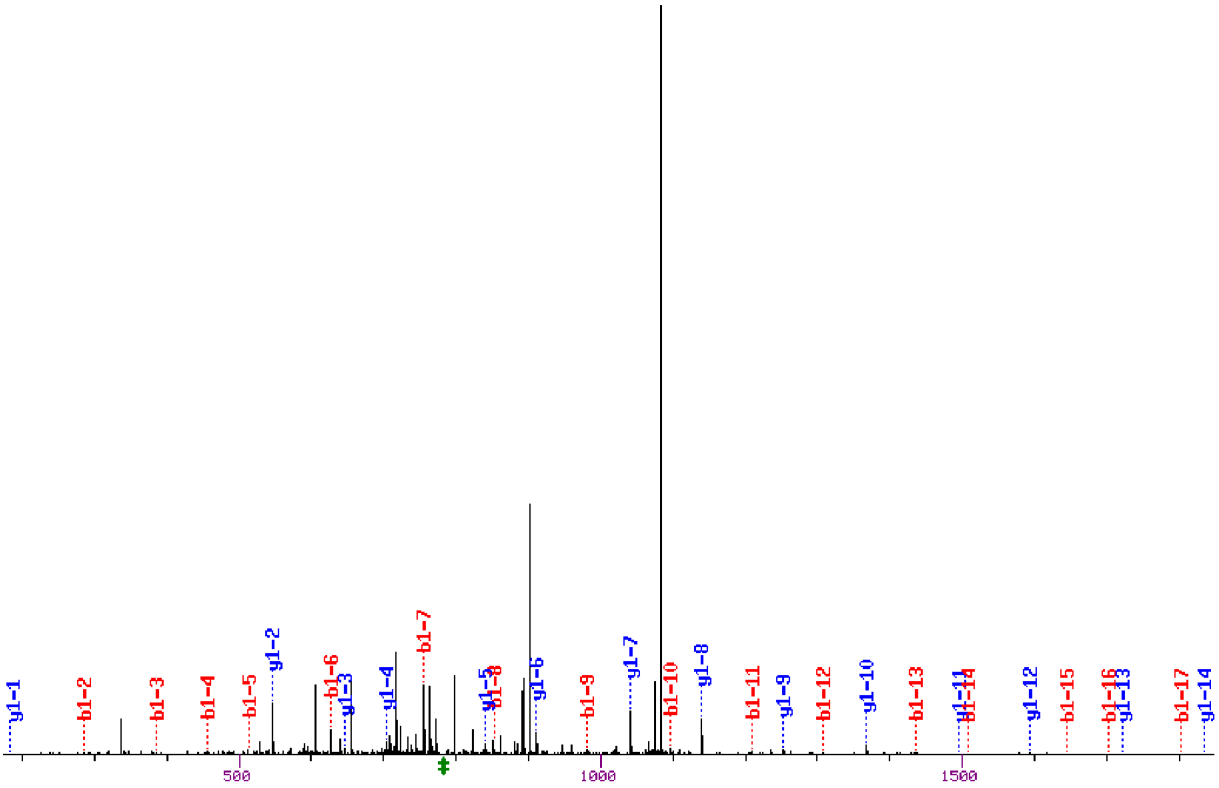
Sequence	#	b	y	#
A	1	72.0	1268.6	9
K	2	200.1	1197.6	8
E	3	329.2	1069.5	7
L	4	442.3	940.4	6
Y#	5	821.4	827.4	5
P	6	918.5	448.2	4
G	7	975.5	351.2	3
Q	8	1103.5	294.1	2
F	9	1250.6	166.1	1

Peptide: ^{136}K.ELY$^{\#}$PGQFK.P^{145}



Sequence	#	b	y	#
E	1	130.1	1197.6	8
L	2	243.1	1068.5	7
Y#	3	622.3	955.5	6
P	4	719.3	576.3	5
G	5	776.3	479.3	4
Q	6	904.4	422.2	3
F	7	1051.5	294.2	2
K	8	1179.6	147.1	1

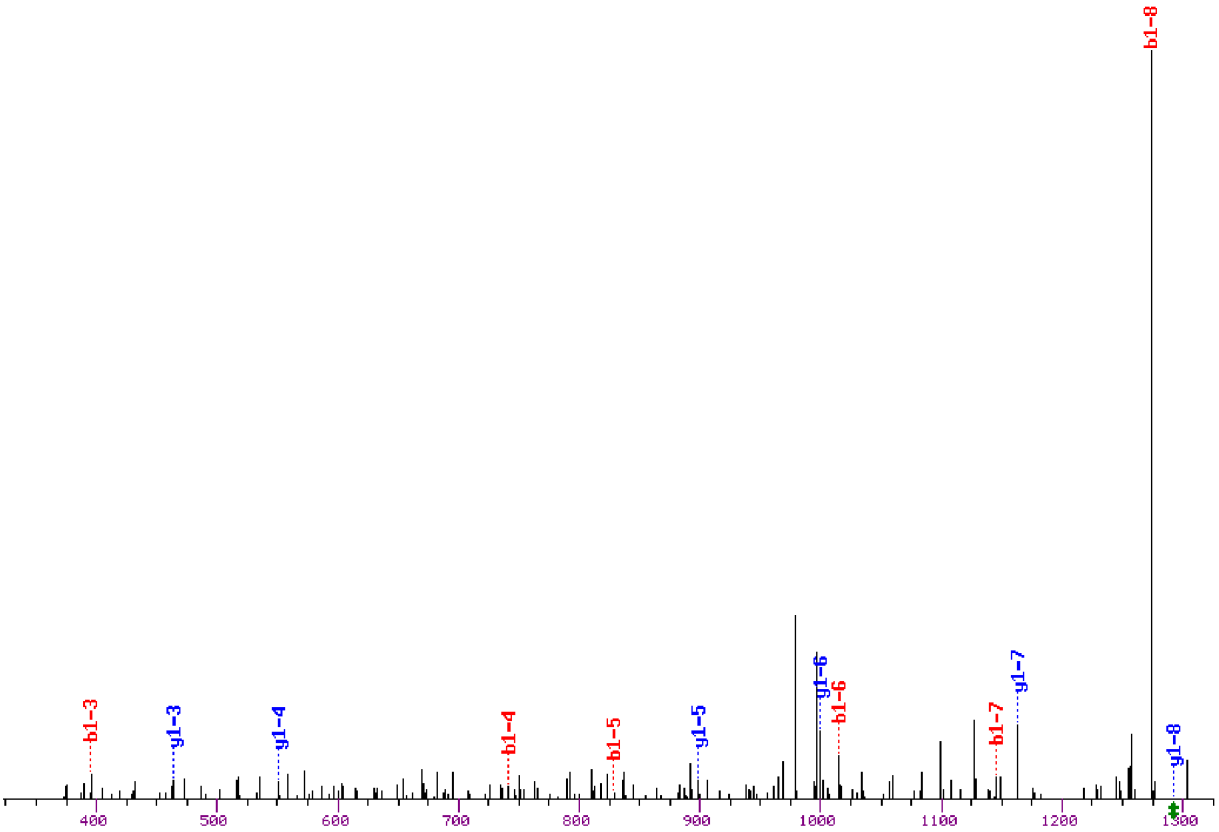
Peptide: ^{172}L.ERVAGLEPQDLVEAHGTF$^{\#}$Y.T^{192}



Sequence	#	b	y	#
E	1	130.1	2347.1	19
R	2	286.2	2218.1	18
V	3	385.2	2062.0	17
A	4	456.3	1962.9	16
G	5	513.3	1891.9	15
L	6	626.4	1834.9	14
E	7	755.4	1721.8	13
P	8	852.5	1592.7	12
Q	9	980.5	1495.7	11
D	10	1095.5	1367.6	10
L	11	1208.6	1252.6	9
V	12	1307.7	1139.5	8
E	13	1436.7	1040.4	7
A	14	1507.8	911.4	6
H	15	1644.8	840.4	5
G	16	1701.9	703.3	4
T	17	1802.9	646.3	3
F#	18	2166.0	545.2	2
Y	19	2329.2	182.0	1

note: the peaks at *m/z* = 902.0 and 1083.5 are b17 and b18 +2 fragment ions, respectively

Peptide: ^{202}K.EYTM$^{\#}$SWMK.E^{211}



Sequence	#	b	y	#
E	1	130.1	1291.5	8
Y	2	293.1	1162.5	7
T	3	394.2	999.4	6
M#	4	741.3	898.4	5
S	5	828.3	551.3	4
W	6	1014.4	464.2	3
M	7	1145.4	278.2	2
K	8	1273.5	147.1	1