SUPPLEMENTAL DATA I. Tryptic Peptides Mass Spectrometric Identification Data

(Numbers refer to the designation in Table 1 and Figure 3 of the main text; all the spots from identical gene products were listed sequentially)

HSP #1

gi|149063018 Mass: 22794 Score: 647 Queries matched: 8

heat shock 27kDa protein 1 [Rattus norvegicus]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
14	987.6119	986.6046	986.6025	2.13	1	16	63	1	R.RVPFSLLR.S
25	1075.5895	1074.5822	1074.5669	14.2	0	82	2.1e-05	1	R.QLSSGVSEIR.Q
30	1104.5233	1103.5160	1103.4996	14.9	0	54	0.014	1	R.QDEHGYISR.C
38	1149.6195	1148.6122	1148.5979	12.5	0	86	7.8e-06	1	R.LFDQAFGVPR.F
51	1358.6802	1357.6729	1357.6474	18.8	0	81	2.8e-05	1	R.AQIGGPESEQSGAK.-
57	1482.7737	1481.7664	1481.7474	12.8	1	49	0.04	1	K.EGVVEITGKHEER.Q
67	1797.9697	1796.9624	1796.9309	17.6	0	119	5.7e-09	1	R.VSLDVNHFAPEELTVK.T
73	1833.0039	1831.9966	1831.9680	15.6	0	160	3.7e-13	1	K.AVTQSAEITIPVTFEAR.A

HSP #2

gi|149063018 Mass: 22794 Score: 222 Queries matched: 3

heat shock 27kDa protein 1 [Rattus norvegicus]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
12	1149.6101	1148.6028	1148.5979	4.33	0	61	0.0028	1	R.LFDQAFGVPR.L
15	1797.9692	1796.9619	1796.9309	17.3	0	65	0.0012	1	R.VSLDVNHFAPEELTVK.T
17	1832.9781	1831.9708	1831.9680	1.56	0	98	7.1e-07	1	K.AVTQSAEITIPVTFEAR.A

CRMP2 #3

gi|157786744 Mass: 62273 Score: 499 Queries matched: 10

dihydropyrimidinase-like 2 [Rattus norvegicus]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1	908.5043	907.4970	907.4916	6.000		34	1.1	1	K.VFNLYPR.K
5	1015.5644	1014.5571	1014.5458	11.20		39	0.36	1	K.SAAEVIAQAR.K
22	1294.7053	1293.6980	1293.6864	9.020		17	59	2	R.MVIPGGIDVHTR.F
26	1323.7328	1322.7255	1322.7558	22.890		30	3.4	1	K.QIGENLIVPGGVK.T
31	1620.8092	1619.8019	1619.7865	9.500		86	9.8e-06	1	R.GLYDGPVCEVSVTPK.T + Carbamidomethyl (C)
34	1682.8883	1681.8810	1681.8635	10.40		72	0.00023	1	K.IVLEDGTLHVTEGSGR.Y

39	1793.8214	1792.8141	1792.8115	1.450	71	0.00032	1	K.DNFTLIPEGTNGTEER.M + Deamidated (NQ)
41	1822.9554	1821.9481	1821.9295	10.20	41	0.34	1	R.SITIANQTNCPLYVTK.V + Carbamidomethyl (C)
44	1915.9980	1914.9907	1914.9575	17.40	49	0.056	1	R.ISVGSDADLVIWDPDSVK.T
46	2149.0493	2148.0420	2148.0335	3.981	63	0.002	1	K.AVGKDNFTLIPEGTNGTEER.M + Deamidated (NQ)

Serum Albumin #4

gi|124028612 Mass: 68686 Score: 185 Queries matched: 4

Serum albumin precursor [Rattus norvegicus]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
14	1266.6349	1265.6276	1265.6292	1.23	0	58	0.0049	1	R.FPNAEFAEITK.L
20	1439.7874	1438.7801	1438.7780	1.49	0	45	0.11	1	K.APQVSTPTLVEAAR.N
24	1465.7865	1464.7792	1464.7725	4.59	0	44	0.16	1	K.LGEYGFQNAVLVR.Y
36	1960.0610	1959.0537	1959.0425	5.72	1	40	0.39	1	R.YTQKAPQVSTPTLVEAAR.N

Serum Albumin #5

gi|124028612 Mass: 68686 Score: 878 Queries matched: 11

Serum albumin precursor [Rattus norvegicus]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
16	1075.4691	1074.4618	1074.4804	17.30	0	28	4.3	1	K.CPYEEHIK.L + Carbamidomethyl C
22	1134.4912	1133.4839	1133.4958	10.44	0	29	3.5	1	K.CCTLPEAQR.L + 2 Carbamidomethyl C
24	1149.5880	1148.5807	1148.6077	23.52	0	78	5.2e-05	1	K.LVQEVTDFAK.T
33	1248.6077	1247.6004	1247.6299	23.60	1	59	0.0046	1	R.FKDLGEQHFK.G
35	1266.6090	1265.6017	1265.6292	21.69	0	90	3.2e-06	1	R.FPNAEFAEITK.L
44	1439.7590	1438.7517	1438.7780	18.25	0	135	1.1e-10	1	K.APQVSTPTLVEAAR.N
47	1455.7710	1454.7637	1454.7994	24.51	1	58	0.006	1	R.RHPDYSVSLLLR.L
50	1465.7448	1464.7375	1464.7725	23.88	0	122	2e-09	1	K.LGEYGFQNAVLVR.Y
54	1609.7461	1608.7388	1608.7824	27.09	0	107	8e-08	1	K.DVFLGTFLYEYSR.R
64	1882.8923	1881.8850	1881.9295	23.63	0	85	1.4e-05	1	R.RPCFSALTVDETYVPK.E + Carbamidomethyl C
68	1948.8788	1947.8715	1947.9109	20.19	1	90	4.5e-06	1	K.AADKDNCFATEGPNLVAR.S + Carbamidomethyl C

Serum Albumin #6

gi|124028612 Mass: 68686 Score: 547 Queries matched: 10

Serum albumin precursor [Rattus norvegicus]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
21	1299.6725	1298.6652	1298.6983	25.45	0	22	23	1	R.HPDYSVSLLLR.L
28	1439.7544	1438.7471	1438.7780	21.45	0	49	0.04	1	K.APQVSTPTLVEAAR.N
31	1455.7753	1454.7680	1454.7994	21.55	1	67	0.00064	1	R.RHPDYSVSLLLR.L
33	1465.7471	1464.7398	1464.7725	22.31	0	73	0.0002	1	K.LGEYGFQNAVLVR.Y
44	1609.7517	1608.7444	1608.7824	23.61	0	100	3.9e-07	1	K.DVFLGTFLYEYSR.R
47	1662.7997	1661.7924	1661.8447	31.44	0	59	0.0046	1	R.LPCVEDYLSAILNR.L +Carbamidomethyl C
53	1768.8278	1767.8205	1767.8614	23.11	1	16	1.1e+02	2	R.MSQRFPNAEFAEITK.L
56	1882.8949	1881.8876	1881.9295	22.25	0	60	0.0045	1	R.RPCFSALTVDETYVPK.E +Carbamidomethyl C
60	1959.9961	1958.9888	1959.0425	27.41	1	74	0.00017	1	R.YTQKAPQVSTPTLVEAAR.N
63	2059.9758	2058.9685	2059.0203	25.14	1	31	3.3	1	R.RHPYFYAPELLYYAEK.Y

Serum Albumin #7

gi|124028612 Mass: 68686 Score: 332 Queries matched: 6

Serum albumin precursor [Rattus norvegicus]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
7	1017.5113	1016.5040	1016.5291	24.67	0	37	0.79	1	K.SIHTLFGDK.L
15	1075.4612	1074.4539	1074.4804	24.65	0	42	0.18	1	K.CPYEEHIK.L + Carbamidomethyl C
20	1149.5874	1148.5801	1148.6077	24.04	0	78	5e-05	1	K.LVQEVTDFAK.T
29	1177.5747	1176.5674	1176.5999	27.63	1	70	0.00036	1	R.EAHKSEIAHR.F
40	1248.6028	1247.5955	1247.6299	27.53	1	42	0.22	1	R.FKDLGEQHFK.G
69	2059.9719	2058.9646	2059.0203	27.04	1	64	0.0018	1	R.RHPYFYAPELLYYAEK.Y

Serum Albumin #16

gi|124028612 Mass: 68686 Score: 523 Queries matched: 8

Serum albumin precursor [Rattus norvegicus]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
22	1149.5984	1148.5911	1148.6077	14.47	0	17	65	2	K.LVQEVTDFAK.T
33	1299.6838	1298.6765	1298.6983	16.75	0	24	14	1	R.HPDYSVSLLLR.L
41	1439.7607	1438.7534	1438.7780	17.07	0	53	0.019	1	K.APQVSTPTLVEAAR.N
44	1455.7813	1454.7740	1454.7994	17.43	1	64	0.0013	1	R.RHPDYSVSLLLR.L
47	1465.7472	1464.7399	1464.7725	22.24	0	84	1.5e-05	1	K.LGEYGFQNAVLVR.Y
55	1609.7550	1608.7477	1608.7824	21.56	0	97	8e-07	1	K.DVFLGTFLYEYSR.R
63	1882.8944	1881.8871	1881.9295	22.51	0	69	0.0005	1	R.RPCFSALTVDETYVPK.E + Carbamidomethyl (C)
68	1960.0078	1959.0005	1959.0425	21.44	1	118	5.8e-09	1	R.YTQKAPQVSTPTLVEAAR.N

Serum Albumin #17

gi|30794280 Mass: 69278 Score: 110 Queries matched: 4

Albumin [Bos taurus]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
5	927.4915	926.4842	926.4861	2.06	0	17	45	2	K.YLYEIAR.R
10	1163.6276	1162.6203	1162.6234	2.62	0	17	74	1	K.LVNELTEFAK.T
12	1479.8082	1478.8009	1478.7881	8.64	0	46	0.09	1	K.LGEYGFQNALIVR.Y

18	1639.9380	1638.9307	1638.9305	0.15	1	31	2.6	1	R.KVPQVSTPTLVEVSR.S

Also consistent with Serum albumin precursor protein (gi|1351907).

α-2-HS-glycoprotein #8

gi|6978477 Mass: 37979 Score: 115 Queries matched: 1

alpha-2-HS-glycoprotein [Rattus norvegicus]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
54	1846.8783	1845.8710	1845.9156	24.14	0	115	1.4e-08	1	K.VGQPGDAGAAGPVAPLCPGR.V + Carbamidomethyl (C)

Apolipoprotein E #9

gi|37805241 Mass: 35741 Score: 729 Queries matched: 10

Apolipoprotein E [Rattus norvegicus]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1	899.4150	898.4077	898.4337	28.95	0	40	0.17	1	R.FWDYLR.W
8	968.5255	967.5182	967.5451	27.75	0	85	7.5e-06	1	R.LGPLVEQGR.Q
13	1019.4564	1018.4491	1018.4753	25.73	0	43	0.15	1	R.LGADMEDLR.N
24	1075.5571	1074.5498	1074.5822	30.10	0	76	9.4e-05	1	R.LQAEIFQAR.I
38	1228.6041	1227.5968	1227.6320	28.63	1	68	0.0005	1	R.GRLEEVGNQAR.D
40	1239.6470	1238.6397	1238.6731	26.95	0	110	3.3e-08	1	R.TANLGAGAAQPLR.D
44	1289.5870	1288.5797	1288.6194	30.75	1	25	9.8	1	R.LGADMEDLRNR.L
59	1510.7625	1509.7552	1509.8012	30.43	1	81	3.2e-05	1	R.TANLGAGAAQPLRDR.A
62	1599.7375	1598.7302	1598.7787	30.35	0	111	2.9e-08	1	K.ELEEQLGPVAEETR.A
66	1720.7742	1719.7669	1719.8097	24.89	0	92	2.8e-06	1	R.NEVNTMLGQSTEELR.S

Serine Protease Inhibitor 1 #10

gi|32563565 Mass: 68180 Score: 104 Queries matched: 2

serine protease inhibitor 1 [Rattus norvegicus]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
22	1150.5529	1149.5456	1149.5778	28.02	0	47	0.062	1	K.VFSQQADLSR.I
38	1321.6136	1320.6063	1320.6561	37.70	0	57	0.0065	1	K.IAELFSDLEER.T

Peptides were consistent with other serpin family members:

A. Serine protease inhibitor 1	gil207042
B. Serpin A3L	gil2507387
C. Unnamed protein product	gil57231
D. Ab1-021	gil33086444

except that A, B, and C were published as smaller than the ~68 kD size observed on size separation.

Translocase OMM 70A #11

gi|47058988 Mass: 67402 Score: 94 Queries matched: 2

translocase of outer mitochondrial membrane 70 homolog A

[Rattus norvegicus]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
17	1079.5823	1078.5750	1078.5845	8.75	0	31	2.6	1	K.YMAEALLLR.A
41	1328.6102	1327.6029	1327.6157	9.59	0	64	0.0014	1	K.NADLSTFYQNR.A

Vimentin #12

gi|14389299 Mass: 53700 Score: 184 Queries matched: 7

vimentin [Rattus norvegicus]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
7	1081.5103	1080.5030	1080.4948	7.61	1	26	7	2	K.QESNEYRR.Q
11	1125.6171	1124.6098	1124.5978	10.7	1	25	8.6	1	R.FANYIDKVR.F
16	1254.5874	1253.5801	1253.5598	16.2	0	63	0.0016	1	R.LGDLYEEEMR.E
23	1309.6489	1308.6416	1308.5986	32.9	0	21	24	2	K.NLQEAEEWYK.S
30	1570.9180	1569.9107	1569.8878	14.6	0	31	2.5	1	R.ISLPLPNFSSLNLR.E
33	1688.8463	1687.8390	1687.8199	11.3	1	(19)	47	3	R.VEVERDNLAEDIMR.L
35	1704.8341	1703.8268	1703.8148	7.05	1	21	32	2	R.VEVERDNLAEDIMR.L + Oxidation (M)

α-ketoglutarate dehydrogenase #13A (same spot as α-KDH #13B)

gi|157819765 Mass: 116638 Score: 273 Queries matched: 6

oxoglutarate dehydrogenase-like [Rattus norvegicus]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2	**897.4280**	**896.4207**	**896.4392**	**20.62**	**0**	**31**	**1.6**	**2**	**R.FEDFLAR.K**
14	1011.6084	1010.6011	1010.6236	22.28	0	40	0.16	1	R.LNVLANVIR.K
24	1092.5159	1091.5086	1091.5247	14.76	0	37	0.72	1	R.SSPYPTDVAR.V
48	1492.8064	1491.7991	1491.8409	28.01	0	42	0.23	1	K.LVEDHLAVQSLIR.A
55	**1705.8571**	**1704.8498**	**1704.8909**	**24.09**	**0**	**23**	**22**	**2**	**R.LEQISPFPFDLIMR.E**
59	**1806.9137**	**1805.9064**	**1805.9523**	**25.42**	**0**	**102**	**2.9e-07**	**1**	**R.LPTTTFIGGSENTLSLR.E**

Present in OGDH-like only: Q2; Q55; Q59. Present in both OGDH & OGDH-like: Q14, Q24; Q48.

α-ketoglutarate dehydrogenase #13B (same spot as α-KDH #13A)

gi|62945278 Mass: 116221 Score: 117 Queries matched: 7

oxoglutarate dehydrogenase (lipoamide) [Rattus norvegicus]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1	**886.5294**	**885.5221**	**885.5436**	**24.26**	**0**	**19**	**31**	**1**	**R.QILLPFR.K**
10	**968.4639**	**967.4566**	**967.4763**	**20.36**	**0**	**28**	**3.2**	**1**	**R.FEEFLQR.K**
14	1011.6084	1010.6011	1010.6236	22.28	0	40	0.16	1	R.LNVLANVIR.K
24	1092.5159	1091.5086	1091.5247	14.76	0	37	0.72	1	R.SSPYPTDVAR.V
48	1492.8064	1491.7991	1491.8409	28.01	0	42	0.23	1	K.LVEDHLAVQSLIR.A

52	**1665.7374**	**1664.7301**	**1664.7617**	**18.97**	**0**	**24**	**14**	**1**	**R.TSFDEMLPGTHFQR.V**
66	**2001.9438**	**2000.9365**	**2000.9915**	**27.50**	**0**	**72**	**0.00028**	**1**	**R.NTNAGAPPGTAYQSPLSLSR.S**

Present in OGDH only: Q1; Q10; Q52; Q66. Present in both OGDH & OGDH-like: Q14, Q24; Q48.

α-ketoglutarate dehydrogenase #19 (different spot from α-KDH #1A,B)

gi|62945278 Mass: 116221 Score: 117 Queries matched: 3

oxoglutarate dehydrogenase (lipoamide) [Rattus norvegicus]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
62	1312.6390	1311.6317	1311.6571	19.37	1	20	35	3	R.STRFEEFLQR.K
70	1665.7367	1664.7294	1664.7617	19.39	0	41	0.31	1	R.TSFDEMLPGTHFQR.V
72	2001.9685	2000.9612	2000.9915	15.15	0	56	0.011	1	R.NTNAGAPPGTAYQSPLSLSR.S

Moesin #14

gi|13540689 Mass: 67697 Score: 111 Queries matched: 3

moesin [Rattus norvegicus]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
4	976.5310	975.5237	975.5389	15.60	0	25	12	6	K.QLFDQVVK.T
9	1104.5703	1103.5630	1103.5764	12.09	0	19	42	2	K.IGFPWSEIR.N
13	1182.5837	1181.5764	1181.5869	8.90	0	67	0.00059	1	K.APDFVFYAPR.L

Also consistent with proteins Radixin(gi|40804379), ezrin(gi|40804381), cytovillin(gi|340217)

MS observed:	**KQLFDQVVKT**	**KIGFPWSEIRN**	**KAPDFVFYAPRL**
Moesin:	KQLFDQVVKT	KIGFPWSEIRN	KAPDFVFYAPRL
Radixin:	KQLFDQVVKT	KIGFPWSEIRN	KAPDFVFYAPRL
Ezrin/Cytovillin:	KQLFDQVVKT	KIGFPWSEIRN	KAPDFVFYAPRL

LOH 11q2A #15

gi|38454250 Mass: 91425 Score: 299 Queries matched: 6

loss of heterozygosity, 11, chromosomal region 2, gene A homolog [Rattus norvegicus]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
24	1155.6625	1154.6552	1154.6812	22.45	0	52	0.017	1	R.YLLPAVLNPR.Y
29	1183.6149	1182.6076	1182.6284	17.61	0	57	0.0065	1	R.DVELLIYYR.E
45	1372.6124	1371.6051	1371.6315	19.26	0	28	5	1	K.VCGEFVFLMDR.S + Carbamidomethyl (C)
51	1467.6772	1466.6699	1466.6889	12.92	0	54	0.014	1	K.YTQETIEEAVER.V
54	1589.7897	1588.7824	1588.8097	17.14	0	75	0.00013	1	R.YVQELPLESDGALR.Y
62	1739.9294	1738.9221	1738.9577	20.48	1	33	1.7	1	K.RLDADLGGTEILTPLR.N

T-kininogen I #18

gi|205085 Mass: 47674 Score: 195 Queries matched: 3

LMW T-kininogen I precursor [Rattus norvegicus]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
5	994.5385	993.5312	993.5508	19.73	0	48	0.04	1	K.HTHLFALR.E
62	1802.8336	1801.8263	1801.8635	20.62	0	101	3e-07	1	K.YNAELESGNQFVLYR.V
67	1930.9301	1929.9228	1929.9584	18.45	1	46	0.12	1	K.KYNAELESGNQFVLYR.V

Also consistent with T-kininogen 1 precursor (T-kininogen I, gi|60392582); kininogen 1 (gi|80861401); major acute phase alpha-1 (gi|758263); and rCG36716, isoform CRA_e (gi|149019924).

Notes

1. Albumin:

- SA#17 is unlikely to be rat albumin, as comparisons below show:

65..........76...160......168...420...........434.436...........452

MS observed:	**KLVNELTEFAKT**	**KYLYEIARR**	**KLGEYGFQNALIVRY**t**RKVPQVSTPTLVEVSRS**
Bovine Albumin:	KLVNELTEFAKT	KYLYEIARR	KLGEYGFQNALIVRYtRKVPQVSTPTLVEVSRS
Rat Albumin:	KLVQEVTDFAKT	HYLHEVARR	KLGEYGFQNALIVRYtRKVPQVSTPTLVEVSRS
Rat Albumin Precursor:	KLVQEVTDFAKT	HYLHEVARR	KLGEYGFQNAVLVRYtQKAPQVSTPTLVEAARN

- All spots except SA#4 had peptides identified as unshared by one or more albumin spots.
- Serum Albumin peptides shared between different spots:

SA#4,5,6,7,16,17:	K.LGEYGFQNAVLVR.Y
SA#4,5,6,16:	K.APQVSTPTLVEAAR.N
SA#4,6,16:	R.YTQKAPQVSTPTLVEAAR.N
SA#4,5:	R.FPNAEFAEITK.L
SA#5,7,16,17:	K.LVQEVTDFAK.T (K.LV**N**ELT**E**FAK.T in Bos taurus #17)
SA#5,6,16:	K.DVFLGTFLYEYSR.R
SA#5,6,16:	R.RHPDYSVSLLLR.L
SA#5,7:	K.CPYEEHIK.L+Carbamidomethyl(C)
SA#5,7:	R.FKDLGEQHFK.G
SA#6,7:	R.RHPYFYAPELLYYAEK.Y
SA#6,16:	R.RPCFSALTVDETYVPK.E+Carbamidomethyl(C)
SA#6,16:	R.HPDYSVSLLLR.L

2. It also must be noted that among the 31 spots analyzed, 4 were associated with human keratin (contamination, see Supplemental Data II below), 1 was associated with bovine albumin, and α2-HS-glycoprotein (#8**)** was identified by only a single peptide, despite repeated attempts.

3. The suitability of this gel analysis approach was borne out in the results; of 25 distinct spots chosen for MALDI-TOF analyses, 19 rat proteins were identified (4 were human keratin contaminations, spot #8 had only 1 identifiable peptide, and 1 remained unidentified; 6 spots were reanalyzed due to insufficient protein). Furthermore, 15 of the 19 protein isoforms identified proved to be regulated both with age × injury (**Table 2**, A•B interactions). And each of the three proteins examined by immunoblot were regulated with age and injury (**Figs. 4, 5**)

Supplemental Data II. Keratin Data

gi|453155 **Mass:** 61950 **Score:** 120 **Queries matched:** 4
keratin 9 [Homo sapiens]

Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
897.4219	896.4146	896.4062	9.39	0	16	45	1	R.MTLDDFR.I
1307.6848	1306.6775	1306.6703	5.51	1	63	0.0019	1	R.IKFEMEQNLR.Q
1323.6757	1322.6684	1322.6652	2.41	1	(17)	74	5	R.IKFEMEQNLR.Q + Oxidation (M)
1851.9169	1850.9096	1850.9196	5.39	1	42	0.29	1	K.TLNDMRQEYEQLIAK.N

gi|119395750 **Mass:** 65999 **Score:** 87 **Queries matched:** 3
keratin 1 [Homo sapiens]

Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1065.5045	1064.4972	1064.5138	15.58	0	30	2.8	1	K.AQYEDIAQK.S
1277.7013	1276.6940	1276.7027	6.77	0	27	7.3	1	K.LALDLEIATYR.T
1716.8480	1715.8407	1715.8438	1.80	0	31	3.2	2	K.QISNLQQSISDAEQR.G

gi|40354192 **Mass:** 58792 **Score:** 392 **Queries matched:** 9
keratin 10 [Homo sapiens]

Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
995.5181	994.5108	994.5123	1.53	1	33	1.5	2	K.IKEWYEK.H
1090.5382	1089.5309	1089.5237	6.65	0	41	0.28	1	K.VTMQNLNDR.L
1109.5031	1108.4958	1108.4825	12.0	0	46	0.062	1	K.DAEAWFNEK.S
1165.5895	1164.5822	1164.5775	4.08	0	51	0.026	1	R.LENEIQTYR.S
1234.6843	1233.6770	1233.6717	4.32	1	56	0.008	1	R.LKYENEVALR.Q
1300.5818	1299.5745	1299.5877	10.14	1	43	0.17	1	K.NHEEEMKDLR.N
1357.7280	1356.7207	1356.7110	7.20	1	47	0.069	1	R.QSVEADINGLRR.V
1434.7761	1433.7688	1433.7626	4.32	1	49	0.041	1	K.IRLENEIQTYR.S
1707.7869	1706.7796	1706.7649	8.62	0	26	10	1	K.GSLGGGFSSGGFSGGSFSR.G

gi|547754 **Mass:** 65825 **Score:** 288 **Queries matched:** 5
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin-2e) (K2e) (CK 2e) (keratin-2)

Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1037.5304	1036.5231	1036.5189	4.07	0	38	0.48	1	R.YLDGLTAER.T
1082.6035	1081.5962	1081.5920	3.88	1	44	0.099	1	K.FASFIDKVR.F
1193.6245	1192.6172	1192.6088	7.07	0	77	6.7e-05	1	K.YEELQVTVGR.H
1320.5878	1319.5805	1319.5756	3.73	0	94	1.4e-06	1	R.HGGGGGGFGGGGFGSR.S
1329.6737	1328.6664	1328.6320	25.9	0	38	0.6	1	K.NVQDAIADAEQR.G

Supp. Data III. Fold induction of age- and injury-related protein isoforms.

COMPARISONS:		**A. INJURED vs. SHAM**				**B1. SHAMS by AGE**			**B2. INJUREDS by AGE**				**A•B INTER-ACTION**
Gene	**Spot#**	**Juvenile**	**Adult**	**Geriatric**	***P-value***	**J. vs A.**	**J. vs G.**	**A. vs G.**	**J. vs A.**	**J. vs G.**	**A. vs G.**	***P-value***	***P-value***
HSP	**2**	**2.72**	**2.20**	**2.41**	***0.0270***	**0.47**	**0.76**	**0.47**	**0.69**	**1.01**	**1.08**	*0.2300*	***0.0339***
SAP	**6**	**17.33**	**3.62**	**4.72**	***$4.2x10^{-6}$***	**0.63**	**1.04**	**0.64**	**0.56**	**0.71**	**0.76**	*0.3800*	*0.0715*
α2-HS-GP	**8**	**6.50**	**3.43**	**1.14**	***0.0024***	**0.39**	**0.66**	**0.41**	**0.37**	**1.87**	**1.99**	***0.0035***	***0.0011***
Apo E	**9**	**2.80**	**1.70**	**1.83**	*0.0700*	**0.32**	**0.36**	**0.22**	**0.61**	**0.63**	**0.67**	*0.3100*	***0.0297***
Moesin	**14**	**6.12**	**2.54**	**2.04**	***0.0027***	**0.34**	**0.32**	**0.20**	**0.43**	**0.51**	**0.54**	*0.1600*	***0.0155***
LOH11CR2A	**15**	**5.74**	**1.98**	**1.12**	***0.0180***	**0.32**	**0.29**	**0.18**	**0.51**	**0.83**	**0.89**	*0.0970*	***0.0126***
BSA	**17**	**11.64**	**1.21**	**0.42**	***0.0028***	**0.36**	**0.24**	**0.15**	**0.95**	**1.87**	**2.00**	***$6.8\ x10^{-6}$***	***0.0005***
SAP	**7**	**4.59**	**1.46**	**3.72**	***0.0035***	**0.26**	**4.33**	**2.68**	**0.58**	**3.75**	**4.00**	***$6.7x10^{-9}$***	***0.0006***
Serpin1	**10**	**5.99**	**1.71**	**4.13**	***0.0035***	**0.16**	**0.96**	**0.60**	**0.31**	**0.75**	**0.80**	***0.0110***	***0.0014***
Vimentin	**12**	**15.57**	**1.80**	**644.2**	***$2.6x10^{-5}$***	**0.27**	**99.98**	**61.83**	**0.48**	**0.50**	**0.53**	*0.4100*	*0.0594*
SAP	**16**	**4.48**	**4.02**	**24.68**	***0.0003***	**0.37**	**70.80**	**43.79**	**0.30**	**9.25**	**9.87**	***$3.4x10^{-15}$***	***0.0001***
HSP	**1**	**3.23**	**5.56**	**1.36**	***0.0290***	**1.62**	**0.39**	**0.24**	**0.94**	**0.92**	**0.98**	*0.1900*	***0.0383***
CRMP2	**3**	**5.52**	**3.81**	**2.79**	***0.0011***	**0.78**	**0.58**	**0.36**	**0.66**	**0.68**	**0.72**	*0.3600*	*0.0625*
SAP	**4**	**2.91**	**1.60**	**0.84**	*0.3100*	**0.18**	**0.12**	**0.08**	**0.36**	**0.47**	**0.50**	*0.4700*	***0.0293***
SAP	**5**	**3.45**	**3.12**	**1.02**	*0.0620*	**0.24**	**0.11**	**0.07**	**0.24**	**0.36**	**0.39**	*0.5000*	***0.0238***
T-kininogen1	**18**	**0.91**	**2.98**	**0.91**	*0.9800*	**0.71**	**0.06**	**0.04**	**0.77**	**0.22**	**0.24**	***$3.2\ x10^{-5}$***	*0.1092*
TOM70A	**11**	**1.93**	**0.77**	**0.40**	*0.2200*	**0.13**	**0.07**	**0.04**	**0.56**	**0.56**	**0.60**	***0.0065***	***0.0173***
αKGD	**13**	**0.24**	**0.81**	**0.30**	***0.0170***	**0.16**	**0.07**	**0.04**	**0.65**	**0.73**	**0.78**	***0.0005***	***0.0020***
αKGD	**19**	**1.57**	**0.77**	**0.58**	*0.7200*	**0.14**	**0.09**	**0.06**	**0.60**	**0.52**	**0.55**	*0.0610*	***0.0238***

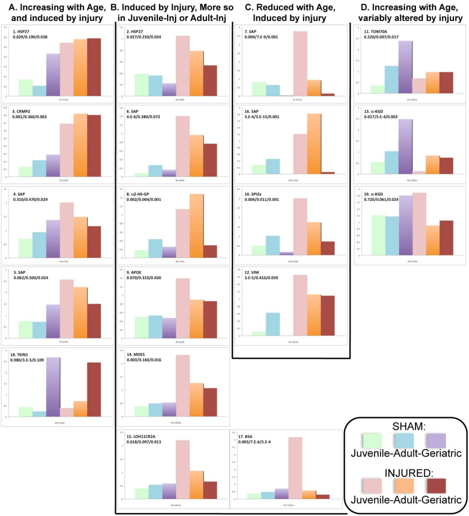
In this supplement to Table 2, each section above (A, B1, B2) compares the relative expression in the first group with the second group listed ($R.E._1/R.E._2$). Two-way analysis of variance showed significant differences in expression with age and injury between the 6 groups compared: juvenile-sham, juvenile injured; adult-sham, adult-injured; geriatric-sham, geriatric-injured. P-values for the two-way ANOVAs are in the columns to the right of each set of comparisons. Protein gene names and spot numbers as in **Table 1**.

Supplemental Data IV. Apparent Sham Effects Among Differentially Expressed Protein Isoforms.

In this analysis, the mean relative expression across all shams were compared to the mean naïves. Sham effects were inferred when the mean value differed by more than 3•SEM. The mean sham R.E. value across age groups deviated from the naïves by greater than 2 standard errors of the mean in 17 of the 19 spots, and by more than 3•SEM in 8 of the 19 spots (shaded boxes overlap with naïve relative expression value, 100%). SEM was deduced from the coefficient of variation returned by Z3 software across all groups using n = 8 per group.

Only 3 of the spots showed increased levels in shams compared to naïves (#18, 11, 13). All of the latter differed by more than 6•SEM from the naïve relative expression value, implying a virtual lack of expression in untreated animals.

Gene	Spot#	Average Shams	Average Injureds	C.V.	Shams ± 2•SEM	Shams ± 3•SEM	Injureds ±2•SEM	Injureds ± 3•SEM
HSP	#2	30.7%	75.5%	51%	67%	85%	111%	
SAP	#6	17.5%	107%	79%	73%	101%	51%	
α2-HS-GP	#8	24.5%	82.7%	79%	81%	109%	139%	
Apo E	#9	44.9%	94.5%	42%	75%	89%	124%	
Moesin	#14	26.3%	87.5%	66%	73%	97%	134%	
LOH11q2A	#15	25.2%	65.8%	68%	74%	98%	114%	
BSA	#17	4.8%	16.0%	127%	94%	139%	105%	
SAP	#7	0.9%	3.1%	119%	85%	127%	87%	129%
SPI2a	#10	13.9%	44.7%	79%	70%	98%	101%	
Vimentin	#12	20.4%	108%	77%	75%	102%	54%	
SAP	#16	10.8%	46.0%	104%	85%	121%	120%	
HSP	#1	86.0%	209%	49%	120%		174%	157%
CRMP2	#3	56.7%	209%	59%	98%	119%	167%	147%
SAP	#4	73.1%	115%	33%	97%	108%	90%	
SAP	#5	57.0%	122%	45%	89%	104%	91%	
T-kininogen1	#18	3251%	3439%	89%	3189%	3157%	3376%	3345%
TL70A	#11	390%	256%	58%	349%	329%	215%	194%
αKGD	#13	689%	289.7%	76%	634%	607%	236%	209%
αKGD	#19	95.3%	87.3%	28%	115%		107%	


A. Increasing with Age, and induced by injury
B. Induced by Injury, More so in Juvenile-Inj or Adult-Inj
C. Reduced with Age, Induced by injury
D. Increasing with Age, variably altered by injury
1. HSP27
0.029/0.190/0.038
2. HSP27
0.027/0.230/0.034
7. SAP
0.004/7.E-9/0.001
11. TOM70A
0.220/0.007/0.017
3. CRMP2
0.001/0.360/0.063
6. SAP
4.E-6/0.380/0.072
16. SAP
3.E-4/3.E-15/0.001
13. α-KGD
0.017/5.E-4/0.002
4. SAP
0.310/0.470/0.029
8. α2-HS-GP
0.002/0.004/0.001
10. SPI2a
0.004/0.011/0.001
19. α-KGD
0.720/0.061/0.024
5. SAP
0.062/0.500/0.024
9. APOE
0.070/0.310/0.030
12. VIM
3.E-5/0.410/0.059
18. TKIN1
0.980/3.E-5/0.109
14. MOES
0.003/0.160/0.016
15. LOH11CR2A
0.018/0.097/0.013
17. BSA
0.003/7.E-6/5.E-4
SHAM:
Juvenile-Adult-Geriatric
INJURED:
Juvenile-Adult-Geriatric

Supplemental Figure I. Expression trends of 19 spots identified by two-dimensional gel electrophoresis and mass-spectrometry of tryptic peptides as changing with both age and traumatic brain injury