

Supporting information

Identification of Altered Proteins in the Plasma of Rats with Chronic Prostatic Inflammation
Induced by Estradiol Benzoate and Sex Hormones

Zhijun Cao, Daniel T. Sloper[†], Noriko Nakamura*

Division of Systems Biology, National Center for Toxicological Research, U.S. Food and Drug
Administration, Jefferson, AR 72079, USA

[†] Current address: Independent researcher.

Table S1. Top ten proteins that mostly contribute to component 1 for each time point

PND 90	PND 100	PND 145	PND 200
Alpha-2 antiplasmin	AP-2 complex subunit beta	Angiotensinogen	Alpha-1-antiproteinase
			Antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5 (predicted)
Apolipoprotein M	ATP synthase subunit alpha, mitochondrial	Calmodulin-1	
	Biorientation of chromosomes in cell division 1-like 1	Carboxylic ester hydrolase	Apolipoprotein A-IV
Complement C5	Complement C3	Carboxypeptidase Q	Carboxypeptidase Q
Complement factor D	Complement C5	Complement factor H-related protein	Hemopexin
Fas apoptotic inhibitory molecule 3	Complement C8 alpha chain	Leukemia inhibitory factor receptor	Ig-like domain-containing protein
Gelsolin	Histidine-rich glycoprotein	Major urinary protein	Leukemia inhibitory factor receptor
Globin a4	Leukemia inhibitory factor receptor	Maltase-glucoamylase	LOC500183 protein
Hemoglobin subunit beta-2	Plasma protease C1 inhibitor	Myosin-9	Proline-rich 32
Pentaxin		Phosphatidylinositol glycan anchor biosynthesis, class A	
Secreted phosphoprotein 24	Serum paraoxonase/arylesterase 1		RCG27669

Table S2. Ingenuity canonical pathways in rat plasma significantly altered on PND 90, 100, 145, or 200 [-log(p-value)]

Ingenuity Canonical Pathways	PND 90	PND 100		PND 145		PND 200		Identified proteins
		EB	EB+T+E	EB	EB+T+E	EB	EB+T+E	
Significantly altered pathways on PNDs 90, 100, 145, and/or 200								
LXR/RXR activation	8.73	1.68	6	8.37	12.6	n.s.	15.3	SERPINF1
FXR/RXR activation	8.62	1.66	5.93	10.1	14.2	n.s.	15.1	SERPINF1
Coagulation system	7.39	n.s.	3.62	3.14	4.6	n.s.	4.84	SERPINF1
Complement system	7.29	n.s.	3.57	5	n.s.	1.89	6.74	CFB
Acute phase response signaling	6.07	n.s.	3.69	5.79	9.4	n.s.	13.6	CFB, SERPINF1
Systemic lupus erythematosus signaling	4.12	1.4	2.01	1.55	n.s.	n.s.	2.43	
Atherosclerosis signaling	3.56	1.65	2.51	4.9	5.72	n.s.	4.59	
IL-12 signaling and production in macrophages	3.51	1.64	2.48	4.83	5.64	n.s.	4.52	
Intrinsic prothrombin activation pathway	3.09	n.s.	1.56	1.33	n.s.	n.s.	2.82	
Production of nitric oxide and reactive oxygen species in macrophages	3.06	1.49	2.18	4.23	4.89	n.s.	3.92	
Clathrin-mediated endocytosis signaling	3.03	1.47	3.6	4.19	6.19	n.s.	6.67	AP2B1
Extrinsic prothrombin activation pathway	1.79	n.s.	1.98	1.74	n.s.	n.s.	3.67	
Actin cytoskeleton signaling	1.69	n.s.	n.s.	n.s.	1.31	n.s.	n.s.	GSN, MYH9
Iron homeostasis signaling pathway	2.08	n.s.	n.s.	n.s.	n.s.	n.s.	5.95	
Docosahexaenoic Acid (DHA) signaling	1.42	n.s.	1.61	n.s.	n.s.	n.s.	n.s.	SERPINF1
Xenobiotic metabolism AHR signaling pathway	n.s.	1.83	n.s.	2.37	n.s.	n.s.	n.s.	
Specifically altered pathway on PND 90								
Selenocysteine Biosynthesis II (archaea and eukaryotes)	2.22	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	
Specifically altered pathway on PND 100								
Lipid antigen presentation by CD1	n.s.	n.s.	1.77	n.s.	n.s.	n.s.	n.s.	AP2B1
PXR/RXR activation	n.s.	n.s.	1.38	n.s.	n.s.	n.s.	n.s.	
Glioma invasiveness signaling	n.s.	n.s.	1.32	n.s.	n.s.	n.s.	n.s.	
CNTF signaling	n.s.	2	n.s.	n.s.	n.s.	n.s.	n.s.	
Mouse embryonic stem cell pluripotency	n.s.	1.74	n.s.	n.s.	n.s.	n.s.	n.s.	

Role of NANOG in mammalian embryonic stem cell pluripotency	n.s.	1.68	n.s.	n.s.	n.s.	n.s.	n.s.	
Specifically altered pathway on PND 145								
Maturity onset diabetes of Young (MODY) signaling	n.s.	n.s.	n.s.	n.s.	3.92	n.s.	n.s.	
Cellular effects of sildenafil (Viagra)	n.s.	n.s.	n.s.	n.s.	2.9	n.s.	n.s.	MYH9
Hepatic fibrosis / hepatic stellate cell activation	n.s.	n.s.	n.s.	n.s.	2.47	n.s.	n.s.	MYH9
MSP-RON signaling pathway	n.s.	n.s.	n.s.	n.s.	2.4	n.s.	n.s.	
SPINK1 pancreatic cancer pathway	n.s.	n.s.	n.s.	n.s.	2.37	n.s.	n.s.	
LPS/IL-1 mediated inhibition of RXR function	n.s.	n.s.	n.s.	3.94	2.24	n.s.	n.s.	
Epithelial Adherens junction signaling	n.s.	n.s.	n.s.	n.s.	1.6	n.s.	n.s.	MYH9
Tight junction signaling	n.s.	n.s.	n.s.	n.s.	1.52	n.s.	n.s.	MYH9
ILK signaling	n.s.	n.s.	n.s.	n.s.	1.42	n.s.	n.s.	MYH9
Agranulocyte adhesion and diapedesis	n.s.	n.s.	n.s.	n.s.	1.41	n.s.	n.s.	MYH9
Apelin liver signaling pathway	n.s.	n.s.	n.s.	n.s.	1.38	n.s.	n.s.	
Calcium signaling	n.s.	n.s.	n.s.	n.s.	1.35	n.s.	n.s.	MYH9
Arsenate Detoxification I (glutaredoxin)	n.s.	n.s.	n.s.	2.34	n.s.	n.s.	n.s.	
Ascorbate recycling (cytosolic)	n.s.	n.s.	n.s.	2.34	n.s.	n.s.	n.s.	
Glutathione-mediated detoxification	n.s.	n.s.	n.s.	1.44	n.s.	n.s.	n.s.	
nNOS signaling in skeletal muscle cells	n.s.	n.s.	n.s.	1.34	n.s.	n.s.	n.s.	
NRF2-mediated oxidative stress response	n.s.	n.s.	n.s.	1.71	n.s.	n.s.	n.s.	
Senescence pathway	n.s.	n.s.	n.s.	1.41	n.s.	n.s.	n.s.	
Superoxide radicals degradation	n.s.	n.s.	n.s.	2.04	n.s.	n.s.	n.s.	
Synaptogenesis signaling pathway	n.s.	n.s.	n.s.	1.31	n.s.	n.s.	n.s.	
Vitamin-C transport	n.s.	n.s.	n.s.	1.57	n.s.	n.s.	n.s.	
Xenobiotic metabolism CAR signaling pathway	n.s.	n.s.	n.s.	1.71	n.s.	n.s.	n.s.	
Xenobiotic metabolism signaling	n.s.	n.s.	n.s.	1.37	n.s.	n.s.	n.s.	
Specifically altered pathway on PND 200								
Maturity onset diabetes of Young (MODY) signaling	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	2.53	
Airway pathology in chronic obstructive pulmonary disease	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	1.95	
Pyrimidine deoxyribonucleotides <i>de novo</i> Biosynthesis I	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	1.53	
Agrin interactions at neuromuscular junction	n.s.	n.s.	n.s.	n.s.	n.s.	1.57	n.s.	

Airway pathology in chronic obstructive pulmonary disease	n.s.	n.s.	n.s.	n.s.	n.s.	1.39	n.s.	
Asparagine Biosynthesis I	n.s.	n.s.	n.s.	n.s.	n.s.	3.45	n.s.	
Caveolar-mediated endocytosis signaling	n.s.	n.s.	n.s.	n.s.	n.s.	1.6	n.s.	
Cellular effects of sildenafil (Viagra)	n.s.	n.s.	n.s.	n.s.	n.s.	1.34	n.s.	
Crosstalk between dendritic cells and natural killer cells	n.s.	n.s.	n.s.	n.s.	n.s.	1.51	n.s.	
Death receptor signaling	n.s.	n.s.	n.s.	n.s.	n.s.	1.5	n.s.	
FAK signaling	n.s.	n.s.	n.s.	n.s.	n.s.	1.48	n.s.	
Fcγ receptor-mediated phagocytosis in macrophages and monocytes	n.s.	n.s.	n.s.	n.s.	n.s.	1.49	n.s.	
IGF-1 signaling	n.s.	n.s.	n.s.	n.s.	n.s.	1.44	n.s.	
Mechanisms of viral exit from host cells	n.s.	n.s.	n.s.	n.s.	n.s.	1.84	n.s.	
MSP-RON signaling pathway	n.s.	n.s.	n.s.	n.s.	n.s.	1.69	n.s.	
Paxillin signaling	n.s.	n.s.	n.s.	n.s.	n.s.	1.43	n.s.	
Remodeling of epithelial Adherens junctions	n.s.	n.s.	n.s.	n.s.	n.s.	1.63	n.s.	
RhoA signaling	n.s.	n.s.	n.s.	n.s.	n.s.	1.37	n.s.	
SPINK1 pancreatic cancer pathway	n.s.	n.s.	n.s.	n.s.	n.s.	1.68	n.s.	
VDR/RXR activation	n.s.	n.s.	n.s.	n.s.	n.s.	1.57	n.s.	
VEGF signaling	n.s.	n.s.	n.s.	n.s.	n.s.	1.46	n.s.	
Virus entry via endocytic pathways	n.s.	n.s.	n.s.	n.s.	n.s.	1.43	n.s.	

n.s.: No significances

Table S3. List of quantified proteins in rat plasma in the EB-treated group on PND 90 and the EB and EB+T+E group on PNDs 100, 145, and 200. In column stat_status 0, 1 and NA indicates no significant change, significant change, or no quantitative comparison for the following comparisons: PND90 EB vs control, PND 100 EB vs control, PND 100 EBTE vs Control, PND 145 EB vs control, PND 145 EBTE vs control, PND 200 EB vs control based on fold change ≥ 1.5 , $p < 0.05$, and FDR < 0.2 .

distinct Protein	differentia leProtein	protein Set	prote protein in_id	description	gene_name	stat_status	PND90 EB-vs.CTRL			PND100 EB-vs.CTRL			PND145 EB-vs.CTRL			PND200 EB-vs.CTRL													
							Ratio	P Value	FDR	Ratio	P Value	FDR	Ratio	P Value	FDR	Ratio	P Value	FDR											
1	0	481	P55159	544	Serum paraoxonase/arylesterase 1	Pon1	1111000	2.386	0.012	0.094	5.760	0.000	0.004	2.870	0.002	0.023	1.971	0.046	0.190	1.321	0.481	0.658	0.768	0.451	0.813	1.013	0.986	1.000	
0	0	213	P17475	531	Alpha-1-antiprotease	Serpina1	1011101	0.540	0.031	0.152	0.972	0.984	1.000	0.306	0.002	0.029	0.410	0.006	0.065	0.218	0.000	0.003	0.743	0.356	0.730	0.278	0.002	0.031	
0	0	345	P53813	309	Vitamin K-dependent protein 5	Pros1	1011000	0.354	0.040	0.168	1.514	0.073	0.387	0.356	0.002	0.023	0.539	0.047	0.190	0.876	0.956	1.000	0.516	0.079	0.470	1.159	0.927	1.000	
0	1	63	AOA096P6i	128	Complement C5	C5	1010001	0.154	0.004	0.066	1.887	0.130	0.422	2.809	0.017	0.159	1.047	0.961	0.998	0.950	0.847	0.921	1.049	0.991	1.000	1.951	0.019	0.101	
1	1	369	F1M4Q1	596	Cylicin_N domain-containing protein	Cyic2	101NANANANA	1.996	0.007	0.070	0.530	0.166	0.468	0.143	0.002	0.023													
1	1	257	Q80ZA3	331	Alpha-2 antiplasmin	Serpinf1	1010000	0.066	0.000	0.000	1.553	0.019	0.214	2.262	0.000	0.008	1.115	0.825	0.998	0.488	0.153	0.330	1.042	0.803	0.963	0.738	0.860	1.000	
0	1	156	P20762	458	Ig gamma-2C chain C region		10010NANA	1.626	0.013	0.094	0.382	0.458	0.741	13.462	0.154	0.604	0.070	0.022	0.124	0.350	0.937	0.991							
0	0	156	B1H2A4	135	Pnpt1 protein	Pnpt1	10010NANA	1.626	0.013	0.094	0.382	0.129	0.422	2.200	0.479	0.948	0.246	0.007	0.065	1.234	0.739	0.848							
0	0	90	AOA0G2K9	260	Carboxylic ester hydrolase	LOC501233	1000100	0.507	0.032	0.152	0.370	0.091	0.399	0.703	0.641	0.988	0.605	0.130	0.355	0.312	0.002	0.012	0.435	0.184	0.636	0.413	0.106	0.274	
0	1	11	Q91WX0	459	Complement factor H-related protein		1000100	3.477	0.019	0.105	3.100	0.170	0.469	0.512	0.213	0.608	4.095	0.216	0.479	17.103	0.001	0.007	6.183	0.030	0.277	7.310	0.067	0.198	
0	0	217	Q64268	361	Heparin cofactor 2	Serpind1	1000100	4.183	0.008	0.072	0.591	0.157	0.458	0.711	0.987	1.000	1.301	0.290	0.569	0.416	0.002	0.014	1.675	0.531	0.841	0.673	0.439	0.696	
0	0	6	Q5M7V3	290	LOC367586 protein	LOC367586	1000100	3.432	0.036	0.154	0.593	0.263	0.586	1.856	0.200	0.608	0.576	0.114	0.326	4.044	0.003	0.016	0.778	0.949	1.000	3.078	0.155	0.356	
0	0	54	AOA0G2J5i	115	Globin a4	Hbb	100NANA01	0.009	0.000	0.000	0.351	0.076	0.387	0.804	0.996	1.000													
0	1	2	D4ADK7	58	Antigen p97 (Melanoma associated) ident	Melft	1000001	0.626	0.048	0.199	0.879	0.843	1.000	0.850	0.633	0.988	0.809	0.901	0.998	0.606	0.231	0.431	0.701	0.219	0.648	0.255	0.000	0.027	
0	0	26	Q62930	157	Complement component C9	C9	1000001	2.856	0.034	0.154	19.443	0.306	0.616	14.074	0.565	0.962	0.964	0.916	0.998	1.361	0.438	0.637	0.395	0.032	0.279	0.305	0.022	0.105	
0	1	19	AOA0G2J5i	329	Globin c2	Hba-a2	1000001	0.109	0.006	0.070	0.239	0.148	0.447	0.248	0.045	0.274	0.750	0.577	0.856	0.411	0.293	0.483	1.110	0.768	0.963	0.021	0.032	0.119	
0	1	19	P01946	30	Hemoglobin subunit alpha-1/2	Hba1	1000001	0.108	0.006	0.070	0.249	0.141	0.438	0.228	0.041	0.270	0.750	0.577	0.856	0.411	0.293	0.483	1.031	0.756	0.963	0.020	0.032	0.119	
0	0	174	Q5M871	414	Fas apoptotic inhibitory molecule 3	Fcmr	1NANANANANANA	0.325	0.003	0.049																			
0	0	199	Q5UDQ9	653	Liprin beta 2		1NANANANANANA	0.185	0.019	0.105																			
1	1	248	D3E3E5	577	Phosphoseryl-tRNA kinase	Pstk	1NANANANANANA	0.075	0.014	0.094																			
0	0	177	AOA0G2K9	423	Secreted phosphoprotein 24	Spp2	1NANANANANANA	4.027	0.001	0.035																			
0	1	54	P11517	139	Hemoglobin subunit beta-2		100NANANANA	0.278	0.004	0.062	0.189	0.512	0.774	1.067	0.355	0.863													
0	0	289	G3V7N9	296	Adiponectin a	C1qb	10000NANA	2.159	0.020	0.106	1.029	0.679	0.914	3.340	0.405	0.274	0.644	0.293	0.569	1.571	0.639	0.776							
1	1	269	P14630	185	Apolipoprotein M	Apom	1000000	0.305	0.000	0.014	0.665	0.491	0.756	0.629	0.480	0.948	1.823	0.055	0.208	1.777	0.058	0.168	1.377	0.408	0.767	2.518	0.077	0.213	
0	1	354	Q811M5	207	Complement component C6	C6	1000000	2.651	0.019	0.105	3.256	0.081	0.387	2.126	0.201	0.608	0.412	0.093	0.307	1.634	0.940	0.991	0.366	0.482	0.817	1.793	0.312	0.574	
0	0	11	F1M983	315	Complement factor H	Cfh	1000000	0.528	0.036	0.154	0.793	0.550	0.808	0.977	0.984	1.000	0.644	0.712	0.940	1.260	0.448	0.642	0.939	0.983	1.000	1.433	0.287	0.550	
0	1	429	Q68FP1	60	Gelsolin	Gsn	1000000	0.456	0.001	0.035	1.205	0.709	0.940	1.015	0.999	1.000	0.743	0.383	0.674	0.803	0.516	0.678	0.925	0.857	0.963	1.163	0.752	1.000	
0	1	46	P08934	438	Kinogen-1	Kng1	1000000	0.568	0.005	0.066	1.975	0.459	0.741	2.376	0.141	0.591	0.956	0.991	0.998	1.158	0.721	0.841	0.847	0.841	0.847	0.524	0.945	0.965	1.000
0	1	46	Q5M8A0	480	Kng2 protein	Kng2l1	1000000	0.492	0.014	0.094	2.752	0.419	0.728	3.019	0.183	0.608	1.055	0.948	0.998	1.301	0.552	0.700	0.962	0.984	1.000	1.036	0.904	1.000	
0	0	3	H6X2X0	84	Pentaxin	crp	1000000	0.561	0.002	0.049	2.222	0.663	0.914	0.862	0.617	0.988	1.644	0.148	0.370	1.994	0.106	0.273	0.760	0.402	0.767	0.869	0.971	1.000	
0	0	144	P23680	322	Serum amyloid P-component	Apcs	1000000	3.955	0.026	0.133	0.181	0.371	0.680	0.318	0.686	1.000	0.852	0.866	0.998	1.607	0.305	0.499	1.629	0.062	0.430	1.131	0.706	0.970	
0	0	95	AOA0G2K2	1091	Tropomyosin alpha-4 chain	Tpm4	1000000	0.213	0.015	0.096	1.012	0.777	0.993	0.837	0.716	1.000	0.417	0.102	0.312	0.514	0.119	0.282	0.628	0.123	0.580	0.661	0.149	0.354	
0	0	63	P08650	66	Complement C5	C5	NA110001	1.822	0.001	0.042	2.566	0.000	0.007	0.823	0.740	0.952	1.084	0.889	0.949	1.029	0.958	0.781	0.963	1.818	0.023	0.109			
1	1	398	M0RC54	398	Biorientation of chromosomes in cell divi	Bod1l1	NA1100NANA	2.660	0.001	0.042	3.281	0.000	0.008	1.140	0.480	0.778	0.956	0.995	1.000										
0	0	37	G3V7K2	684	Leukemia inhibitory factor receptor	Lifr	NA100101	6.480	0.001	0.042	2.791	0.036	0.254	1.132	0.956	0.998	28.037	0.001	0.009	1.881	0.231	0.651	12.611	0.001	0.031				
1	1	302	D3Z5G2	393	Tetratricopeptide repeat and ankyrin rep	Trank1	NA011100	0.946	0.960	1.000	0.391	0.000	0.008	1.616	0.003	0.053	0.595	0.003	0.015	1.274	0.506	0.833	1.079	0.999	1.000				
1	1	167	Q9QYJ4	395	ATP-binding cassette sub-family B membe	Abcb9	0011100	1.596	0.089	0.246	1.279	0.920	1.000	0.250	0.011	0.023	3.629	0.010	0.083	4.408	0.017	0.061	1.958	0.851	0.963	0.947	0.863	1.000	
1	1	205	D3ZWD6	513	Complement C8 alpha chain	C8a	0011000	0.518	0.133	0.329	4.099	0.019	0.214	3.905	0.011	0.117	1.894	0.023	0.124	1.076	0.704	0.833	1.258	0.279	0.681	1.566	0.700	0.203	
0	0	120	AOA0G2K9	262	Histidine-rich glycoprotein	Hrg	0010100	2.864	0.052	0.205	0.210	0.010	0.214	0.249	0.020	0.175	1.312	0.464	0.766	0.518	0.019	0.068	0.901	0.847	0.963	1.077	0.875	1.000	
0	0	204	P62944	512	AP-2 complex subunit beta	Ap2b1	NA01NANANANA	5.323	0.028	0.240	7.625	0.006	0.069																
1	1	230	D4A1D3	18	Sacsin molecular chaperone	Sacs	NA0100NANA	0.800	0.435	0.728	0.226	0.000	0.008	1.632	0.951	0.998	0.536	0.440	0.637	</									

0	0	1	Q7TPI9	413	Ac2-248		0001001	0.944	0.561	0.739	1.328	0.653	0.914	2.264	0.340	0.841	1.772	0.000	0.009	1.007	0.999	1.000	0.693	0.360	0.730	0.469	0.032	0.119
1	1	293	F7FA5Y	313	Similar to alpha-fetoprotein	LOC360919	0001001	1.302	0.014	0.094	0.779	0.322	0.620	1.609	0.107	0.475	0.568	0.004	0.056	1.147	0.544	0.695	1.178	0.539	0.841	1.607	0.020	0.102
1	1	311	P55314	415	Complement component C8 beta chain	C8b	0001000	4.832	0.344	0.550	0.422	0.620	0.895	0.755	0.928	1.000	6.953	0.003	0.053	1.389	0.785	0.892	2.445	0.461	0.813	1.995	0.960	1.000
0	1	1	P31211	1	Corticosteroid-binding globulin	Serpin6	0001000	1.574	0.088	0.246	1.122	0.955	1.000	0.825	0.992	1.000	2.666	0.000	0.008	1.351	0.127	0.292	2.028	0.809	0.963	1.042	0.995	1.000
1	1	475	Q08420	451	Extracellular superoxide dismutase [Cu-Zn SOD3]		0001000	1.758	0.057	0.208	0.720	0.655	0.914	1.588	0.524	0.962	0.365	0.032	0.145	0.632	0.330	0.534	0.566	0.809	0.963	0.591	0.833	1.000
0	0	310	AOA096MJ	517	Glutathione S-transferase omega 1, isoform Gsto1		0001000	0.942	0.545	0.209	0.741	0.153	0.453	1.545	0.091	0.475	1.799	0.200	0.124	1.018	0.989	1.000	1.098	0.680	0.963	1.161	0.587	0.854
1	1	457	D4A0W2	327	Lysozyme f1	RGD1306474	0001000	1.047	0.602	0.757	0.373	0.040	0.265	0.613	0.491	0.948	0.419	0.047	0.190	0.384	0.112	0.281	0.551	0.748	0.963	0.583	0.694	0.964
0	0	171	Q5M878	410	Serum amyloid A protein	Saa4	0001000	0.808	0.593	0.757	0.985	0.868	1.000	1.222	0.808	1.000	0.614	0.021	0.124	1.376	0.172	0.353	0.687	0.241	0.651	1.138	0.968	1.000
1	1	262	D3ZTX4	175	Maltase-glucoamylase	Mgam	NANANA0111										0.994	0.945	0.998	0.440	0.000	0.001	4.959	0.009	0.189	8.022	0.003	0.035
0	0	103	P63259	299	Actin, cytoplasmic 2	Actg1	0000111	1.481	0.129	0.324	0.856	0.855	1.000	0.806	0.988	1.000	0.716	0.937	0.998	5.320	0.025	0.086	0.536	0.014	0.197	0.513	0.012	0.083
0	0	455	AOA0G2JV	270	Insulin-like growth factor-binding protein	Igfbp5	NANANA0110										1.047	0.758	0.968	1.502	0.025	0.086	0.617	0.003	0.117	0.743	0.051	0.170
0	1	90	D3ZGK7	171	Carboxylic ester hydrolase	Ces1c	0000101	0.598	0.079	0.236	0.346	0.088	0.399	0.584	0.538	0.962	0.651	0.173	0.410	0.284	0.001	0.008	0.412	0.137	0.580	0.311	0.048	0.161
0	1	42	AOA0G2JSI	251	RCG20603	Serpina3c	0000101	1.085	0.656	0.769	0.530	0.041	0.265	0.868	0.785	1.000	0.703	0.023	0.124	0.551	0.001	0.009	0.782	0.322	0.705	0.529	0.025	0.111
0	1	42	P05545	99	Serine protease inhibitor A3K	Serpina3k	0000101	1.085	0.656	0.769	0.530	0.041	0.265	0.868	0.785	1.000	0.703	0.023	0.124	0.551	0.001	0.009	0.782	0.322	0.705	0.528	0.025	0.111
1	1	317	P20767	642	Ig lambda-2 chain C region		NANANA01NANA										1.288	0.739	0.952	5.766	0.011	0.044						
0	1	129	Q62812	533	Myosin-9	Myh9	NANANA01NANA										2.216	0.268	0.554	39.501	0.001	0.006						
1	1	333	D4AAY7	547	Phosphatidylinositol glycan anchor biosyn Piga		NANANA01NANA										1.157	0.008	0.070	0.657	0.000	0.000						
1	1	359	F1LXF5	1450	Guided entry of tail-anchored proteins FatG4		NAO001NANA				1.024	0.936	1.000	0.928	0.886	1.000	1.196	0.299	0.569	0.498	0.002	0.012						
0	1	145	P14046	166	Alpha-1-inhibitor 3	A1i3	0000100	1.027	0.794	0.876	0.607	0.237	0.536	0.501	0.216	0.608	1.353	0.081	0.279	0.612	0.006	0.025	1.169	0.320	0.705	1.161	0.419	0.696
0	0	34	M0RDX2	1455	Amyloid-like protein 2	Aplp2	0000100	1.407	0.088	0.246	4.004	0.028	0.240	0.467	0.384	0.906	0.854	0.392	0.680	0.601	0.004	0.021	1.320	0.266	0.671	1.191	0.542	0.801
1	1	178	P01015	247	Angiotensinogen	Agt	0000100	0.960	0.926	0.962	0.305	0.037	0.265	0.640	0.770	1.000	0.699	0.222	0.480	0.224	0.000	0.003	1.122	0.796	0.963	0.523	0.290	0.550
1	1	391	G3V8D4	328	Apolipoprotein C-II (Predicted)	ApoC2	0000100	0.434	0.141	0.339	2.679	0.435	0.728	0.379	0.596	0.982	0.511	0.208	0.468	2.065	0.044	0.138	0.909	0.629	0.914	0.753	0.799	1.000
0	0	250	P26644	109	Beta-2-glycoprotein 1	ApoH	0000100	1.286	0.119	0.304	0.918	0.941	1.000	1.767	0.626	0.988	0.649	0.099	0.312	0.553	0.015	0.057	0.848	0.571	0.858	0.940	0.842	1.000
0	0	165	G3V836	42	Clusterin	Clu	0000100	1.058	0.977	0.983	0.630	0.366	0.677	0.382	0.101	0.475	0.636	0.349	0.630	0.316	0.050	0.153	1.359	0.468	0.813	0.995	0.974	1.000
0	0	105	D3ZBS2	224	Inter-alpha-trypsin inhibitor heavy chain I th3		0000100	0.857	0.524	0.717	1.005	0.977	1.000	1.046	0.892	1.000	1.040	0.971	0.998	0.661	0.043	0.136	1.128	0.657	0.947	1.193	0.338	0.608
0	0	35	P97569	205	Kallistatin		0000100	0.495	0.153	0.357	0.530	0.267	0.587	0.439	0.437	0.948	1.511	0.119	0.337	0.270	0.000	0.003	1.396	0.391	0.760	0.744	0.355	0.627
0	1	145	Q03626	182	Murineoglobulin-1	Mug1	0000100	0.999	0.983	0.983	0.605	0.218	0.516	0.493	0.201	0.608	1.321	0.063	0.230	0.623	0.003	0.016	1.257	0.153	0.580	1.205	0.303	0.564
0	0	164	P14272	62	Plasma kallikrein	Klk1b	0000100	0.800	0.293	0.518	1.096	0.998	1.000	0.448	0.485	0.948	1.223	0.358	0.639	2.427	0.017	0.061	1.987	0.137	0.580	1.799	0.161	0.358
0	0	363	G3V8K8	787	Protein Z, vitamin K-dependent plasma gl	ProZ	0000100	0.587	0.239	0.485	4.189	0.021	0.214	2.023	0.164	0.608	0.677	0.331	0.610	2.281	0.026	0.089	0.524	0.089	0.498	1.107	0.963	1.000
1	1	370	D3Z977	220	T-box 19 (Predicted)	Tbx19	0000100	0.689	0.467	0.675	0.849	0.862	1.000	0.852	0.589	0.980	0.513	0.148	0.370	0.328	0.010	0.041	0.525	0.768	0.963	1.018	0.647	0.933
1	1	442	M0R6K3	162	Proline-rich 32	Prr32	NANANA0011										0.634	0.080	0.279	0.624	0.058	0.168	0.508	0.000	0.000	0.329	0.000	0.000
1	1	406	D3ZPI8	434	Complement C8 gamma chain	C8g	NAO000011				1.027	0.857	1.000	1.355	0.956	1.000	0.901	0.947	0.998	0.566	0.737	0.848				0.127	0.011	0.083
1	1	226	P49088	10	Asparagine synthetase [glutamine-hydro] Asn		NANANANANA10																0.601	0.002	0.092	1.046	0.800	1.000
0	0	330	AOA0G2JA	770	Neubulette		NANANANANA10																0.639	0.013	0.197	0.974	0.912	1.000
0	1	313	P19939	943	Apolipoprotein C-I	ApoC1	0000010	1.299	0.337	0.548	1.307	0.431	0.728	1.501	0.176	0.608	1.478	0.096	0.312	0.785	0.396	0.593	2.188	0.007	0.189	1.482	0.178	0.386
1	1	416	Q9EQV9	245	Carboxypeptidase B2	Cpb2	0000010	1.312	0.296	0.518	1.482	0.323	0.620	1.244	0.750	1.000	0.826	0.562	0.855	0.724	0.510	0.678	1.662	0.011	0.197	1.369	0.077	0.213
0	0	194	Q63515	472	C4b-binding protein beta chain		NANANANANA01																0.745	0.881	0.972	2.673	0.028	0.117
0	0	94	P31394	203	Vitamin K-dependent protein C	Proc	NAO0NANA01				7.341	0.189	0.488	11.821	0.032	0.246							1.248	0.367	0.730	1.802	0.030	0.119
0	1	6	F1LXV6	703	Ig-like domain-containing protein		NAO000001				0.797	0.182	0.488	0.843	0.397	0.925	0.605	0.079	0.279	0.670	0.094	0.245	0.498	0.026	0.277	0.306	0.002	0.031
0	1	6	F1LW00	1277	Ig-like domain-containing protein		NAO000001				0.797	0.185	0.488	0.836	0.368	0.883	0.605	0.084	0.284	0.657	0.085	0.229	0.498	0.024	0.277	0.301	0.002	0.031
0	0	57	Q4KM66	353	LOC500183 protein	LOC500183	NAO000001				2.875	0.129	0.422	2.386	0.638	0.988	0.455	0.777	0.978	1.630	0.886	0.949	2.924	0.016	0.208	11.834	0.002	0.031
0	0	2	Q7TMC7	388	Ab2-417		0000001	1.228	0.214	0.464	0.795	0.485	0.752	0.652	0.103	0.475	0.743	0.509	0.796	0.663	0.161	0.344	0.814	0.586	0.866	0.281	0.002	0.031
0	1	192	Q7TPK2	394	Ac2-120	F5	0000001	0.688	0.172	0.382	0.340	0.013	0.214	0.734	0.506	0.948	0.670	0.868	0.998	0.534	0.240	0.432	0.703	0.164	0.580	0.492	0.012	0.083
0	0	29	F1M632	241	Adenylate kinase 9	Ak9	0000001	0.977	0.947	0.962	2.145	0.107	0.399	1.709	0.244	0.671	0.690	0.272	0.554	0.808	0.354	0.561	0.772	0.268	0.671	0.468	0.004	0.045
0	0	22	P02764	239	Alpha-1-acid glycoprotein	Orm1	0000001	0.209	0.107	0.284	50.332	0.099	0.399	31.508	0.108	0.475	0.481	0.181	0.418	0.712	0.248	0.432	0.286	0.085	0.492	0.120	0.015	0.087
0	1	251	P02651	124	Apolipoprotein A-IV	ApoA4	0000001	0.658	0.074	0.236	1.034	0.921	1.000	1.253	0.541	0.962	1.168	0.690	0.936	1.419	0.252	0.432	0.635	0.163	0.580	0.362	0.004	0.045
0	1	133	F1M6Z1	346	Apolipoprotein B-100	ApoB	0000001	0.170	0.445	0.652	2.611	0.997	1.000	1.072	0.999	1.000	1.220	0.576	0.856	0.36								

