

Supplementary Material

Table 1S. MALDI-ToF MS identification details for differentially expressed proteins in livers N, HFD and HFD+T2 rats using Protein Lynx Global Server 2.3 software (Waters Corporation, Manchester, UK). Spot numbers refer to Table 2. CAM-Cys: CAM-Cysys; Met Ox: Methionine oxidation.

No. 1 Glutamate dehydrogenase 1								
m/z	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Start	End	Sequence	Modifications
1730.908	1729.900	1729.959	-0.059	-34	35	51	(R)GQPSAVPQPGLTPVARR(H)	
1011.481	1010.473	1010.435	0.038	38	61	68	(R)EDDPNFFK(M)	
1000.449	999.441	999.448	-0.007	-7	69	76	(K)MVEGFFDR(G)	
1016.423	1015.415	1015.443	-0.028	-27	69	76	(K)MVEGFFDR(G)	Met Ox (1)
1033.485	1032.477	1032.484	-0.007	-7	91	98	(K)TRENEEQK(R)	
1894.079	1893.071	1893.066	0.006	3	108	123	(R)IIKPCNHVLSLSFPIR(R)	CAM-Cys (5)
2050.144	2049.136	2049.167	-0.031	-15	108	124	(R)IIKPCNHVLSLSFPIRR(D)	CAM-Cys (5)
1581.735	1580.727	1580.722	0.005	3	124	136	(R)RDDGSWEVIEGYR(A)	
1425.620	1424.612	1424.621	-0.009	-6	125	136	(R)DDGSWEVIEGYR(A)	
997.505	996.497	996.531	-0.035	-35	163	171	(K)ALASLMTYK(C)	
2198.115	2197.107	2197.127	-0.020	-9	163	183	(K)ALASLMTYKCAVVDVPPFGGAK(A)	CAM-Cys (10)
2044.025	2043.017	2043.010	0.007	4	212	231	(K)KGFIPGIDVPAPDMSTGER(E)	
1915.926	1914.918	1914.915	0.004	2	213	231	(K)GFIGPGIDVPAPDMSTGER(E)	
1748.893	1747.885	1747.883	0.002	1	303	318	(K)TFVVQGFQGNVGLHSMR(Y)	
1764.870	1763.863	1763.878	-0.015	-9	303	318	(K)TFVVQGFQGNVGLHSMR(Y)	Met Ox (15)
1958.048	1957.040	1957.031	0.010	5	347	363	(K)ELEDFKLQHGSI LGFPK(A)	
1196.648	1195.641	1195.671	-0.031	-26	353	363	(K)LQHGSI LGFPK(A)	
2293.109	2292.101	2292.119	-0.019	-8	366	386	(K)VYEGSILEADCDILIPAASEK(Q)	CAM-Cys (11)
2242.172	2241.165	2241.164	0.000	0	400	420	(K)IIAEGANGPTTPEADKIFLER(N)	
2742.504	2741.496	2741.414	0.082	30	421	444	(R)NIMVIPDLYLNAGGVTVSYFEWLK(N)	
1059.515	1058.507	1058.526	-0.019	-18	445	453	(K)NLNHVSYGR(L)	
956.509	955.501	955.513	-0.011	-12	454	460	(R)LTFKYER(D)	
2369.209	2368.201	2368.112	0.090	38	458	476	(K)YERDSNYHLLMSVQESLER(K)	
1920.919	1919.911	1919.905	0.006	3	461	476	(R)DSNYHLLMSVQESLER(K)	
2056.040	2055.032	2055.054	-0.022	-11	478	496	(K)FGKHGGTIPVVPTAEFQDR(I)	
1723.869	1722.861	1722.869	-0.008	-5	481	496	(K)HGGTIPVVPTAEFQDR(I)	
2164.105	2163.097	2163.063	0.034	16	497	516	(R)ISGASEKDIVHSGLAYTMER(S)	
1491.715	1490.707	1490.719	-0.011	-8	504	516	(K)DIVHSGLAYTMER(S)	

1394.728	1393.720	1393.739	-0.019	-14	524	535	(R)TAMKYNLGLDLR(T)
963.511	962.503	962.519	-0.016	-16	528	535	(K)YNLGLDLR(T)
1079.540	1078.533	1078.566	-0.033	-31	536	545	(R)TAAYVNAIEK(V)

No. 2 ATP synthase alpha chain

m/z	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Start	End	Sequence	Modifications
1020.494	1019.486	1019.507	-0.021	-20	252	260	(K)RLTDADAMK(Y)	
1287.670	1286.662	1286.687	-0.025	-19	296	306	(K)HALIIYDDLK(Q)	
1553.759	1552.752	1552.731	0.020	13	325	337	(R)EAYPGDVFYLSR(L)	
1096.503	1095.495	1095.542	-0.047	-43	415	424	(R)AMKQVAGTMK(L)	2 Met Ox
2338.148	2337.141	2337.160	-0.020	-8	432	453	(R)EVAFAAQFGSLLDAATQQLLSR(G)	
2309.140	2308.132	2308.152	-0.020	-9	463	483	(K)QGQYSPMAIEEQVAVIYAGVR(G)	
2325.173	2324.165	2324.147	0.018	8	463	483	(K)QGQYSPMAIEEQVAVIYAGVR(G)	Met Ox (7)
2711.441	2710.433	2710.455	-0.022	-8	494	517	(K)ITKFESAFVSHVVSQHQSLGNIR(S)	
2369.210	2368.202	2368.229	-0.027	-11	497	517	(K)FESAFVSHVVSQHQSLGNIR(S)	
1577.819	1576.811	1576.850	-0.039	-25	530	543	(K)LKEIVTNFLAGFEP(-)	

No. 3 Carnitine O palmitoyltransferase 2

m/z	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Start	End	Sequence	Modifications
1063.586	1062.578	1062.583	-0.005	-5	1	8	(-)MMPRLFR(A)	
1964.046	1963.038	1963.028	0.010	5	63	78	(K)RYLNAQKPLLDLSQFR(R)	
1807.960	1806.952	1806.926	0.026	14	64	78	(R)YLNAQKPLLDLSQFR(R)	
2415.234	2414.226	2414.148	0.079	33	105	124	(K)QNKHTSYISGPWFDMYLTAR(D)	
2431.179	2430.171	2430.143	0.029	12	105	124	(K)QNKHTSYISGPWFDMYLTAR(D)	Met Ox (15)
2044.989	2043.981	2043.951	0.030	15	108	124	(K)HTSYISGPWFDMYLTAR(D)	
2060.978	2059.970	2059.946	0.024	12	108	124	(K)HTSYISGPWFDMYLTAR(D)	Met Ox (12)
2066.000	2064.992	2064.998	-0.005	-3	125	142	(R)DSIVLNFNPFMAFNPDPK(S)	
2082.021	2081.013	2080.993	0.020	10	125	142	(R)DSIVLNFNPFMAFNPDPK(S)	Met Ox (11)
1125.521	1124.513	1124.510	0.003	3	143	151	(K)SEYNDQLTR(A)	
1031.593	1030.586	1030.577	0.008	8	152	161	(R)ATNLTSAVR(F)	
1993.066	1992.058	1992.068	-0.010	-5	165	182	(K)TLQAGLLEPEVFHLNPSK(S)	
939.450	938.442	938.446	-0.003	-4	183	190	(K)SDTDAFKR(L)	
1701.896	1700.888	1700.885	0.003	2	226	239	(R)IPRPNRDELFTDTK(A)	
2484.242	2483.234	2483.222	0.012	5	275	296	(K)YILSDSSPVPEFPVAYLTSENR(D)	

1144.659	1143.652	1143.604	0.048	42	297	305	(R)DVWAE LRQK(L)	
1278.633	1277.625	1277.650	-0.025	-20	306	316	(K)LIFDGNEETLK(K)	
967.481	966.473	966.502	-0.029	-30	432	439	(K)EKFDTTVK(T)	
1999.019	1998.011	1998.042	-0.031	-15	434	450	(K)FDTTVKTLSIDSIQFQR(G)	
1307.650	1306.642	1306.688	-0.046	-35	440	450	(K)TLSIDSIQFQR(G)	
1549.813	1548.805	1548.826	-0.021	-13	440	453	(K)TLSIDSIQFQRGGK(E)	
2150.117	2149.109	2149.135	-0.026	-12	459	477	(K)KQLSPDAVAQLAFQMAFLR(Q)	Met Ox (15)
2022.096	2021.088	2021.040	0.048	24	460	477	(K)QLSPDAVAQLAFQMAFLR(Q)	Met Ox (14)
1519.844	1518.836	1518.852	-0.016	-10	499	511	(R)TETIRPASIFTKR(C)	
1024.495	1023.487	1023.492	-0.005	-5	511	518	(K)RCSEAFVR(D)	CAM-Cys (2)
2171.054	2170.046	2169.961	0.085	39	519	537	(R)DPSKHSV GELQHMM AECSK(Y)	CAM-Cys (17)
1401.709	1400.701	1400.698	0.003	2	632	642	(R)NAREFLHC VQK(C)	CAM-Cys (8)
1409.639	1408.631	1408.654	-0.023	-17	643	654	(K)CLE DIFDALE GK(A)	CAM-Cys (1)

No. 4 Purine nucleoside phosphorilase

m/z	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Start	End	Sequence	Modifications
2915.532	2914.524	2914.400	0.124	43	42	67	(K)LTQPQAFDYNEIPNFPQSTVQGHAGR(L)	
1022.545	1021.537	1021.571	-0.034	-33	68	76	(R)LVFGFLNGR(S)	
1987.982	1986.974	1986.959	0.015	8	68	84	(R)LVFGFLNGRSCVMMQGR(F)	CAM-Cys (11), Met Ox
968.386	967.378	967.404	-0.026	-26	77	84	(R)SCVMMQGR(F)	CAM-Cys (2)
1361.575	1360.567	1360.612	-0.045	-33	85	95	(R)FHM YEGYSLSK(V)	
1192.621	1191.614	1191.632	-0.019	-16	124	133	(K)FEVGDIMLIR(D)	
1737.861	1736.853	1736.842	0.011	6	134	148	(R)DHINLPGFCGQNPLR(G)	CAM-Cys (9)
1172.543	1171.535	1171.497	0.038	32	159	168	(R)FPAMSDAYDR(D)	
1574.652	1573.644	1573.665	-0.021	-13	159	171	(R)FPAMSDAYDRDMR(Q)	
992.538	991.530	991.524	0.006	6	172	179	(R)QKAFNAWK(Q)	
1465.681	1464.673	1464.693	-0.020	-14	174	185	(K)AFNAWKQMGEQR(E)	
2802.407	2801.399	2801.325	0.074	27	186	210	(R)ELQEGTYIMSAGPTFETVAESCLR(M)	CAM-Cys (22)
2818.440	2817.432	2817.320	0.113	40	186	210	(R)ELQEGTYIMSAGPTFETVAESCLR(M)	Met Ox (9), CAM-Cys (22)
1916.021	1915.013	1914.991	0.022	12	211	229	(R)MLGADAVGMSTVPEVIVAR(H)	
1748.905	1747.898	1747.919	-0.022	-13	230	244	(R)HCGLRVFGFSLITNK(V)	CAM-Cys (2)
1240.627	1239.620	1239.580	0.039	32	245	254	(K)VVM DYN NLEK(A)	Met Ox (3)
1168.594	1167.586	1167.589	-0.003	-2	255	265	(K)ASHQEVLEAGK(A)	
2228.212	2227.204	2227.203	0.001	0	266	285	(K)AAAQKLEQFVSILMESIPPR(E)	
2244.188	2243.180	2243.199	-0.019	-8	266	285	(K)AAAQKLEQFVSILMESIPPR(E)	Met Ox (14)

1758.953	1757.945	1757.939	0.007	4	271	285	(K)LEQFVSILMESIPPR(E)	
1774.933	1773.925	1773.933	-0.008	-4	271	285	(K)LEQFVSILMESIPPR(E)	Met Ox (9)
2044.079	2043.071	2043.082	-0.012	-6	271	287	(K)LEQFVSILMESIPPRER(A)	

No. 5 Sulfotransferase 1 A1

m/z	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Start	End	Sequence	Modifications
1439.787	1438.780	1438.776	0.004	3	1	12	(-)MEFSRPPLVHVK(G)	
2387.154	2386.146	2386.155	-0.009	-4	45	65	(K)SGTTWMSEILDMIYQGGKLEK(C)	
1909.921	1908.913	1908.925	-0.012	-6	82	99	(K)CPGVPSGLETLEETPAPR(L)	CAM-Cys (1)
1803.024	1802.017	1802.030	-0.014	-8	103	118	(K)THLPLSLLPQSLLDQK(V)	
918.433	917.425	917.440	-0.015	-16	174	179	(K)EWWELR(H)	
1774.895	1773.887	1773.909	-0.022	-13	180	193	(R)HTHPVLYLFYEDIK(E)	
2243.156	2242.148	2242.142	0.005	2	180	197	(R)HTHPVLYLFYEDIKENPK(R)	
975.553	974.545	974.591	-0.046	-47	202	209	(K)KILEFLGR(S)	
1925.940	1924.932	1924.953	-0.021	-11	210	226	(R)SLPEETVDSIVHHTSFK(K)	
1924.914	1923.906	1923.908	-0.001	-1	255	271	(K)GTTGDWKNFTVAQNER(F)	
1179.570	1178.563	1178.568	-0.005	-5	262	271	(K)NTFTVAQNER(F)	

No. 6 Hydroxymethylglutaryl-CoA synthase

m/z	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Start	End	Sequence	Modifications
1141.676	1140.668	1140.654	0.014	12	36	46	(R)FSTIPPAPLAK(T)	
2626.363	2625.355	2625.321	0.034	13	53	75	(K)DVGILALEVYFPAQYVDQTDLEK(F)	
994.527	993.519	993.524	-0.005	-5	84	92	(K)YTVGLGQTR(M)	
2356.118	2355.111	2355.102	0.008	4	93	112	(R)MGFCSVQEDINSLCLTVVQR(L)	CAM-Cys (4, 14)
2372.188	2371.180	2371.097	0.083	35	93	112	(R)MGFCSVQEDINSLCLTVVQR(L)	Met Ox (1), CAM-Cys (4, 14)
1142.598	1141.591	1141.624	-0.034	-30	117	126	(R)TKLPWDAVGR(L)	
1217.615	1216.608	1216.655	-0.048	-39	127	137	(R)LEVGTETIIDK(S)	
1432.724	1431.716	1431.782	-0.066	-46	127	139	(R)LEVGTETIIDKSK(A)	
1095.658	1094.650	1094.645	0.005	4	222	231	(K)APLVLEQGLR(G)	
1052.574	1051.566	1051.549	0.017	16	257	264	(K)LSIQCYLR(A)	CAM-Cys (5)
959.464	958.456	958.444	0.012	12	269	275	(R)CYAAYRR(K)	CAM-Cys (1)
932.510	931.502	931.527	-0.025	-27	307	314	(K)MVQKSLAR(L)	
2251.094	2250.086	2250.063	0.023	10	315	333	(R)LMFNDFLSSSSDKQNNLYK(G)	

925.428	924.420	924.438	-0.017	-19	359	366	(K)ASLDMFNK(K)	
941.472	940.464	940.432	0.032	34	359	366	(K)ASLDMFNK(K)	Met Ox (5)
1885.007	1883.999	1883.920	0.079	42	407	424	(R)IGAFSYGSGLAASFFSFR(V)	
1000.532	999.524	999.487	0.037	37	428	437	(K)DASPGSPLEK(L)	

No. 7 Hydroxymethylglutaryl-CoA synthase

m/z	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Start	End	Sequence	Modifications
2626.347	2625.340	2625.321	0.019	7	53	75	(K)DVGILALEVYFPAQYVDQTDLEK(F)	
1853.910	1852.902	1852.943	-0.041	-22	76	92	(K)FNNVEAGKYTVGLGQTR(M)	
994.502	993.495	993.524	-0.030	-30	84	92	(K)YTVGLGQTR(M)	
2356.102	2355.095	2355.102	-0.008	-3	93	112	(R)MGFCSVQEDINSLCLTVVQR(L)	CAM-Cys (4, 14)
2372.105	2371.097	2371.097	0.000	0	93	112	(R)MGFCSVQEDINSLCLTVVQR(L)	Met Ox (1), CAM-Cys (4,14)
1142.600	1141.592	1141.624	-0.033	-29	117	126	(R)TKLPWDAVGR(L)	
913.464	912.456	912.482	-0.026	-29	119	126	(K)LPWDAVGR(L)	
1095.616	1094.608	1094.645	-0.037	-34	222	231	(K)APLVLEQGLR(G)	
2859.448	2858.440	2858.322	0.118	41	232	256	(R)GTHMENAYDFYKPNLASEYPLVDGK(L)	
1052.523	1051.515	1051.549	-0.033	-32	257	264	(K)LSIQCYLR(A)	CAM-Cys (5)
959.455	958.447	958.444	0.003	3	269	275	(R)CYAAYRR(K)	CAM-Cys (1)
2871.445	2870.437	2870.316	0.121	42	283	306	(K)QAGNNQPFTLDDVQYMIFHTPFCK(M)	CAM-Cys (23)
1490.650	1489.642	1489.676	-0.034	-23	315	327	(R)LMFNDFLSSSSDK(Q)	
2251.095	2250.087	2250.063	0.024	11	315	333	(R)LMFNDFLSSSSDKQNNLYK(G)	
997.452	996.444	996.476	-0.032	-33	343	350	(K)LEETYTNK(D)	
925.435	924.427	924.438	-0.010	-11	359	366	(K)ASLDMFNK(K)	
1053.522	1052.514	1052.533	-0.019	-18	359	367	(K)ASLDMFNKK(T)	
2397.257	2396.249	2396.144	0.106	44	474	494	(K)VNFSPPGDTSNLFPGTWYLER(V)	
958.459	957.451	957.445	0.006	7	495	501	(R)VDEMHRK(K)	Met Ox (4)

No. 8 Ornithine aminotransferase

m/z	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Start	End	Sequence	Modifications
1767.867	1766.859	1766.848	0.011	6	32	46	(K)KTEQGPPSSEYIFER(E)	
1736.880	1735.873	1735.879	-0.007	-4	50	64	(K)YGAHNYHPLVALER(G)	
1410.698	1409.690	1409.676	0.014	10	65	76	(R)GKGIYMWDVEGR(Q)	
1225.559	1224.551	1224.560	-0.009	-7	67	76	(K)GIYMWDVEGR(Q)	

1241.576	1240.568	1240.555	0.014	11	67	76	(K)GIYMWDVEGR(Q)	Met Ox (4)
2312.063	2311.055	2311.048	0.007	3	77	96	(R)QYFDLSAYGAVSQGHCHK(I)	CAM-Cys (17)
1277.680	1276.673	1276.670	0.003	2	97	107	(K)IIEAMKSQVDK(L)	Met Ox (5)
1247.645	1246.637	1246.688	-0.051	-41	103	113	(K)SQVDKLTLSR(A)	
1952.934	1951.927	1951.921	0.006	3	114	129	(R)AFYNNVLGEYEEYITK(L)	
909.467	908.459	908.487	-0.028	-30	155	161	(R)RWGYTVK(G)	
1464.768	1463.760	1463.804	-0.043	-30	168	180	(K)AKIVFAVGNFWGR(T)	
1265.666	1264.658	1264.672	-0.013	-11	170	180	(K)IVFAVGNFWGR(T)	
1810.974	1809.966	1809.974	-0.008	-4	256	271	(R)HQVLFIADEIQTGLAR(T)	
2074.145	2073.137	2073.137	0.000	0	275	292	(R)WLAVDHENVRPDI VLLGK(A)	
2178.119	2177.111	2177.122	-0.010	-5	332	351	(R)IAIAALEVLEEEHLAENADK(M)	
2819.562	2818.554	2818.490	0.064	23	332	357	(R)IAIAALEVLEEEHLAENADKMGAILR(K)	
1056.584	1055.576	1055.598	-0.022	-21	363	372	(K)LPSDVVTAVR(G)	
1153.711	1152.704	1152.734	-0.031	-27	373	383	(R)GKGLLNAIVIR(E)	
968.605	967.597	967.618	-0.021	-21	375	383	(K)GLLNAIVIR(E)	
1889.053	1888.045	1888.065	-0.020	-10	397	413	(R)LRDNGLLAKPTHGDIIR(L)	
1619.862	1618.854	1618.879	-0.026	-16	399	413	(R)DNGLLAKPTHGDIIR(L)	
1492.866	1491.859	1491.866	-0.008	-5	414	426	(R)LAPPLVIKEDIIR(E)	

No. 9 Heat shock protein 75 kDa

m/z	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Start	End	Sequence	Modifications
989.511	988.503	988.461	0.042	42	90	97	(K)HEFQAETK(K)	
927.570	926.562	926.591	-0.029	-32	98	105	(K)KLLDIVAR(S)	
1506.791	1505.783	1505.845	-0.062	-41	99	111	(K)LLDIVARSLYSEK(E)	
1370.707	1369.699	1369.724	-0.025	-18	106	116	(R)SLYSEKEVFIR(E)	
2326.096	2325.088	2325.098	-0.010	-5	134	153	(R)VCEGQVLPMEIHLQTDAEK(G)	CAM-Cys (2)
2342.149	2341.141	2341.093	0.048	21	134	153	(R)VCEGQVLPMEIHLQTDAEK(G)	CAM-Cys (2), Met Ox (10)
2718.414	2717.407	2717.427	-0.021	-8	154	179	(K)GTITIQDTGIGMTKEELVSNLGTIAR(S)	
1687.825	1686.817	1686.833	-0.016	-9	184	198	(K)AFLEALQHQAEISSR(I)	
1328.555	1327.548	1327.546	0.001	1	261	271	(K)SDCKDFANESR(V)	CAM-Cys (3)
1676.826	1675.818	1675.836	-0.018	-11	279	292	(K)YSNFVSFPLYLNGR(R)	
1716.863	1715.855	1715.885	-0.030	-18	293	306	(R)RINTLQAIWMMDPK(D)	
1732.873	1731.865	1731.880	-0.015	-9	293	306	(R)RINTLQAIWMMDPK(D)	Met Ox
1560.756	1559.748	1559.784	-0.036	-23	294	306	(R)INTLQAIWMMDPK(D)	
1599.691	1598.683	1598.700	-0.017	-10	307	318	(K)DISEFQHEEFYR(Y)	

1224.615	1223.607	1223.630	-0.022	-18	319	328	(R)YIAQAYDKPR(F)	
2032.980	2031.972	2031.980	-0.008	-4	343	359	(R)SIFYVPEMKPSMFDVSR(E)	
2048.970	2047.962	2047.975	-0.012	-6	343	359	(R)SIFYVPEMKPSMFDVSR(E)	Met Ox
2064.935	2063.927	2063.970	-0.042	-20	343	359	(R)SIFYVPEMKPSMFDVSR(E)	2 Met Ox
1513.760	1512.752	1512.778	-0.027	-18	391	404	(R)GVVDESDIPLNLSR(E)	
1171.639	1170.631	1170.661	-0.030	-25	405	414	(R)ELLQESALIR(K)	
1686.783	1685.775	1685.791	-0.016	-9	439	451	(K)YAKFFEDYGLFMR(E)	
1324.581	1323.574	1323.596	-0.022	-17	442	451	(K)FFEDYGLFMR(E)	
1340.578	1339.570	1339.591	-0.021	-15	442	451	(K)FFEDYGLFMR(E)	Met Ox (9)
1303.699	1302.691	1302.667	0.024	19	452	463	(R)EGIVTTAEQDIK(E)	
2116.003	2114.995	2115.012	-0.017	-8	472	491	(R)YESSALPAGQLTSLSDYASR(M)	
1283.605	1282.597	1282.613	-0.015	-12	498	507	(R)NIYYLCAPNR(H)	CAM-Cys (6)
1575.712	1574.704	1574.719	-0.015	-9	508	520	(R)HLAEHSPYYEAMK(Q)	
1591.721	1590.713	1590.714	-0.001	0	508	520	(R)HLAEHSPYYEAMK(Q)	Met Ox (12)
2554.281	2553.273	2553.257	0.016	6	523	542	(K)QTEVLFICYEQFDELTLHLR(E)	CAM-Cys (7)
2017.038	2016.030	2016.042	-0.011	-6	549	565	(K)LISVETDIVVDHYKEEK(F)	
1108.481	1107.473	1107.483	-0.010	-9	566	575	(K)FEDTSPAGER(L)	
1565.760	1564.753	1564.737	0.016	10	566	579	(K)FEDTSPAGERLSEK(E)	
1752.820	1751.812	1751.822	-0.010	-6	576	589	(R)LSEKETEELMAWMR(N)	
1768.800	1767.792	1767.817	-0.025	-14	576	589	(R)LSEKETEELMAWMR(N)	Met Ox
1295.564	1294.556	1294.569	-0.013	-10	580	589	(K)ETEELMAWMR(N)	
1811.909	1810.901	1810.907	-0.006	-3	605	621	(R)LDTHPAMVTVLEMGAAR(H)	
1827.899	1826.891	1826.902	-0.011	-6	605	621	(R)LDTHPAMVTVLEMGAAR(H)	Met Ox
2397.224	2396.216	2396.209	0.007	3	605	625	(R)LDTHPAMVTVLEMGAARHFLR(M)	2 Met Ox
1492.825	1491.817	1491.841	-0.024	-16	637	649	(R)AQLLQPTLEINPR(H)	

No. 30 Catalase

m/z	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Start	End	Sequence	Modifications
1320.585	1319.577	1319.578	-0.001	-1	1	12	(-)ADSRDPASDQMK(Q)	
2278.152	2277.144	2277.171	-0.028	-12	16	37	(K)EQRAPQKPDVLTGGGNPIGDK(L)	
2818.553	2817.545	2817.481	0.064	23	19	46	(R)APQKPDVLTGGGNPIGDKLNIMTAGPR(G)	
972.517	971.509	971.522	-0.014	-14	38	46	(K)LNIMTAGPR(G)	
988.491	987.483	987.517	-0.034	-35	38	46	(K)LNIMTAGPR(G)	Met Ox (4)
2189.072	2188.064	2188.062	0.002	1	47	65	(R)GPLLVQDVVFTDEMAHFDR(E)	
2474.218	2473.210	2473.206	0.004	2	47	67	(R)GPLLVQDVVFTDEMAHFDRER(I)	

1048.576	1047.568	1047.619	-0.051	-49	68	76	(R)IPERVVHAK(G)	
2275.163	2274.155	2274.155	0.000	0	72	92	(R)VVHAKGAGAFGYFEVTHDITR(Y)	
1740.837	1739.829	1739.827	0.002	1	77	92	(K)GAGAFGYFEVTHDITR(Y)	
985.542	984.534	984.551	-0.016	-17	98	105	(K)VFEHIGKR(T)	
1483.681	1482.674	1482.695	-0.022	-15	112	126	(R)FSTVAGESGSADTVR(D)	
1851.901	1850.893	1850.876	0.017	9	112	129	(R)FSTVAGESGSADTVRDPR(G)	
2518.203	2517.196	2517.196	-0.001	0	135	155	(K)FYTEDGNWDLVGNNTPIFFIR(D)	
1520.742	1519.734	1519.749	-0.015	-10	156	168	(R)DAMLFPSFIHSQK(R)	
1676.839	1675.831	1675.851	-0.019	-12	156	169	(R)DAMLFPSFIHSQKR(N)	
1692.893	1691.885	1691.845	0.039	23	156	169	(R)DAMLFPSFIHSQKR(N)	Met Ox (3)
2010.949	2009.941	2009.928	0.013	7	203	220	(R)GIPDGHHRMNGYGSHTFK(L)	
1278.607	1277.600	1277.561	0.038	30	210	220	(R)HMNGYGSHTFK(L)	
1337.651	1336.643	1336.645	-0.001	-1	221	232	(K)LVNANGEAVYCK(F)	CAM-Cys (11)
1912.946	1911.938	1911.930	0.008	4	221	236	(K)LVNANGEAVYCKFHYK(T)	CAM-Cys (11)
984.499	983.492	983.504	-0.012	-12	243	251	(K)NLPVEEAGR(L)	
2242.172	2241.164	2241.102	0.062	27	243	262	(K)NLPVEEAGRLAQEDPDYGLR(D)	
1276.616	1275.609	1275.610	-0.001	-1	252	262	(R)LAQEDPDYGLR(D)	
1655.775	1654.767	1654.788	-0.021	-13	287	300	(K)EAETFPFNPFDLTK(V)	
2303.132	2302.124	2302.142	-0.018	-8	287	305	(K)EAETFPFNPFDLTKVWPHK(D)	
1648.921	1647.913	1647.914	-0.001	-1	301	314	(K)VWPHKDYPLIPVGK(L)	
2097.103	2096.095	2096.074	0.021	10	363	379	(R)HRLGPNYLQIPVNCPYR(A)	CAM-Cys (14)
977.486	976.478	976.520	-0.042	-43	380	387	(R)ARVANYQR(D)	
1493.714	1492.706	1492.691	0.016	10	431	443	(R)FNSANEDNVTQVR(T)	
1016.532	1015.524	1015.530	-0.006	-6	449	456	(K)VLNEEERK(R)	

Table 2S. MALDI-ToF MS identification details for differentially expressed proteins in livers N, HFD and HFD+T2 rats using Mascot software (www.matrixscience.com). Spot numbers refer to Table 2.

No. 1 Glutamate dehydrogenase 1							
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	Modifications
35 - 51	1730.908	1729.900	1729.959	-0.059	1	R.GQPSAVPQPGLTPVARR.H	
52 - 60	1049.434	1048.427	1048.457	-0.031	0	R.HYSEAATDR.E	
61 - 68	1011.481	1010.473	1010.435	0.039	0	R.EDDPNFFK.M	
69 - 76	1000.449	999.442	999.448	-0.007	0	K.MVEGFFDR.G	
69 - 76	1016.423	1015.416	1015.443	-0.027	0	K.MVEGFFDR.G	Oxidation (M)
91 - 98	1033.485	1032.477	1032.484	-0.006	1	K.TRENEEQK.R	
108 - 123	1894.079	1893.072	1893.066	0.006	0	R.IIKPCNHVLSLSFPIR.R	
108 - 124	2050.144	2049.136	2049.167	-0.031	1	R.IIKPCNHVLSLSFPIRR.D	
124 - 136	1581.735	1580.727	1580.722	0.005	1	R.RDDGSWEVIEGYR.A	
125 - 136	1425.620	1424.613	1424.621	-0.008	0	R.DDGSWEVIEGYR.A	
163 - 171	997.505	996.497	996.531	-0.034	0	K.ALASLMTYK.C	
163 - 183	2198.115	2197.107	2197.128	-0.020	1	K.ALASLMTYKCAVVDVPFGGAK.A	
172 - 183	1219.533	1218.525	1218.607	-0.082	0	K.CAVVDVPFGGAK.A	
212 - 231	2044.025	2043.017	2043.010	0.008	1	K.KGFIGPGIDVPAPDMSTGER.E	
213 - 231	1915.926	1914.919	1914.915	0.004	0	K.GFIGPGIDVPAPDMSTGER.E	
303 - 318	1748.893	1747.886	1747.883	0.003	0	K.TFVVQGFQGNVGLHSMR.Y	
303 - 318	1764.870	1763.863	1763.878	-0.015	0	K.TFVVQGFQGNVGLHSMR.Y	Oxidation (M)
347 - 363	1958.048	1957.041	1957.031	0.010	1	K.ELEDFKLQHGSILGFPA.A	
353 - 363	1196.648	1195.641	1195.671	-0.030	0	K.LQHGSILGFPA.A	
366 - 386	2293.109	2292.101	2292.120	-0.018	0	K.VYEGSILEADCDILIPAASEK.Q	
400 - 420	2242.172	2241.165	2241.164	0.001	1	K.IIAEGANGPTTPEADKIFLER.N	
421 - 444	2742.504	2741.496	2741.414	0.083	0	R.NIMVIPDLYLNAGGVTVSYFEWLK.N	
445 - 453	1059.515	1058.508	1058.526	-0.018	0	K.NLNHVSYGR.L	
454 - 460	956.509	955.502	955.513	-0.011	1	R.LTFKYER.D	
458 - 476	2369.209	2368.202	2368.112	0.090	1	K.YERDSNYHLLMSVQESLER.K	
461 - 476	1920.919	1919.912	1919.905	0.007	0	R.DSNYHLLMSVQESLER.K	
478 - 496	2056.040	2055.032	2055.054	-0.022	1	K.FGKHGGTIPVVPTAEFQDR.I	
481 - 496	1723.869	1722.862	1722.869	-0.007	0	K.HGGTIPVVPTAEFQDR.I	

497 - 516	2164.105	2163.097	2163.063	0.034	1	R.ISGASEKDIVHSGLAYTMER.S	
504 - 516	1491.715	1490.708	1490.719	-0.011	0	K.DIVHSGLAYTMER.S	
520 - 527	994.446	993.439	993.510	-0.071	1	R.QIMRTAMK.Y	Oxidation (M)
524 - 535	1394.728	1393.721	1393.739	-0.018	1	R.TAMKYNLGLDLR.T	
528 - 535	963.511	962.503	962.519	-0.015	0	K.YNLGLDLR.T	
536 - 545	1079.540	1078.533	1078.566	-0.033	0	R.TAAYVNAIEK.V	

No. 2 ATP synthase subunit alpha

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	Modifications
24 - 34	1108.484	1107.477	1107.567	-0.091	0	K.NALGSSFVGTR.N	
232 - 239	925.326	924.319	924.383	-0.064	0	R.FNDGTDEK.K	
262 - 270	1020.494	1019.487	1019.507	-0.020	1	K.RLTDADAMK.Y	
306 - 316	1287.670	1286.663	1286.687	-0.024	0	K.HALIIYDDLSK.Q	
335 - 347	1553.759	1552.752	1552.731	0.021	0	R.EAYPGDVFLHSR.L	
428 - 441	1607.773	1606.766	1606.850	-0.084	1	K.QVAGTMKLELAQYR.E	
442 - 463	2338.148	2337.141	2337.160	-0.019	0	R.EVAFAAQFGSDLDAATQQLSR.G	
473 - 493	2309.140	2308.132	2308.152	-0.020	0	K.QGQYSPMAIEEQVAVIYAGVR.G	
504 - 527	2711.441	2710.434	2710.456	-0.022	1	K.ITKFESAFLSHVVSQHQSSLGNIR.S	
507 - 527	2369.210	2368.202	2368.229	-0.026	0	K.FESAFLSHVVSQHQSSLGNIR.S	
540 - 553	1577.819	1576.812	1576.850	-0.038	1	K.LKEIVTNFLAGFEP.-	

No. 3 Carnitine O-palmitoyltransferase 2

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	Modifications
1 - 8	1063.586	1062.579	1062.583	-0.004	1	-.MMPRLLFR.A	
2 - 8	932.582	931.575	931.543	0.032	1	M.MPRLLFR.A	
64 - 78	1807.960	1806.953	1806.926	0.026	0	R.YLNAQKPLLDDSQFR.R	
64 - 79	1964.046	1963.039	1963.028	0.011	1	R.YLNAQKPLLDDSQFRR.T	
80 - 93	1553.680	1552.673	1552.756	-0.083	1	R.TEALCKNFETGVGK.E	
94 - 104	1274.611	1273.604	1273.678	-0.074	0	K.ELHAHLLAQDK.Q	
105 - 124	2415.234	2414.227	2414.148	0.079	1	K.QNKHTSYISGPWFDMYLAR.D	
108 - 124	2044.989	2043.982	2043.951	0.030	0	K.HTSYISGPWFDMYLAR.D	
125 - 142	2066.000	2064.993	2064.998	-0.005	0	R.DSIVLNFNPFMAFNPK.S	
143 - 151	1125.521	1124.514	1124.510	0.004	0	K.SEYNDQLTR.A	

152 - 161	1031.593	1030.586	1030.577	0.009	0	R.ATNLTVSAVR.F	
165 - 182	1993.066	1992.059	1992.068	-0.010	0	K.TLQAGLLEPEVFHNLNPSK.S	
183 - 190	939.450	938.443	938.446	-0.003	1	K.SDTDAFKR.L	
226 - 239	1701.896	1700.888	1700.885	0.004	1	R.IPRPNRDELFTDTK.A	
232 - 239	968.360	967.353	967.450	-0.097	0	R.DELFTDTK.A	
275 - 296	2484.242	2483.234	2483.222	0.012	0	K.YILSDSSPVPEFPVAYLTSEN.R.D	
297 - 305	1144.659	1143.652	1143.604	0.049	1	R.DVWAE LRQK.L	
306 - 316	1278.633	1277.626	1277.650	-0.025	0	K.LIFDGN EETLK.K	
432 - 439	967.481	966.473	966.502	-0.029	1	K.EKFDTTVK.T	
434 - 450	1999.019	1998.012	1998.042	-0.030	1	K.FDTTVKTL SIDS IQFQR.G	
440 - 450	1307.650	1306.643	1306.688	-0.045	0	K.TLSIDS IQFQR.G	
440 - 453	1549.813	1548.806	1548.826	-0.020	1	K.TLSIDS IQFQRGGK.E	
499 - 511	1519.844	1518.837	1518.852	-0.015	1	R.TETIRPASIFTKR.C	
511 - 518	1024.495	1023.487	1023.492	-0.005	1	K.RCSEAFVR.D	
519 - 537	2171.054	2170.047	2169.961	0.086	1	R.DPSKHSV GELQHMM AECSK.Y	
632 - 642	1401.709	1400.702	1400.698	0.003	1	R.NAREFLHCVQK.C	
643 - 654	1409.639	1408.632	1408.654	-0.023	0	K.CLEDIFDALEGK.A	

No. 4 Purine nucleoside phosphorylase

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	Modifications
2 - 12	1493.613	1492.606	1492.611	-0.005	0	M.ENEFTYEDYQR.T	
68 - 76	1022.545	1021.538	1021.571	-0.033	0	R.LVFGFLNGR.S	
68 - 84	1987.982	1986.975	1986.959	0.016	1	R.LVFGFLNGRSCVMMQGR.F	Oxidation (M)
77 - 84	968.386	967.379	967.404	-0.025	0	R.SCVMMQGR.F	
77 - 84	984.324	983.317	983.399	-0.082	0	R.SCVMMQGR.F	Oxidation (M)
85 - 95	1361.575	1360.568	1360.612	-0.044	0	R.FHMYEGYLSK.V	
124 - 133	1192.621	1191.614	1191.632	-0.018	0	K.FEVGDIMLIR.D	
124 - 133	1208.573	1207.566	1207.627	-0.061	0	K.FEVGDIMLIR.D	Oxidation (M)
134 - 148	1737.861	1736.853	1736.842	0.012	0	R.DHINLPGFCGQNPLR.G	
159 - 168	1172.543	1171.535	1171.497	0.039	0	R.FPAMSDAYDR.D	
159 - 171	1574.652	1573.645	1573.665	-0.021	1	R.FPAMSDAYDRDMR.Q	
172 - 179	992.538	991.531	991.524	0.007	1	R.QKAFNAWK.Q	
174 - 185	1465.681	1464.673	1464.693	-0.020	1	K.AFNAWKQMGEQR.E	
186 - 210	2802.407	2801.400	2801.325	0.075	0	R.ELQEGTYIMSAGPTFETVAESCLLR.M	
211 - 229	1916.021	1915.013	1914.991	0.023	0	R.MLGADAVGMSTVPEVIVAR.H	

230 - 244	1748.905	1747.898	1747.919	-0.021	1	R.HCGLRVFGFSLITNK.V	
245 - 254	1240.627	1239.620	1239.581	0.040	0	K.VVMDYNNLEK.A	Oxidation (M)
255 - 265	1168.594	1167.586	1167.588	-0.002	0	K.ASHQEVLKAGK.A	
266 - 285	2228.212	2227.205	2227.203	0.001	1	K.AAAQKLEQFVSILMESIPPR.E	
266 - 285	2244.188	2243.180	2243.198	-0.018	1	K.AAAQKLEQFVSILMESIPPR.E	Oxidation (M)
271 - 285	1758.953	1757.946	1757.939	0.007	0	K.LEQFVSILMESIPPR.E	
271 - 285	1774.933	1773.926	1773.934	-0.008	0	K.LEQFVSILMESIPPR.E	Oxidation (M)
271 - 287	2044.079	2043.071	2043.082	-0.011	1	K.LEQFVSILMESIPPRER.A	

No. 5 Sulfotransferase 1A1

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	Modifications
1 - 12	1439.787	1438.780	1438.776	0.005	0	-.MEFSRPPLVHVK.G	
45 - 65	2387.154	2386.146	2386.155	-0.009	1	K.SGTTWMSEILDMIYQGKLEK.C	
82 - 99	1909.921	1908.914	1908.925	-0.012	0	K.CPGVPSGLETLEETPAPR.L	
103 - 118	1803.024	1802.017	1802.030	-0.013	0	K.THLPLSLLPQSLLDQK.V	
174 - 179	918.433	917.425	917.440	-0.014	0	K.EWWELR.H	
180 - 193	1774.895	1773.888	1773.909	-0.022	0	R.HTHPVLYLFYEDIK.E	
180 - 197	2243.156	2242.148	2242.142	0.006	1	R.HTHPVLYLFYEDIKENPK.R	
202 - 209	975.553	974.546	974.591	-0.046	1	K.KILEFLGR.S	
210 - 226	1925.940	1924.933	1924.953	-0.020	0	R.SLPEETVDSIVHHTSFK.K	
255 - 271	1924.914	1923.907	1923.908	-0.001	1	K.GTTGDWKNFTVAQNER.F	
262 - 271	1179.570	1178.563	1178.568	-0.005	0	K.NFTVAQNER.F	

No. 6 Hydroxymethylglutaryl-CoA synthase

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	Modifications
1 - 9	1055.472	1054.465	1054.607	-0.142	1	-.MQRLLAPAR.R	
36 - 46	1141.676	1140.669	1140.654	0.014	0	R.FSTIPPAPLAK.T	
53 - 75	2626.363	2625.356	2625.321	0.034	0	K.DVGILALEVYFPAQYVDQTDLEK.F	
84 - 92	994.527	993.520	993.524	-0.004	0	K.YTVGLGQTR.M	
93 - 112	2356.118	2355.111	2355.102	0.009	0	R.MGFCSVQEDINSLCLTVVQR.L	
117 - 126	1142.598	1141.591	1141.624	-0.033	1	R.TKLPWDAVGR.L	
119 - 126	913.562	912.555	912.482	0.073	0	K.LPWDAVGR.L	
127 - 137	1217.615	1216.608	1216.655	-0.047	0	R.LEVGTETIIDK.S	

127 - 139	1432.724	1431.717	1431.782	-0.065	1	R.LEVGTETIIDKSK.A
222 - 231	1095.658	1094.650	1094.645	0.005	0	K.APLVLEQGLR.G
232 - 256	2859.478	2858.471	2858.322	0.148	0	R.GTHMENAYDFYKPNLASEYPLVDGK.L
257 - 264	1052.574	1051.566	1051.548	0.018	0	K.LSIQCYLR.A
269 - 275	959.464	958.457	958.444	0.012	1	R.CYAAAYRR.K
276 - 282	944.343	943.336	943.524	-0.188	1	R.KIQNQWK.Q
283 - 306	2871.473	2870.466	2870.316	0.150	0	K.QAGNNQPFTLDDVQYMIFHTPFCK.M
307 - 314	932.510	931.502	931.527	-0.025	1	K.MVQKSLAR.L
315 - 333	2251.094	2250.087	2250.063	0.024	1	R.LMFNDFLSSSSDKQNNLYK.G
343 - 350	997.579	996.572	996.476	0.096	0	K.LEETYTNK.D
351 - 358	901.411	900.403	900.528	-0.125	1	K.DVDKALLK.A
359 - 366	925.428	924.421	924.438	-0.017	0	K.ASLDMFNK.K
407 - 424	1885.007	1884.000	1883.921	0.079	0	R.IGAFSYGSGLAASFFSFR.V
428 - 437	1000.532	999.525	999.487	0.038	0	K.DASPGSPLEK.L
474 - 494	2397.344	2396.337	2396.144	0.193	0	K.VNFSPPGDTSNLFPGTWYLER.V
495 - 501	942.606	941.599	941.450	0.149	1	R.VDEMHRK.K

No. 7 Hydroxymethylglutaryl-CoA synthase

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	Modifications
53 - 75	2626.347	2625.340	2625.321	0.019	0	K.DVGILALEVYFPAQYVDQTDLEK.F	
76 - 92	1853.910	1852.902	1852.943	-0.041	1	K.FNNVEAGKYTVGLGQTR.M	
84 - 92	994.502	993.495	993.524	-0.029	0	K.YTVGLGQTR.M	
93 - 112	2356.102	2355.095	2355.102	-0.007	0	R.MGFCSVQEDINSLCLTVVQR.L	
117 - 126	1142.600	1141.592	1141.624	-0.032	1	R.TKLPWDAVGR.L	
119 - 126	913.464	912.456	912.482	-0.026	0	K.LPWDAVGR.L	
222 - 231	1095.616	1094.608	1094.645	-0.037	0	K.APLVLEQGLR.G	
257 - 264	1052.523	1051.516	1051.548	-0.033	0	K.LSIQCYLR.A	
269 - 275	959.455	958.448	958.444	0.003	1	R.CYAAAYRR.K	
276 - 282	944.484	943.477	943.524	-0.047	1	R.KIQNQWK.Q	
315 - 327	1490.650	1489.643	1489.676	-0.033	0	R.LMFNDFLSSSSDK.Q	
315 - 333	2251.095	2250.088	2250.063	0.025	1	R.LMFNDFLSSSSDKQNNLYK.G	
343 - 350	997.452	996.445	996.476	-0.032	0	K.LEETYTNK.D	
359 - 366	925.435	924.428	924.438	-0.010	0	K.ASLDMFNK.K	
359 - 367	1053.522	1052.514	1052.532	-0.018	1	K.ASLDMFNKK.T	

No. 8 Ornithine aminotransferase

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	Modifications
32 - 46	1767.867	1766.859	1766.848	0.012	1	K.KTEQGPPSSEYIFER.E	
33 - 46	1639.857	1638.849	1638.753	0.097	0	K.TEQGPPSSEYIFER.E	
50 - 64	1736.880	1735.873	1735.879	-0.006	0	K.YGAHNYHPLPVALER.G	
65 - 76	1410.698	1409.691	1409.676	0.015	1	R.GKGIYMWDVEGR.Q	
67 - 76	1225.559	1224.552	1224.560	-0.008	0	K.GIYMWDVEGR.Q	
67 - 76	1241.576	1240.569	1240.555	0.014	0	K.GIYMWDVEGR.Q	Oxidation (M)
77 - 96	2312.063	2311.056	2311.048	0.008	0	R.QYDFLSAYGAVSQGHCHKP.I	
97 - 107	1277.680	1276.673	1276.670	0.003	1	K.IIEAMKSQVDK.L	Oxidation (M)
103 - 113	1247.645	1246.638	1246.688	-0.051	1	K.SQVDKLTLSR.A	
114 - 129	1952.934	1951.927	1951.920	0.007	0	R.AFYNNVLGEYEEYITK.L	
155 - 161	909.467	908.460	908.487	-0.027	1	R.RWGYTVK.G	
156 - 165	1179.569	1178.561	1178.645	-0.084	1	R.WGYTVKGIQK.Y	
168 - 180	1464.768	1463.761	1463.804	-0.043	1	K.AKIVFAVGNFWGR.T	
170 - 180	1265.666	1264.659	1264.672	-0.013	0	K.IVFAVGNFWGR.T	
256 - 271	1810.974	1809.967	1809.974	-0.007	0	R.HQVLFIADEIQTGLAR.T	
275 - 292	2074.145	2073.138	2073.137	0.001	0	R.WLAVDHENVRPDIVLLGK.A	
332 - 351	2178.119	2177.112	2177.122	-0.010	0	R.IAIAALEVLEEEHLAENADK.M	
332 - 357	2819.562	2818.554	2818.490	0.064	1	R.IAIAALEVLEEEHLAENADKMGAILR.K	
363 - 372	1056.584	1055.576	1055.598	-0.021	0	K.LPSDVVTAVR.G	
373 - 383	1153.711	1152.704	1152.734	-0.030	1	R.GKGLLNAIVIR.E	
375 - 383	968.605	967.598	967.618	-0.020	0	K.GLLNAIVIR.E	
397 - 413	1889.053	1888.045	1888.064	-0.019	1	R.LRDNGLLAKPTHGDIIR.L	
399 - 413	1619.862	1618.854	1618.879	-0.025	0	R.DNGLLAKPTHGDIIR.L	
414 - 426	1492.866	1491.859	1491.866	-0.007	1	R.LAPPLVIKEDEIR.E	

No. 9 Heat shock protein 75 kDa

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	Modifications
90 - 97	989.511	988.504	988.461	0.042	0	K.HEFQAETK.K	
90 - 98	1117.478	1116.471	1116.556	-0.085	1	K.HEFQAETKK.L	
98 - 105	927.570	926.562	926.591	-0.029	1	K.KLLDIVAR.S	
99 - 111	1506.791	1505.784	1505.845	-0.062	1	K.LLDIVARSLYSEK.E	

106 - 116	1370.707	1369.699	1369.724	-0.025	1	R.SLYSEKEVFIR.E	
117 - 130	1558.755	1557.748	1557.836	-0.089	1	R.ELISNASDALEKLR.H	
134 - 153	2326.096	2325.088	2325.098	-0.010	0	R.VCEGQVLPMEIHLQTDAEK.G	
134 - 153	2342.149	2341.142	2341.093	0.049	0	R.VCEGQVLPMEIHLQTDAEK.G	Oxidation (M)
154 - 179	2718.414	2717.407	2717.427	-0.020	1	K.GTITIQDTGIGMTKEELVSNLGTIAR.S	
168 - 179	1301.631	1300.623	1300.699	-0.075	0	K.EELVSNLGTIAR.S	
184 - 198	1687.825	1686.818	1686.833	-0.015	0	K.AFLEALQHQETSSR.I	
261 - 271	1328.555	1327.548	1327.546	0.002	1	K.SDCKDFANESR.V	
279 - 292	1676.826	1675.819	1675.836	-0.017	0	K.YSNFVSFPLYLNGR.R	
293 - 306	1716.863	1715.856	1715.885	-0.029	1	R.RINTLQAIWMMDPK.D	
293 - 306	1732.873	1731.865	1731.880	-0.015	1	R.RINTLQAIWMMDPK.D	Oxidation (M)
294 - 306	1560.756	1559.749	1559.784	-0.035	0	R.INTLQAIWMMDPK.D	
307 - 318	1599.691	1598.684	1598.700	-0.016	0	K.DISEFQHEEFYR.Y	
319 - 328	1224.615	1223.608	1223.630	-0.022	0	R.YIAQAYDKPR.F	
329 - 342	1700.853	1699.846	1699.941	-0.095	1	R.FILHYKTDAPLNIR.S	
343 - 359	2032.980	2031.972	2031.980	-0.008	0	R.SIFYVPEMKPSMFDVSR.E	
343 - 359	2048.970	2047.963	2047.975	-0.012	0	R.SIFYVPEMKPSMFDVSR.E	Oxidation (M)
343 - 359	2064.935	2063.928	2063.970	-0.042	0	R.SIFYVPEMKPSMFDVSR.E	2 Oxidation (M)
391 - 404	1513.760	1512.752	1512.778	-0.026	0	R.GVVDSEDIPLNLSR.E	
405 - 414	1171.639	1170.632	1170.661	-0.029	0	R.ELLQESALIR.K	
427 - 434	1012.492	1011.485	1011.539	-0.054	1	K.FFIDQSKK.D	
439 - 451	1686.783	1685.776	1685.791	-0.016	1	K.YAKFFEDYGLFMR.E	
442 - 451	1324.581	1323.574	1323.596	-0.022	0	K.FFEDYGLFMR.E	
442 - 451	1340.578	1339.571	1339.591	-0.020	0	K.FFEDYGLFMR.E	Oxidation (M)
452 - 463	1303.699	1302.692	1302.667	0.025	0	R.EGIVTTAEQDIK.E	
472 - 491	2116.003	2114.995	2115.012	-0.017	0	R.YESSALPAGQLTSLSDYASR.M	
498 - 507	1283.605	1282.598	1282.613	-0.015	0	R.NIYYLCAPNR.H	
508 - 520	1575.712	1574.705	1574.719	-0.014	0	R.HLAEHSPYYEAMK.Q	
508 - 520	1591.721	1590.714	1590.714	0.000	0	R.HLAEHSPYYEAMK.Q	Oxidation (M)
523 - 542	2554.281	2553.274	2553.257	0.016	0	K.QTEVLFCYEQFDELTLHLR.E	
549 - 565	2017.038	2016.031	2016.042	-0.011	1	K.LISVETDIVVDHYKEEK.F	
566 - 575	1108.481	1107.474	1107.483	-0.010	0	K.FEDTSPAGER.L	
566 - 579	1565.760	1564.753	1564.737	0.016	1	K.FEDTSPAGERLSEK.E	
576 - 589	1752.820	1751.813	1751.822	-0.009	1	R.LSEKETEELMAWMR.N	
576 - 589	1768.800	1767.793	1767.817	-0.025	1	R.LSEKETEELMAWMR.N	Oxidation (M)
580 - 589	1295.564	1294.556	1294.569	-0.012	0	K.ETEELMAWMR.N	
605 - 621	1811.909	1810.902	1810.907	-0.005	0	R.LDTHPAMVTVLEMGAAR.H	

605 - 621	1827.899	1826.892	1826.902	-0.010	0	R.LDTHPAMVTVLEMGAAR.H	Oxidation (M)
605 - 625	2397.224	2396.217	2396.209	0.008	1	R.LDTHPAMVTVLEMGAARHFLR.M	2 Oxidation (M)
626 - 636	1361.758	1360.751	1360.677	0.074	1	R.MQQLAKTQEER.A	
637 - 649	1492.825	1491.817	1491.841	-0.024	0	R.AQLLQPTLEINPR.H	

No. 30 Catalase

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	Modifications
2 - 13	1320.585	1319.577	1319.578	0.000	1	M.ADSRDPASDQMK.Q	
6 - 13	907.313	906.305	906.375	-0.070	0	R.DPASDQMK.Q	Oxidation (M)
17 - 38	2278.152	2277.144	2277.171	-0.027	1	K.EQRAPQKPDVLTGGGNPIGDK.L	
20 - 47	2818.553	2817.545	2817.481	0.065	1	R.APQKPDVLTGGGNPIGDKLNIMTAGPR.G	
39 - 47	972.517	971.509	971.522	-0.013	0	K.LNIMTAGPR.G	
39 - 47	988.491	987.483	987.517	-0.034	0	K.LNIMTAGPR.G	Oxidation (M)
48 - 66	2189.072	2188.065	2188.062	0.002	0	R.GPLLVQDVVFTDEMAHFDR.E	
48 - 68	2474.218	2473.211	2473.206	0.005	1	R.GPLLVQDVVFTDEMAHFDRER.I	
69 - 77	1048.576	1047.568	1047.619	-0.051	1	R.IPERVVHAK.G	
73 - 93	2275.163	2274.155	2274.155	0.001	1	R.VVHAKGAGAFGYFEVTHDITR.Y	
78 - 93	1740.837	1739.830	1739.827	0.003	0	K.GAGAFGYFEVTHDITR.Y	
99 - 106	985.542	984.535	984.551	-0.016	1	K.VFEHIGKR.T	
113 - 127	1483.681	1482.674	1482.695	-0.021	0	R.FSTVAGESGSADTVR.D	
113 - 130	1851.901	1850.894	1850.876	0.018	1	R.FSTVAGESGSADTVRDPR.G	
136 - 156	2518.203	2517.196	2517.197	0.000	0	K.FYTEDGNWDLVGNNTPIFFIR.D	
157 - 169	1520.742	1519.735	1519.749	-0.015	0	R.DAMLFPSFIHSQK.R	
157 - 170	1676.839	1675.832	1675.850	-0.019	1	R.DAMLFPSFIHSQKR.N	
157 - 170	1692.893	1691.885	1691.845	0.040	1	R.DAMLFPSFIHSQKR.N	Oxidation (M)
170 - 177	993.479	992.472	992.552	-0.080	1	K.RNPQTHLK.D	
204 - 221	2010.949	2009.942	2009.928	0.014	1	R.GIPDGHRHMNGYGSHTFK.L	
211 - 221	1278.607	1277.600	1277.561	0.039	0	R.HMNGYGSHTFK.L	
222 - 233	1337.651	1336.644	1336.645	-0.001	0	K.LVNANGEAVYCK.F	
222 - 237	1912.946	1911.939	1911.930	0.009	1	K.LVNANGEAVYCKFHYK.T	
244 - 252	984.499	983.492	983.504	-0.012	0	K.NLPVEEAGR.L	
244 - 263	2242.172	2241.164	2241.103	0.062	1	K.NLPVEEAGRLAQEDPDYGLR.D	
253 - 263	1276.616	1275.609	1275.610	-0.001	0	R.LAQEDPDYGLR.D	
288 - 301	1655.775	1654.767	1654.788	-0.021	0	K.EAETFPFNPFDLTK.V	
288 - 306	2303.132	2302.125	2302.142	-0.018	1	K.EAETFPFNPFDLTKVWPHK.D	

302 - 315	1648.921	1647.913	1647.914	-0.001	1	K.VWPHKDYPLIPVGK.L
355 - 363	1119.652	1118.645	1118.551	0.094	0	R.LFAYPDTHR.H
364 - 380	2097.103	2096.096	2096.074	0.022	1	R.HRLGPNYLQIPVNCPYR.A
381 - 388	977.486	976.479	976.520	-0.041	1	R.ARVANYQR.D
432 - 444	1493.714	1492.707	1492.691	0.016	0	R.FNSANEDNVTQVR.T
450 - 457	1016.532	1015.524	1015.530	-0.005	1	K.VLNEEERK.R
459 - 468	1211.556	1210.549	1210.613	-0.064	0	R.LCENIANHLK.D
