Supplemental Table 1. STZ-induced diabetes and duration mediated erectile tissue protein profiles.

No	Gene name	Protein identities	Accession number	MW (KDa), pI[1]	Fold Change[2]				One way ANOVA[3] p-value	Two way ANOVA p-value [4]		
					2/1	4/3	3/1	4/2		Treatment	Time	Interact
1	*A2U*	alpha2u globulin	gi| 66730407|	20.74, 5.55	**-4.77**	**-5.2**	-1.88	-2.14	0.00086	0.00031	0.02	0.75
2	*Alb*	Albumin	P002770	68.73, 6.09	1.34	**1.56**	1.34	**1.56**	0.00012	0.0004	0.00036	0.33
3	*Andpro (crp1)*	Cystatin-related protein 1 precursor	P22282	21.06, 8.7	**-2.31**	**-2.75**	-3.24	-3.86	7.0E-04	0.0046	6.4E-04	0.66
4	*Apcs*	seum amyloid P component	P23680	26.20, 5.4	**2.04**	**1.63**	1.48	1.18	3.9E-04	0.00015	0.024	0.29
5	*Apeh*	acyl-peptide hydrolase	P13676	80.95, 5.4	1.21	**1.55**	1.04	1.26	0.019	0.0074	0.14	0.31
6	*apoA-I*	Apolipoprotein A-I precursor	P04639	30.1, 5.5	**2.89**	**3.39**	1.01	1.18	0.00013	1.3E-05	0.63	0.58
7	*apoA-IV*	Apolipoprotein A-IV	P02651	44.5, 4.98	**2.24**	**2.03**	1.21	1.1	0.00027	4.0E-05	0.17	0.6
8	*apoE*	Apolipoprotein E precursor	P02650	35.8, 5.2	**-1.97**	-1.12	**-2.21**	-1.26	0.011	0.031	0.018	0.1
9	*Bpgm*	2,3-bisphosphoglycerate mutase	Q6P6G4	18.1, 6.6	**1.58**	1.18	1.38	1.03	0.011	0.0069	0.098	0.14
10	*C3*	Complement C3	P01026	186.3, 6.1	**1.63**	**1.91**	1.18	1.38	0.0033	0.00098	0.072	0.61
11	*C5*	Complement C5	gi| 109468076|	189.8, 6.1	1.2	**2.02**	1.35	**2.15**	0.00051	0.0023	0.00081	0.093
12	*Ca2*	Carbonic anhydrase 2	P27139	29.09, 7.02	**1.67**	1.11	1.31	-1.15	0.012	0.0098	0.49	0.073
13	*Car1*	similar to Carbonic anhydrase I	gi|27689031|	28.3, 6.9	**1.72**	1.17	1.46	-1.01	0.031	0.02	0.19	0.14
14	*Cc1-8*	liver regeneration-related protein LRRG161	gi|33086660|	107.34, 8.35	**-1.73**	-1.14	**-2.33**	**-1.54**	0.0015	0.12	0.00039	0.06
15	*Cct4*	Chaperonin containing Tcp1, subunit 4 (delta)	gi|50927753|	58.09, 8.24	1.42	**1.85**	**1.66**	**2.13**	0.001	0.01	0.00075	0.35
16	*Cct5*	Chaperonin containing Tcp1, subunit 5 (epsilon)	Q6B436	59.49, 5.44	1.27	**1.72**	-1.05	1.29	0.0372	0.0034	0.53	0.098
17	*Col14a1*	Collagen, type XIV, alpha 1	gi|109480777|	193.22, 4.9	-1.11	**-1.68**	-1.11	**-1.69**	0.0032	0.017	0.0037	0.1
18	*Col1a1*	Collagen, type 1, alpha 1	P02454	137.86, 5.7	**-1.68**	**-2.02**	**-2.57**	**-3.12**	4.10E-05	0.00056	2.20E-05	0.34
19	*Col1a2*	Collagen, type 1, alpha 2	P02466	129.48, 9.6	**-1.96**	**-2.04**	-2.62	-1.41	0.0003	0.021	0.00026	0.013
20	*Col6a2*	Collagen, type 6, alpha 2	Q5EB88	109.5, 6.2	**-1.52**	**-2.02**	-1.7	-1.15	0.0096	0.04	0.0067	0.084
21	*Col6a3*	Procollagen, type 6, alpha 3	gi|157817857|	324.91, 5.8	1.32	**1.62**	1.3	**1.6**	0.0035	0.0022	0.022	0.2
22	*Crmp4*	collapsin response mediator protein 4	gi|14518293|	61.92, 6.03	1.48	**2.09**	1.01	1.43	0.0002	5.50E-05	0.025	0.029
23	*Ethe1*	ethylmalonic encephalopathy 1	B0BNJ4	27.66, 6.6	1.21	**2.18**	1.36	**2.44**	0.00063	0.0029	0.0003	0.041

Supplemental Table 1 continued

Pos.	Gene name	Protein identities	Accession number	MW (KDa), pI[1]	Fold Change[2]				One way ANOVA[3] p-value	Two way ANOVA p-value [4]		
					2/1	4/3	3/1	4/2		Treatment	Time	Interact
24	*Fetub*	fetuin beta	Q9QX79	42.40, 6.7	**1.51**	**2.08**	1.06	1.45	0.00056	0.00015	0.0519	0.15
25	*Fga*	Fibrinogen alpha chain precursor	P06399	61.00, 7.8	1.34	**1.81**	**1.84**	**2.49**	0.00025	0.0092	0.00012	0.31
26	*Fgb*	Fibrinogen beta chain precursor	P14480	54.80, 8.2	1.37	**1.63**	1.35	**1.6**	0.0034	0.0064	0.0058	0.47
27	*Fgg*	Fibrinogen gamma chain precursor	P02680	51.2, 5.4	1.31	**2.03**	1.33	**2.05**	0.0011	0.0033	0.0028	0.13
28	*Fhl1*	LIM protein	gi|4894849|	31.88, 8.76	-1.02	**-3.66**	2.01	-1.78	0.028	0.027	0.69	0.021
29	*Ganab*	alpha glucosidase 2 alpha neutral subunit	gi|109463536|	109.39, 5.7	**1.51**	**1.79**	1.44	**1.71**	9.6E-05	0.0002	0.00041	0.46
30	*Gda*	guanine deaminase	gi|7533042|	51.50, 5.5	1.08	**1.68**	-1.14	1.37	0.0075	0.0034	0.32	0.015
31	*Gpx3*	glutathione peroxidase 3	P23764	25.25, 8.2	**1.73**	1.71	1.09	-1	0.025	0.004	0.86	0.64
32	*Gsta6*	Glutathione S-transferase A6	Q6AXY0	25.79, 5.9	**-1.69**	-1.09	**-1.59**	1.02	0.0024	0.0069	0.023	0.016
33	*Hadha*	mitochondrial trifunctional protein, alpha subunit	gi|148747393|	82.66, 9.16	1.22	**2.08**	-1.09	**1.57**	0.003	0.0014	0.089	0.024
34	*Hbb*	Hemoglobin subunit beta-1	P02091	15.90, 8.2	**1.68**	2.27	-1.25	-1.3	0.012	0.0047	0.038	0.33
35	*Hsp47*	Heat shock protein 47	P29457	46.6, 9.2	**-2.94**	**-7.79**	**-6.09**	**- 4.17**	9.30E-07	9.30E-05	5.20E-07	0.29
36	*Hp*	Haptoglobin	P06866	38.53, 6.1	-1.13	2.23	1.9	**4.76**	0.0011	0.34	0.00038	0.052
37	*Hpx*	Hemopexin	P20059	52.00, 7.9	1.52	**2.35**	**1.82**	**2.81**	0.00011	0.0011	0.00014	0.2
38	*Igc*	anti-NGF30 antibody light-chain	gi|4096754|	23.80, 5.9	**1.86**	**2.02**	1.66	1.69	0.0015	0.0018	0.0053	0.99
39	*Lamb2*	Laminin subunit beta-2 precursor	P15800	196.34, 6.3	**-1.73**	-1.69	**-2.02**	-1.53	0.0033	0.011	0.0026	0.28
40	*Ldhb*	*lactate dehydrogenase B*	P42123	36.58, 5.65	**1.57**	**1.56**	1.18	1.04	0.0059	0.0012	0.24	0.54
41	*lmna*	Lamin-A	P48679	71.9, 6.20	1.15	**2.32**	-1.26	1.6	0.034	0.038	0.71	0.10
42	*Mad1*	similar to Mitotic spindle assembly checkpoint protein MAD1	gi|109496662|	83.27, 5.51	1.26	1.53	1.44	**1.63**	0.0018	0.015	0.0011	0.55
43	*Map1*	T-kininogen 1 precursor	P01048	46.90, 6.0	**2.29**	**2.21**	**7.17**	**6.91**	1.60E-05	0.0028	4.20E-06	0.76
44	*Mpz*	myelin protein zero	P06907	27.65, 9.8	**1.99**	**1.8**	1.35	1.22	8.5E-06	2.30E-06	0.0043	0.55
45	*Otud6b*	OTU domain containing 6B	gi|157820311|	37.08, 5.9	1.37	**1.68**	**1.74**	**2.03**	1.40E-05	0.00058	9.10E-06	0.45

Supplemental Table 1 continued

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					2/1	4/3	3/1	4/2		Treatment	Time	Interact
46	*Prelp*	Proline arginine-rich end leucine-rich repeat protein	gi|47938987|	43.12, 9.8	**-2.2**	-1.04	-1.47	1.47	0.0096	0.0091	0.94	0.0056
47	*Psmb4*	proteasome (prosome, macropain) subunit, beta type 4	P34067	25.77, 6.4	1.19	**-2.14**	1.34	**-1.9**	0.0076	0.035	0.20	0.0029
48	*Puf60*	Poly(U)-binding-splicing factor PUF60	Q9WV25	59.77, 5.4	1.87	**2..5**	1.27	1.69	0.0071	0.0026	0.074	0.53
49	*Pzp*	pregnancy-zone protein	Q63041	168.4, 6.46	**2.19**	**1.75**	**1.58**	1.26	0.00016	3.70E-05	0.014	0.56
50	*Serpina1*	Serine protease inhibitor alpha 1	P17475	46.3, 5.5	2.33	**2.74**	1.91	2.25	0.0036	0.0035	0.011	0.81
51	*Serpina3n*	Serine (or cysteine) peptidase inhibitor, clade A, member 3N	P09006	46.6, 5.19	1.84	**3.40**	1.17	2.16	0.0012	0.00049	0.041	0.16
52	*Serpinf1*	Alpha-2 antiplasmin	Q80ZA3	46.50, 6.0	1.61	**2.42**	1.64	**2.47**	0.00021	0.00031	0.0012	0.088
53	*sid23p*	similar to sid23p	gi|27703460 |	18.60, 7.7	-1.08	-1.55	**2.85**	**1.98**	0.00066	0.11	8.500E-05	0.29
54	*Smc3*	Structural maintenance of chromosomes protein 3	P97690	138.36, 7.8	-1.19	**1.77**	**-1.66**	1.12	0.017	0.28	0.057	0.009
55	*Snx1*	sorting nexin 1	Q99N27	59.0, 5.0	1.11	**1.53**	1.2	**1.66**	0.0009	0.0083	0.0012	0.069
56	*Tf*	Serotransferrin	P12346	78.1, 8.2	**1.59**	**2.19**	1.32	**1.63**	0.00054	0.00041	0.0057	0.39
57	*Ywhag*	14-3-3 protein gamma	P61983	28.30, 4.80	**1.97**	**1.47**	1.3	-1.03	0.00045	9.90E-05	0.18	0.16

[1] The theoretical molecular weight (MW) and isoelectric point (pI) were calculated using ExPASY compute pI/Mw tool from the data base entries.

[2,3,4] The difference in the standardized abundance for the proteins between the groups are expressed as fold change that are calculated by taking the means of standardized volume values, from four independent biological replicates per group, for the protein spot in the corresponding group (Group 1 = one week control, Group 2 = one week STZ-induced diabetic, Group 3 = two months control, Group 4 = two months STZ-induced diabetic), Values are displayed in the range of -∞ to -1 for decreases in expression and +1 to + ∞ for increases in expression. One-way and two-way analysis of variances (ANOVA) p-values calculated using DeCyder software version 6.5.

[a] Boldface for ratios indicating statistically significant fold changes ($p \le 0.05$).