

Supplementary Information

HDAC1 and HDAC2 are bidirectional enzymes that catalyze histone sorbylation to induce epigenetic alteration

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Supplementary Information

Supplementary Figures 1-7

Supplementary Tables 1-4

H2A: NP_003508.1

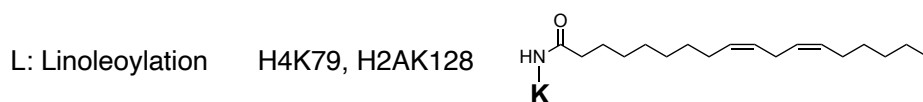
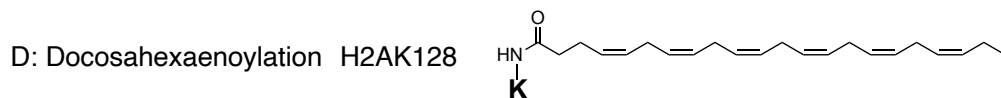
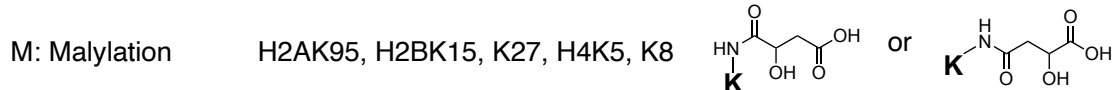
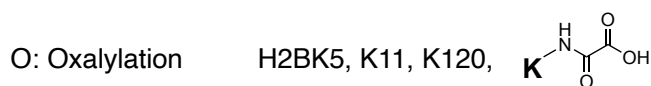
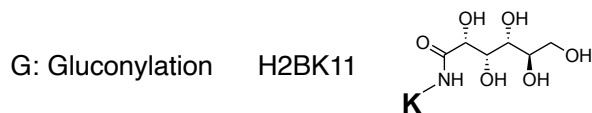
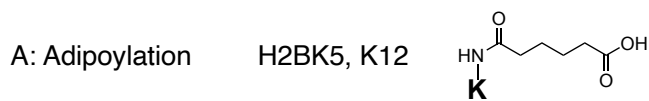
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H2B: NP_003515.1

NH₂- PDPAK^ASAPAP^OK^GSGS^{OA}K^MKAVTKAQKKG^MKKRKRSRKESYSVYV--KAVTKYTSSK-COOH
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H4: NP_001029249.1

NH₂- SGRGK^MGGK^MGKGLGKGGAKRHRK--YTEHAKR^LKTVTAMDVVYALKRQGR^LTLYGFGG-COOH
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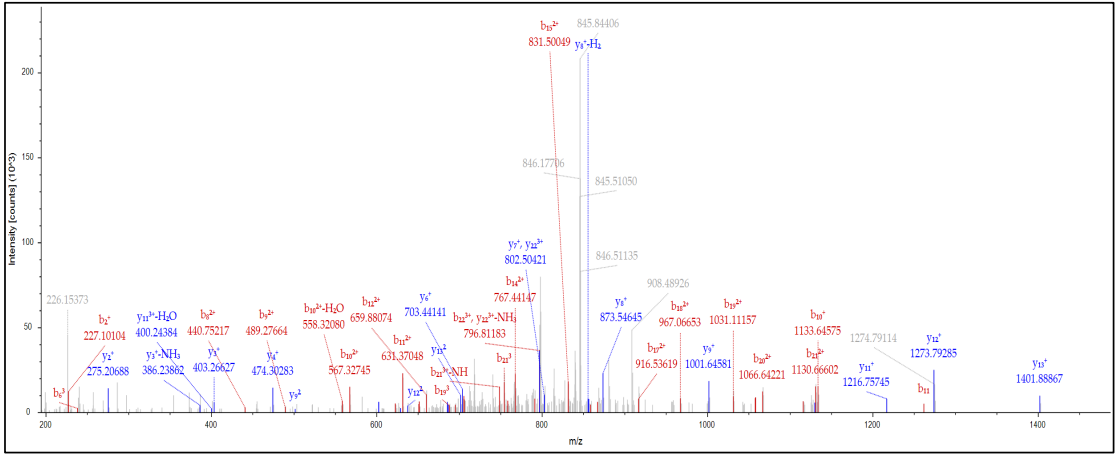


Supplementary Figure 1. Histone lysine modifications induced by carboxylic acids derived from food ingredients.

A schematic representation of lysine residues in core histones modified by carboxylic acids derived from food ingredients, as identified through LC-MS/MS analysis, and chemical structures of lysine acylation derived from each carboxylic acid.

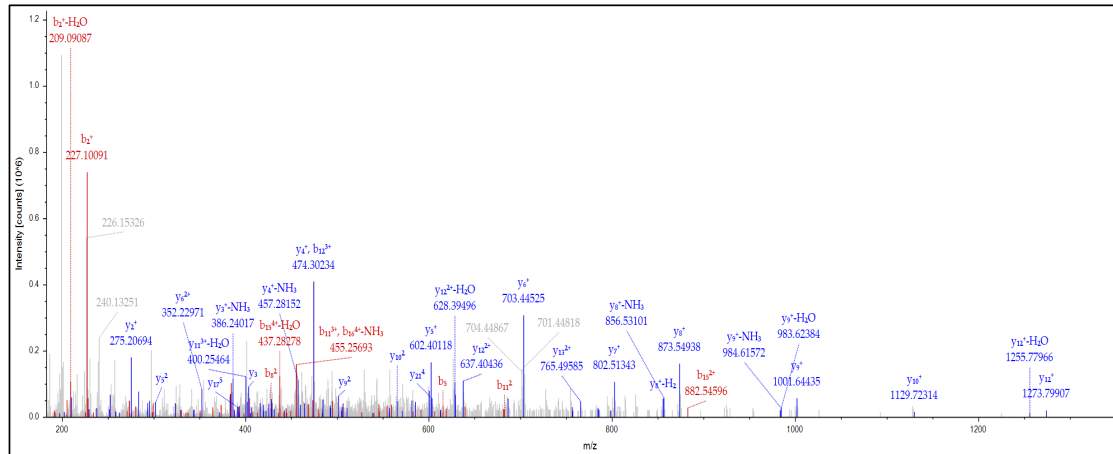
HepG2, 3 mM Adipic acid, H2BK5ad

Sequence: EPAKSAPAPKKGSKKAVTKAQKK, K10-Dimethyl (28.03130 Da), K4-adipic acid (128.04734 Da)
Charge: +3, Monoisotopic m/z: 845.51738 Da (+11.59 mmu/+13.71 ppm), MH+: 2534.53758 Da, RT: 24.6298 min,
Identified with: Mascot (v1.36); Ions Score:16, Percolator q-Value:1.3e-3, Percolator PEP:6.7e-4, Ions matched by search engine: 19/248
Fragment match tolerance used for search: 30 mmu
Fragments used for search: -H₂O; y; -NH₃; y; b; b; -H₂O; b; -NH₃; y



HepG2, 3 mM Adipic acid, H2BK12ad

Sequence: EPAKFAPAPKKGSKKAVTKAQKK, K10-Dimethyl (28.03130 Da), K4-Trimethyl (42.04695 Da), K11-adipic acid (128.04734 Da)
Charge: +6, Monoisotopic m/z: 440.26870 Da (-1.73 mmu/-3.93 ppm), MH+: 2636.57581 Da, RT: 24.7197 min,
Identified with: Mascot (v1.36); Ions Score:27, Percolator q-Value:1.3e-3, Percolator PEP:2.5e-3, Ions matched by search engine: 8/248
Fragment match tolerance used for search: 30 mmu
Fragments used for search: -H₂O; y; -NH₃; y; b; b; -H₂O; b; -NH₃; y

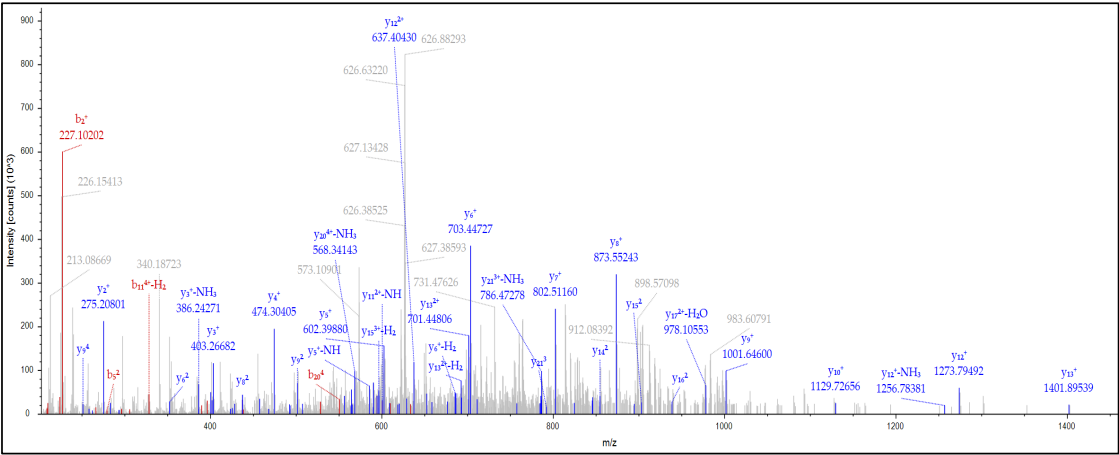


#1	b	b ²	b ³	b ⁴	b ⁵	b ⁶	Seq.	y	y ²	y ³	y ⁴	y ⁵	y ⁶	#2
1	130.04987	65.52857	44.02147	33.26792	26.81590	22.51438	E							23
2	227.10263	114.05498	76.37240	57.53112	46.22635	38.68884	P	2507.54357	1254.27543	836.51938	627.64135	502.31454	418.76333	22
3	280.13873	145.57351	100.05143	75.29439	60.45377	50.82836	A	2410.49381	1205.74904	804.16845	603.32418	482.30368	402.58787	21
4	468.28168	234.64447	156.76540	117.62587	94.49215	78.86634	K-Trimethyl	2339.45370	1170.23049	780.48542	585.61889	469.69556	390.74935	20
5	615.35007	306.17868	205.78621	154.59298	123.87584	103.39774	F	2169.31178	1085.15953	723.77545	543.06340	434.66818	362.38136	19
6	686.38718	343.69723	229.48725	172.35225	138.08326	115.23726	A	2022.24337	1011.62532	674.75284	506.31630	405.25450	337.87996	18
7	763.43956	382.22861	251.81817	186.61545	157.45381	131.41272	P	1851.20528	926.10677	631.07360	488.55702	391.04107	326.04044	17
8	854.47707	427.74211	285.48721	214.37472	171.70123	143.25294	A	1854.15349	927.58038	618.72288	484.28383	371.63850	309.86488	16
9	951.52983	476.26858	317.84813	238.63791	191.11178	159.42770	P	1783.11638	892.06183	595.04364	446.53455	357.42910	298.02546	15
10	1107.65608	554.33168	369.89022	277.68948	222.33704	185.44875	K-Dimethyl	1686.06362	843.53545	562.69272	422.27136	338.01851	281.85000	14
11	1363.79840	682.40282	455.27088	341.70536	273.56550	228.13813	K-adipic acid	1529.93735	765.47231	510.65684	383.73988	306.79329	253.62865	13
12	1420.81988	710.91357	474.27814	355.96042	284.98979	237.64271	G	1273.79505	637.40116	425.26987	319.20422	255.56483	213.13857	12
13	1507.85180	754.42958	503.28881	377.71843	302.37620	252.14805	S	1216.77358	608.88043	406.26271	304.94885	244.18054	203.63490	11
14	1635.94685	818.47707	545.88714	409.74217	327.99518	273.49721	K	1120.74155	565.37441	377.25204	283.16085	226.75413	189.12956	10
15	1764.04182	882.52455	588.68636	441.16601	353.61418	294.84637	K	1001.64659	501.32683	334.55371	251.18711	201.13514	167.78050	9
16	1835.07893	918.04310	612.36449	469.62519	367.82161	306.88589	A	873.55183	437.27945	291.85539	219.14336	175.51615	146.43134	8
17	1934.14734	967.57731	645.38730	484.29229	387.63529	323.19729	V	802.51451	401.76090	268.17636	201.38409	161.30872	134.59182	7
18	2035.19502	1018.10115	679.06986	509.55421	407.84885	340.03857	L	703.44810	352.22858	235.15355	178.61698	141.49804	118.08041	6
19	2163.28969	1082.14963	721.76818	541.67765	433.46382	361.38773	K	602.39842	301.70285	201.47089	151.35506	121.28551	101.23913	5
20	2234.32710	1117.66719	745.44722	559.33723	447.67124	373.22725	A	474.30346	237.65537	158.77267	119.33132	95.66551	79.88997	4
21	2362.38568	1181.68648	788.13341	581.35188	473.28298	394.57034	O	403.29634	202.13681	135.09363	101.57204	81.45906	68.05045	3
22	2490.48069	1245.74396	830.63173	623.37562	498.90195	415.91950	K	275.20771	138.10752	92.40744	68.58740	55.84747	46.70738	2
23								147.11280	74.06004	49.70512	37.53368	30.22838	25.35620	1

Fig. S1

HepG2, 10 mM Gluconic acid, H2BK11gl

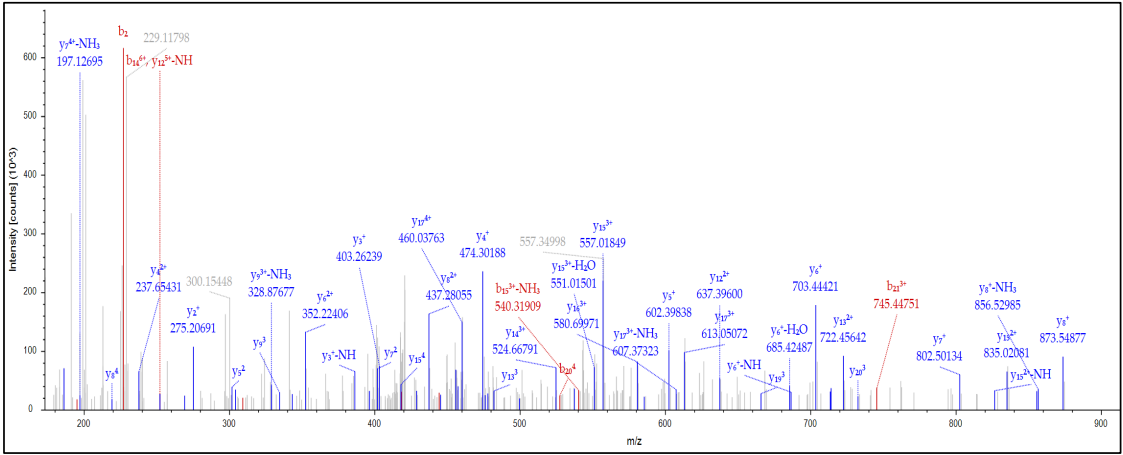
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Fragment match tolerance used for search: 30 mmu
Fragments used for search: -H₂O; y; -NH₃; y; b; b; -H₂O; b; -NH₃; y



#1	b	b ²	b ³	b ⁴	Seq.	y	y ²	y ³	y ⁴	#2
1	130.04987	65.52857	44.02147	33.26792	E					23
2	227.10263	114.05496	76.37240	57.53112	P	2471.45555	1236.23141	824.49003	618.61934	22
3	314.13466	157.57097	105.38307	79.28912	S	2374.40278	1187.70503	792.13911	594.35615	21
4	470.26092	235.63410	157.42516	118.32069	K-Dimethyl	2287.37076	1144.18902	763.12844	572.59815	20
5	557.29295	279.15011	186.43584	140.07870	S	2131.24449	1066.12588	711.08635	533.56658	19
6	628.33007	314.66867	210.11487	157.83797	A	2044.21246	1022.60987	682.07557	511.80857	18
7	725.38283	363.19505	242.46579	182.10117	P	1973.17535	987.09131	658.34953	494.04930	17
8	796.41934	398.71361	266.14483	199.86044	A	1876.12259	938.56493	626.04571	469.76810	16
9	893.47271	447.23999	298.49575	224.12383	P	1805.09547	903.04637	602.36658	452.02893	15
10	1199.61541	600.31134	400.54332	300.65931	K-Gluconic acid	1708.03271	854.51999	570.01575	427.76383	14
11	1327.71037	664.35882	443.24164	332.68305	K	1401.89001	701.44864	467.96819	351.22796	13
12	1384.73184	692.86956	462.24880	346.93842	G	1273.79505	637.40116	425.26987	319.20422	12
13	1471.76386	736.38557	491.25947	368.69642	S	1216.77358	608.89043	406.26271	304.94885	11
14	1599.85883	800.43305	533.95779	400.72016	K	1129.74155	565.37441	377.25204	283.19085	10
15	1727.95379	864.48053	576.65611	432.74391	K	1001.64659	501.32693	334.55371	251.16711	9
16	1793.99030	899.99008	600.33515	450.50318	A	873.55163	437.27945	281.85539	219.14336	8
17	1893.05932	949.53330	633.35736	475.27029	V	802.51451	401.76090	268.17636	201.38409	7
18	1999.10700	1000.05714	667.04052	500.53221	T	703.44610	352.22689	235.15355	176.61698	6
19	2127.20196	1064.10462	709.73884	532.55595	K	602.39842	301.70285	201.47099	151.35508	5
20	2198.23907	1099.62317	733.41788	550.31523	A	474.30346	237.65537	158.77267	119.33132	4
21	2326.29765	1163.65246	776.10407	582.32987	O	403.26634	202.13681	135.09363	101.57204	3
22	2454.39261	1227.69994	818.80239	614.35361	K	275.20777	138.10752	92.40744	69.55740	2
23					K	147.11280	74.06004	49.70912	37.53366	1

HepG2, 5 mM sodium Oxalate, H2BK5ox

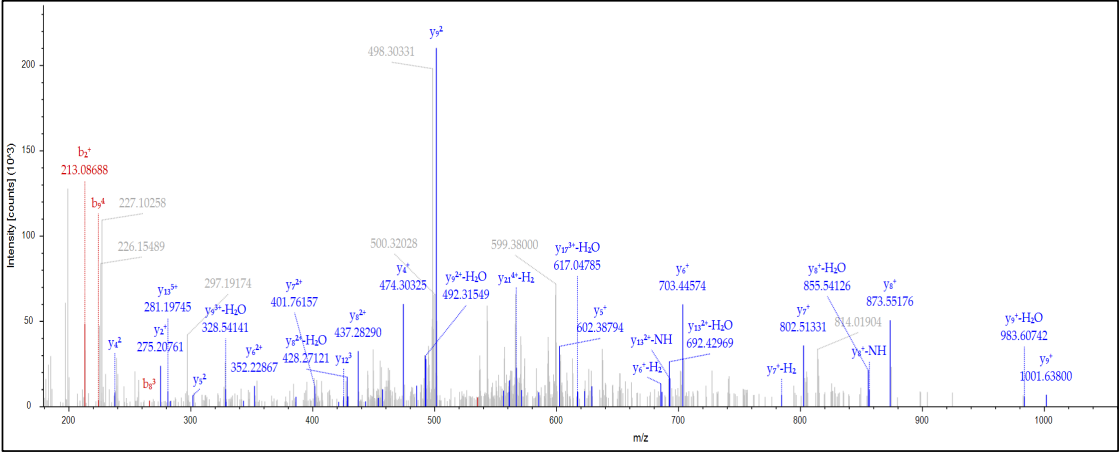
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Charge: +6, Monoisotopic m/z: 418.90955 Da (-4.99 mmu/-11.92 ppm), MH+: 2508.42089 Da, RT: 24.7796 min,
Identified with: Mascot (v1.36); Ions Score:14, Ions matched by search engine: 8/248
Fragment match tolerance used for search: 30 mmu
Fragments used for search: -H₂O; y; -NH₃; y; b; b; -H₂O; b; -NH₃; y



#1	b	b*	b*	b*	b*	b*	Seq.	y	y*	y*	y*	y*	y*	#2
1	130.04097	65.52857	44.02147	33.26792	26.81586	22.51438	P	2379.40820	1190.20774	793.80759	595.60751	476.68746	397.40743	23
2	227.10263	114.05496	76.37240	57.53112	46.22635	38.68984	P	2282.35544	1141.68136	761.45666	571.34432	457.27691	381.23197	21
3	314.13468	157.57097	105.38307	79.28912	63.63275	53.19517	S	2195.32341	1088.16534	732.44399	543.58631	439.87050	366.72663	20
4	514.21237	257.61082	172.07631	129.30965	103.64870	86.54178	K-Oxalic Acid	1995.24371	998.12549	669.75275	499.56638	399.85458	333.38001	19
5	601.24640	301.12884	201.08869	151.08706	121.05510	101.04713	S	1908.21168	954.60948	636.74208	477.80838	382.44816	318.87468	18
6	672.28351	336.64539	224.76902	168.82634	135.26257	112.88665	A	1837.17455	919.09032	613.06304	460.04910	368.24073	307.03516	17
7	769.33627	385.17178	257.11694	193.08953	154.67308	128.06211	P	1740.12180	870.56458	580.71214	435.76621	348.63018	290.85970	16
8	849.37339	424.68633	280.79558	210.84960	168.68050	140.90163	A	1669.08465	835.04588	557.03305	418.02653	334.92776	275.02018	15
9	937.42515	469.21671	313.14680	235.11200	188.25105	157.07705	P	1443.93666	722.47212	481.96384	361.73970	289.59321	241.49556	13
10	1065.52112	533.26420	355.84522	267.13574	213.91004	178.42625	K	1218.77358	609.89043	408.28271	304.94885	244.16054	203.63499	11
11	1235.66303	618.33515	412.55918	309.67121	247.93843	206.76324	K-Trimethyl	1129.74155	565.37441	377.25204	283.19085	226.75413	189.12966	10
12	1292.68449	646.84580	431.58635	323.92659	259.34272	218.28681	S	1001.64659	501.32633	334.85471	251.16711	201.13513	167.78050	9
13	1379.71652	690.38190	460.57702	345.68459	276.75515	230.79219	S	802.51451	401.76030	268.17636	201.38409	161.30872	134.59182	7
14	1507.81148	754.40938	503.27535	377.70833	302.36812	252.18131	K	703.44810	352.22659	235.15355	176.61698	141.49504	118.08041	6
15	1635.90645	818.45695	545.97367	409.73207	327.48711	273.49047	K	602.39847	301.10283	201.47029	151.35508	121.28551	101.23913	5
16	1709.94356	853.97542	569.65270	427.49155	342.19453	285.30961	A	474.30349	237.65537	158.77267	119.33132	95.66651	79.89957	4
17	1806.01197	903.50963	602.67551	452.25845	362.00822	301.84139	V	403.26634	202.13681	135.09363	101.57204	81.45909	68.05045	3
18	1807.05965	954.03346	636.35807	477.62037	382.21775	318.68267	T	275.20777	138.10752	92.40744	69.56740	55.84747	46.70736	2
19	2035.15482	1018.08029	679.95638	509.54411	407.83674	340.03183	K	147.11281	74.06034	49.70912	37.53369	30.22838	25.35820	1
20	2106.19173	1053.69950	702.13543	527.30339	422.04117	351.81138	A							
21	2234.25031	1117.62879	745.42162	559.31803	447.65588	373.21445	O							
22	2362.34527	1181.67827	788.11994	591.34177	473.27488	394.56361	K							
23							K							

HepG2, 5 mM sodium Oxalate, H2BK11ox

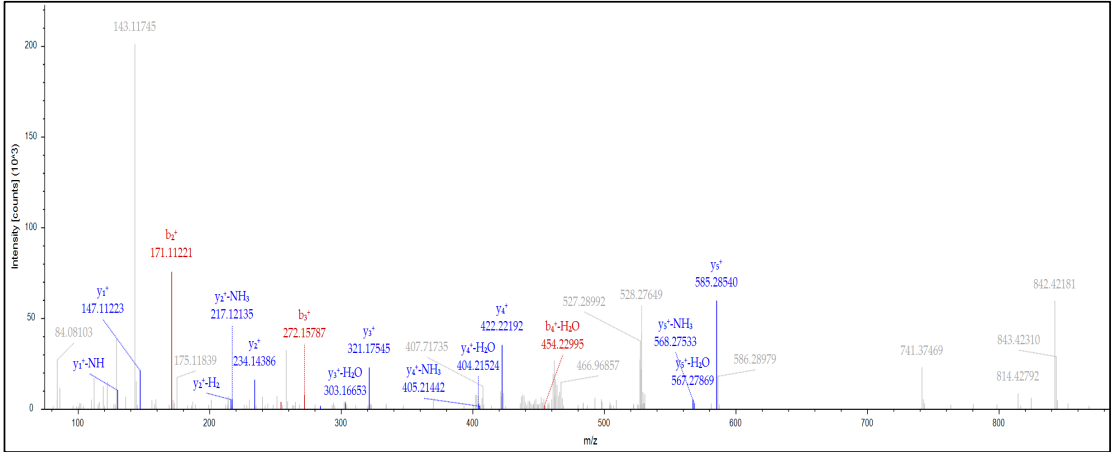
Sequence: DPSKSAPAPKKGSKKAVTKAQKK, K4-Acetyl (42.01057 Da), K10-Oxalic Acid (71.98474 Da)
Charge: +5, Monoisotopic m/z: 499.68845 Da (+2.88 mmu/+5.76 ppm), MH+: 2494.41312 Da, RT: 24.9382 min,
Identified with: Mascot (v1.36); Ions Score:17, Ions matched by search engine: 12/248
Fragment match tolerance used for search: 30 mmu
Fragments used for search: -H₂O; y; -NH₃; y; b; b; -H₂O; b; -NH₃; y



#1	b	b ⁺	b ⁺	b ⁺	b ⁺	Seq.	v	v ⁺	v ⁺	v ⁺	v ⁺	#2
1	116.03422	58.52075	39.34959	29.76401	24.01267	D	2379.37182	1190.18855	793.79546	595.58841	476.68019	23
2	213.08688	107.04713	71.70051	54.02720	43.42322	P	2282.31906	1141.66317	761.44454	571.33522	457.26963	21
3	300.11901	150.56314	100.71119	75.78521	60.82962	S	2195.28703	1098.14715	732.43386	549.57721	439.86323	20
4	470.22454	235.61591	157.41303	118.81159	94.85073	K-Acetyl	2025.18150	1013.09439	675.73202	507.05083	405.84212	19
5	557.25657	279.13192	186.42371	140.06960	112.25713	S	1938.14947	969.57837	646.72134	485.29283	388.43572	18
6	628.29368	314.65048	210.10275	157.82888	126.46456	A	1867.11236	934.05882	623.04230	467.53355	374.22829	17
7	725.34645	363.17696	242.45367	182.09207	145.87511	P	1770.05959	885.53343	590.68138	443.27036	354.81774	16
8	796.38356	398.69542	266.13270	199.85135	160.08253	A	1699.02248	850.01488	567.01234	426.51108	340.61032	15
9	893.43632	447.22180	298.48363	224.11454	179.49309	P	1601.86872	801.48850	534.66142	401.24789	321.19376	14
10	1093.51603	547.26165	365.17686	274.13447	219.50903	K-Oxalic	1401.89201	701.44884	467.98819	351.22796	281.18392	13
11	1221.61099	611.30813	407.87518	306.15921	245.12802	K	1273.78505	637.40116	425.26887	319.20422	255.56483	12
12	1278.63246	639.81987	426.88234	320.41357	256.53231	G	1216.77358	608.89043	406.26271	304.94885	244.16054	11
13	1365.66449	683.33588	455.89301	342.17158	273.93872	S	1129.74155	565.37441	377.25204	283.19085	226.75413	10
14	1493.75945	747.38336	498.59133	374.19532	298.55771	K	1001.64659	501.32693	334.55371	251.16711	201.13514	9
15	1621.85441	811.43084	541.28955	406.21908	325.17670	K	873.55163	437.27945	291.85539	219.14336	175.51815	8
16	1692.89152	846.94940	564.96869	423.97834	339.38413	A	802.51451	401.76090	268.17638	201.84009	161.30872	7
17	1791.85934	896.48361	597.99160	448.74544	358.19781	V	703.44810	352.22660	235.15355	176.81698	141.49504	6
18	1893.00762	947.00745	631.67406	474.00736	379.40734	T	602.39842	301.70285	201.47099	151.35506	121.28551	5
19	2021.10258	1011.05493	674.37238	506.03110	405.02634	K	474.30346	237.65537	158.77267	119.33132	95.66551	4
20	2092.13969	1046.57349	698.05142	523.79038	419.23376	A	403.26634	202.13681	135.09363	101.57204	81.45908	3
21	2220.19827	1110.60277	740.73761	555.80503	444.84548	O	275.20777	138.10752	92.40744	69.55740	55.84737	2
22	2348.29233	1174.65026	783.43593	587.82877	470.46447	K	147.11280	74.06004	49.70912	37.53366	30.22838	1
23						K						

HepG2, 5 mM sodium Oxalate, H2BK120ox

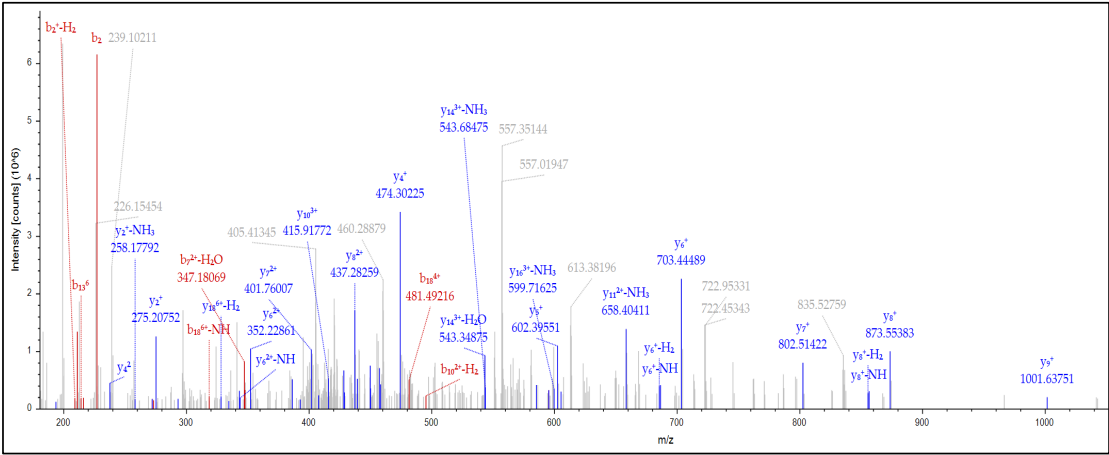
Sequence: AVTKYTSSK, K4-Oxalic acid (71.98474 Da)
Charge: +2, Monoisotopic m/z: 528.76424 Da (+0.21 mmu/+0.41 ppm), MH+: 1056.52121 Da, RT: 27.1918 min,
Identified with: Mascot (v1.36); Ions Score:33, Ions matched by search engine: 5/84
Fragment match tolerance used for search: 30 mmu
Fragments used for search: -H₂O; y; -NH₃; y; b; b; -H₂O; y



#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	72.04439	36.52583	A			9
2	171.11280	86.06004	V	985.48367	493.24547	8
3	272.16048	136.58388	T	886.41525	443.71126	7
4	472.24019	236.62373	K-Oxalic acid	785.36757	393.18743	6
5	635.30352	318.15540	Y	585.28787	293.14757	5
6	736.35120	368.67924	T	422.22454	211.61591	4
7	823.38322	412.19525	S	321.17686	161.09207	3
8	910.41525	455.71126	S	234.14483	117.57605	2
9			K	147.11280	74.06004	1

HepG2, 5 mM Malic acid , H2BK15ma

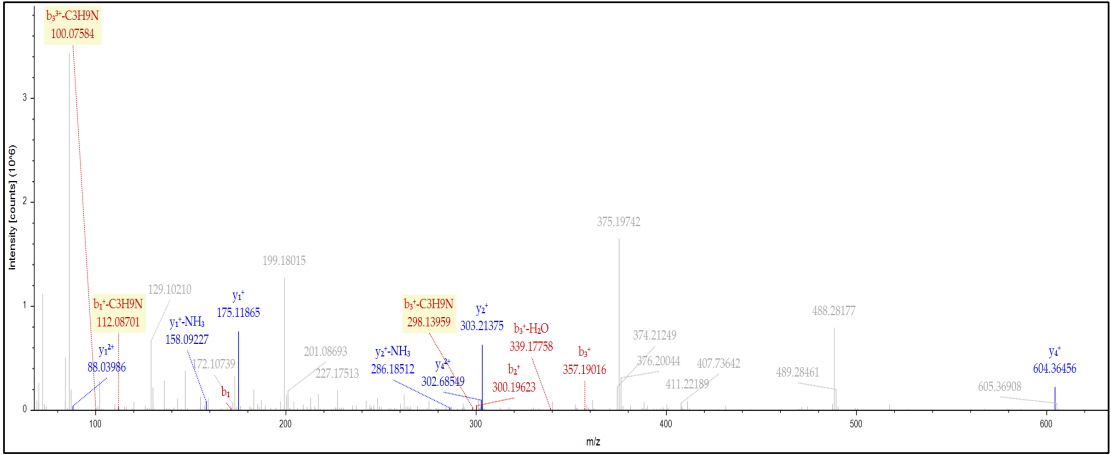
Sequence: EPTKSAPAPKKGSKKAVTKAQKK, K14-Malic acid (116.01096 Da)
Charge: +6, Monoisotopic m/z: 421.57418 Da (-6.18 mmu/-14.65 ppm), MH+: 2524.40872 Da, RT: 26.2320 min,
Identified with: Mascot (v1.36); Ions Score:13, Ions matched by search engine: 6/248
Fragment match tolerance used for search: 30 mmu
Fragments used for search: -H₂O; y; -NH₃; y; b; b; -H₂O; b; -NH₃; y



#1	b ⁺	b ²⁺	b ³⁺	b ⁴⁺	b ⁵⁺	b ⁶⁺	Seq.	y ⁺	y ²⁺	y ³⁺	y ⁴⁺	y ⁵⁺	y ⁶⁺	#2
1	130.04987	65.52857	44.02147	33.26792	26.81580	22.51438	E							23
2	227.10263	114.05496	76.37240	57.53112	46.22635	38.68984	P	2395.40312	1198.20520	799.13922	599.60624	479.88645	400.07325	22
3	328.15031	164.57879	110.05496	82.79304	66.43568	55.53112	T	2296.35036	1149.67862	766.78832	575.34336	460.47589	383.89719	21
4	458.24527	229.62629	152.75329	114.81878	92.05485	76.88029	K	2197.30299	1098.15498	733.10574	560.08113	440.25636	367.05651	20
5	543.27730	272.14229	181.76399	136.57478	108.46128	91.38561	S	2069.20771	1035.10750	690.40742	518.05739	414.64736	345.70735	19
6	614.31442	307.66085	205.44299	154.33406	123.66870	103.22513	A	1982.17569	991.59148	661.39675	496.29938	397.24096	331.20201	18
7	711.38718	356.18723	237.79391	178.59723	143.07928	119.40059	P	1911.13857	956.07292	637.71771	478.54010	383.03354	319.36249	17
8	782.40429	391.70575	261.47295	196.35653	157.28668	131.24011	A	1814.08581	907.54654	605.36675	454.27691	365.62298	303.18703	16
9	879.45708	440.23211	293.82381	220.81972	176.69723	147.41551	P	1743.04669	872.02798	581.68772	436.51763	349.41556	291.34751	15
10	1007.55202	504.27965	336.52219	252.84346	202.31623	168.78473	K	1645.99593	823.50160	549.33685	412.25444	330.02501	275.17205	14
11	1135.64698	568.32713	379.22051	284.66720	227.93522	190.11389	K	1517.90097	759.45412	506.63851	380.23070	304.38601	253.82289	13
12	1192.66845	596.83786	398.22767	298.92257	239.33951	199.61747	G	1389.80600	695.40664	463.94010	348.20696	278.76702	232.47373	12
13	1279.70048	640.35388	427.23834	320.88058	256.74592	214.12281	S	1332.78454	666.89591	444.93303	333.95159	267.36273	222.97015	11
14	1523.80640	762.40684	508.60698	381.70708	305.56710	254.80713	K-Malic acid	1245.75251	623.37989	415.92235	312.19359	249.95632	208.46482	10
15	1651.90136	826.45432	551.30533	413.73093	331.18039	276.15629	K	1001.84683	501.32893	334.55377	251.16711	201.13514	167.78030	9
16	1722.93847	861.97288	574.98434	431.49008	345.39352	287.99581	A	873.55163	437.27943	291.85539	219.14336	175.51615	146.43134	8
17	1822.00689	911.50708	608.00715	456.25718	365.20720	304.50721	V	802.51451	401.76090	268.17636	201.38409	161.30872	134.59182	7
18	1923.05457	962.03092	641.68971	481.51913	385.41673	321.34840	T	703.44610	352.22669	235.15350	176.61609	141.49504	118.08041	6
19	2051.14953	1026.07840	684.38803	513.54284	411.03573	342.69765	K	602.39842	301.70285	201.47099	151.35506	121.28551	101.23913	5
20	2122.18664	1061.59699	708.96707	531.30212	425.24318	354.53710	A	474.30340	237.65357	158.77267	119.33132	95.66851	79.88997	4
21	2259.24522	1129.62625	750.75329	563.31679	450.85487	375.88027	Q	403.26634	202.13681	135.09365	101.57204	81.45909	68.05040	3
22	2378.34018	1189.87373	793.45158	595.34050	478.47388	397.22943	K	275.20777	138.10752	92.40744	69.55740	55.84737	46.70736	2
23							K	147.11280	74.06004	49.70912	37.53366	30.22838	25.35820	1

HepG2, 5 mM Malic acid , H2BK37ma

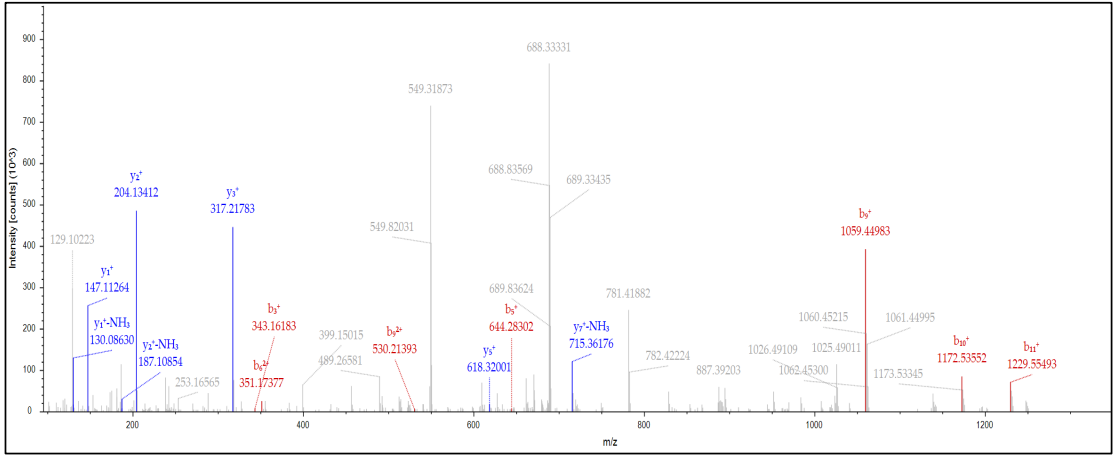
Sequence: KEGKKR, K1-Trimethyl (42.04695 Da), K4-Malic acid (116.01096 Da)
Charge: +3, Monoisotopic m/z: 301.84301 Da (-3.79 mmu/-12.55 ppm), MH+: 903.51447 Da, RT: 26.9917 min,
Identified with: Mascot (v1.36); Ions Score:12, Ions matched by search engine: 5/50
Fragment match tolerance used for search: 30 mmu
Fragments used for search: -H₂O; y; -NH₃; y; b; b; -H₂O; b; -NH₃; y



#1	b ⁺	b ²⁺	b ³⁺	Seq.	y ⁺	y ²⁺	y ³⁺	#2
1	171.14919	86.07823	57.72125	K-Trimethyl				6
2	300.19178	150.59953	100.73545	E	733.38389	367.19559	245.13282	5
3	357.21325	179.11026	119.74260	G	604.34130	302.67429	202.11862	4
4	601.31917	301.16322	201.11124	K-Malic acid	547.31984	274.16356	183.11146	3
5	729.41413	365.21070	243.80956	K	303.21392	152.11060	101.74282	2
6				R	175.11895	88.06311	59.04450	1

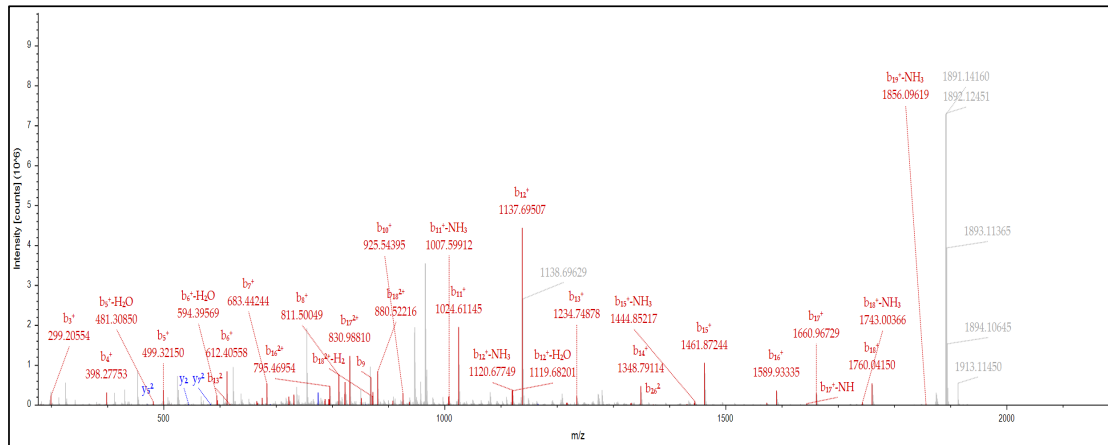
HepG2, 5 mM Malic acid , H4K5ma,K8ma

Sequence: SGRGKGGKGLGK, S1-Acetyl (42.01057 Da), K5- K4-Malic acid (116.01096 Da), K8- K4-Malic acid (116.01096 Da)
Charge: +2, Monoisotopic m/z: 688.33528 Da (-8.96 mmu/-13.02 ppm), MH+: 1375.66329 Da, RT: 33.5022 min,
Identified with: Mascot (v1.36); Ions Score:9, Ions matched by search engine: 3/106
Fragment match tolerance used for search: 30 mmu
Fragments used for search: -NH₃; y; b; b; -NH₃; y



#1	b+	b2+	Seq.	y+	y2+	#2
1	130.04987	65.52857	S-Acetyl			12
2	187.07133	94.03931	G	1246.63861	623.82294	11
3	343.17244	172.08986	R	1189.61714	595.31221	10
4	400.19391	200.60059	G	1033.51603	517.26165	9
5	644.29983	322.65355	K-Malic acid	976.49457	488.75092	8
6	701.32129	351.16429	G	732.38864	366.69796	7
7	758.34276	379.67502	G	675.36718	338.18723	6
8	1002.44868	501.72798	K-Malic acid	618.34572	309.67650	5
9	1059.47014	530.23871	G	374.23980	187.62354	4
10	1172.55421	586.78074	L	317.21833	159.11280	3
11	1229.57567	615.29147	G	204.13427	102.57077	2
12			K	147.11280	74.06004	1

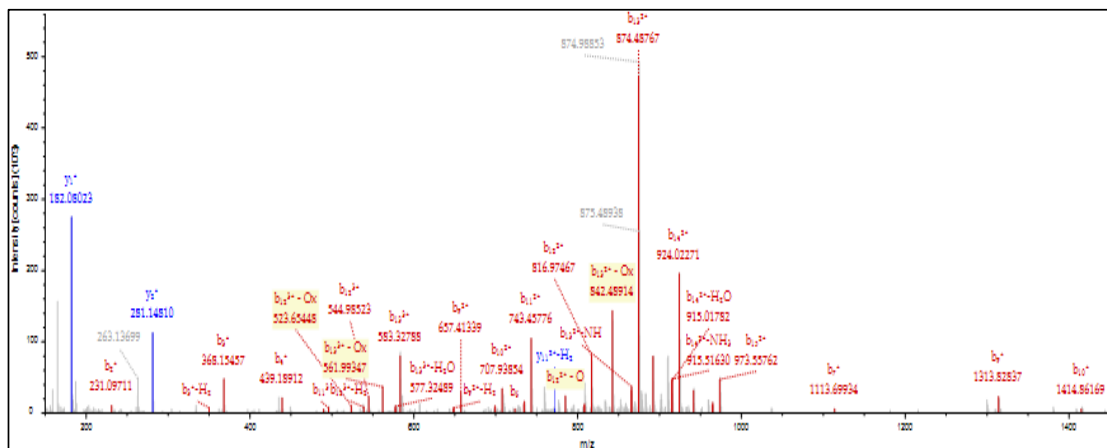
Sequence: LGKVITIAQGGLVLPNIQAVLLPKKTESHKAKSK, K22-Acetyl (42.01057 Da), K23-Acetyl (42.01057 Da), K28-Acetyl (42.01057 Da), K30-Dimethyl (28.03130 Da), K32-DHA (310.22967 Da)
Charge: +3, Monoisotopic m/z: 1273.42196 Da (-13.62 mmu/-10.7 ppm), MH+: 3818.25131 Da, RT: 11.7268 min, Identified with: Mascot (v1.36); Ions Score:50, Percolator q-Value:7.1e-4, Percolator PEP:2.8e-3, Ions matched by search engine: 14/358
Fragment match tolerance used for search: 30 mmu
Fragments used for search: -H₂O; y; -NH₃; y; b; b; -H₂O; b; -NH₃; y



#1	b	b ²	b ³	Seq.	v	v ²	v ³	#2
1	14 09134	57 54931	38 70198					32
2	171 11288	86 06004	57 70912	G	3705 20810	1853 10769	1235 74088	31
3	269 20777	150 10752	100 40744	K	3648 18654	1824 69696	1216 73373	30
4	398 27618	199 64173	133 43024	V	3520 99168	1760 54948	1174 03541	29
5	499 32398	250 16657	167 11280	T	3421 02326	1711 01527	1141 01260	28
6	612 40792	306 70702	204 80745	I	3319 97558	1660 49143	1107 33005	27
7	683 44504	342 22616	228 48653	A	3206 89152	1603 94940	1069 63636	26
8	811 50361	405 25543	271 17272	G	3135 85441	1568 43084	1045 95632	25
9	889 52918	433 12638	293 76583	G	3062 76883	1504 73153	1007 01302	24
10	925 54654	453 67891	309 10703	G	2980 77438	1475 89025	984 26297	23
11	1024 61498	152 81112	342 20584	V	2883 75290	1447 38079	965 25582	22
12	1137 69902	569 35315	379 90452	L	2794 68448	1387 84588	932 23301	21
13	1234 75178	617 87953	412 25545	P	2681 68042	1341 30395	894 53833	20
14	1348 79471	674 90089	450 26975	N	2584 54766	1292 77747	862 18749	19
15	1461 87877	731 44303	487 96444	I	2470 50473	1235 75600	824 17305	18
16	1589 93735	795 47231	530 65009	O	2357 42067	1179 21397	786 47841	17
17	1660 97444	830 98087	554 32369	A	2229 36208	1115 18468	743 19221	16
18	1750 04298	880 52508	587 35248	V	2158 32698	1079 66613	720 11318	15
19	1873 12618	943 12618	626 26566	L	2068 26566	1009 01362	679 01362	14
20	1986 21101	993 60914	662 74185	P	1946 17250	977 58899	649 35653	13
21	2083 26377	1042 13557	695 05277	P	1833 08943	913 04726	611 70710	12
22	2253 36930	1127 18829	751 79462	K-Aceyl	1736 03567	868 52 147	579 35007	11
23	2423 47483	1212 24103	808 49648	K-Aceyl	1665 93014	878 46871	522 64820	10
24	2524 52251	1262 76489	842 17902	T	1396 82461	698 41595	465 94639	9
25	2653 56510	1327 28619	885 19322	E	1294 77694	647 89211	432 26383	8
26	2740 59713	1370 80220	914 20389	S	1165 73434	583 30781	389 24963	7
27	2877 65004	1438 33166	959 80802	H	1078 70232	535 85480	360 23896	6
28	3047 76157	1524 38424	1016 95204	K-Aceyl	941 64340	471 49534	314 52565	5
29	3118 76688	1554 74088	1040 75788	K	771 63788	379 25808	234 11778	4
30	3274 92494	1637 98611	1092 31311	K-Dimethyl	700 50078	350 75402	214 55269	3
31	3361 95509	1681 48212	1121 32384	S	544 37452	272 89039	182 12968	2
32				K-DHA	447 34247	229 17497	153 11901	1

HeLa, 10 mM Linoleic acid, H4K80lino

Sequence: TEHAKRKTVTAMDVVY, M12-Oxidation (15.99492 Da), K7-linoleic acid (262.22967 Da)
Charge: +3, Monoisotopic m/z: 709.73341 Da (-0.85 mmu/-1.19 ppm), MH+: 2127.18568 Da, RT: 46.3679 min,
Identified with: Mascot (v1.36); Ions Score:13, q-Value:4.9e-4, PEP:6.9e-3, SVM Score:5.0e-1, Ions matched by search engine: 9/148
Fragment match tolerance used for search: 30 mmu
Fragments used for search: y-H₂O; y-NH₂; b; b-H₂O; b-NH₂; y

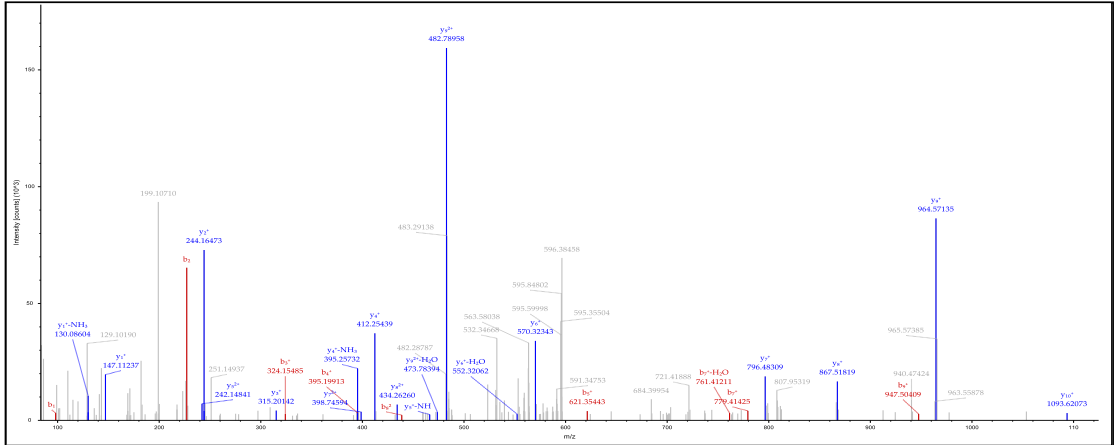


#1	b ⁺	b ²⁺	b ³⁺	Seq.	y ⁺	y ²⁺	y ³⁺	#2
1	102.05496	51.53112	34.68984	T				16
2	231.09755	116.05241	77.70403	E	2026.14055	1013.57391	676.05170	15
3	368.15646	184.58187	123.39034	H	1897.09795	949.05261	633.03750	14
4	439.19357	220.10043	147.06938	A	1760.03904	880.52316	587.35120	13
5	567.28854	284.14791	189.76770	K	1689.00193	845.00460	563.67216	12
6	723.38965	362.19846	241.80140	R	1560.90696	780.95712	520.97384	11
7	1113.71428	557.36078	371.90961	K-linoleic acid	1404.80585	702.90657	468.94014	10
8	1214.76195	607.88462	405.59217	T	1014.48122	507.74425	338.83193	9
9	1313.83037	657.41882	438.61497	V	913.43355	457.22041	305.14937	8
10	1414.87805	707.94266	472.29753	T	814.36513	407.68620	272.12656	7
11	1485.91516	743.46122	495.97657	A	713.31745	357.16237	238.44400	6
12	1632.95056	816.97892	544.98837	M-Oxidation	642.28034	321.64381	214.76496	5
13	1747.97750	874.49239	583.3069	D	495.24494	248.12611	165.75316	4
14	1847.04592	924.02660	616.35349	V	380.21800	190.61264	127.41085	3
15	1946.11433	973.56080	649.37629	V	281.14958	141.07843	94.38805	2
16				Y	182.08117	91.54422	61.36524	1

MS/MS spectra of each peptide from histones extracted from cultured cells treated with the indicated carboxyl group-containing food component compounds.

HepG2, d₄-sorbate, H2BK5sor

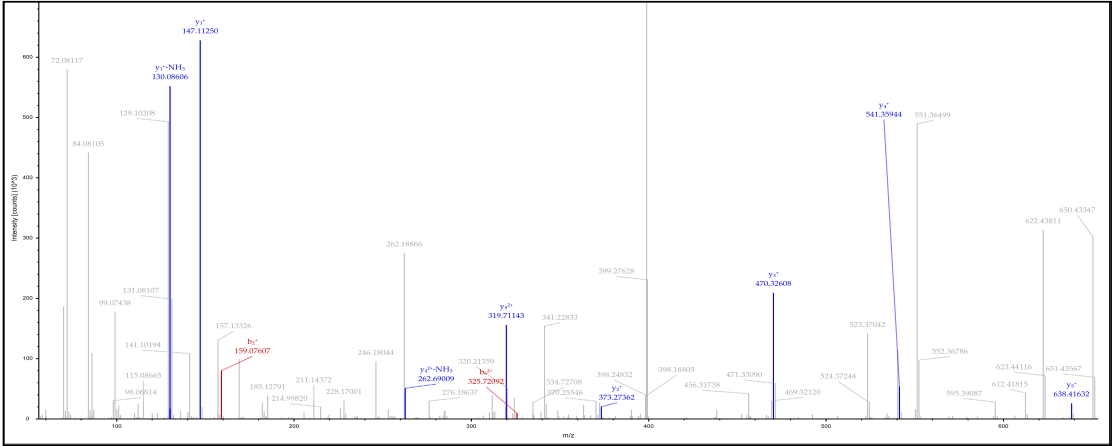
Sequence: PEPKSAAPAPK, K5- Sorbyl (²H₄) (98.06697 Da)
Charge: +2, Monoisotopic m/z: 595.83488 Da (-4.64 mmu/-7.78 ppm), MH⁺: 1190.66249 Da, RT: 60.1625 min,
Identified with: Mascot (v1.36); Ions Score:54, Percolator q-Value:2.7e-4, Percolator PEP:4.0e-3, Ions matched by search engine: 9/100
Fragment match tolerance used for search: 30 mmu
Fragments used for search: y-H₂O; y-NH₃; b; b-H₂O; y



#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	98.06004	49.53366	P			11
2	227.10263	114.05496	E	1093.61899	547.31313	10
3	324.15540	162.58134	P	964.57640	482.79184	9
4	395.19251	198.09989	A	867.52364	434.26546	8
5	621.35445	311.18086	K-Sorbyl (² H ₄)	796.48652	398.74690	7
6	708.38647	354.69688	S	570.32459	285.66593	6
7	779.42359	390.21543	A	483.29256	242.14992	5
8	876.47635	438.74181	P	412.25545	206.63136	4
9	947.51347	474.26037	A	315.20268	158.10498	3
10	1044.56623	522.78675	P	244.16557	122.58642	2
11			K	147.11280	74.06004	1

HepG2, d₄-sorbate, H2BK11sor

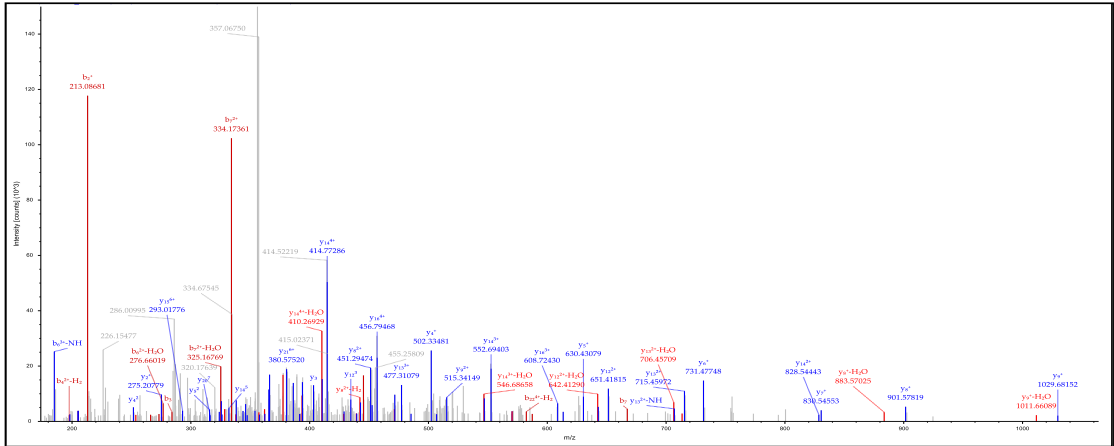
Sequence: SAPAPKK, K6- Sorbyl (²H₄) (98.06697 Da)
Charge: +2, Monoisotopic m/z: 398.74560 Da (-1.3 mmu/-3.26 ppm), MH+: 796.48393 Da, RT: 50.6111 min,
Identified with: Mascot (v1.36); Ions Score:13, Percolator q-Value:1.1e-2, Percolator PEP:1.7e-1, Ions matched by search engine: 6/50
Fragment match tolerance used for search: 30 mmu
Fragments used for search: y-NH₃⁺; b; b-H₂O; y



#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	88.03930	44.52329	S			7
2	159.07642	80.04185	A	709.45449	355.23089	6
3	256.12918	128.56823	P	638.41738	319.71233	5
4	327.16630	164.08679	A	541.36462	271.18595	4
5	424.21906	212.61317	P	470.32750	235.66739	3
6	650.38100	325.69414	K-Sorbyl (² H ₄)	373.27474	187.14101	2
7			K	147.11280	74.06004	1

HepG2, d₄-sorbate, H2BK11 sor

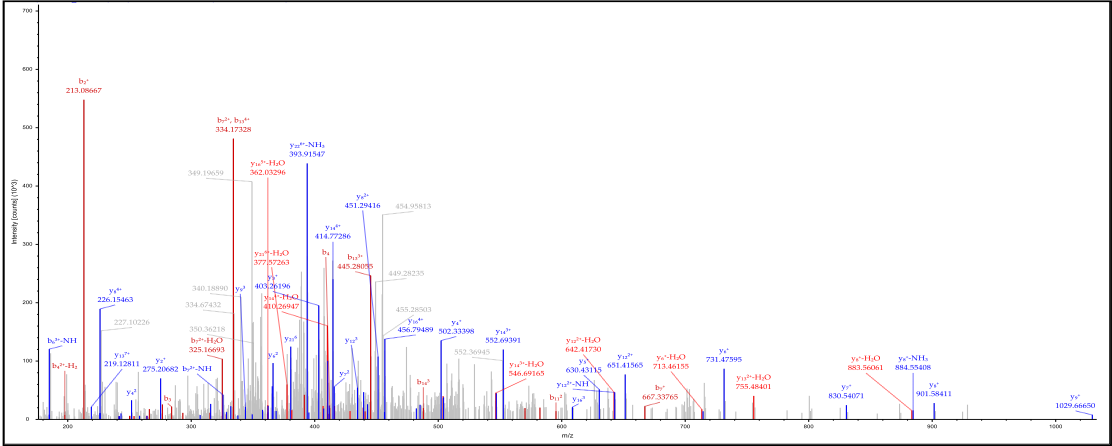
Sequence: DPAKSAPAPKKGSKKAVTKVQKK, K10-Sorbyl (2H₂) (98.06697 Da)
Charge: +7, Monoisotopic m/z: 356.64715 Da (-2.92 mmu/-8.19 ppm), MH+: 2490.48640 Da, RT: 16.6040 min,
Identified with: Mascot (v1.36); Ions Score:17, Percolator q-Value:1.2e-3, Percolator PEP:8.5e-3, Ions matched by search engine: 5/248
Fragment match tolerance used for search: 30 mmu
Fragments used for search: y-H₂O; y-NH₃; b; b-H₂O; b-NH₃; y



#1	b ⁺	b ²⁺	b ³⁺	b ⁴⁺	b ⁵⁺	b ⁶⁺	b ⁷⁺	Seq.	y ⁺	y ²⁺	y ³⁺	y ⁴⁺	y ⁵⁺	y ⁶⁺	y ⁷⁺	#2
1	116.03422	58.52075	39.34959	29.76401	24.01267	20.17843	17.43970	D								23
2	213.08698	107.04713	71.70051	54.02720	43.42322	36.35389	31.30438	P	2375.47987	1188.24357	792.49814	594.62542	475.90179	396.75271	340.21765	22
3	284.12410	142.56589	95.37955	71.78648	57.63064	48.19341	41.45254	A	2278.42710	1139.71719	760.14722	570.36225	456.49124	380.57725	326.35297	21
4	412.21906	206.61317	138.07797	103.81022	83.24963	69.54257	59.75182	K	2207.38999	1104.19983	730.46816	552.60225	442.28382	368.73773	318.25489	20
5	489.25105	250.12918	167.08653	125.58522	100.63600	84.04791	72.18498	S	2078.23953	1040.15113	693.75988	520.57921	416.88483	347.38857	297.90553	19
6	570.28820	285.64774	190.76752	143.32751	114.88346	95.88743	82.33312	A	1992.26300	996.63514	654.75910	498.82121	399.25842	332.88322	285.47292	18
7	657.34007	334.17412	223.11851	167.59070	134.27401	112.06289	96.10780	P	1921.22588	961.11658	641.08015	481.06193	385.05100	321.04371	275.32422	17
8	738.37808	369.89288	246.79754	185.34939	148.48144	123.90241	106.34588	A	1824.17312	912.59020	608.72322	458.73874	365.54043	304.88825	251.45954	16
9	835.43084	418.21905	279.14847	209.61317	167.89199	140.07787	120.21064	P	1753.13601	877.07164	585.05019	439.03948	351.43302	293.02872	251.31138	15
10	1061.59278	531.30003	354.53678	266.15365	213.12438	177.77153	152.51949	K-Sorbyl (2H ₂)	1656.08324	828.54526	552.69927	414.77827	332.02247	276.85327	237.44670	14
11	1189.68774	595.34751	397.23410	298.17739	238.74337	199.12069	170.81877	K	1429.92131	715.46429	477.31195	358.23578	286.79008	239.15962	205.13785	13
12	1246.70921	623.85824	416.24125	312.43276	250.14766	208.62426	178.96469	G	1301.82635	651.41681	434.61362	326.21204	261.17109	217.81045	186.63857	12
13	1333.74123	667.37426	445.25193	334.19077	267.55407	223.12960	191.39784	S	1244.80488	622.90608	415.60648	311.95668	249.76680	208.30688	178.69285	11
14	1461.83620	731.42174	487.95025	366.21451	293.17306	244.47876	209.69712	K	1157.77285	579.39007	386.59580	290.19867	232.36039	193.80154	166.25950	10
15	1589.93116	795.46922	530.64857	398.23825	318.79205	265.82792	227.99640	K	1029.67788	515.34258	343.89748	258.17493	206.74140	172.45238	147.96022	9
16	1660.96827	830.98777	554.32761	415.99753	332.99948	277.66744	238.14456	A	901.58293	451.29510	301.19916	226.15119	181.12241	151.10322	129.66094	8
17	1760.03669	880.52198	587.35041	440.76463	352.81316	294.17885	252.29719	V	830.54581	415.77655	277.52012	208.39191	166.91498	139.26370	119.51278	7
18	1861.08437	931.04582	621.03297	466.02655	373.02269	311.02012	266.73258	T	731.47746	366.24234	244.48732	183.62481	147.10130	122.75230	105.36013	6
19	1989.17933	995.09330	663.73125	498.05029	398.64166	332.36929	285.03186	K	630.42972	315.71853	210.81476	158.36289	126.89177	105.91102	90.92477	5
20	2088.34777	1044.02751	699.73410	522.81735	418.43537	348.86069	299.18440	V	592.33478	291.67102	198.11644	128.33915	101.27277	84.56188	72.65540	4
21	2216.93632	1108.65880	739.44025	554.83204	444.08709	370.22378	317.47857	O	493.28653	202.13681	136.09363	101.57204	81.45809	68.05043	58.47289	3
22	2344.40128	1172.70428	782.13861	586.85578	469.68606	391.57294	335.77785	K	275.50777	138.10752	92.40744	69.55740	55.84737	48.70739	40.17870	2
23								K	147.11280	74.06004	49.70912	37.53369	30.22638	25.35820	21.87940	1

HepG2, d₄-sorbate, H2BK12sor

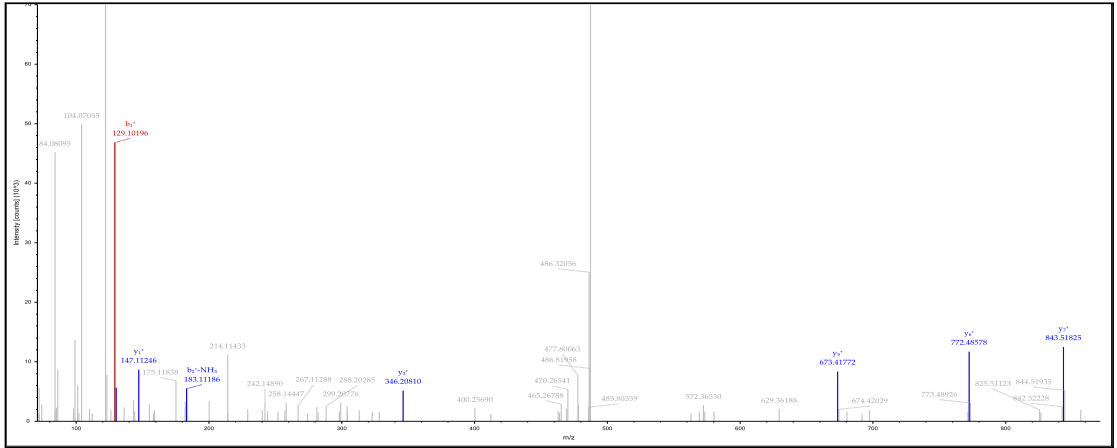
Sequence: DPAKSAPAPKKGSKKAVTKVQKK, K11-Sorbyl (2H₄) (98.06697 Da)
Charge: +7, Monoisotopic m/z: 356.64758 Da (-2.49 mmu/-6.99 ppm), MH+: 2490.48939 Da, RT: 15.1117 min,
Identified with: Mascot (v1.36); Ions Score:15, Percolator q-Value:1.2e-3, Percolator PEP:9.6e-4, Ions matched by search engine: 4/248
Fragment match tolerance used for search: 30 mmu
Fragments used for search: y-H₂O; y-NH₃; b; b-H₂O; b-NH₃; y



#1	b ¹⁺	b ²⁺	b ³⁺	b ⁴⁺	b ⁵⁺	b ⁶⁺	b ⁷⁺	Seq.	y ¹⁺	y ²⁺	y ³⁺	y ⁴⁺	y ⁵⁺	y ⁶⁺	y ⁷⁺	#2
1	116.03422	58.52075	39.34955	29.76401	24.01267	20.17843	17.43970	D								23
2	213.06697	107.04715	71.70051	54.02726	43.42322	36.35399	31.30438	P	2075.47987	1188.24357	792.49814	594.62542	475.90170	396.75271	340.21765	22
3	284.12415	142.56559	95.37955	71.78548	57.63064	48.19341	41.45254	A	2278.42710	1139.71712	760.14722	570.36222	458.49121	380.57725	326.35291	21
4	412.21905	206.61317	138.07787	103.81022	83.24963	69.54257	59.75182	K	2207.38995	1104.19663	736.46818	552.60292	442.28382	368.73773	316.20481	20
5	489.25103	250.12918	167.08853	125.58823	100.65604	84.04791	72.18498	S	2079.29503	1040.15115	693.76985	520.57921	416.66483	347.38857	297.90553	19
6	570.28823	285.64774	190.76759	143.32751	114.86348	95.88743	82.33312	A	1992.26300	996.63514	664.75918	498.82121	399.25842	332.88328	285.47298	18
7	667.34097	334.17412	223.11851	167.59070	134.27401	112.06289	96.19780	P	1921.22588	961.11658	641.08015	481.06193	385.05100	321.04371	275.32422	17
8	738.37808	369.69268	246.79754	185.34998	148.48144	123.90241	106.34598	A	1824.17312	912.59020	608.72922	458.79874	365.64043	304.86825	261.45954	16
9	835.43084	418.21905	279.14847	209.81317	167.89199	140.07787	120.21064	P	1753.13601	877.07164	585.05019	439.03945	351.43302	293.02873	251.31138	15
10	963.52581	482.26654	321.84678	241.63691	193.51098	161.42703	138.50992	K	1656.08324	828.54526	552.69927	414.77627	332.02247	276.85327	237.44670	14
11	1189.68774	595.34751	397.23410	298.17738	238.74337	199.12069	170.81877	K-Sorbyl (H)	1527.98828	764.49778	510.00094	382.75253	306.40348	255.50411	219.14742	13
12	1246.70921	623.85824	416.24125	312.43278	250.14768	208.62428	178.96488	Q	1301.82832	651.41681	434.61362	326.21204	261.17109	217.81043	186.83851	12
13	1333.74123	667.37426	445.25193	334.19077	267.55407	223.12560	191.30784	S	1244.80488	622.90609	415.60640	311.85669	249.76680	208.30689	178.89253	11
14	1481.83820	731.42174	487.35023	366.21451	293.17308	244.47876	209.69712	K	1157.77285	579.38007	386.52680	290.19897	232.36039	193.80154	166.25950	10
15	1589.93118	795.46922	530.64857	398.23825	318.79205	265.82792	227.99640	K	1029.67789	515.34258	343.89748	258.17493	206.74140	172.45238	147.96022	9
16	1660.96827	830.98777	554.32761	415.99763	332.99948	277.66744	238.14458	A	901.58293	451.29510	301.19916	226.15119	181.12241	151.10322	129.66094	8
17	1760.03669	880.52198	587.35041	440.76463	352.81316	294.17885	252.29719	V	830.54581	415.77655	277.52012	208.39191	166.91498	139.26370	119.51278	7
18	1861.08437	931.04582	621.03297	466.02655	373.02269	311.02012	266.73258	T	731.47740	366.24234	244.49732	183.62481	147.10130	122.75230	105.36015	6
19	1989.17933	995.09330	663.73129	498.05029	398.64169	332.36929	285.03186	K	630.42972	315.71850	210.81476	158.36289	126.89177	105.91102	90.92477	5
20	2088.24774	1044.62751	696.75410	522.81739	418.45537	348.88069	299.18449	V	502.33478	251.67102	168.11644	126.33915	101.27277	84.56186	72.62540	4
21	2216.30632	1108.65680	739.44029	554.83204	444.06709	370.22376	317.47857	Q	403.26634	202.13681	135.09363	101.57204	81.45909	68.05045	58.47286	3
22	2344.40128	1172.70428	782.13861	586.85578	469.68608	391.57294	335.77785	K	275.20777	138.10752	92.40744	69.55740	55.84737	46.70736	40.17878	2
23								K	147.11285	74.06004	49.70912	37.53366	30.22638	25.35820	21.87948	1

HepG2, d₄-sorbate, H2BK20sor

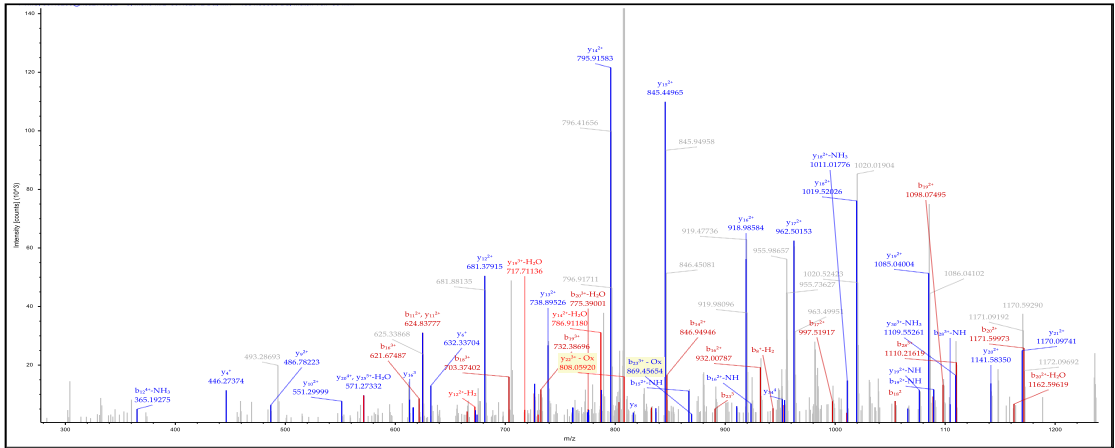
Sequence: KAVTKAQK, K5-Sorbyl (²H₄) (98.06697 Da)
Charge: +2, Monoisotopic m/z: 486.31267 Da (-0.27 mmu/-0.55 ppm), MH⁺: 971.61806 Da, RT: 40.8390 min,
Identified with: Mascot (v1.36); Ions Score:20, Percolator q-Value:9.9e-3, Percolator PEP:2.0e-1, Ions matched by search engine: 9/70
Fragment match tolerance used for search: 30 mmu
Fragments used for search: y-H₂O; y-NH₃; b; b-H₂O; b-NH₃; y



#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	129.10224	65.05476	K			8
2	200.13935	100.57331	A	843.52364	422.26546	7
3	299.20777	150.10752	V	772.48652	386.74690	6
4	400.25545	200.63136	T	673.41811	337.21269	5
5	626.41738	313.71233	K-Sorbyl (² H ₄)	572.37043	286.68885	4
6	697.45449	349.23089	A	346.20850	173.60789	3
7	825.51307	413.26017	Q	275.17138	138.08933	2
8			K	147.11280	74.06004	1

HepG2, d₄-sorbate, H2BK46sor/K57sor

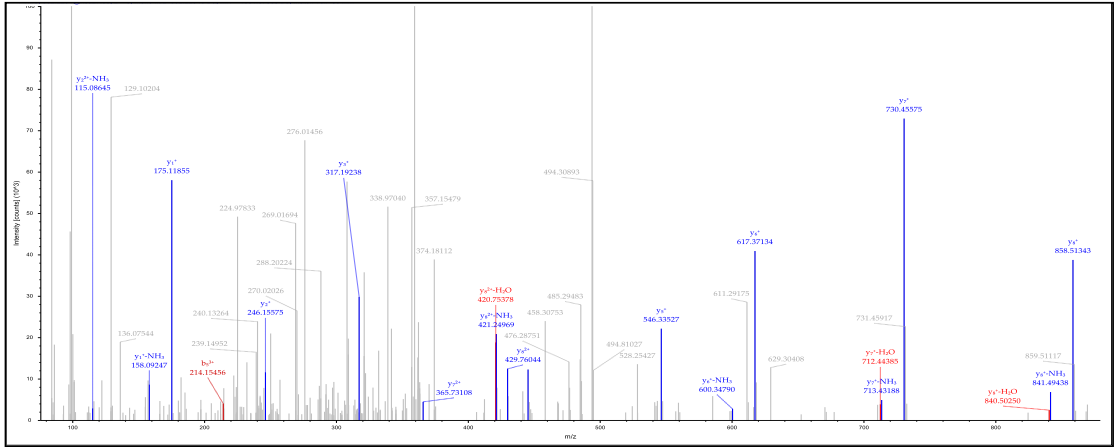
Sequence: KQVHPDTGISSKAMGIMNSFVNDIFERIAGEASRL,
M14-Oxidation (15.99492 Da), K1-Sorbyl (²H₄) (98.06697 Da), K12-Sorbyl (²H₄) (98.06697 Da)
Charge: +5, Monoisotopic m/z: 807.02312 Da (+5.21 mmu/+6.45 ppm), MH+: 4031.08650 Da, RT: 81.1515 min,
Identified with: Mascot (v1.36); Ions Score:25, Percolator q-Value:7.9e-4, Percolator PEP:2.1e-2, Ions matched by search engine: 9/392
Fragment match tolerance used for search: 30 mmu
Fragments used for search: y-H₂O; y-NH₃; b; b-H₂O; b-NH₃; y



#1	b ⁺	b ⁺	b ⁺	b ⁺	b ⁺	Seq	y ⁺	y ⁺	y ⁺	y ⁺	y ⁺	#2
1	227.1882	114.0852	76.3642	57.5476	46.2309	K-Sorbyl (16)	984.8889	1907.9599	1386.9704	961.8890	761.7855	34
2	265.2679	176.1716	119.1879	89.2692	71.8976	G	967.6399	1836.2636	1326.2636	919.2636	736.7756	35
3	454.2925	227.6674	152.1039	114.0267	87.6624	V	927.7775	1769.3624	1135.3624	855.3624	715.3624	36
4	591.3511	295.1812	197.7659	148.1392	110.1392	D	944.7126	1729.8597	1147.3764	860.9386	686.9386	37
5	686.4076	344.7076	236.1408	172.8742	136.4874	D	944.6999	1672.3359	1115.2369	836.6704	666.5376	38
6	883.4345	402.2912	268.4874	207.6147	167.4876	V	933.6324	1614.6211	1035.6211	807.6104	636.5237	39
7	904.4825	436.7455	302.1525	226.6762	181.7026	G	917.5882	1556.2587	1046.1994	785.6576	616.3268	40
8	961.5039	481.2552	321.1726	241.1312	191.1026	G	907.5929	1504.1927	1004.1927	746.5924	574.9756	41
9	1074.5885	537.7976	358.4074	268.4074	216.7254	I	897.5929	1452.1824	952.1824	692.1824	524.9756	42
10	1151.6202	581.8126	381.8126	291.1526	241.1526	S	887.5929	1400.1724	900.1724	642.1724	474.9756	43
11	1248.6520	624.8326	416.8888	312.9126	255.5264	S	877.5929	1348.1624	848.1624	592.1624	424.9756	44
12	1474.8142	757.9126	492.9126	389.4926	295.7868	K-Sorbyl (16)	867.5929	1296.1524	796.1524	542.1524	374.9756	45
13	1456.8116	742.8126	477.8126	374.8126	280.7868	H Oxidation	857.5929	1244.1424	744.1424	492.1424	324.9756	46
14	1622.8885	846.8488	584.9676	424.9776	339.3876	G	847.5929	1192.1324	692.1324	442.1324	274.9756	47
15	1749.9090	975.4674	684.9746	498.2324	360.7874	G	837.5929	1140.1224	642.1224	392.1224	224.9756	48
16	1862.9204	1047.8126	746.8126	536.8126	391.8126	M	827.5929	1088.1124	592.1124	342.1124	174.9756	49
17	1994.1025	1097.5188	806.5488	589.2626	422.4266	N	817.5929	1036.1024	542.1024	292.1024	124.9756	50
18	2108.0947	1164.5412	868.5612	627.7742	453.4266	S	807.5929	984.0924	492.0924	242.0924	74.9756	51
19	2116.1076	1166.5412	870.5612	629.7742	455.4266	F	797.5929	932.0824	442.0824	192.0824	24.9756	52
20	2242.7159	1271.5816	981.5916	736.2916	560.2916	V	787.5929	880.0724	392.0724	142.0724	19.9756	53
21	2441.3443	1321.1556	1041.1556	786.1556	615.1556	D	777.5929	828.0624	342.0624	92.0624	14.9756	54
22	2522.3776	1396.1476	1116.1476	861.1476	695.1476	I	767.5929	776.0524	292.0524	82.0524	9.9756	55
23	2670.8748	1436.6674	1156.6674	901.6674	735.6674	A	757.5929	724.0424	242.0424	32.0424	4.9756	56
24	2763.3963	1502.3277	1222.3277	967.3277	801.3277	A	747.5929	672.0324	192.0324	22.0324	3.9756	57
25	2907.6999	1552.1659	1272.1659	1017.1659	851.1659	A	737.5929	620.0224	142.0224	12.0224	2.9756	58
26	3039.1029	1602.5079	1322.5079	1067.5079	901.5079	A	727.5929	568.0124	92.0124	2.0124	1.9756	59
27	3215.6103	1668.3088	1388.3088	1133.3088	967.3088	A	717.5929	516.0024	42.0024	1.0024	0.9756	60
28	3338.8244	1744.8094	1464.8094	1209.8094	1043.8094	A	707.5929	464.0024	32.0024	0.9756	0.9756	61
29	3399.7319	1760.3694	1480.3694	1224.3694	1058.3694	A	697.5929	412.0024	22.0024	0.9756	0.9756	62
30	3456.7933	1782.8876	1502.8876	1246.8876	1080.8876	A	687.5929	360.0024	12.0024	0.9756	0.9756	63
31	3566.7561	1832.4112	1552.4112	1296.4112	1130.4112	A	677.5929	308.0024	2.0024	0.9756	0.9756	64
32	3696.8377	1882.9348	1602.9348	1346.9348	1180.9348	A	667.5929	256.0024	1.0024	0.9756	0.9756	65
33	3743.8676	1912.4584	1632.4584	1376.4584	1210.4584	A	657.5929	204.0024	0.9756	0.9756	0.9756	66
34	3929.8557	1992.4820	1712.4820	1456.4820	1290.4820	A	647.5929	152.0024	0.9756	0.9756	0.9756	67
35							637.5929	100.0024	0.9756	0.9756	0.9756	68

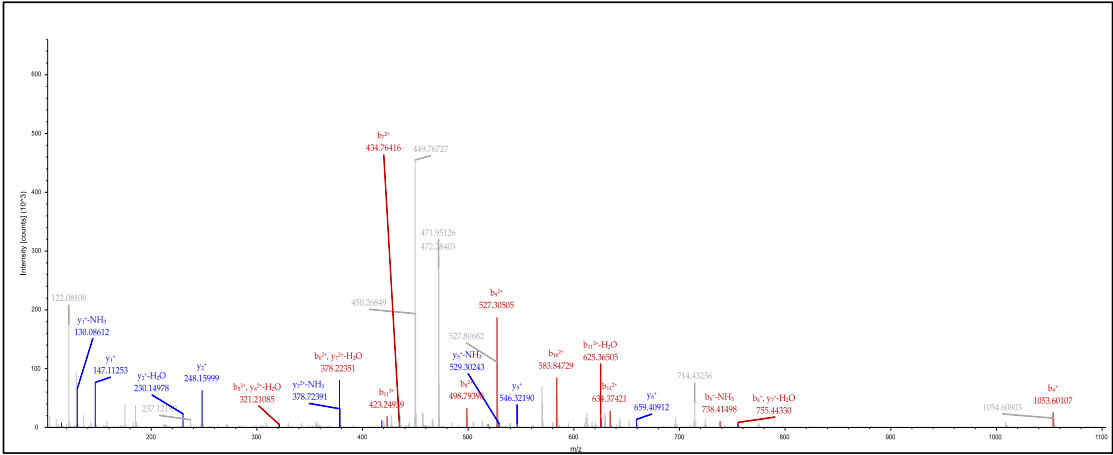
HepG2, d₄-sorbate, H3K18sor

Sequence: KQLATKAAR, K1-Sorbyl (²H₄) (98.06697 Da)
Charge: +3, Monoisotopic m/z: 362.22940 Da (-1.29 mmu/-3.56 ppm), MH+: 1084.67365 Da, RT: 53.0412 min,
Identified with: Mascot (v1.36); Ions Score:23, Percolator q-Value:1.1e-3, Percolator PEP:4.3e-2, Ions matched by search engine: 8/80
Fragment match tolerance used for search: 30 mmu
Fragments used for search: y-H₂O; y-NH₃; b; b-H₂O; b-NH₃; y



HepG2, d4-sorbate, H4K20sor

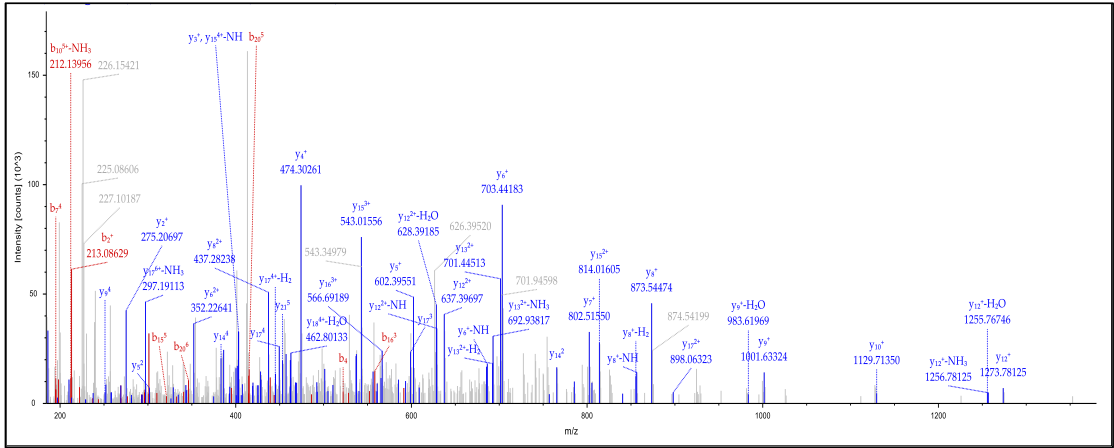
Sequence: KVLSDNIQGITK, K1-Sorbic acid label(2H4) (98.06697 Da)
Charge: +3, Monoisotopic m/z: 471.95196 Da (+5.46 mmu/+11.57 ppm), MH+: 1413.84132 Da, RT: 55.0976 min,
Identified with: Mascot (v1.36); Ions Score:16, Percolator q-Value:2.5e-1, Percolator PEP:1.0e0, Ions matched by search engine: 5/124
Fragment match tolerance used for search: 30 mmu
Fragments used for search: -H₂O; y; -NH₃; y; b; b; -H₂O; b; -NH₃; y



#1	b ⁺	b ²⁺	b ³⁺	Seq.	y ⁺	y ²⁺	y ³⁺	#2
1	227.16921	114.08824	76.39459	K-Sorbyl (² H4)				12
2	326.23763	163.62245	109.41739	V	1187.66303	594.33515	396.55919	11
3	439.32169	220.16448	147.11208	L	1088.59461	544.80095	363.53639	10
4	526.35372	263.68050	176.12276	S	975.51055	488.25891	325.84170	9
5	641.38066	321.19397	214.46507	D	888.47852	444.74290	296.83103	8
6	755.42359	378.21543	252.47938	N	773.45158	387.22943	258.48871	7
7	868.50765	434.75746	290.17407	I	659.40865	330.20796	220.47440	6
8	996.56623	498.78675	332.86026	Q	546.32459	273.66593	182.77971	5
9	1053.58769	527.29748	351.86742	G	418.26601	209.63664	140.09352	4
10	1166.67176	583.83952	389.56210	I	361.24455	181.12591	121.08637	3
11	1267.71944	634.36336	423.24466	T	248.16048	124.58388	83.39168	2
12				K	147.11280	74.06004	49.70912	1

HepG2, sorbic acid, H2BK5sor

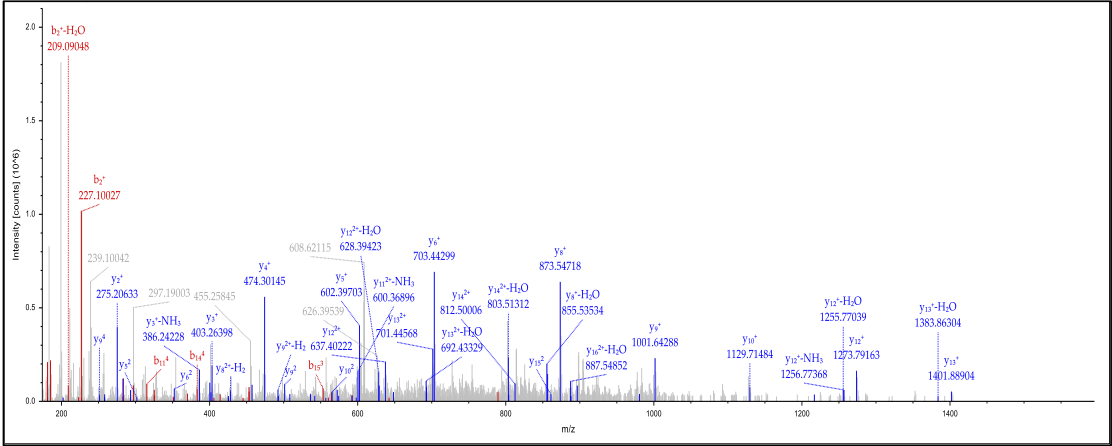
Sequence: DPSKSAPAPKKGSKKAVTKAQKK, K4-Sorbyl (94.04187 Da)
Charge: +6, Monoisotopic m/z: 413.24930 Da (+2.35 mmu/+5.7 ppm), MH+: 2474.45942 Da, RT: 20.9084 min,
Identified with: Mascot (v1.36); Ions Score:37, Percolator q-Value:4.5e-4, Percolator PEP:5.7e-6, Ions matched by search engine: 8/248
Fragment match tolerance used for search: 30 mmu
Fragments used for search: -H₂O; y; -NH₃; y; b; b; -H₂O; b; -NH₃; y



#1	b ¹	b ²	b ³	b ⁴	b ⁵	b ⁶	Seq.	y ¹	y ²	y ³	y ⁴	y ⁵	y ⁶	#2
1	116.03422	58.52075	39.34959	29.76401	24.01267	20.17843	D							23
2	213.08698	107.04713	71.70051	54.02720	43.42322	36.35389	P	2359.41837	1180.21283	787.14431	590.61005	472.68950	394.07579	22
3	300.11901	150.56314	100.71119	75.78521	60.82962	50.85920	S	2262.36561	1131.68644	754.79339	566.34686	453.27894	377.90033	21
4	522.25584	261.63156	174.75680	131.31942	105.25699	87.88204	K-Sorbyl	2175.33358	1088.17043	725.78271	544.58895	435.87254	363.39498	20
5	609.26787	305.14757	203.76747	153.07742	122.66339	102.38738	S	1953.19675	977.10202	651.73710	489.05495	391.44517	326.37219	19
6	680.32498	340.66613	227.44651	170.83670	136.87082	114.22899	A	1856.16473	933.58600	622.72643	467.29694	374.03877	311.86685	18
7	777.37775	389.19251	259.79743	195.09889	156.28137	130.40236	P	1795.12761	898.06744	599.04739	449.53736	359.83134	300.02733	17
8	848.41486	424.71107	283.47647	212.85917	170.48879	142.24187	A	1698.07485	849.54106	566.59647	425.27417	340.42079	283.85187	16
9	945.46762	473.23745	315.82739	237.12236	189.89935	158.41733	P	1627.03774	814.02251	543.01743	407.51489	326.21337	272.01235	15
10	1073.56259	537.28493	358.52571	269.14610	215.51834	179.76640	K	1529.28497	765.49612	510.56951	383.25170	306.80282	255.83686	14
11	1201.65755	601.33241	401.22403	301.16984	241.13733	201.11596	K	1401.89001	701.44864	467.56819	351.22796	281.18382	234.48773	13
12	1256.67901	629.84314	420.23119	315.42521	252.54162	210.61923	G	1273.79505	637.40116	425.26987	319.20422	255.56483	213.13857	12
13	1345.71104	673.35916	449.24186	337.18322	269.94803	225.12457	S	1216.77358	608.89043	406.26271	304.94885	244.16054	203.63496	11
14	1473.80600	737.40664	491.94019	369.20596	295.56702	246.47373	K	1129.74155	565.37441	377.25204	283.19085	226.75413	189.12956	10
15	1601.90007	801.45412	534.63851	401.23070	321.18901	267.82289	K	1001.64658	501.32693	334.55371	251.16711	201.13514	167.78050	9
16	1672.93806	836.97268	558.31754	418.98996	335.39344	279.66241	A	873.55163	437.27945	291.85539	219.14336	175.51615	146.43134	8
17	1772.00649	886.50689	591.34035	443.75709	355.20712	296.17381	V	802.51451	401.76090	268.17636	201.38409	161.30872	134.59182	7
18	1873.05417	937.03072	625.02291	469.01900	375.41666	313.01500	T	703.44810	352.22669	235.15355	176.61698	141.49504	118.08041	6
19	2001.14914	1001.07821	667.72123	501.04274	401.03565	334.36426	K	602.39843	301.70289	201.47099	151.35506	121.66551	101.23913	5
20	2072.18625	1036.59676	691.40027	518.80202	415.24307	346.20377	A	474.30348	237.65537	158.77267	119.33132	95.66551	79.88997	4
21	2200.34483	1100.62605	734.08646	550.81666	440.85479	367.54687	Q	403.29634	202.13681	135.09363	101.57204	81.45909	66.05045	3
22	2326.33979	1164.67353	776.78478	582.84041	466.47378	388.89603	K	275.20777	138.10752	92.40744	69.55740	55.84737	46.70736	2
23							K	147.11280	74.06004	49.70912	37.53366	30.22838	25.35820	1

HepG2, sorbic acid, H2BK11sor

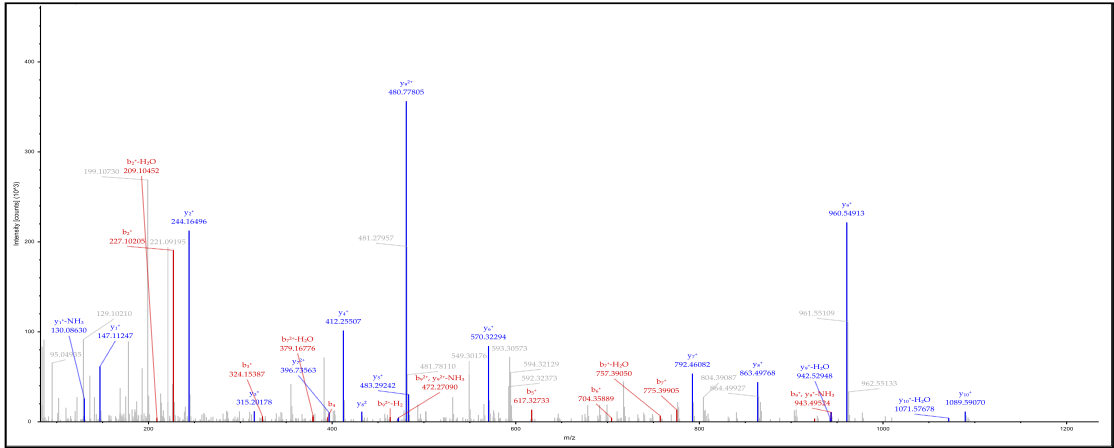
Sequence: EPSKSAPAPKKGSKKAVTKAQKK, K4-Acetyl (42.01057 Da), K10-Sorbyl (94.04187 Da)
Charge: +4, Monoisotopic m/z: 633.36759 Da (-5.76 mmu/-9.09 ppm), MH+: 2530.44852 Da, RT: 23.0393 min,
Identified with: Mascot (v1.36); Ions Score:37, Percolator q-Value:6.5e-4, Percolator PEP:1.2e-2, Ions matched by search engine: 11/248
Fragment match tolerance used for search: 30 mmu
Fragments used for search: -H₂O; y; -NH₃; y; b; b; -H₂O; b; -NH₃; y



#1	b ⁻	b ²⁻	b ³⁻	b ⁴⁻	Seq.	y ⁻	y ²⁻	y ³⁻	y ⁴⁻	#2
1	130.04987	65.52857	44.02147	33.26792	E					23
2	227.10293	114.05496	76.37240	57.53112	P	2401.42894	1201.21811	801.14783	601.11269	22
3	314.13466	157.57097	105.36307	79.28912	S	2304.37618	1152.69173	768.79691	576.84950	21
4	484.24019	242.62373	162.08491	121.81550	K-Acetyl	2217.34415	1109.17571	739.78623	555.09149	20
5	571.27222	286.13975	191.09559	143.57351	S	2047.23862	1024.12295	683.08439	512.56511	19
6	642.30533	321.65830	214.77463	161.33279	A	1960.20659	980.60693	654.07371	490.80711	18
7	739.36210	370.18469	247.12555	185.59598	P	1889.16946	945.08838	630.39468	473.04783	17
8	810.39921	405.70324	270.80459	203.35526	A	1792.11671	896.58200	598.04372	448.78464	16
9	907.45197	454.22962	303.15551	227.61845	P	1721.07960	861.04344	574.38472	431.02536	15
10	1129.58880	565.29804	377.20112	283.15298	K-Sorbyl	1624.02894	812.51709	542.01380	406.76217	14
11	1257.68376	629.34552	419.89944	315.17540	K	1401.89001	701.44864	467.96819	351.22796	13
12	1314.70523	657.85625	438.90659	329.43176	G	1273.79505	637.40118	425.26987	319.20422	12
13	1401.73726	701.37227	467.91727	351.18977	S	1216.77358	608.89043	406.26271	304.94885	11
14	1529.83222	765.41975	510.81559	383.21351	K	1129.74155	565.37441	377.25204	283.19085	10
15	1657.92718	829.46723	553.31391	415.23725	K	1001.84659	501.32693	334.55371	251.16711	9
16	1728.96430	864.98570	576.99295	432.99653	A	873.55163	437.27945	291.85530	219.14336	8
17	1828.03271	914.51999	610.01575	457.76393	V	802.51451	401.76090	265.17636	201.38409	7
18	1929.08039	965.04383	643.89831	483.02555	T	703.44610	352.22699	235.15355	176.81699	6
19	2057.17335	1029.09131	686.39963	515.04930	K	602.39842	301.70299	201.47099	151.35506	5
20	2128.21346	1064.60987	710.07567	532.80857	A	474.30346	237.65537	158.77267	119.31352	4
21	2256.27104	1128.63916	752.76187	564.82322	Q	403.29634	202.13691	135.09363	101.87204	3
22	2384.36601	1192.68664	795.46019	596.84696	K	275.20777	138.10752	92.40744	69.55740	2
23					K	147.11280	74.06004	49.70912	37.53366	1

HeLa, sorbic acid, H2BK5sor

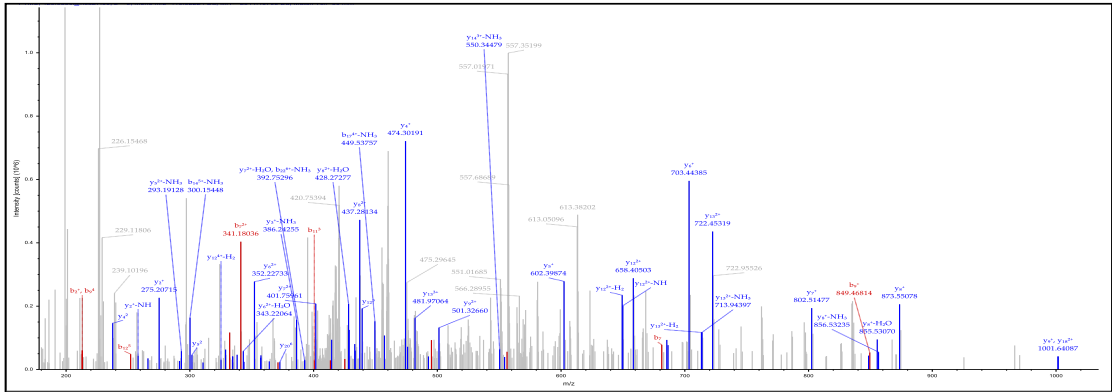
Sequence: PEPKSAAPAPK, K5-Sorbyl (94.04187 Da)
Charge: +2, Monoisotopic m/z: 593.82712 Da (+0.15 mmu/+0.26 ppm), MH+: 1186.64696 Da, RT: 28.4397 min,
Identified with: Mascot (v1.36); Ions Score:43, Percolator q-Value:3.3e-4, Percolator PEP:3.7e-4, Ions matched by search engine: 10/100
Fragment match tolerance used for search: 30 mmu
Fragments used for search: y-H₂O; y-NH₃; b; b-H₂O; y



#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	98.06004	49.53366	P			11
2	227.10263	114.05496	E	1089.59389	545.30058	10
3	324.15540	162.58134	P	960.55129	480.77928	9
4	395.19251	198.09989	A	863.49853	432.25290	8
5	617.32934	309.16831	K-Sorbyl	792.46142	396.73435	7
6	704.36137	352.68432	S	570.32459	285.66593	6
7	775.39848	388.20288	A	483.29256	242.14992	5
8	872.45124	436.72926	P	412.25545	206.63136	4
9	943.48836	472.24782	A	315.20268	158.10498	3
10	1040.54112	520.77420	P	244.16557	122.58642	2
11			K	147.11280	74.06004	1

HeLa, sorbic acid, H2BK11sor

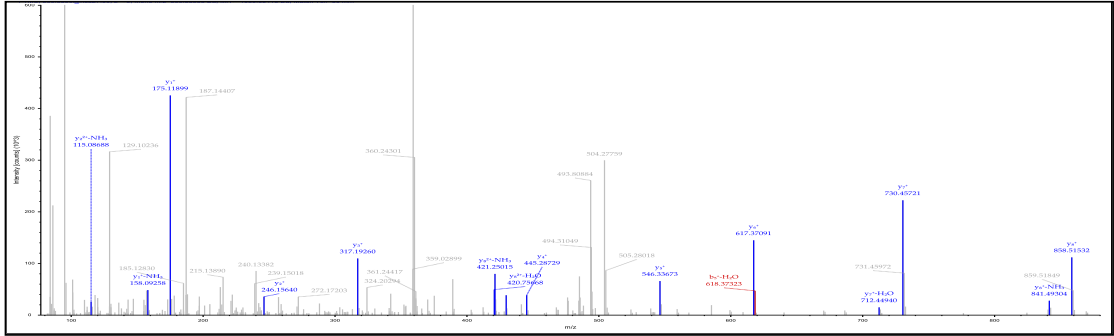
Sequence: DPAKSAPAPKKGSKKAVTKAQKK, K14-Acetyl (42.01057 Da), K4-Methyl (14.01565 Da), K10-Sorbyl (94.04187 Da)
Charge: +6, Monoisotopic m/z: 419.92224 Da (+3.41 mmu/+8.13 ppm), MH+: 2514.49705 Da, RT: 23.0305 min,
Identified with: Mascot (v1.36); Ions Score:15, Percolator q-Value:1.6e-3, Percolator PEP:1.6e-2, Ions matched by search engine: 12/248
Fragment match tolerance used for search: 30 mmu
Fragments used for search: y-H₂O; y-NH₃; b; b-H₂O; b-NH₃; y



#1	b ⁺	b ²⁺	b ³⁺	b ⁴⁺	b ⁵⁺	b ⁶⁺	Seq.	y ⁻	y ²⁺	y ³⁺	y ⁴⁺	y ⁵⁺	y ⁶⁺	#2
1	116.03422	58.52075	39.34959	29.76401	24.01267	20.17843	D							23
2	213.08698	107.04713	71.70051	54.02720	43.42322	36.35389	P	2399.44968	1200.22848	800.48808	600.61788	480.69576	400.74768	22
3	284.12410	142.56569	95.37955	71.78648	57.63064	48.19341	A	2302.39691	1151.70209	768.13715	576.35469	461.28520	384.57222	21
4	426.23471	213.62099	142.74975	107.31413	86.05276	71.87852	K-Methyl	2231.35980	1116.18354	744.45812	558.59541	447.07778	372.73270	20
5	513.26674	257.13701	171.76043	129.07214	103.45917	86.38385	S	2089.24918	1045.12823	697.08791	523.06775	418.65566	349.04759	19
6	584.30385	292.65556	195.43947	146.83142	117.86659	98.22337	A	2002.21716	1001.61222	668.07724	501.30975	401.24925	334.54226	18
7	681.35662	341.18195	227.79039	171.09461	137.07714	114.39883	P	1931.18004	966.09366	644.39820	483.55047	387.04183	322.70274	17
8	732.39373	376.70050	251.48943	188.83389	151.28457	126.23835	A	1834.12728	917.56728	612.04728	459.28728	367.53128	306.52728	16
9	849.44449	425.22889	283.82035	213.11708	170.89512	142.41381	P	1763.08017	882.04872	588.38824	441.52800	353.42385	294.88776	15
10	1071.58332	536.29530	357.86595	268.65129	215.12249	179.43662	K-Sorbyl	1666.03740	833.52234	556.01732	417.26481	334.01330	278.51230	14
11	1199.67828	600.34278	400.56428	300.67503	240.74148	200.78578	K	1443.90057	722.45392	481.97171	361.73060	289.58694	241.48948	13
12	1256.69975	628.85351	418.57143	314.93039	252.14577	210.28836	G	1315.80561	658.40644	439.27339	329.70689	263.96694	220.14033	12
13	1343.73178	672.36953	448.58211	336.68840	269.55216	224.79469	S	1258.78415	629.89571	420.26623	315.45149	252.56285	210.63675	11
14	1513.83730	757.42229	505.28395	379.21478	303.57328	253.14561	K-Acetyl	1171.75212	586.37970	391.25556	293.69349	235.15624	196.13142	10
15	1641.93227	821.46977	547.98227	411.23852	329.19227	274.49478	K	1001.64659	501.32693	334.55371	251.16711	201.13514	167.78050	9
16	1712.96938	856.98833	571.66131	428.99780	343.39970	286.33429	A	873.55163	437.27945	291.85539	219.14336	175.51615	146.43134	8
17	1812.03780	906.52254	604.68412	453.76491	363.21338	302.84570	V	802.51451	401.76090	268.17636	201.38409	161.30872	134.59182	7
18	1913.08547	957.04638	638.36668	479.02683	383.42292	319.68698	T	703.44610	352.22668	235.15355	176.61698	141.49504	118.08041	6
19	2041.18044	1021.09386	681.06500	511.05057	409.04191	341.03614	K	602.39842	301.70285	201.47099	151.35506	121.28551	101.23913	5
20	2112.21755	1056.61241	704.74403	528.80985	423.24933	352.87566	A	474.30348	237.65537	158.77267	119.33132	95.66651	79.88997	4
21	2240.27613	1120.64170	747.43023	560.82449	448.86105	374.21875	Q	403.26634	202.13681	135.09363	101.57204	81.45909	68.05045	3
22	2368.37109	1184.68918	790.12655	592.84823	474.48004	395.56791	K	275.20777	138.10752	92.40744	69.55740	55.84737	46.70736	2
23							K	147.11280	74.06004	49.70912	37.53366	30.22836	25.35820	1

HeLa, sorbic acid, H3K18sor

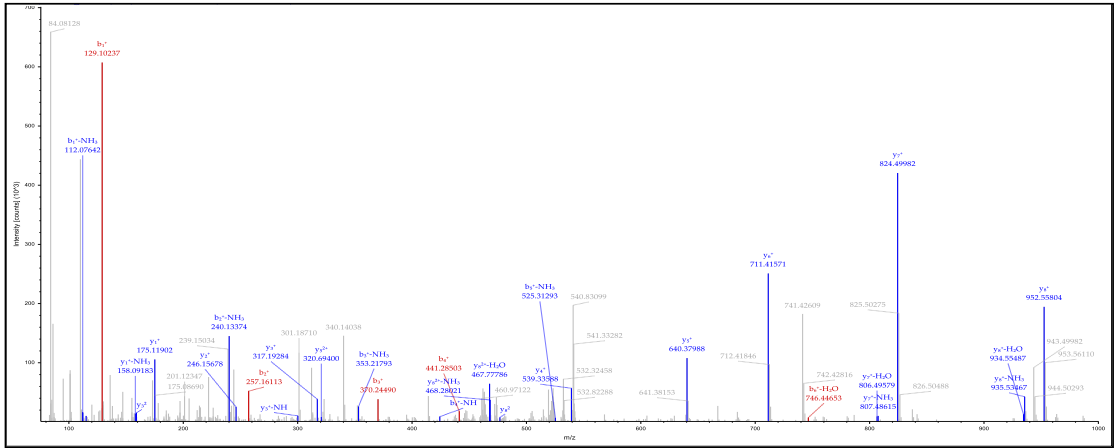
Sequence: KQLATKAAR, K1-Sorbyl (94.04187 Da)
Charge: +3, Monoisotopic m/z: 360.88958 Da (+0.59 mmu/+1.64 ppm), MH+: 1080.65418 Da, RT: 27.2244 min,
Identified with: Mascot (v1.36); Ions Score:25, Percolator q-Value:3.3e-4, Percolator PEP:6.9e-3, Ions matched by search engine: 7/80
Fragment match tolerance used for search: 30 mmu
Fragments used for search: y-H₂O; y-NH₃; b; b-H₂O; b-NH₃; y



#1	b ⁺	b ²⁺	b ³⁺	Seq.	y ⁺	y ²⁺	y ³⁺	#2
1	223.14410	112.07569	75.05289	K-Sorbyl				9
2	351.20268	176.10498	117.73908	Q	858.51558	429.76143	286.84338	8
3	464.28675	232.64701	155.43377	L	730.45700	365.73214	244.15718	7
4	535.32386	268.16557	179.11280	A	617.37293	309.19011	206.46250	6
5	636.37154	318.68941	212.79536	T	546.33582	273.67155	182.78346	5
6	764.46650	382.73689	255.49368	K	445.28814	223.14771	149.10090	4
7	835.50361	418.25545	279.17272	A	317.19318	159.10023	106.40258	3
8	906.54073	453.77400	302.85176	A	246.15607	123.58167	82.72354	2
9				R	175.11895	88.06311	59.04450	1

HeLa, sorbic acid, H3K23sor

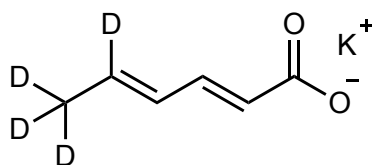
Sequence: KQLATKAAR, K6-Sorbyl (94.04187 Da)
Charge: +2, Monoisotopic m/z: 540.83135 Da (+1.51 mmu/+2.79 ppm), MH+: 1080.65541 Da, RT: 27.2259 min,
Identified with: Mascot (v1.36); Ions Score:23, Percolator q-Value:6.4e-4, Percolator PEP:1.2e-2, Ions matched by search engine: 5/80
Fragment match tolerance used for search: 30 mmu
Fragments used for search: y-H₂O; y-NH₃; b; b-H₂O; b-NH₃; y



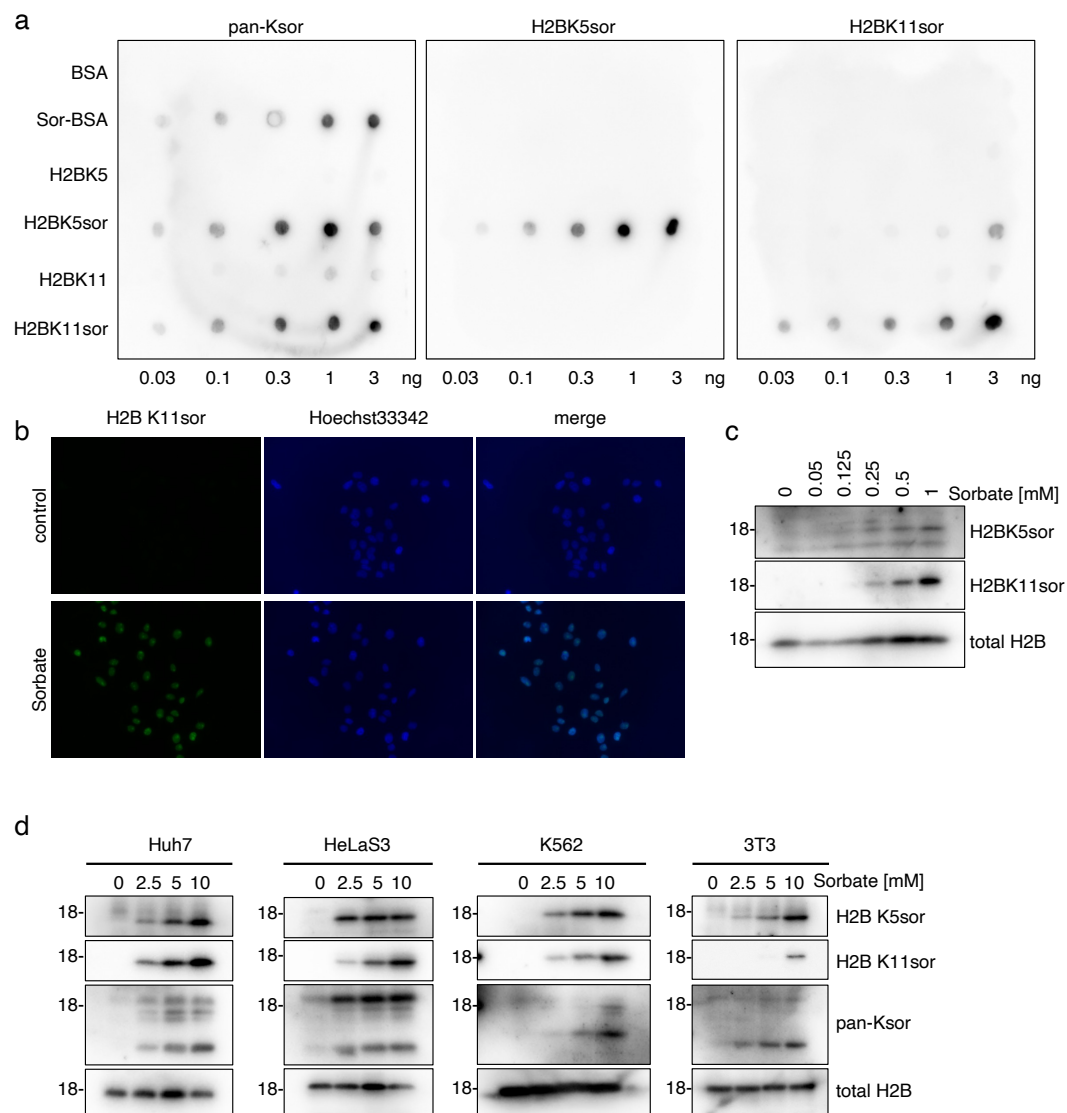
#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	129.10224	65.05476	K			9
2	257.16082	129.08405	Q	952.55744	476.78236	8
3	370.24488	185.62608	L	824.49886	412.75307	7
4	441.28199	221.14464	A	711.41480	356.21104	6
5	542.32967	271.66847	T	640.37769	320.69248	5
6	764.46650	382.73689	K-Sorbyl	539.33001	270.16864	4
7	835.50361	418.25545	A	317.19318	159.10023	3
8	906.54073	453.77400	A	246.15607	123.58167	2
9			R	175.11895	88.06311	1

Supplementary Figure 3. MS/MS spectra of histone sorbylated lysine containing peptides.

MS/MS spectra of each peptide from sorbic acid, potassium sorbate, or d₄-containing potassium sorbate-treated cells.

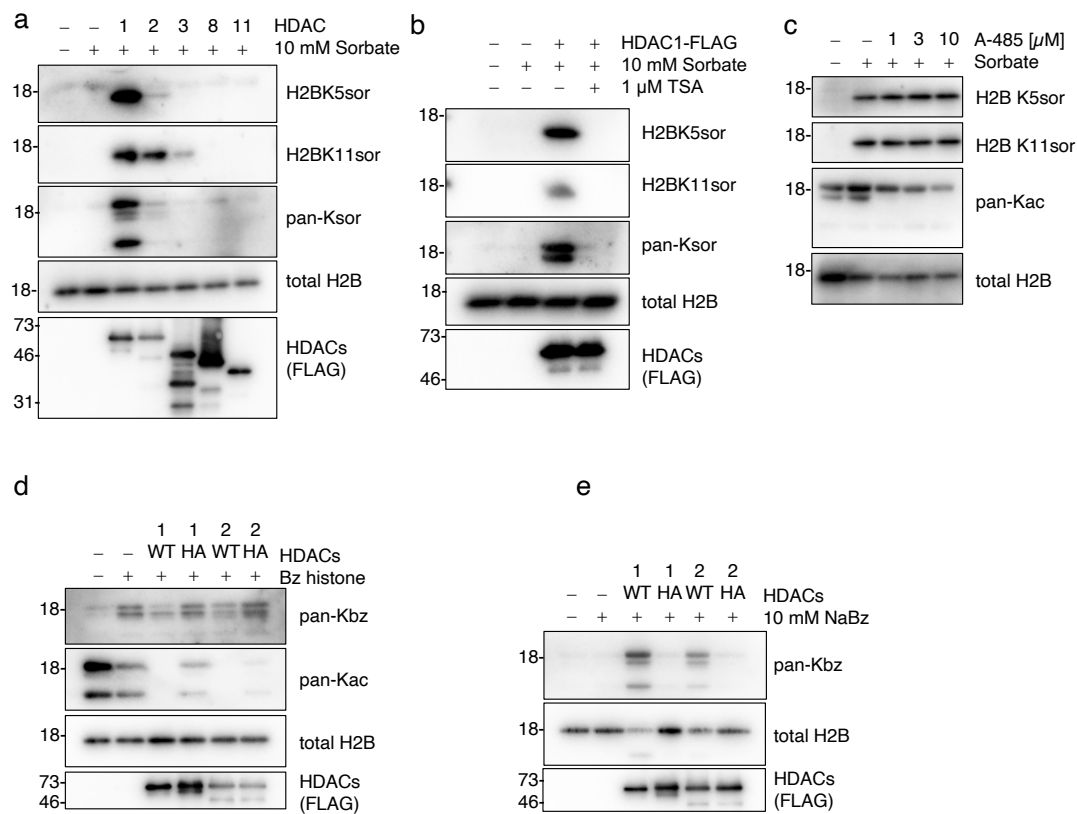


Supplementary Figure 4. Chemical structure of deuterium-labeled potassium sorbate.



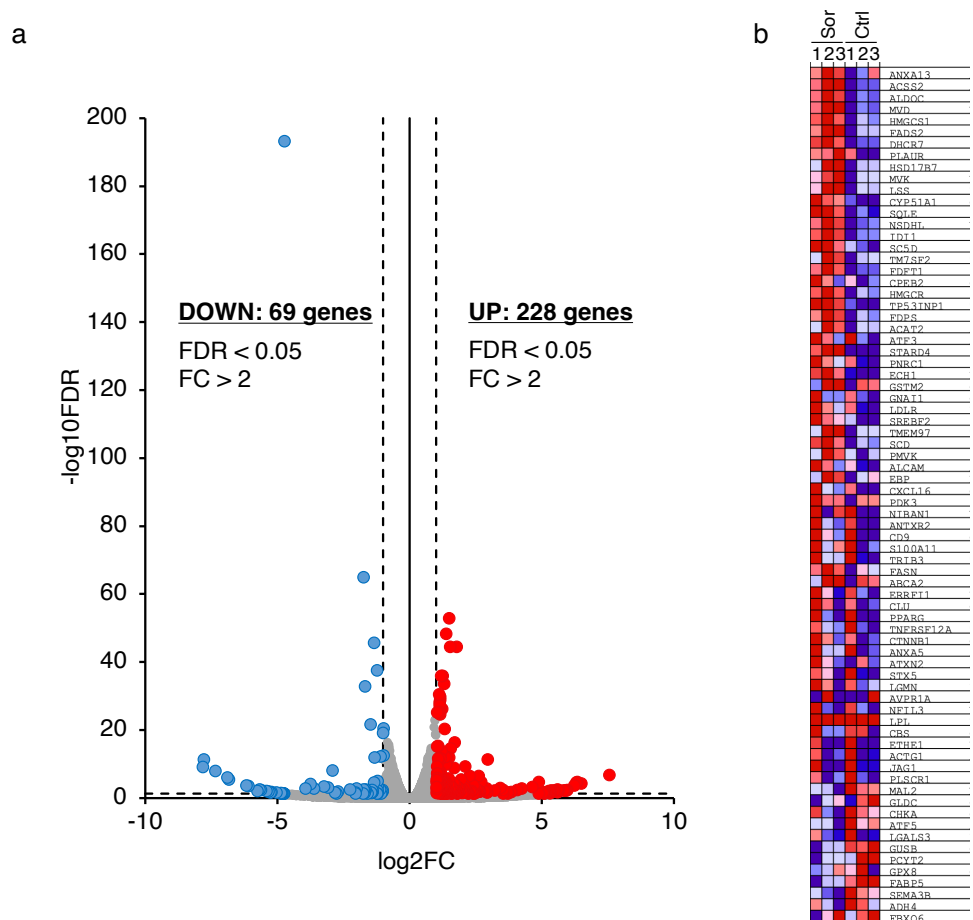
Supplementary Figure 5. Detection of sorbic acid induced histone sorbylation.

a Dot blot against BSA, sorbylated BSA, and BSA-conjugated peptides using antibodies generated in this study. **b** Immunofluorescence using H2BK11sor antibody. COS-7 cells were treated with 10 mM potassium sorbate for 24 h, and immunofluorescence was performed. **c** Sorbylation was induced in HepG2 cells by treatment with low-dose potassium sorbate. **d** Histone sorbylation in various cell lines. Human and mouse-derived cell lines were treated with the indicated concentrations of potassium sorbate for 24 h.



Supplementary Figure 6. HDAC1/2 catalyze histone acylation using carboxylic acids, depending on the deacetylation activity.

a Histone sorbylation by class I and IV KDACs *in vitro*. HDAC1-3, 8 or 11 and histones extracted from HEK293T cells were incubated with 10 mM potassium sorbate for 3 h. **b** Effect of HDAC activity inhibition on HDAC1-catalyzing sorbylation *in vitro*. Histone sorbylation was performed for 1 h as described in a, with or without 1 μ M TSA treatment. **c** Effect of p300 inhibition on histone sorbylation. HepG2 cells were treated with the indicated concentrations of A-485 for 1 h followed by treatment with 10 mM potassium sorbate for 6 h. Sorbylation and acetylation levels were determined by western blotting using the indicated antibodies. **d** Histone debenzoylation by HDAC1/2 *in vitro*. HDAC1 or HDAC2 and histones extracted from HEK293T cells treated with or without 20 mM sodium benzoate were incubated for 3 h. **e** Histone benzoylation by HDAC1/2 using sodium benzoate *in vitro*. The assay was performed as described in b using 10 mM sodium benzoate. Histone benzoylation levels were determined using western blotting



Supplementary Figure 7. Effect of sorbate on gene expression in HepG2 cells.

a Volcano plot visualizing the RNA-seq results. Thresholds of $-\log_{10}FDR$ and $\log_2FC$ are shown as dashed lines. **b** Heatmap of mRNA expression levels in HALLMARK_CHOLESTEROL_HOMEOSTASIS of GSEA.

Supplementary Table 1. DEGs list in RNA-seq analysis.

gene_id	gene_name	gene_type	logFC	logCPM	LR	FDR
ENSG00000276077.4	ENSG00000276077	lncRNA	7.545496319	-0.406250044	38.61169205	1.51E-07
ENSG00000255073.8	ZFP91-CNTF	protein_coding	6.480858254	-1.282508259	26.06671216	4.08E-05
ENSG00000244617.3	ASPRV1	protein_coding	6.323634307	-1.409442005	27.69013079	2.00E-05
ENSG00000284874.1	ENSG00000284874	protein_coding	6.294665664	-1.431076215	27.06642411	2.62E-05
ENSG00000259040.5	BLOC1S5-TXNDC5	protein_coding	6.21438232	-1.460584712	22.93064056	0.000165879
ENSG00000269693.1	ENSG00000269693	protein_coding	5.958574097	-1.544883481	16.00343817	0.003480462
ENSG00000198211.8	ENSG00000198211	protein_coding	5.91384799	-1.624218285	15.21602263	0.004856136
ENSG00000244255.5	ENSG00000244255	protein_coding	5.859758204	-1.661119042	14.68617133	0.006166243
ENSG00000274611.4	TBC1D3	protein_coding	5.824495605	-1.631072688	14.7522628	0.005982194
ENSG00000288606.1	ENSG00000288606	lncRNA	5.625859551	-1.868846577	16.06608318	0.003394568
ENSG00000213402.3	PTPRCAP	protein_coding	5.586873058	-1.828041449	12.75155259	0.013975312
ENSG00000212932.3	RPL23AP4	processed_pseudogene	5.563131466	-1.842221767	12.58880155	0.014984037
ENSG00000288698.1	ENSG00000288698	protein_coding	5.562491722	-1.905661577	16.41717478	0.002917885
ENSG00000248235.6	ENSG00000248235	protein_coding	5.454494566	-1.968968562	15.25893271	0.004762753
ENSG00000268400.6	ENSG00000268400	protein_coding	5.415137089	-1.989206504	14.36075544	0.007104228
ENSG00000176595.4	KBTBD11	protein_coding	5.342998706	-2.031742249	14.72457662	0.00606587
ENSG00000288234.1	ENSG00000288234	lncRNA	5.319905977	-2.031489089	13.95470126	0.008409571
ENSG00000244457.2	ENO1P1	transcribed_processed_pseudogene	5.313264948	-1.985199263	10.94655556	0.02997376
ENSG00000235884.4	LINC00941	lncRNA	5.281136625	-1.960143292	10.96402069	0.029738988
ENSG00000285218.1	ENSG00000285218	protein_coding	5.267795954	-1.967574587	10.88066283	0.030786799
ENSG00000133106.15	EPSTI1	protein_coding	5.254601467	-2.086627788	13.9001566	0.008600587
ENSG00000283549.1	ENSG00000283549	lncRNA	5.191024503	-2.076392169	12.14725712	0.01804898
ENSG00000251246.1	ENSG00000251246	protein_coding	5.140081234	-2.098889313	11.67120358	0.022193467
ENSG00000288550.3	ENSG00000288550	protein_coding	5.138434699	-2.135608678	11.59737144	0.022857931
ENSG00000217576.7	ENSG00000217576	lncRNA	5.091535166	-2.145360749	11.30724767	0.025874881
ENSG00000261771.5	DNAAF4-CCPG1	lncRNA	5.079321583	-2.068854671	9.744568518	0.049352182
ENSG00000255330.9	ENSG00000255330	protein_coding	5.072195761	-2.142072685	11.29684177	0.025947791
ENSG00000250011.1	HMGB1P3	processed_pseudogene	5.032918233	-2.200008823	11.55456641	0.023272214
ENSG00000182257.8	PRR34	lncRNA	5.032250977	-2.201681392	11.85507037	0.020500917
ENSG00000270249.2	ENSG00000270249	protein_coding	5.02851047	-2.181334097	11.07555846	0.028462107
ENSG00000248406.1	ENSG00000248406	transcribed_unprocessed_pseudogene	4.86745684	-2.263275662	10.16593946	0.041592051
ENSG00000162738.7	VANGL2	protein_coding	4.863605713	-1.087724875	28.42258339	1.46E-05
ENSG00000262481.5	TMEM256-PLSCR3	protein_coding	4.632764288	-1.213251685	20.46555974	0.000497968

ENSG00000004799.8	PDK4	protein_coding	4.229877138	-1.500542968	18.13396485	0.001393017
ENSG00000185739.13	SRL	protein_coding	4.062793386	-1.616586116	15.90695159	0.003617089
ENSG00000126467.11	TSKS	protein_coding	3.828910656	-1.785865188	12.19579746	0.017714791
ENSG00000182568.18	SATB1	protein_coding	3.703201954	-1.881250885	10.31870568	0.039062746
ENSG00000142185.18	TRPM2	protein_coding	3.699998306	-1.833228931	11.69978938	0.021892478
ENSG00000160460.17	SPTBN4	protein_coding	3.521787005	-1.979313693	10.06575772	0.043199861
ENSG00000122592.8	HOXA7	protein_coding	3.518823317	-1.430300058	15.80577602	0.003782267
ENSG00000179855.9	GIPC3	protein_coding	3.410234949	-1.142282929	19.02806473	0.000938678
ENSG00000148600.15	CDHR1	protein_coding	3.209982765	-1.297409419	14.77008691	0.005935339
ENSG00000103522.17	IL21R	protein_coding	2.936039492	0.764874975	61.08965266	4.19E-12
ENSG00000250282.1	ENSG00000250282	lncRNA	2.923007236	-1.502689474	12.0585392	0.018771822
ENSG00000147100.11	SLC16A2	protein_coding	2.895998734	-0.954542854	17.89691783	0.001536856
ENSG00000135625.8	EGR4	protein_coding	2.798802935	-0.924681409	14.15513792	0.007734677
ENSG00000127743.6	IL17B	protein_coding	2.699210995	-0.201410787	28.17864477	1.65E-05
ENSG00000063438.20	AHRR	protein_coding	2.635877156	-1.163254842	13.14538684	0.011857932
ENSG00000184730.12	APOBR	protein_coding	2.634475171	-1.142682626	13.26963768	0.011264872
ENSG00000100078.4	PLA2G3	protein_coding	2.606985274	0.567519052	36.80748274	3.37E-07
ENSG00000181577.16	C6orf223	lncRNA	2.601174777	-0.905721226	14.2911864	0.007315611
ENSG00000242173.10	ARHGDIG	protein_coding	2.55319598	-0.829511742	14.63663967	0.006300477
ENSG00000105088.9	OLFM2	protein_coding	2.508972472	-0.344185016	17.90983381	0.001529995
ENSG00000285160.1	THSD1P1	transcribed_unprocessed_pseudogene	2.471627494	-0.78014989	11.30214575	0.025916966
ENSG00000163072.16	NOSTRIN	protein_coding	2.468469659	-1.231496724	11.5498228	0.023305538
ENSG00000243709.1	LEFTY1	protein_coding	2.429145593	-0.899453125	14.26425229	0.007387476
ENSG00000229484.3	LINC02766	lncRNA	2.421592075	-1.295458616	10.09612922	0.042784552
ENSG00000180340.7	FZD2	protein_coding	2.416828935	-0.29337544	22.59777904	0.000193211
ENSG00000075340.23	ADD2	protein_coding	2.381634888	-1.32610884	9.765026519	0.049033397
ENSG00000288787.1	ENSG00000288787	lncRNA	2.331489049	-0.830981677	14.13893925	0.007778292
ENSG00000262633.2	ENSG00000262633	protein_coding	2.28849086	-0.509312148	12.94580276	0.012941873
ENSG00000105419.18	MEIS3	protein_coding	2.266885578	0.624888576	37.05845142	3.01E-07
ENSG00000162367.12	TAL1	protein_coding	2.209114343	-0.900601593	10.82886122	0.031449307
ENSG00000167207.15	NOD2	protein_coding	2.204079516	-1.00871645	9.856132071	0.047394579
ENSG00000228705.4	LINC00659	lncRNA	2.147950784	-0.615124896	11.62849484	0.022631313
ENSG00000135299.17	ANKRD6	protein_coding	2.108035775	-0.636676814	13.90783078	0.008596758
ENSG00000205978.6	NYNRIN	protein_coding	2.090667566	1.264592873	50.79897889	5.24E-10
ENSG00000257921.6	ENSG00000257921	protein_coding	2.08269482	0.209863816	16.23994291	0.003159645

ENSG00000214491.9	SEC14L6	protein_coding	2.054442785	0.233125875	24.29765279	9.10E-05
ENSG00000157657.15	ZNF618	protein_coding	2.044865803	-0.046350983	19.47956651	0.000768328
ENSG00000120324.9	PCDHB10	protein_coding	2.023138679	-0.630439368	12.84686241	0.013441305
ENSG00000197479.7	PCDHB11	protein_coding	1.987400772	-0.334013334	15.62126104	0.004081517
ENSG00000273238.3	TMEM271	protein_coding	1.981476097	-0.20063188	17.3525826	0.001930482
ENSG00000108852.16	MPP2	protein_coding	1.972178904	-0.80920311	10.76219407	0.032304657
ENSG00000185585.20	OLFML2A	protein_coding	1.929490072	0.736578605	31.99603699	2.99E-06
ENSG00000154040.21	CABYR	protein_coding	1.923614878	-0.251097715	15.8843105	0.003650927
ENSG00000108947.5	EFNB3	protein_coding	1.858969343	0.146557263	17.75997719	0.001624734
ENSG00000116329.12	OPRD1	protein_coding	1.840891762	-0.346473143	12.45754078	0.015894726
ENSG00000100321.15	SYNGR1	protein_coding	1.830540911	0.246265209	18.81363165	0.001036815
ENSG00000188620.11	HMX3	protein_coding	1.830424018	-0.384405521	10.84321904	0.031254421
ENSG00000113211.6	PCDHB6	protein_coding	1.812379456	-0.098611447	16.62262482	0.002670667
ENSG00000168280.18	KIF5C	protein_coding	1.801296172	0.408407173	19.93461784	0.00062553
ENSG00000231528.3	FAM225A	lncRNA	1.786299859	-0.137989275	11.14878266	0.027608885
ENSG00000198157.11	HMGNS	protein_coding	1.779869544	-0.314090847	10.72597059	0.032859819
ENSG00000065717.15	TLE2	protein_coding	1.777036127	-0.679519481	9.878020459	0.046941118
ENSG00000169174.11	PCSK9	protein_coding	1.771026949	7.092367145	217.9410084	2.60E-45
ENSG00000091879.14	ANGPT2	protein_coding	1.768228612	-0.320739583	12.20956078	0.017616395
ENSG00000170921.16	TANC2	protein_coding	1.759455056	-0.343725477	13.31833687	0.011043607
ENSG00000145882.11	PCYOX1L	protein_coding	1.726113496	0.244504827	18.00739146	0.001466165
ENSG00000213190.4	MLLT11	protein_coding	1.724088086	0.685589384	23.65805327	0.00012001
ENSG00000167664.9	TMIGD2	protein_coding	1.722721316	0.346818566	16.46266975	0.002851357
ENSG00000172380.6	GNG12	protein_coding	1.697059631	-0.324482498	11.92471619	0.019877151
ENSG00000213648.11	SULT1A4	protein_coding	1.691051174	2.699382782	85.6421167	3.71E-17
ENSG00000166589.13	CDH16	protein_coding	1.680802037	1.745011452	49.02097632	1.20E-09
ENSG00000109586.12	GALNT7	protein_coding	1.678882681	0.417056413	16.68844157	0.00259692
ENSG00000157514.18	TSC22D3	protein_coding	1.650230366	0.157992713	15.9805968	0.003513264
ENSG00000136274.9	NACAD	protein_coding	1.649760496	1.011989416	26.24110029	3.80E-05
ENSG00000283183.4	ENSG00000283183	lncRNA	1.626154362	-0.34517305	11.14705842	0.027619797
ENSG00000137078.10	SIT1	protein_coding	1.593939734	0.60237417	19.64015038	0.000718762
ENSG00000186998.16	EMID1	protein_coding	1.575143388	-0.327775297	11.05709548	0.028701328
ENSG00000040608.14	RTN4R	protein_coding	1.574056351	-0.156550637	12.32046934	0.016854038
ENSG00000180739.15	S1PR5	protein_coding	1.573882629	-0.282230617	10.31284004	0.03914929
ENSG00000010310.9	GIPR	protein_coding	1.572906574	0.621107545	18.64340474	0.001105155

ENSG00000182162.11	P2RY8	protein_coding	1.548143596	3.236015384	76.75933253	2.70E-15
ENSG00000285901.2	ENSG00000285901	protein_coding	1.544925795	2.222710153	10.85234771	0.031132672
ENSG00000113248.6	PCDHB15	protein_coding	1.53834218	0.037247353	11.21116402	0.026861875
ENSG00000148082.10	SHC3	protein_coding	1.532168541	0.016643414	12.55873837	0.015160322
ENSG00000182013.18	PNMA8A	protein_coding	1.529178797	0.192926586	13.36767073	0.010823494
ENSG00000112972.15	HMGCS1	protein_coding	1.516023108	7.870357586	217.4427528	2.87E-45
ENSG00000015568.13	RGPD5	protein_coding	1.510867081	3.395975046	16.85648604	0.00241389
ENSG00000101670.12	LIPG	protein_coding	1.484379877	1.407659553	29.13374474	1.06E-05
ENSG00000131069.20	ACSS2	protein_coding	1.480740587	6.082491066	257.7833792	1.07E-53
ENSG00000186115.13	CYP4F2	protein_coding	1.477626653	2.663510669	64.14223848	1.08E-12
ENSG00000274750.3	H3C6	protein_coding	1.472669907	1.292229437	24.42835344	8.55E-05
ENSG00000085741.14	WNT11	protein_coding	1.469795828	0.043702335	11.92774361	0.019877151
ENSG00000167191.12	GPRC5B	protein_coding	1.456737825	1.648962234	33.41921884	1.58E-06
ENSG00000135052.16	GOLM1	protein_coding	1.424296478	0.464713078	13.24439486	0.011371207
ENSG00000271943.4	ENSG00000271943	transcribed_processed_pseudogene	1.412780631	0.302059215	13.49334742	0.010227733
ENSG00000196132.14	MYT1	protein_coding	1.411907964	0.09460378	10.37880837	0.038087224
ENSG00000176884.16	GRIN1	protein_coding	1.384987364	0.719949954	14.82632709	0.005783949
ENSG00000161082.13	CELF5	protein_coding	1.384223362	1.284826108	26.02878015	4.15E-05
ENSG00000289027.1	ENSG00000289027	protein_coding	1.380842332	0.974204831	17.0746008	0.002194684
ENSG00000007264.15	MATK	protein_coding	1.38054977	1.173513118	21.32425954	0.000338393
ENSG00000087085.16	ACHE	protein_coding	1.376471406	1.47203703	28.42769677	1.46E-05
ENSG00000105255.11	FSD1	protein_coding	1.369984703	0.099678315	10.40656196	0.037682797
ENSG00000173930.9	SLCO4C1	protein_coding	1.368147497	2.888058039	63.58373417	1.39E-12
ENSG00000253686.2	LINC01484	lncRNA	1.366260455	2.681852833	54.02802283	1.15E-10
ENSG00000167508.12	MVD	protein_coding	1.361301399	6.781862212	235.715892	5.19E-49
ENSG00000167964.13	RAB26	protein_coding	1.355366361	1.414782674	25.57687954	5.08E-05
ENSG00000286001.1	ENSG00000286001	protein_coding	1.349352304	0.257889226	10.46217977	0.036890512
ENSG00000168916.16	ZNF608	protein_coding	1.348018632	2.946614446	65.04430469	7.26E-13
ENSG00000154277.13	UCHL1	protein_coding	1.341241805	0.484903775	13.25712045	0.011330878
ENSG00000230863.3	ENSG00000230863	transcribed_processed_pseudogene	1.338971874	0.035430224	9.724584959	0.049775079
ENSG00000260807.7	CEROX1	lncRNA	1.334104958	1.846220176	23.38433606	0.000136732
ENSG00000176204.14	LRRIM4	protein_coding	1.330586636	0.043460024	10.55182505	0.035387704
ENSG00000174672.16	BRSK2	protein_coding	1.317003804	1.787682803	29.73802511	8.22E-06
ENSG00000272674.4	PCDHB16	protein_coding	1.311695983	1.433412925	25.4378876	5.44E-05
ENSG00000088881.22	EBF4	protein_coding	1.311359968	1.19541922	21.84573893	0.000268512

ENSG00000173918.15	C1QTNF1	protein_coding	1.309101313	0.629069812	14.65661515	0.006248873
ENSG00000162512.16	SDC3	protein_coding	1.30362105	3.985082622	103.8814621	4.55E-21
ENSG00000172893.18	DHCR7	protein_coding	1.287330974	7.203974799	166.7284552	2.14E-34
ENSG00000163898.10	LIPH	protein_coding	1.287049025	0.291424815	9.948134943	0.04554013
ENSG00000247081.8	BAALC-AS1	lncRNA	1.278825865	0.934817434	15.47697167	0.004351646
ENSG00000140107.12	SLC25A47	protein_coding	1.276883533	0.794963443	15.84338052	0.003724176
ENSG00000286053.2	ASDURF	protein_coding	1.263833825	1.564674866	11.1063105	0.028098191
ENSG00000248508.10	SRP14-DT	lncRNA	1.258815328	0.198257746	10.28299743	0.039539608
ENSG00000103316.12	CRYM	protein_coding	1.256772227	0.335302238	10.6011202	0.034697618
ENSG00000114923.17	SLC4A3	protein_coding	1.248497064	1.505093962	24.11528928	9.83E-05
ENSG00000228451.5	SDAD1P1	transcribed_processed_pseudogene	1.246315613	0.508658005	12.08828256	0.018500734
ENSG00000052802.13	MSMO1	protein_coding	1.233262297	7.271468179	177.2509799	1.19E-36
ENSG00000132010.16	ZNF20	protein_coding	1.232300048	0.365092209	10.4130308	0.037588938
ENSG00000204681.11	GABBR1	protein_coding	1.224468691	1.171452995	17.74283796	0.001633456
ENSG00000287542.1	HERC3	protein_coding	1.222085313	0.644448425	10.69707622	0.03227592
ENSG00000112406.5	HECA	protein_coding	1.221449262	2.217340052	36.64685406	3.62E-07
ENSG00000109107.14	ALDOC	protein_coding	1.214006146	4.994487592	131.4843656	6.27E-27
ENSG00000196391.11	ZNF774	protein_coding	1.211238248	0.384984268	10.1618855	0.041656867
ENSG00000132003.10	ZSWIM4	protein_coding	1.211017767	1.984347428	30.15180567	6.82E-06
ENSG00000115085.15	ZAP70	protein_coding	1.210832591	1.510388685	20.90632379	0.00040366
ENSG00000155428.12	TRIM74	protein_coding	1.208159849	0.604239014	12.02068073	0.01906874
ENSG00000231683.6	ENSG00000231683	lncRNA	1.200398475	2.114252469	28.13047497	1.66E-05
ENSG00000124466.9	LYPD3	protein_coding	1.196291398	0.305691455	9.813075253	0.04807887
ENSG00000130528.12	HRC	protein_coding	1.195928962	3.571286571	73.54991633	1.28E-14
ENSG00000116701.16	NCF2	protein_coding	1.195622137	1.712146791	20.05086611	0.000593156
ENSG00000118971.9	CCND2	protein_coding	1.189976236	0.873260888	12.86481704	0.013347512
ENSG00000160285.15	LSS	protein_coding	1.183535848	7.442630096	177.3200168	1.19E-36
ENSG00000182472.9	CAPN12	protein_coding	1.168408144	2.67198021	42.39247644	2.64E-08
ENSG00000182247.10	UBE2E2	protein_coding	1.168221136	0.710310871	10.56660581	0.035193189
ENSG00000159164.10	SV2A	protein_coding	1.161443567	3.347709999	62.80525581	1.92E-12
ENSG00000052344.16	PRSS8	protein_coding	1.152618127	2.629565143	31.75452329	3.33E-06
ENSG00000137285.11	TUBB2B	protein_coding	1.152190593	5.856512906	133.947517	1.91E-27
ENSG00000134824.14	FADS2	protein_coding	1.148189056	6.27714099	148.2096505	1.87E-30
ENSG000000001630.18	CYP51A1	protein_coding	1.144506541	7.346139377	144.1725992	1.33E-29
ENSG00000187550.9	SBK2	protein_coding	1.140059202	1.396370982	16.86510871	0.002405292

ENSG00000149269.10	PAK1	protein_coding	1.139847561	1.806348226	24.17128877	9.60E-05
ENSG00000134324.12	LPIN1	protein_coding	1.132504269	5.39845637	123.8112131	2.47E-25
ENSG00000151690.15	MFSD6	protein_coding	1.12976981	2.373679121	33.33350648	1.64E-06
ENSG00000165716.11	DIPK1B	protein_coding	1.128040792	1.93852145	23.71178985	0.000117503
ENSG00000163586.10	FABP1	protein_coding	1.122119668	7.151027588	140.930337	6.40E-29
ENSG00000104549.12	SQLE	protein_coding	1.120082175	7.527656516	136.6884708	5.10E-28
ENSG00000125848.10	FLRT3	protein_coding	1.115421644	2.248792353	29.8215368	7.95E-06
ENSG00000170522.10	ELOVL6	protein_coding	1.114634324	5.37639098	127.6856089	4.04E-26
ENSG00000174669.12	SLC29A2	protein_coding	1.1136352	2.554083827	37.91169244	2.09E-07
ENSG00000179292.5	TMEM151A	protein_coding	1.113196337	0.834732088	12.30424423	0.01695964
ENSG00000079459.13	FDFT1	protein_coding	1.111903503	8.118793653	151.9542495	3.06E-31
ENSG00000198892.7	SHISA4	protein_coding	1.11060589	1.196603931	16.05192341	0.003413879
ENSG00000049192.15	ADAMTS6	protein_coding	1.109579465	3.456346557	43.94164404	1.34E-08
ENSG00000105227.16	PRX	protein_coding	1.107171983	1.759718599	16.2692399	0.003122682
ENSG00000184922.15	FMNL1	protein_coding	1.104226749	1.468758139	18.24660708	0.001324688
ENSG00000287709.3	ENSG00000287709	lncRNA	1.103119811	0.835675111	11.29595563	0.025947791
ENSG00000105048.18	TNNT1	protein_coding	1.099654199	2.093361693	27.7774916	1.94E-05
ENSG00000087245.13	MMP2	protein_coding	1.098728918	2.979404822	39.69346111	9.08E-08
ENSG00000275496.4	ENSG00000275496	lncRNA	1.096303597	2.41599861	31.04862042	4.53E-06
ENSG00000244062.1	ENSG00000244062	processed_pseudogene	1.094599247	4.264452476	35.3258075	6.72E-07
ENSG00000205744.10	DENND1C	protein_coding	1.089893475	1.276181518	13.32784449	0.011010346
ENSG00000110090.13	CPT1A	protein_coding	1.089006082	5.499249963	125.7848807	9.57E-26
ENSG00000176490.5	DIRAS1	protein_coding	1.086949911	2.888958751	34.82624517	8.45E-07
ENSG00000060566.14	CREB3L3	protein_coding	1.08579756	3.547594362	58.19914737	1.60E-11
ENSG00000185215.11	TNFAIP2	protein_coding	1.084042742	0.748362958	11.02519028	0.029107191
ENSG00000085831.16	TTC39A	protein_coding	1.081160426	1.893161188	23.71655712	0.000117413
ENSG00000077585.14	GPR137B	protein_coding	1.077636722	2.198196814	28.94743867	1.16E-05
ENSG00000130477.16	UNC13A	protein_coding	1.077334392	0.9694924	13.28717757	0.011190401
ENSG00000149212.12	SESN3	protein_coding	1.070595779	1.879552598	22.37673222	0.000211772
ENSG00000100344.11	PNPLA3	protein_coding	1.068647798	4.484549996	62.89465524	1.86E-12
ENSG00000188385.13	JAKMIP3	protein_coding	1.065028327	0.894446682	11.22731529	0.026678619
ENSG00000105219.10	CCNP	protein_coding	1.064675206	1.885439299	23.77666045	0.000114391
ENSG00000104081.14	BMF	protein_coding	1.060838226	4.289817028	80.40839783	4.92E-16
ENSG00000204396.11	VWA7	protein_coding	1.059544072	1.973121638	24.11230985	9.83E-05
ENSG00000114698.15	PLSCR4	protein_coding	1.058402727	3.052062105	40.7729194	5.43E-08

ENSG00000135709.14	KIAA0513	protein_coding	1.052582739	1.050712159	12.31473093	0.016895585
ENSG00000072071.17	ADGRL1	protein_coding	1.044686102	3.502109929	42.41846907	2.62E-08
ENSG00000100100.13	PIK3IP1	protein_coding	1.043565681	2.62052295	33.25685024	1.69E-06
ENSG00000166415.15	WDR72	protein_coding	1.040969552	1.390439236	13.57242714	0.009910592
ENSG00000139112.11	GABARAPL1	protein_coding	1.036379094	4.808635865	80.12898685	5.52E-16
ENSG00000067064.13	ID1I	protein_coding	1.034626198	7.18420735	126.757991	6.14E-26
ENSG00000100027.17	YPEL1	protein_coding	1.032004479	1.029151538	12.43119972	0.016060591
ENSG00000159753.15	CARMIL2	protein_coding	1.028843128	3.357243074	50.98550949	4.80E-10
ENSG00000170537.13	TMC7	protein_coding	1.028585976	4.641291572	40.93922342	5.08E-08
ENSG00000147889.18	CDKN2A	protein_coding	1.02824456	2.80476026	34.10532597	1.15E-06
ENSG00000074181.9	NOTCH3	protein_coding	1.02614886	1.177770001	13.54713891	0.009993465
ENSG00000101115.13	SALL4	protein_coding	1.023669044	1.924190221	20.1743654	0.000564009
ENSG00000024422.12	EHD2	protein_coding	1.021397779	1.869941073	20.03119243	0.000597759
ENSG00000144488.15	ESPNL	protein_coding	1.020579971	1.552902542	16.57567646	0.002722034
ENSG00000274180.1	NATD1	protein_coding	1.02018399	2.465257709	28.71830461	1.29E-05
ENSG00000144355.15	DLX1	protein_coding	1.018089081	0.81148669	10.65739878	0.03826621
ENSG00000196542.9	SPTSSB	protein_coding	1.01246497	1.670576982	17.14454749	0.002125893
ENSG00000249790.3	LINC02972	lncRNA	1.009096068	2.319410988	26.93425023	2.77E-05
ENSG00000131650.14	KREMEN2	protein_coding	1.007908708	2.733298845	31.23583431	4.22E-06
ENSG00000260630.9	SNAI3-AS1	lncRNA	1.002671121	1.891415481	20.08439348	0.00058736
ENSG00000111665.12	CDCA3	protein_coding	-1.004330309	4.679363199	66.93545039	3.08E-13
ENSG00000123975.5	CKS2	protein_coding	-1.005111629	6.740937948	104.7072593	3.11E-21
ENSG00000274588.2	DGKK	protein_coding	-1.012870193	5.557331778	98.32470828	7.27E-20
ENSG00000272599.2	ENSG00000272599	lncRNA	-1.032743789	1.36115548	13.62572599	0.009710289
ENSG00000259112.2	NDUFC2-KCTD14	protein_coding	-1.033818282	2.459027648	15.31800614	0.00464686
ENSG00000176919.13	C8G	protein_coding	-1.05757025	1.174908438	13.71469928	0.009330234
ENSG00000172201.12	ID4	protein_coding	-1.088622709	0.743146475	9.90271531	0.046423622
ENSG00000178150.10	ZNF114	protein_coding	-1.108437816	4.035380733	65.97810847	4.83E-13
ENSG00000205670.12	SMIM11	protein_coding	-1.138828824	3.00877231	16.52768354	0.002770793
ENSG00000167774.2	ENSG00000167774	protein_coding	-1.21785656	1.966743089	21.41657876	0.000323403
ENSG00000277957.1	SENP3-EIF4A1	protein_coding	-1.219442369	1.863358694	29.58345907	8.74E-06
ENSG00000243679.1	ENSG00000243679	processed_pseudogene	-1.227205482	0.887079835	14.91288526	0.005551132
ENSG00000263276.1	ENSG00000263276	lncRNA	-1.232849795	0.413860304	9.766445575	0.049025803
ENSG00000115738.10	ID2	protein_coding	-1.236154832	6.628921195	185.1646533	2.77E-38
ENSG00000228412.9	LNC-LBCS	lncRNA	-1.238308844	0.378574035	9.918792566	0.046114731

ENSG00000276168.1	RN7SL1	misc_RNA	-1.333236083	4.349006613	64.41913645	9.73E-13
ENSG00000125968.9	ID1	protein_coding	-1.357959783	7.812015764	223.5154193	1.90E-46
ENSG00000168874.13	ATOH8	protein_coding	-1.357974482	1.493688708	27.56170423	2.11E-05
ENSG00000165376.12	CLDN2	protein_coding	-1.412463975	0.117492524	12.22459883	0.017517232
ENSG00000285314.1	ENSG00000285314	lncRNA	-1.415057603	0.645652333	14.04516632	0.008109386
ENSG00000272617.3	ENSG00000272617	protein_coding	-1.428577956	2.068438168	15.48206911	0.0043473
ENSG00000283293.1	RN7SK	snRNA	-1.461262708	-0.019668266	10.69954629	0.03265106
ENSG00000258604.1	ENSG00000258604	lncRNA	-1.475174389	0.053012453	11.52270914	0.023514717
ENSG00000274012.1	RN7SL2	misc_RNA	-1.484749694	4.470026745	110.0622188	2.24E-22
ENSG00000289750.1	ENSG00000289750	lncRNA	-1.604859664	-0.219680687	9.944612817	0.045570513
ENSG00000170458.15	CD14	protein_coding	-1.683495894	0.23603952	16.64565925	0.002643471
ENSG00000287765.1	ENSG00000287765	lncRNA	-1.692930014	0.07876065	13.97755813	0.008326207
ENSG00000177984.7	LCN15	protein_coding	-1.694163957	5.476158694	162.9425613	1.32E-33
ENSG00000278771.1	RN7SL3	misc_RNA	-1.708651202	0.257200329	10.93273751	0.030151629
ENSG00000242288.9	BMS1P4-AGAP5	lncRNA	-1.730227967	0.224841617	15.19893736	0.004888181
ENSG00000184260.6	H2AC20	protein_coding	-1.756855222	0.271600684	16.65781	0.002631618
ENSG00000117318.9	ID3	protein_coding	-1.763707169	5.945484037	314.0339577	8.87E-66
ENSG00000281358.1	RASSF1-AS1	lncRNA	-1.78084481	-0.485259069	10.22920239	0.040378819
ENSG00000284377.2	ENSG00000284377	lncRNA	-2.025220714	0.028950331	18.08317719	0.001419727
ENSG00000275713.3	H2BC9	protein_coding	-2.048377855	-0.788095711	11.60638818	0.022798754
ENSG00000233154.6	LINC01762	lncRNA	-2.061231132	-0.85866407	10.40928772	0.037646796
ENSG00000064489.23	BORCS8-MEF2B	protein_coding	-2.260811387	-0.0771051	16.37026183	0.002982642
ENSG00000268744.1	ENSG00000268744	lncRNA	-2.719264591	-0.95300896	13.55657569	0.009972103
ENSG00000200534.1	SNORA33	snoRNA	-2.772314395	-1.57846034	10.46228264	0.036890512
ENSG00000230715.3	ENSG00000230715	processed_pseudogene	-2.833345479	-0.958202493	12.05432873	0.018783016
ENSG00000283782.2	ENSG00000283782	protein_coding	-2.933841604	0.634200411	45.3299765	7.11E-09
ENSG00000270276.3	H4C15	protein_coding	-3.09810749	-0.739365718	19.32026727	0.000825017
ENSG00000243302.3	ENSG00000243302	processed_pseudogene	-3.250556608	-0.051119267	21.23348312	0.000352799
ENSG00000288602.1	C8orf44-SGK3	protein_coding	-3.630579936	-1.109022567	17.74301413	0.001633456
ENSG00000267059.2	ENSG00000267059	protein_coding	-3.75934816	0.893815305	24.92932507	6.84E-05
ENSG00000274944.4	ENSG00000274944	protein_coding	-3.95096449	-0.751610539	17.98441358	0.001480758
ENSG00000105697.9	HAMP	protein_coding	-4.752526759	4.568280934	904.8911964	5.21E-194
ENSG00000204540.11	PSORS1C1	protein_coding	-4.756624984	-2.328665934	9.959396747	0.045331623
ENSG00000267246.1	ENSG00000267246	lncRNA	-4.757785312	-2.335062128	9.989543225	0.044774728
ENSG00000214300.7	SPDYE3	protein_coding	-4.783711057	-2.327333785	10.29561078	0.039367695

ENSG00000270617.1	URGCP-MRPS24	protein_coding	-4.828340435	-2.304728922	10.50329196	0.036235454
ENSG00000241020.1	RPL32P24	processed_pseudogene	-4.85176438	-2.256392039	9.744319397	0.049352182
ENSG00000234231.4	ANAPC1P4	transcribed_unprocessed_pseudogene	-4.857738396	-2.255402096	9.835272829	0.047734714
ENSG00000288735.2	ENSG00000288735	lncRNA	-4.881053195	-2.264343405	10.60188484	0.034697618
ENSG00000137970.7	RPL7P9	processed_pseudogene	-5.046932345	-2.19355831	11.84068518	0.020613868
ENSG00000269110.1	ENSG00000269110	lncRNA	-5.241643236	-2.068607595	12.56479179	0.015120755
ENSG00000267281.3	ATF7-NPFF	protein_coding	-5.271013741	-2.018374203	11.84340394	0.020595719
ENSG00000248101.2	ENSG00000248101	lncRNA	-5.357288042	-2.006671699	13.54745179	0.009993465
ENSG00000287856.1	ENSG00000287856	protein_coding	-5.436577489	-1.956523677	14.39264923	0.007006383
ENSG00000255513.1	ENSG00000255513	transcribed_processed_pseudogene	-5.632352464	-1.833030744	15.66808628	0.004001148
ENSG00000253366.3	GUSBP16	unprocessed_pseudogene	-5.683867825	-1.797435068	16.29653389	0.00308945
ENSG00000258830.1	ENSG00000258830	protein_coding	-5.770959215	-1.690835448	14.09405112	0.007924768
ENSG00000280852.2	ENSG00000280852	transcribed_processed_pseudogene	-6.102282938	-1.532738996	21.60287967	0.000298567
ENSG00000283977.1	ENSG00000283977	protein_coding	-6.185917713	-1.470004484	22.47115368	0.000203176
ENSG00000288637.1	ENSG00000288637	protein_coding	-6.85199159	-0.973541224	32.00546172	2.99E-06
ENSG00000244563.1	RPS26P19	processed_pseudogene	-6.90177241	-0.937640508	34.52637048	9.53E-07
ENSG00000176020.9	AMIGO3	protein_coding	-7.366613942	-0.574673118	44.52377906	1.03E-08
ENSG00000261459.1	ENSG00000261459	protein_coding	-7.798792745	-0.192827474	60.95078518	4.44E-12
ENSG00000125954.13	CHURC1-FNTB	protein_coding	-7.838434436	-0.134179795	50.26672077	6.60E-10

Supplementary Table 2. Primer sets used in RT-qPCR.

genes		sequences 5' -> 3'		amplicon size
HMGCR	NM_001130996	F	tgattgacctttccagagcaag	102
		R	ctaaaattgccattccacgagc	
HMGCS1	NM_001098272	F	ctcttgggatggacggtatgc	90
		R	gctccaactccacctgtagg	
ACSS2	NM_018677	F	tcattcctacgtcacctatgg	141
		R	gtgggtgctgtgtagaactg	
GAPDH	NM_002046.3	F	agccacatcgctcagacac	66
		R	gcccaatacgaccaaatec	

Supplementary Table 3. Mapping results of Bowtie2 in CUT&Tag.

Treat	Antibody	SequencingDepth	FilteredFragNum_fastp	Aligned_Frag_Num	Unique_Frag_Num	AlignmentRate
Sor	H2BK11sor_N1	49,334,261	48869152	47269045	40667167	96.73%
ctrl	H2BK11sor_N1	1,689,361	1642707	1489492	818370	90.67%
Sor	H2BK11sor_N2	72,030,702	70999158	69102285	59470002	97.33%
ctrl	H2BK11sor_N2	690,826	681262	627939	507623	92.17%
Sor	H3K27ac	59,092,385	58471816	57196911	52085740	97.82%
ctrl	H3K27ac	47,487,723	46979461	46148348	42137150	98.23%
Sor	PolII S2/5p	66,204,432	65118982	63653801	56577913	97.75%
ctrl	PolII S2/5p	40,275,883	39756705	39277125	34612628	98.79%

Supplementary Table 4. Annotated H2BK11sor peaks around gene locus (ratio in Fig. 5d).

Feature	Total	Up
Promoter (≤ 1 kb)	73.68	82.62
Promoter (1-2kb)	1.32	0.78
Promoter (2-3kb)	1.41	0.59
5' UTR	0.84	1.37
3' UTR	3.45	3.52
1st Exon	3.76	0.98
Other Exon	4.58	3.71
1st Intron	3.38	3.32
Other Intron	5.27	2.93
Distal Intergenic	2.32	0.20