

Accession	Description	Sequence coverage (%)	Score	Ratio+SD	P-value
P0CG51	Polyubiquitin-B	97.05	355.41	1.412437	0.046024
P63018	Heat shock cognate 71 kDa protein	87.62	2685.68	1.73033	0.007834
M0RCB1	Heat shock cognate 71 kDa protein	79.88	2488.48	1.765353	0.000408
P14659	Heat shock-related 70 kDa protein2	30.49	399.97	1.743284	0.00182
M0R8M9	Heat shock cognate 71 kDa protein	81.89	1822.2	1.77616	0.031028
P04906	Glutathione S-transferase P	91.9	966.55	2.846058	0.043078
P00173	Cytochrome b5	92.54	228.05	2.072059	0.040968
O35244	Peroxisomal oxidase	85.27	575.5	2.407127	0.038773
P10960	Sulfated glycoprotein 1	45.49	201.84	1.855984	0.00029
P07335	Creatine kinase B-type	77.95	511.43	1.538768	0.034791
P05982	NAD(P)H dehydrogenase [quinone] 1	92.34	189.83	3.209328	0.006881
P02767	Transthyretin	67.35	220.79	1.630304	0.04253
M0RCX0	Pterin-4- α -carbinolamine dehydratase	64.57	54.22	1.718009	0.027559
P01836	Ig kappa chain C region, A allele	57.55	108.22	2.023165	0.033602
F1LP60	Moesin (Fragment)	65.1	166.63	3.509945	0.022846
P31977	Ezrin	26.79	97.73	3.509945	0.022846
D3ZTR5	Protein Zbed5 transcription factor	15.59	56.67	1.359699	0.012188
P62161	Calmodulin	76.51	140.66	1.623685	0.035661
Q6AYH5	Dynactin subunit 2	81.34	102.55	2.544214	0.04482
Q68FU3	Electron transfer flavoprotein subunit β	68.24	102.02	1.378183	0.027853
Q6P9V6	Proteasome subunit α type	43.98	76.38	22.21342	0.041745
F1MAB9	Protein Tpd52	40.18	31.66	4.239866	0.004339
P51886	Lumican	38.46	101.04	2.450671	0.002599
B0BNK1	Protein Rab5c	53.7	51.71	2.516557	0.029638
B2RYS8	NADH dehydrogenase (Ubiquinone) 1 β subcomplex 8	40.32	2.83	8.503979	0.036967
F1LMP7	Granulins	19.08	36.77	5.902347	0.039249
P09527	Ras-related protein Rab-7a	72.95	46.13	2.241089	0.020963
B0K010	Thioredoxin Domain Containing protein 17	60.16	14.55	2.773801	0.040354

Q5M7T9	Threonine synthase-like 2	62.06	124.03	1.83096	0.017857
Q5EBC7	Rab GTPase-binding effector protein 2	55.96	59.65	2.768731	0.026171
D3ZBB2	RCG64160	28.69	5.77	8.554427	0.01725
P62074	Mitochondrial import inner membrane translocase subunit Tim10	61.11	27.29	2.724346	0.001188
P14841	Cystatin-C	20	13.63	2.360779	0.005784
Q5U1X1	Oligoribonuclease, mitochondrial	57.38	42.9	3.79982	0.043906
Q9WVH8	Fibulin-5	28.13	29.59	3.101038	0.028942
F1LV94	Protein Asap2 (Fragment)	8.63	2.37	47.45525	0.032682
B5DF55	Protein Stam	28.34	34.87	8.030781	0.049278
D3ZWN1	Protein Zfp259	56.21	27.72	3.194902	0.025782
P36972	Adenine phosphoribosyltransferase	71.67	34.37	8.227029	0.023299
Q6AXW2	Protein Tmod3	51.99	44.7	4.827979	0.030639
P50411	Protein phosphatase inhibitor 2	14.15	15.16	12.17887	0.045397
G3V6D3	ATP synthase subunit beta	80.34	28	24.27784	0.000709
Q64428	Trifunctional enzyme subunit alpha, mitochondrial	52.56	63.12	3.293405	0.012022
Q99PD6	Transforming growth factor beta-1-induced transcript 1 protein	41.43	17.42	3.282076	0.016727
P50408	V-type proton ATPase subunit F	81.51	34.46	2.71806	0.015603
Q5PQK2	Fusion, derived from t(1216) malignant liposarcoma (Human)	20.27	28.43	2.777947	0.01493
Q60587	Trifunctional enzyme subunit beta, mitochondrial	45.89	29.01	2.431164	0.025443
P23965	Enoyl-CoA delta isomerase 1, mitochondrial	61.59	16.53	2.80938	0.041896
Q5M9G3	Caprin-1	49.65	18.07	26.78835	0.017034
D3ZXY4	Protein Aldh8a1	62.83	24.32	8.020514	0.034677
D3ZWJ1	Protein Dnlz	5.2	2.42	3.645078	0.033616
Q66H94	Peptidyl-prolyl cis-trans isomerase FKBP9	23.86	2.46	14.32083	0.024593
Q9Z2L0	Voltage-dependent anion-selective channel protein 1	57.6	4.08	2.218091	0.004565
P52847	Sulfotransferase family cytosolic 1B member 1	28.43	11.2	73.47571	0.00632
P31430	Dipeptidase 1	41.95	3.87	3.711116	0.016513

P62994	Growth factor receptor-bound protein 2	51.15	12.84	1.900879	0.00403
Q5FWT9	Suppressor of IKBKE 1	52.17	8.57	7.401652	0.030314
P05964	Protein S100-A6	47.19	5.79	9.993081	0.036439
D4ABI6	Protein RGD1561252	56.96	8.64	5.983627	0.025687
Q6MG76	Protein Skiv2l	6.69	4.75	1.709551	0.022702
P32551	Cytochrome b-c1 complex subunit 2, mitochondrial	62.61	3.52	6.89386	0.028782
Q499P2	Leukotriene A-4 hydrolase	26.19	5	1.546276	0.049539
F1M0L7	Annexin (Fragment)	62.35	1.79	4.20332	0.0027
Q499S6	Cathepsin F	9.74	2.18	8.784867	0.037444

Table S1. Up-regulated proteins in HG rats liver.

ID	name	Sequence coverage (%)	Score	Ratio+SD	P-value
O88752	Epsilon 1 globin	34.69	264.28	0.436021	0.043763
D3ZKR3	Glyceraldehyde-3-phosphate dehydrogenase	52.99	875.27	0.649527	0.036055
D3ZEN2	Glyceraldehyde-3-phosphate dehydrogenase	47.27	237.84	0.667896	0.040667
P04762	Catalase	94.88	4741.07	0.777087	0.040533
P13255	Glycine N-methyltransferase	89.08	2899.04	0.364228	0.041491
M0R6J1	Glyceraldehyde-3-Phosphate Dehydrogenase	39.39	296.06	0.316538	0.005842
Q920P0	L-xylulose reductase	90.57	1339.47	0.302818	0.036168
Q07523	Hydroxyacid oxidase 2	91.22	1876.48	0.264111	0.024474
B0BN46	Grhpr protein	88.66	1037.74	0.171527	0.016547
Q58FK9	Kynurenine--oxoglutarate transaminase 3	63	761.95	0.548214	0.033444
O08557	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	78.95	287.31	0.430164	0.014069
P60892	Ribose-phosphate pyrophosphokinase 1	76.42	372.76	0.634923	0.011133
P09330	Ribose-phosphate pyrophosphokinase 2	55.35	300.17	0.644624	0.007056
D4A8Z3	Protein Frrs1	26.64	136.26	0.363454	0.002852
M0RBK1	Phosphoribosyl pyrophosphate synthetase 1-like 1 (Predicted)	43.4	200.12	0.605916	0.025146
F1M3E5	Uncharacterized protein (Fragment)	7.37	17.19	0.673743	0.026116
P13803	Electron transfer flavoprotein subunit alpha, mitochondrial	77.18	245.12	0.558185	0.008189
P23457	3-alpha-hydroxysteroid dehydrogenase	70.19	128.74	0.577471	0.028669
G3V9Z4	Putative L-aspartate dehydrogenase	86.06	154.05	0.240566	0.017221
O70593	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	48.41	110.67	0.618784	0.003652
G3V907	Protein LOC100911356	77.93	158.51	0.589961	0.024474
O35077	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic	61.32	74.11	0.230433	0.003939
G3V998	Lanosterol synthase	14.7	4.42	0.768431	0.006074

F1LRV6	GMP reductase	14.49	19.73	0.748249	0.000357
D4ACD4	Protein LOC100911166	40.51	21.42	0.31096	0.049896
D3ZDE4	Deoxyguanosine kinase (Predicted), isoform CRA_a	46.4	17.61	0.459619	0.04782
G3V9C9	Protein Zmiz2	13.04	2.72	0.31375	0.044187

Table S2. Down-regulated proteins in HG rats liver.

Accession	Description	Score	Sequence	Ratio+SD	P-value
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			coverage (%)		
Q6P9V6	Proteasome subunit alpha type	76.38	43.98	22.21342 ± 1.37	0.042
F1LV94	Protein Asap2 (Fragment)	2.37	8.63	47.45525 ± 5.13	0.033
G3V6D3	ATP synthase subunit beta	28	80.34	24.27784 ± 3.27	0.00071
Q5M9G3	Caprin-1	18.07	49.65	26.78835 ± 2.19	0.017
P52840	Sulfotransferase family cytosolic 1A member 1	11.2	28.43	73.47571 ± 5.18	0.0063
Q5XI77	Annexin	48	27.04	21.82555 ± 2.76	0.0092
Q642E6	Tripeptidyl peptidase I	35	24.51	28.14738 ± 3.53	0.033

Table S3. The list of the up-regulated over 20 times proteins in high dose (1500 mg/kg daily) of emodin for seven consecutive days in rat liver.

Accession	Description	Score	Sequence	Ratio+SD	P-value
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			coverage(%)		
P13803	Electron transfer flavoprotein subunit α	245.12	77.18	0.56 ± 0.17	0.0082
O88752	Epsilon 1 globin transfer/carrier protein	264.28	34.69	0.44 ± 0.08	0.044
D3ZEN2	Glyceraldehyde-3-phosphate dehydrogenase I	237.84	47.27	0.67 ± 0.12	0.041
M0R6J1	Glyceraldehyde-3-phosphate dehydrogenase II	296.06	39.39	0.32 ± 0.06	0.0058
O35077	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic	74.11	61.32	0.23 ± 0.08	0.0039
D3ZKR3	Glyceraldehyde-3-phosphate dehydrogenase	875.27	52.99	0.65 ± 0.07	0.0361

Table S4. The list of the down-regulated proteins associated with electron transfer.

Accession	Description	Score	Sequence coverage(%)	Ratio+SD	P-value
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P05982	NAD(P)H quinone dehydrogenase 1(Nqo1)	189.83	92.34	3.21±0.67	0.0069
D3ZXY4	aldehyde dehydrogenase 8 family, member A1(Aldh8a1)	24.32	62.83	8.02±1.21	0.034
P00173	cytochrome b5 type A(Cyb5a)	228.05	92.54	2.07±0.31	0.040
Q68FU3	electron transfer flavoprotein beta subunit(Etfb)	102.02	68.24	1.38±0.47	0.028
Q60587	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase, beta subunit(Hadhb)	29.01	45.89	2.43±0.72	0.025
O35244	peroxiredoxin 6(Prdx6)	575.50	85.27	2.41±0.37	0.039
M0RCX0	pterin-4 alpha-carbinolamine dehydratase 2(Pcbd2)	54.22	64.57	1.72±0.45	0.027
B0K010	thioredoxin domain containing 17(Txndc17)	14.55	60.16	2.77±0.23	0.040

Table S5. The list of the up-regulated proteins associated with oxidation and reduction reaction.

Accession	Description	Sequence coverage	Score	Ratio+SD	P-value
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		(%)			
P63018	Heat shock cognate 71 kDa protein 8	87.62	2685.68	1.73 ± 0.32	0.0078
M0RCB1	Heat shock cognate 71 kDa protein	79.88	2488.48	1.77 ± 0.47	0.00041
P14659	Heat shock-related 70 kDa protein2	30.49	399.97	1.74 ± 0.51	0.0018
M0R8M9	Heat shock cognate 71 kDa protein	81.89	1822.2	1.78 ± 0.22	0.031

Table S6. The list of the up-regulated proteins associated with heat shock 70 kDa proteins.

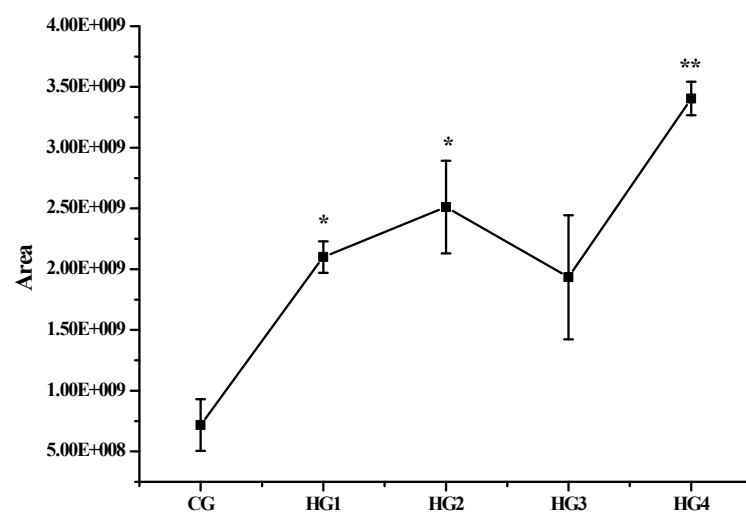


Figure S1. The change of HSP70 in CG, HG1, HG2, HG3 and HG4. * for $P < 0.05$, ** for $P < 0.01$.