

Table 1. Attribution of proteins identified in unfertilized eggs, 16 cell-stage embryos and tadpole larvae to the gene clusters from microarray gene expression profile.

<b>Category*1</b>	<b>Percentage (Protein count)</b>			
	<b>Total</b>	<b>Unfertilized eggs</b>	<b>16 cell-stage embryos</b>	<b>Larvae</b>
a Embryonic gene cluster	7 (16)	6 (3)	0 (0)	10 (13)
b Embryonic and adult gene cluster	16 (36)	9 (5)	15 (6)	20 (25)
c Adult gene cluster	17 (38)	20 (11)	20 (8)	15 (19)
d Stably expressed gene cluster	10 (22)	6 (3)	7 (3)	13 (16)
e Maternal gene cluster	49 (109)	59 (32)	59 (24)	42 (53)

\*1 Category of gene cluster is according to Azumi et al., 2007.

Table 2. List of proteins abundantly expressed in unfertilized eggs, 16 cell-stage embryos and tadpole larvae.

	SSN	Mr (kDa)	QTY	C.V.	Sequence ID	Blast		EST count			Cluster
						Description	E-value	Unfertilized eggs (/ 29444)	Cleaving embryos (/ 26796)	Tadpole larvae (/ 24532)	
<b>Unfertilized eggs</b>											
1	A7109	34.36	833.70	0.21	Not determined						
2	B9202	37.17	833.58	1.28	JGI_286147	apolipoprotein B [Rattus norvegicus] (Vitellogenin)	6.0E-18	0	0	0	00997, 16456
3	A6111	34.44	553.60	0.13	Not determined						
4	A8008	28.98	509.05	0.29	JGI_286147	apolipoprotein B [Rattus norvegicus] (Vitellogenin)	6.0E-18	0	0	0	00997, 16456
5	A6012	30.78	487.48	0.44	JGI_286147	apolipoprotein B [Rattus norvegicus] (Vitellogenin)	6.0E-18	0	0	0	00997, 16456
6	B8401	44.94	431.69	0.43	KYOTOGRAIL2005.55.42.3	elongation factor 1A [Geodia cydonium]	1.0E-37	103	189	187	05079, 14095, 13525, 00080, 10321
7	B7001	24.70	397.41	1.06	KYOTOGRAIL2005.216.2.1	H+ transporting ATP synthase O subunit isoform 1 [Bombyx	1.0E-37	19	16	3	02586, 01736
8	B9201	37.08	389.14	1.02	JGI_286147	apolipoprotein B [Rattus norvegicus] (Vitellogenin)	6.0E-18	0	0	0	00997, 16456
9	B7002	26.93	374.86	1.04	KYOTOGRAIL2005.119.5.1	novel protein (zgc:56136) [Danio rerio]	6.0E-28	20	6	10	36808, 00286
10	A2209	45.10	349.66	0.12	PROCITS_00805_1_2_0	actin [Ciona intestinalis]	0.0E+00	0	0	0	00046
11	B4204	38.12	310.17	0.18	JGI_216024	isocitrate dehydrogenase 3, beta subunit [Mus musculus]	3.0E-122	20	6	0	04248
12	A7302	50.50	299.15	0.20	JGI_298739	mitochondrial citrate synthase precursor [Xiphias gladius]	0.0E+00	38	3	2	02113, 00809
13	B4504	60.69	285.74	1.24	KYOTOGRAIL2005.100.2.1	No similarity (Vitellogenin)		0	0	0	00997
14	B5405	49.24	269.02	0.27	JGI_292814	ATP synthase alpha-subunit [Ciona intestinalis] (mitochondrial F1 complex)	0.0E+00	33	8	4	00396
15	A5808	105.64	268.27	0.14	JGI_286147	apolipoprotein B [Rattus norvegicus] (Vitellogenin)	6.0E-18	0	0	0	00997, 16456
16	A4107	37.55	254.99	0.14	KYOTOGRAIL2005.26.37.1	malate dehydrogenase, mitochondrial [Rattus norvegicus]	3.0E-127	18	9	1	04668
17	A6813	106.34	205.01	0.13	JGI_286147	apolipoprotein B [Rattus norvegicus] (Vitellogenin)	6.0E-18	0	0	0	00997, 16456
18	B9107	34.81	201.88	0.32	JGI_286147	apolipoprotein B [Rattus norvegicus] (Vitellogenin)	6.0E-18	0	0	0	00997, 16456
					JGI_233126 *	No similarity		34	22	1	00034
19	A1005	29.57	197.76	0.19	JGI_224382 *	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1 [Danio rerio]	3.0E-34	34	22	1	00034
20	A5812	104.67	196.95	0.08	KYOTOGRAIL2005.100.11.1	No similarity (Vitellogenin)		NA	NA	NA	NA
21	A8004	28.55	191.93	0.18	JGI_286147	apolipoprotein B [Rattus norvegicus] (Vitellogenin)	6.0E-18	0	0	0	00997, 16456
22	A7206	41.98	190.54	0.33	JGI_294238	isocitrate dehydrogenase 3 (NAD+) alpha [Mus musculus]	4.0E-158	25	9	0	04422
23	A5314	48.77	169.22	0.29	KYOTOGRAIL2005.45.49.1	phosphoglycerate kinase [Halocynthia roretzi]	1.0E-171	7	2	1	05676
24	B7105	29.18	168.16	0.55	KYOTOGRAIL2005.100.2.1	No similarity (Vitellogenin)		0	0	0	00997
25	B7101	31.46	167.36	0.79	KYOTOGRAIL2005.545.3.1	Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVDAC2) (Outer mitochondrial membrane protein porin 2)	7.0E-89	38	61	4	00121, 36613
26	B7004	26.95	166.79	1.17	Not determined						
27	B4107	34.99	160.02	0.35	PROCITS_00881_0_1_0	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	2.0E-154	49	54	19	00881, 37267, 36139
28	A5012	31.00	156.89	0.36	JGI_286147	apolipoprotein B [Rattus norvegicus] (Vitellogenin)	6.0E-18	0	0	0	00997, 16456
29	A7007	28.77	148.48	0.65	KYOTOGRAIL2005.10.70.1	No similarity		3	9	3	00188
30	A9501	65.30	147.24	0.21	KYOTOGRAIL2005.42.4.1	t-complex polypeptide 1 [Danio rerio]	0.0E+00	4	1	0	12274

Table 2. Continued

16 cell-stage embryos											
1	B8401	44.94	1051.94	0.76	KYOTOGRAIL2005.55.42.3	translation elongation factor 1A	8.0E-170	103	189	187	05079, 14095, 13525, 00080, 10321
2	A6111	34.44	642.37	0.46	Not determined						
3	B7001	24.70	592.97	0.28	KYOTOGRAIL2005.216.2.1	H+ transporting ATP synthase O subunit isoform 1 [Bombyx	1.0E-37	19	16	3	02586, 01736
4	B9202	37.17	494.48	2.06	JGI_286147	apolipoprotein B [Rattus norvegicus] (Vitellogenin)	6.0E-18	0	0	0	00997, 16456
5	A2209	45.10	398.13	0.36	PROCITS_00805_1_2_0	actin [Ciona intestinalis]	0.0E+00	0	0	0	00046
6	B7002	26.93	395.50	0.92	KYOTOGRAIL2005.119.5.1	novel protein (zgc:56136) [Danio rerio]	6.0E-28	20	6	10	36808, 00286
7	B5405	49.24	385.05	0.47	JGI_292814	ATP synthase alpha-subunit [Ciona intestinalis] (mitochondrial F1 complex)	0.0E+00	33	8	4	00396
8	A6112	35.03	382.40	0.56	Not determined						
9	B4204	38.12	372.64	0.27	JGI_216024	isocitrate dehydrogenase 3, beta subunit [Mus musculus]	3.0E-122	20	6	0	04248
10	A6012	30.78	324.06	0.70	JGI_286147	apolipoprotein B [Rattus norvegicus] (Vitellogenin)	6.0E-18	0	0	0	00997, 16456
11	A7302	50.50	303.82	0.44	JGI_298739	mitochondrial citrate synthase precursor [Xiphias gladius]	0.0E+00	38	3	2	02113, 00809
12	A5314	48.77	301.30	0.44	KYOTOGRAIL2005.45.49.1	phosphoglycerate kinase [Halocynthia roretzi]	1.0E-171	7	2	1	05676
13	A8001	29.89	266.87	0.33	JGI_286147	apolipoprotein B [Rattus norvegicus] (Vitellogenin)	6.0E-18	0	0	0	00997, 16456
14	A8004	28.55	256.28	0.57	JGI_286147	apolipoprotein B [Rattus norvegicus] (Vitellogenin)	6.0E-18	0	0	0	00997, 16456
15	B4203	40.12	248.23	0.98	KYOTOGRAIL2005.297.4.1	3-ketoacyl-CoA thiolase, mitochondrial (Beta-ketothiolase) (Acetyl-CoA acyltransferase) (Mitochondrial 3-oxoacyl-CoA	5.0E-135	10	9	0	00534, 016553
16	B7913	138.65	237.13	0.35	JGI_286147	apolipoprotein B [Rattus norvegicus] (Vitellogenin)	6.0E-18	0	0	0	00997, 16456
17	B9201	37.08	236.78	1.06	JGI_286147	apolipoprotein B [Rattus norvegicus] (Vitellogenin)	6.0E-18	0	0	0	00997, 16456
18	B4107	34.99	233.87	1.03	PROCITS_00881_0_1_0	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	2.0E-154	49	54	19	00881, 37267, 36139
19	A4107	37.55	224.03	0.45	KYOTOGRAIL2005.26.37.1	malate dehydrogenase, mitochondrial [Rattus norvegicus]	3.0E-127	18	9	1	04668
20	A1005	29.57	205.82	0.29	JGI_224382	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1 [Danio rerio]	3.0E-34	34	22	1	00034
21	B7101	31.46	190.66	0.66	KYOTOGRAIL2005.545.3.1	Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVDAC2) (Outer mitochondrial membrane protein porin 2)	7.0E-89	38	61	4	00121, 36613
22	B9002	24.69	187.74	0.75	KYOTOGRAIL2005.195.15.1	No similarity		4	14	0	03081
23	A2104	38.41	181.17	0.41	PROCITS_00085_1_1_0	Rplp0 protein [Danio rerio] ribosomal P10 protein	1.0E-111	145	149	217	13584
24	A7206	41.98	167.12	0.29	JGI_294238	isocitrate dehydrogenase 3 (NAD+) alpha [Mus musculus]	4.0E-158	25	9	0	04422
25	B7103	31.51	165.41	1.55	KYOTOGRAIL2005.545.3.1	Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVDAC2) (Outer mitochondrial membrane protein porin 2)	7.0E-89	38	61	4	00121, 36613
26	B5002	23.87	163.82	3.94	KYOTOGRAIL2005.416.5.2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d [Danio rerio]	4.0E-24	15	21	2	05392, 16890, 16767
27	A201	41.87	159.40	0.42	PROCITS_00526_1_1_0	67kD laminin receptor precursor [Pinctada fucata]	2.0E-107	20	5	6	00526, 09576
28	A405	54.28	159.01	0.38	KYOTOGRAIL2005.174.27.1	tubulin, beta 4 [Xenopus tropicalis]	0.0E+00	82	43	85	00086, 13299, 14360
29	A407	54.82	151.75	0.39	JGI_206517	alpha-tubulin 1 [Drosophila melanogaster]	0.0E+00	33	29	2	02340
30	A6811	107.93	142.26	0.20	JGI_286147	apolipoprotein B [Rattus norvegicus] (Vitellogenin)	6.0E-18	0	0	0	00997, 16456

Table 2. Continued

Tadpole larvae											
1	B8401	44.94	572.31	0.08	KYOTOGRAIL2005.55.42.3	translation elongation factor 1A	8.0E-170	103	189	187	05079, 14095, 13525, 00080, 10321
2	A2209	45.10	488.82	0.23	PROCITS_00805_1_2_0	actin [Ciona intestinalis]	0.0E+00	0	0	0	00046
3	B7001	24.70	480.47	1.53	KYOTOGRAIL2005.216.2.1	H+ transporting ATP synthase O subunit isoform 1 [Bombyx	1.0E-37	19	16	3	02586, 01736
4	B7002	26.93	351.37	0.40	KYOTOGRAIL2005.119.5.1	novel protein (zgc:56136) [Danio rerio]	6.0E-28	20	6	10	36808, 00286
5	B9202	37.17	340.83	0.30	JGI_286147	apolipoprotein B [Rattus norvegicus] (Vitellogenin)	6.0E-18	0	0	0	00997, 16456
6	B4204	38.12	310.93	0.10	JGI_216024	isocitrate dehydrogenase 3, beta subunit [Mus musculus]	3.0E-122	20	6	0	04248
7	A4107	37.55	302.17	0.39	KYOTOGRAIL2005.26.37.1	malate dehydrogenase, mitochondrial [Rattus norvegicus]	3.0E-127	18	9	1	04668
8	A7302	50.50	252.45	0.12	JGI_298739	mitochondrial citrate synthase precursor [Xiphias gladius]	0.0E+00	38	3	2	02113, 00809
9	B5002	23.87	238.36	1.34	KYOTOGRAIL2005.416.5.2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d [Danio rerio]	4.0E-24	15	21	2	05392, 16890, 16767
10	B9201	37.08	210.16	0.02	KYOTOGRAIL2005.100.11.1	No similarity (Vitellogenin)		NA	NA	NA	NA
11	A5007	30.17	208.82	0.28	Not determined						
12	A2104	38.41	205.66	0.18	PROCITS_00085_1_1_0	Rplp0 protein [Danio rerio] ribosomal P10 protein	1.0E-111	145	149	217	13584
13	A1308	45.83	205.41	0.49	PROCITS_10733_1_1_0	Actin, muscle	0.0E+00	0		1	36868, 10733
14	A1005	29.57	192.67	0.12	JGI_233126	No similarity		34	22	1	00034
15	A1405	55.40	191.95	0.34	KYOTOGRAIL2005.274.14.1	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	0.0E+00	63	20	1	03031
16	B5405	49.24	188.28	0.11	JGI_292814	ATP synthase alpha-subunit [Ciona intestinalis] (mitochondrial F1 complex)	0.0E+00	33	8	4	00396
17	A8008	28.98	169.20	0.26	JGI_286147	apolipoprotein B [Rattus norvegicus] (Vitellogenin)	6.0E-18	0	0	0	00997, 16456
18	A7206	41.98	166.42	0.13	JGI_294238	isocitrate dehydrogenase 3 (NAD+) alpha [Mus musculus]	4.0E-158	25	9	0	04422
19	B7103	31.51	159.05	0.68	KYOTOGRAIL2005.545.3.1	Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVDAC2) (Outer mitochondrial membrane protein porin 2)	7.0E-89	38	61	4	00121, 36613
20	B9602	70.65	149.49	0.39	KYOTOGRAIL2005.116.8.1	mitochondrial trifunctional protein, alpha subunit [Xenopus	0.0E+00	15	5	0	01869,02701
21	B9002	24.69	148.75	0.03	KYOTOGRAIL2005.195.15.1	No similarity		4	14	0	03081
22	A8208	45.01	143.36	0.59	JGI_208156	aldolase C, fructose-bisphosphate [Pan troglodytes]	4.0E-139	5	4	30	00094
23	B9004	24.71	137.92	2.19	Not determined						
24	B4107	34.99	130.93	0.22	PROCITS_00881_0_1_0	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	2.0E-154	49	54	19	00881, 37267, 36139
25	A5001	26.72	124.92	0.62	JGI_291517	peroxiredoxin-like [Ciona intestinalis]	6.0E-112	6	4	18	00138
26	A7104	32.20	124.20	0.44	KYOTOGRAIL2005.182.19.1	Electron-transfer-flavoprotein, beta polypeptide [Xenopus	1.0E-90	12	2	1	14809, 05683
27	A5306	49.68	119.19	0.05	KYOTOGRAIL2005.45_49_1	phosphoglycerate kinase [Halocynthia roretzi]	1.0E-171	7	2	1	05676
28	A3307	51.66	118.66	0.29	KYOTOGRAIL2005.289.16.1	Alpha-enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1)	3.0E-176	3	3	5	03247, 04432, 01662
29	A5010	29.35	118.00	0.29	KYOTOGRAIL2005.103.6.1	glutathione peroxidase [Suberites domuncula]	1.0E-73	9	5	1	02869
30	A2108	32.39	114.84	0.04	JGI_233410	prohibitin [Homo sapiens]	1.0E-74	12	10	0	01295

Table 3. Genes with high occurrence and their corresponding proteins identified in each embryonic stage.

	CLUSTER	Clones	Description	Sequence ID	SSN	QTY
<b>Unfertilized eggs</b>	CLSTR00046	162/29444	cytoplasmic actin 1	PROCITS_00805_1_2_0	A2209	349.66
	CLSTR00424	146/29444	no similarity	not detected.		
	CLSTR00085	144/29444	acidic ribosomal phosphoprotein	PROCITS_00085_1_1_0	A2104	143.81
	CLSTR00333	141/29444	cytochrome P450 monooxygenase	not detected.		
	CLSTR00032	136/29444	no similarity	not detected.		
	CLSTR00020	135/29444	ATP/ADP translocase	not detected.		
	CLSTR00585	112/29444	C9	not detected.		
	CLSTR00081	112/29444	ribosomal protein S1a	not detected.		
	CLSTR00080	103/29444	translational elongation factor-1 alpha	KYOTOGRAIL2005.55.42.3	B8401	431.68
<b>Cleaving embryos</b>	CLSTR00032	365 / 26796	no similarity	not detected.		
	CLSTR00080	189 / 26796	translational elongation factor-1 alpha	KYOTOGRAIL2005.55.42.3	B8401	1051.94
	CLSTR00020	173 / 26796	ATP/ADP translocase	not detected.		
	CLSTR00046	149 / 26796	actin 1	PROCITS_00805_1_2_0	A2209	398.13
	CLSTR00085	149 / 26796	acidic ribosomal phosphoprotein	PROCITS_00085_1_1_0	A2104	181.16
	CLSTR00081	147 / 26796	ribosomal protein S1a	not detected.		
	CLSTR00424	143 / 26796	no similarity	not detected.		
	CLSTR01131	125 / 26796	Splicing factor, arginine/serine-rich 7	not detected.		
	CLSTR01468	125 / 26796	Meprin A beta-subunit precursor	not detected.		
	CLSTR00734	97 / 26796	G2/mitotic-specific cyclin B1	not detected.		
<b>Tadpole larvae</b>	CLSTR00065	1488/25532	no similarity	not detected.		
	CLSTR00046	937/25532	cytoplasmic actin	PROCITS_00805_1_2_0	A2209	488.12
	CLSTR00087	395/25532	no similarity	not detected.		
	CLSTR00419	363/25532	no similarity	not detected.		
	CLSTR00025	290/25532	muscle actin	not detected.		
	CLSTR00085	217/25532	acidic ribosomal protein P0	PROCITS_00085_1_1_0	A2104	205.66
	CLSTR00080	184/25532	translational elongation factor-1 alpha	KYOTOGRAIL2005.55.42.3	B8401	572.31
	CLSTR00081	169/25532	40S ribosomal protein	not detected.		
	CLSTR00359	139/25532	troponin T	not detected.		

Table 4. Protein spots unique in unfertilized eggs, 16 cell-stage embryos and tadpole larvae.

SSN	Mr (observed)	QTY	C.V.	Sequence ID	Description	E-value
<b>Unfertilized eggs</b>						
B6205	39.42	26.90	0.13	JGI_238339	Glutamic-oxaloacetic transaminase 2b, mitochondrial (aspartate aminotransferase 2) [Danio rerio]	6.0E-170
B4302	42.69	17.56	0.38	not determined		
B5503	63.51	9.24	0.66	not determined		
B6605	68.74	7.87	0.39	KYOTOGRAIL2005.221.21.1	ATPase family, AAA domain containing 3A [Xenopus tropicalis]	0.0E+00
A4207	43.58	7.00	0.63	KYOTOGRAIL2005.253.11.1	Isovaleryl Coenzyme A dehydrogenase [Danio rerio]	3.0E-175
<b>16 cell-stage embryos</b>						
A6112	35.03	382.40	0.56	not determined		
B8201	34.56	76.06	1.12	JGI_286147	apolipoprotein B [Rattus norvegicus] (Vitellogenin)	6.0E-18
B8403	44.07	63.32	1.89	not determined		
B3208	37.36	39.89	0.71	KYOTOGRAIL2005.151.18.3	myosin, light chain kinase [Gallus gallus]	0.0E+00
B7401	43.90	38.47	2.70	not determined		
B3306	42.96	27.53	0.98	not determined		
B5304	41.65	18.42	0.80	not determined		
A2105	38.99	13.70	0.34	not determined		
B4408	44.44	11.22	1.99	not determined		
A1101	36.15	2.94	0.99	not determined		
<b>Tadpole larvae</b>						
A5007	30.17	208.82	0.28	not determined		
A5306	49.68	119.19	0.05	KYOTOGRAIL2005.45.49.1	phosphoglycerate kinase [Halocynthia roretzi]	1.0E-171
A3504	62.70	105.63	0.14	not determined		
A3104	38.97	97.97	0.52	JGI_286147	apolipoprotein B [Rattus norvegicus] (Vitellogenin)	6.0E-18
B5201	40.17	87.00	0.70	KYOTOGRAIL2005.297.4.1	3-ketoacyl-CoA thiolase, mitochondrial (Beta-ketothiolase) (Acetyl-CoA acyltransferase) (Mitochondrial 3-oxoacyl-CoA thiolase)	5.0E-135
B4105	34.66	74.28	0.42	not determined		
A2502	63.52	66.78	0.16	KYOTOGRAIL2005.100.11.1	No similarity (Vitellogenin)	
A5107	32.78	51.79	0.54	N. D.		
A5713	95.06	50.10	0.13	KYOTOGRAIL2005.100.11.1	No similarity (Vitellogenin)	
A4105	32.68	49.34	0.62	not determined		

SSNs are spot unique identification numbers that are automatically assigned to each spot by 2-DE analysis software (see Materials and Methods). SSNs beginning with "A" indicate spots in pH4-7 2-DE gel, and those beginning with "B" indicate spots in pH6-11.

Table 5. Up-regulated proteins in the embryogenesis in *C. intestinalis*.

	SSN	Sequence ID	Description	Change in QTY (-fold change)
<b>Egg to 16cell</b>				
1	<b>B4203</b>	KYOTOGRAIL2005.297.4.1	3-ketoacyl-CoA thiolase, mitochondrial (Beta-ketothiolase) (Acetyl-CoA acyltransferase) (Mitochondrial 3-oxoacyl-CoA thiolase)	4.98
2	<b>B5401</b>	KYOTOGRAIL2005.353.8.1	leucyl aminopeptidase, putative [ <i>Aedes aegypti</i> ]	4.84
3	<b>B4406</b>	Not determined		4.81
4	<b>A5602</b>	JGI_293460	ezrin/radixin/moesin (ERM)-like protein [ <i>Ciona intestinalis</i> ]	3.47
5	<b>A2</b>	Not determined		2.97
6	<b>B9302</b>	JGI_286147	apolipoprotein B [ <i>Rattus norvegicus</i> ] (Vitellogenin)	2.95
7	<b>B4403</b>	KYOTOGRAIL2005.198.6.1	fascin 1(55 kDa actin-bundling protein) (p55) [ <i>Homo sapiens</i> ]	2.95
8	<b>B3201</b>	KYOTOGRAIL2005.297.4.1	3-ketoacyl-CoA thiolase, mitochondrial (Beta-ketothiolase) (Acetyl-CoA acyltransferase) (Mitochondrial 3-oxoacyl-CoA thiolase)	2.93
9	<b>A3603</b>	Not determined		2.78
10	<b>A8506</b>	Not determined		2.72
<b>16cell to Tadpole larva</b>				
1	<b>A1308</b>	PROCITS_10733_1_1_0	Actin, muscle	30.77
2	<b>A1210</b>	PROCITS_00249_0_1_0	ATP-specific succinyl-CoA synthetase beta subunit [ <i>Mus musculus</i> ]	29.13
3	<b>A8307</b>	Not determined		25.28
4	<b>A1609</b>	JGI_210507	Plastin-3 (T-plastin)	20.72
5	<b>A2602</b>	Not determined		20.42
6	<b>A7306</b>	Not determined		20.01
7	<b>A4209</b>	JGI_286147	apolipoprotein B [ <i>Rattus norvegicus</i> ] (Vitellogenin)	17.36
8	<b>A4304</b>	KYOTOGRAIL2005.160.3.1	PREDICTED: similar to protein disulfide isomerase-associated 3 [ <i>Ciona intestinalis</i> ]	16.70
9	<b>A5310</b>	Not determined		14.35
10	<b>B7304</b>	Not determined		13.64

SSNs are spot unique identification numbers that are automatically assigned to each spot by 2-DE analysis software (see Materials and Methods). SSNs beginning with "A" indicate spots in pH4-7 2-DE gel, and those beginning with "B" indicate spots in pH6-11.

Table 6. Down-regulated proteins in the embryogenesis in *C. intestinalis*.

	SSN	Sequence ID	Description	Change in QTY (-fold change)
<b>Egg to 16cell</b>				
1	A1210	PROCITS_00249_0_1_0	ATP-specific succinyl-CoA synthetase beta subunit [ <i>Mus musculus</i> ]	0.02
2	A4304	KYOTOGRAIL2005.160.3.1	PREDICTED: similar to protein disulfide isomerase-associated 3 [ <i>Ciona intestinalis</i> ]	0.08
3	A2408	KYOTOGRAIL2005.45.31.1	Chaperonin containing TCP1, subunit 2 (beta) [ <i>Xenopus tropicalis</i> ]	0.10
4	A2307	Not determined		0.10
5	A2509	KYOTOGRAIL2005.117.37.1	programmed cell death 8 [ <i>Gallus gallus</i> ]	0.15
6	A7109	Not determined		0.16
7	A4507	PROCITS_00049_1_1_1	T-complex protein 1 subunit gamma (TCP-1-gamma) (CCT-gamma)	0.18
8	A5313	KYOTOGRAIL2005.53.53.1	fumarate hydratase [ <i>Gallus gallus</i> ]	0.28
9	A7604	JGI_375252	Glycyl-tRNA synthetase [ <i>Mus musculus</i> ]	0.31
10	B4501	KYOTOGRAIL2005.100.2.1	No similarity (Vitellogenin)	0.32
<b>16cell to Tadpole larva</b>				
1	A7211	KYOTOGRAIL2005.100.2.1	No similarity (Vitellogenin)	0.00
2	A7803	JGI_286147	apolipoprotein B [ <i>Rattus norvegicus</i> ] (Vitellogenin)	0.04
3	A5101	KYOTOGRAIL2005.269.21.1	Enoyl Coenzyme A hydratase, short chain, 1, mitochondrial [ <i>Xenopus tropicalis</i> ]	0.04
4	A6811	JGI_286147	apolipoprotein B [ <i>Rattus norvegicus</i> ] (Vitellogenin)	0.10
5	B4504	KYOTOGRAIL2005.100.2.1	No similarity (Vitellogenin)	0.11
6	A7508	Not determined		0.13
7	A1605	Not determined		0.15
8	A2202	Not determined		0.18
9	B4406	Not determined		0.21
10	A5313*	KYOTOGRAIL2005.53.53.1	fumarate hydratase [ <i>Gallus gallus</i> ]	0.22
		JGI_252770	elongation factor-1 gamma [ <i>Diguettia canites</i> ]	0.28