Supplemental TABLE 3. List of *Strongyloides* proteins found only in E/S products from infective larvae

N°	Cluster	BLAST Alignment	Species	Accession Number	E	SP	EST Lgt.	% Cov.	Pep. #	UPS
Oxidative metabolism										
1	SR03650	Superoxide dismutase	*Caenorhabditis elegans*	NP_492290	$7e^{-60}$	no	129	17.8	2	4.00
Carbohydrate metabolism										
2	SR00435	Pyruvate kinase	*Brugia malayi*	XP_001898629	$4e^{-64}$	no	176	16.4	2	4.00
3	SS00237	Carbohydrate phosphorylase	*B. malayi*	XP_001894669	$1e^{-38}$	no	111	54.9	4	8.00
4	SS02195	Carbohydrate phosphorylase	*B. malayi*	XP_001894669	$1e^{-61}$	no	148	39.1	4	6.32
5	SR00710	Trehalase family protein	*B. malayi*	XP_001900224	$2e^{-51}$	yes	281	11.0	2	4.01
6	SR01315	Phosphoenol-pyruvate carboxykinase	*Haemonchus contortus*	P29190	$5e^{-34}$	no	106	32	3	7.55
7	SS02356	Hexokinase family protein	*B. malayi*	XP_001897796	$2e^{-16}$	no	60	81.6	4	8.00
8	SR01676	Hexokinase family protein	*B. malayi*	XP_001897796	$7e^{-68}$	no	189	18.5	2	5.70
9	SR01818	UDP-Galactose 4´epimerase	*B. malayi*	XP_001902615	$4e^{-20}$	yes	81	60.5	2	4.00
Cytosol energy metabolism										
10	SS00138	Adenylate kinase	*B. malayi*	XP_001894222	$4e^{-62}$	no	149	49.6	6	14.00
11	SR00089	Aldehyde dehydrogenase	*C. elegans*	NP_498081	$9e^{-76}$	no	187	31.5	4	8.00
12	SR03043	Aldehyde dehydrogenase	*C. elegans*	NP_503467	$2e^{-56}$	no	162	33.3	4	8.00
13	SS03123	Aldehyde dehydrogenase	*C. elegans*	NP_001022212	$4e^{-33}$	no	134	25.3	2	4.54
14	SR03212	Aldehyde dehydrogenase	*C. elegans*	NP_498081	$7e^{-76}$	no	188	13.8	2	4.44
15	SR00700	Na, K-ATPase alpha subunit	*C. elegans*	AAB02615	$3e^{-101}$	no	233	29.2	4	9.71
16	SS01028	Na, K-ATPase alpha subunit	*B. malayi*	XP_001901816	$4e^{-70}$	no	166	14.5	2	4.00
17	SR00383	Propionyl Coenzyme A Carboxylase	*C. elegans*	NP_509293	$2e^{-17}$	no	76	50.0	3	9.10
18	SR01758	2-oxoglutarate dehydrogenase	*B. malayi*	XP_001897753	$6e^{-76}$	no	185	20.5	2	5.60
19	SS00819	Citrate synthase family member	*C. elegans*	NP_499264	$7e^{-61}$	no	163	16.4	2	5.22
20	SR02784	Acyl-CoA binding protein	*C. elegans*	NP_509822	$3e^{-36}$	no	120	18.3	2	5.40
21	SS00766	Vacuolar H ATPase family member	*C. elegans*	NP508412	$6e^{-98}$	no	255	14.5	2	4.67
22	SS01243	Vacuolar H ATPase protein 16	*B. malayi*	XP_001901105	$5e^{-177}$	no	349	8.6	2	4.00

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23	SS00854	GTP-binding nuclear protein RAN/TC4	*B. malayi*	XP_001900408	$9e^{-95}$	no	172	13.9	2	4.00
Protein digestion and folding										
24	SR11111	Metalloproteinase precursor	*Strongyloides stercoralis*	AAK55800	$2e^{-61}$	truncated	265	43.8	6	13.72
25	SR04474	Peptidase family M1 containing protein	*B. malayi*	XP_001897028	$2e^{-64}$	no	196	32.1	4	10.36
26	SR02466	Calpain family member	*C. elegans*	NP_498741	$1e^{-76}$	no	180	20.6	2	4.00
27	SR02020	Calpain family protein 1	*B. malayi*	XP_001897507	$1e^{-53}$	no	171	36.3	3	6.00
28	SS01570	EF hand family protein	*B. malayi*	XP_001901225	$3e^{-83}$	no	176	26.1	2	4.00
29	SR02697	Zinc carboxy-peptidase family protein	*B. malayi*	XP_001902361	$2e^{-44}$	yes	161	16.1	2	5.41
30	SR03248	Prolyl oligopeptidase	*B. malayi*	XP_001894227	$3e^{-38}$	no	190	8.9	2	5.15
Structural proteins										
31	SR01001	Myosin – filarial antigen	*B. malayi*	AAB35044	0.0	truncated	490	41.2	13	13.67
32	SS02558	Disorganized muscle protein 1	*B. malayi*	XP_001899521	$2e^{-50}$	no	189	16.9	4	8.00
33	SR00587	Histone H2A	*B. malayi*	XP_001895511	$5e^{-59}$	no	129	24.8	2	5.10
34	SR04861	Protein unc-22	*B. malayi*	XP_001899339	$1e^{-32}$	no	193	30.0	3	6.82
35	SR03042	Uncoordinated family ember	*C. elegans*	NP_497044	$2e^{-48}$	yes	170	17.6	2	4.00
36	SR00848	Uncoordinated family member	*C. elegans*	NP_001021093	$2e^{-149}$	no	338	10.7	3	6.00
37	SS00698	Vinculin	*B. malayi*	XP_001899040	$8e^{-65}$	no	163	23.3	2	4.00
38	SS01450	Intermediate filament protein	*A. suum*	CAA60047	0.0	no	381	12.3	4	8.02
39	SR02037	Intermediate filament protein	*B. malayi*	XP_001900185	$1e^{-37}$	no	106	61.3	3	6.00
40	SR00426	Intermediate filament tail domain	*B. malayi*	XP_001901413	$1e^{-36}$	no	310	6.1	2	4.86
41	SS00348	Profilin	*B. malayi*	ACD47109	$9e^{-20}$	no	80	48.8	3	7.06
42	SS01266	Myosin-4	*C. elegans*	P02566	$3e^{-94}$	no	258	26.0	6	11.45
43	SR00998	Myosin light chain family member	*C. elegans*	NP_510828	$2e^{-73}$	no	170	31.8	4	10.60
44	SS01012	Myosin tail family member	*B. malayi*	XP_001901629	$1e^{-99}$	no	311	16.4	4	7.84

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45	SS03393	Filamin/ABP280 repeat family protein	*B. malayi*	XP_001894616	$2e^{-45}$	no	157	19.7	2	5.72
46	SR05180	ERM-1	*C. elegans*	NP_491559	$2e^{-23}$	no	192	16.1	2	4.52
47	SR00624	Tubulin alpha chain	*H. contortus*	P50719	$1e^{-103}$	no	232	12.9	2	4.03
48	SR04696	Tubulin alpha chain	*C. elegans*	NP_496351	$3e^{-57}$	no	136	16.9	2	4.00
49	SR00547	Alpha-tubulin	*B. malayi*	XP_001893894	$1e^{-71}$	no	147	14.3	2	4.00
50	SS01136	Beta-tubulin	*Strongyloides ratti*	AAY16349	0.0	no	375	11.2	3	8.94
51	SR02940	Collagen alpha 2 subunit	*A. suum*	P27393	$3e^{-05}$	yes	150	18.7	2	4.05
52	SS02105	L-Plastin	*B. malayi*	NP_001899119	$1e^{-57}$	no	188	26.0	3	8.84
53	SR02137	L-Plastin	*B. malayi*	NP_001899119	$6e^{-66}$	no	177	16.3	2	5.41
54	SS02310	L-Plastin	*B. malayi*	NP_001899119	$7e^{-51}$	no	146	17.8	2	4.00
Sugar binding										
Fatty acid binding										
55	SR02741	Fatty acid retinoid binding protein	*Wuchereria bancrofti*	AAL33794	0.37	no	139	15.8	4	10.02
56	SS02274	Fatty acid retinol binding protein 1precursor	*W. bancrofti*	Q9WT54	$7e^{-04}$	yes	155	27.7	4	8.56
Developmental processes										
57	SR03164	Reticulon protein family memeber	*C. elegans*	NP_506656	$5e^{-31}$	no	225	16.4	2	5.15
Heat shock proteins										
58	SS01374	Small heat shock protein 12.6	*B. malayi*	XP_001900590	$6e^{-13}$	no	153	16.9	2	4.00
Putative uncharacterized protein										
Cytoplasmatic										
Other functions										
59	SR01976	Prion like protein	*B. malayi*	XP_001902838	$3e^{-08}$	truncated	78	43.6	3	6.00
60	SR00769	Prion like protein	*B. malayi*	XP_001902838	$4e^{-58}$	truncated	213	15.5	2	4.78
61	SR01328	Class V Aminotransferase	*Heterodera glycines*	AAK26375	$3e^{-37}$	no	162	14.2	2	6.42
62	SS02304	ABC transporter family member	*C. elegans*	NP_503175	$2e^{-79}$	yes	182	26.3	4	8.60
63	SR02297	Tyrosinase like protein	*C. elegans*	Q19673	$7e^{-43}$	yes	192	20.8	3	6.00
64	SR01746	Acid phosphatase	*B. malayi*	XP_001901799	$2e^{-28}$	yes	190	19.4	2	4.00

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65	SS02787	Dihydropyrimidinase family member	*C. elegans*	NP_501797	$2e^{-44}$	no	221	19.9	2	5.40
66	SR00906	RAS-related protein O-RAL	*B. malayi*	XP_001900524	$1e^{-76}$	yes	215	13.0	2	5.60
67	SS01511	RAS-related protein RAB-1A	*B. malayi*	XP_001901944	$7e^{-104}$	no	205	57.5	8	16.05
68	SR01803	Thiosulfate sulfurtransferase	*B. malayi*	XP_001901653	$1e^{-15}$	no	174	53.4	7	14.03
69	SS00527	Haloacid dehalogenase like hydrolase	*B. malayi*	XP_001895356	$1e^{-57}$	no	245	14.2	3	6.03
70	SS01895	Glutamate cysteine ligase modifier subunit	*B. malayi*	XP_001899959	$3e^{-29}$	no	182	20.9	3	7.57
71	SS01689	AvL3-1	*Acantocheilonema viteae*	AAA17420	$6e^{-63}$	no	195	12.3	2	4.00
72	SR03954	CAP protein	*B. malayi*	XP_001891888	$2e^{-53}$	no	242	28.1	4	9.22
73	SS00973	Ubiquitin E2 variant family member	*C. elegans*	NP_493578	$8e^{-53}$	no	141	29.0	3	8.02
74	SS00694	Trans thyretin related family member	*C. elegans*	NP_499054	$1e^{-40}$	yes	138	28.9	3	6.01
75	SS00453	Transthyretin-like family protein	*B. malayi*	XP_001899436	$3e^{-44}$	yes	125	17.6	2	4.00
76	SS01698	Patterned expression site family member	*Caenorhabditis elegans*	NP_506610	$3e^{-57}$	no	157	14.6	2	4.12
77	SS00110	Displaced gonad family member	*C. elegans*	NP_741200	$3e^{-30}$	yes	172	15.1	2	4.00
78	SR02558	Lethal family member (let-805)	*C. elegans*	NP_001022641	$1e^{-69}$	yes	190	37.8	5	13.52
79	SS02590	Sensory Axon guidance family member	*C. elegans*	NP_001033397	$3e^{-42}$	yes	169	59.7	6	12.00
80	SR04483	NCAM – neural cell adhesion molecule	*C. elegans*	NP_741708	$4e^{-05}$	yes	191	22.5	3	7.44
81	SR00292	Transmembrane matrix receptor MUP-4	*C. elegans*	AAK69172	$7e^{-50}$	yes	238	18.0	3	8.89
82	SS00025	Rab GDP dissociation inhibitor alpha	*B. malayi*	XP_001893230	$7e^{-73}$	no	169	15.5	2	4.49
83	SR00641	Vacuolar ATP synthase subunit B	*B. malayi*	XP_001893872	$6e^{-142}$	no	266	42.4	5	8.00
84	SS01502	Synaptobrevin	*B. malayi*	XP_001902083	$3e^{-32}$	no	111	18.0	2	4.00
85	SR03602	Nematode Kynurenine Aminotransferase	*C. elegans*	NP_510355	$9e^{-27}$	no	140	33.6	2	5.30

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86	SS02977	Major allergen Anis.1	*Anisakis simplex*	Q7Z1K3	$6e^{-22}$	yes	195	25.6	3	6.00
87	SR01398	Protein Phosphatase 2C	*B. malayi*	XP_001898345	$3e^{-61}$	no	198	14.6	2	4.00
88	SS01495	RAS-related protein RAB-5B	*B. malayi*	XP_001898689	$9e^{-88}$	no	215	13.0	2	4.00
89	SS01382	Cyclase associated protein	*B. malayi*	XP_001891888	$3e^{-69}$	no	208	9.6	2	4.64
90	SS01764	DJ1 mammalian transcriptional regulator	*C. elegans*	NP_493696	$2e^{-32}$	no	161	12.6	2	4.38
91	SS00302	Methylamalonyl CoA epimerase family member	*C. elegans*	NP_492120	$3e^{-54}$	yes	153	21.3	3	8.17
92	SR03037	Trans thyretin related family member	*C. elegans*	NP_499054	$1e^{-30}$	yes	147	50.3	5	11.80
93	SS02764	Trans thyretin related family member	*C. elegans*	NP_509839	$2e^{-35}$	yes	128	24.2	3	6.06
94	SR00166	EF-1 guanine nucleotide exchange domain	*B. malayi*	XP_001897042	$1e^{-34}$	no	195	24.7	3	8.78
95	SR01252	RRN RNA binding domain family member	*C. elegans*	NP_497891	$2e^{-29}$	no	117	23.9	2	4.24
96	SS02951	Glutamate synthase	*B. malayi*	XP_001899642	$1e^{-47}$	no	169	21.8	3	6.77
97	SR02060	Cell division cycle related family member	*C. elegans*	NP_495705	$3e^{-92}$	no	193	32.6	4	9.50
98	SS03239	Cell division cycle related family member	*C. elegans*	NP_496273	$1e^{-92}$	no	206	17.9	2	4.06
99	SS01112	Translational enoplasmatic reticulum ATPase	*B. malayi*	XP_001902553	$3e^{-115}$	no	256	23.0	4	8.00
100	SR03221	Ubiquitin carboxyl terminal hydrolase	*B. malayi*	XP_001902802	$5e^{-55}$	no	178	21.9	3	6.00
101	SS01978	Aconitase 2	*Homo sapiens*	AAH26196	$1e^{-68}$	no	172	20.8	2	4.60
102	SR00196	Threonyl t-RNA synthetase	*B. malayi*	XP_001893343	$1e^{-91}$	no	189	12.1	2	4.00
103	SS02820	Methylmalonyl CoA mutase homolog	*C. elegans*	NP_497786	$5e^{-94}$	no	195	11.7	2	4.00
104	SR01516	N-acetyl-galactosaminyl-transferase	*C. elegans*	AAC13673	$9e^{-88}$	yes	198	32.8	4	8.00
105	SR02185	Bifunctional aminoacyl-tRNA synthase	*B. malayi*	XP_001894567	$2e^{-76}$	no	187	14.9	2	5.17

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106	SS00992	Receptor mediated endocytosis family member	*C. elegans*	NP_001024193	$1e^{-103}$	no	248	10.4	2	4.00
107	SR00606	NAD-dependent malic enzyme	*B. malayi*	XP_001902120	$2e^{-115}$	no	306	25.8	4	8.18
108	SR02855	NAD-dependent malic enzyme	*B. malayi*	XP_001902120	$5e^{-62}$	no	158	12.0	2	4.38
109	SS00946	Protein phosphatase PP2A regulatory subunit	*B. malayi*	XP_001894294	$8e^{-97}$	no	325	6.8	2	4.00
110	SR00901	TPR domain containg protein	*B. malayi*	XP_001902724	$5e^{-48}$	no	226	34.9	6	12.73
111	SS00837	*Brugia malayi* antigen	*B. malayi*	XP_001900036	0.09	yes	269	4.5	2	5.20
112	SR00660	Protein phosphatase methylesterase 1	*B. malayi*	XP_001896165	$3e^{-46}$	no	194	27.8	3	6.46
113	SS02248	Protein phosphatase methylesterase 1	*B. malayi*	XP_001896165	$2e^{-37}$	no	156	7.7	2	4.02
114	SS00421	Eukaryotic type carbonic anhydrase	*B. malayi*	XP_001901136	$8e^{-36}$	no	151	21.8	2	4.30
115	SS01166	Endophilin related protein	*B. malayi*	XP_001898188	$3e^{-89}$	no	277	8.3	2	5.71
116	SR00614	Leucine rich repeat family protein	*B. malayi*	XP_001896670	$5e^{-26}$	no	198	15.1	2	4.06
117	SR03119	Short chain reductase/dehydrogenase	*B. malayi*	XP_001900343	$1e^{-46}$	no	179	30.1	5	11.57
118	SR00255	Ubiquitin fusion degradation protein	*B. malayi*	XP_001902965	$5e^{-49}$	no	174	21.8	3	6.33
119	SR00141	C2 domain containing protein	*B. malayi*	XP_001895890	$3e^{-35}$	no	165	21.8	3	6.02
120	SR02207	Calponin 1	*B. malayi*	XP_001898596	$2e^{-57}$	no	145	22.0	2	5.70
121	SS01425	Ubiquitin ligase complex component	*C. elegans*	NP_492513	$1e^{-58}$	no	167	20.3	2	4.08
122	SS01049	RAS like GTP binding protein RhoA	*B. malayi*	XP_001896906	$2e^{-80}$	no	177	23.1	2	4.00
123	SR01305	Peptide methionine sulfoxide reductase msrB	*B. malayi*	XP_001900393	$2e^{-41}$	no	166	12.0	2	4.00
124	SS00103	17.1 kDa polypeptide	*B. malayi*	XP_001896848	$2e^{-19}$	no	79	41.8	2	4.00
125	SS01330	Vacuolar ATP synthase subunit G	*B. malayi*	XP_001893897	$1e^{-38}$	no	125	21.6	2	4.00

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126	SS02063	Vacuolar H ATPase family member	*C. elegans*	NP_496217	$3e^{-49}$	no	121	33.1	3	6.00
127	SR00694	High mobility group protein	*B. malayi*	NP_001900502	$1e^{-74}$	no	192	19.8	3	6.01
128	SS01022	High mobility group protein	*B. malayi*	NP_001900502	$1e^{-81}$	no	191	13.1	2	6.19
129	SS00814	Small subunit ribosomal protein 21	*Pristionchus sp.* 6 RS5101	ABR87532	$5e^{-34}$	no	90	48.9	2	5.71
130	SR03619	Seryl t-RNA synthetase family member	*C. elegans*	NP_501804	$1e^{-51}$	no	194	14.4	2	4.00
131	SR03176	Hexokinase	*H. contortus*	CAB40412	$4e^{-72}$	no	172	16.3	2	4.00
132	SR02972	Vacuolar H ATPase family member	*C. elegans*	NP_001023451	$4e^{-72}$	no	167	11.4	2	5.23
133	SR01338	Vacuolar ATPase subunit C family protein	*B. malayi*	XP_001899274	$2e^{-16}$	no	66	65.2	3	6.00
Not assigned										
134	SR00386	L3NieAg.01	*S. stercoralis*	AAD46493	0.15	truncated	112	50.8	5	13.50
135	SR02886	Hypothetical 35.6 kDa protein	*B. malayi*	XP_001899587	$1e^{-71}$	no	180	55.0	7	14.10
136	SS01256	Hypothetical protein Bm1_13900	*B. malayi*	XP_001894244	$1e^{-26}$	yes	228	39.0	5	10.00
137	SS01225	GH10174	*Drosophila grimshawi*	EDW04076	$3e^{-04}$	yes	223	15.2	2	4.43
138	SS02094	Hypothetical protein	*B. malayi*	XP_001899474	$3e^{-31}$	no	145	24.8	2	4.01
139	SR01443	Hypothetical protein	*C. elegans*	CAP26647	$3e^{-05}$	no	44	65.9	3	7.70
140	SR02296	Hypothetical protein	*B. malayi*	XP_001896771	$1e^{-33}$	yes	144	20.1	2	6.93
141	SR00103	Hypothetical protein CBG23797	*C. elegans*	CAP20556	$6e^{-47}$	yes	143	16.1	2	4.00
142	SR01197	Hypothetical protein C10G8.3	*C. elegans*	NP_504417	$2e^{-11}$	yes	166	30.7	4	8.47
143	SS01885	Y73B6BL.25	*C. elegans*	NP_500983	$6e^{-23}$	yes	196	18.4	3	6.02
144	SS00215	Hypothetical protein CBG04133	*C. briggsae*	XP_001667008	$2e^{-11}$	yes	204	14.2	2	4.00
145	SS02239	C32F10.8a	*C. elegans*	NP_001021021	$4e^{-54}$	no	140	16.4	2	4.65
146	SR01604	Hypothetical protein CBG08398	*C. briggsae*	XP_001671673	$4e^{-18}$	yes	171	26.9	2	4.00
147	SR03753	K02D10.1b	*C. elegans*	NP_498936	$5e^{-30}$	no	154	14.3	3	10.05
148	SS00711	F15B9.10	*C. elegans*	NP_001122920	$5e^{-48}$	yes	180	14.8	2	4.99

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149	SS00357	Hypothetical protein CBG16364	*C. briggsae*	XP_001667068	$8e^{-29}$	no	132	15.2	2	4.00
150	SR01525	C30C11.4	*C. elegans*	NP_498868	$2e^{-28}$	no	211	11.4	2	4.73
151	SR01791	Y105E8A.19	*C. elegans*	NP_740947	$3e^{-11}$	no	188	16.5	2	5.52
152	SS00863	Hypothetical protein CBG21807	*C. briggsae*	XP_001672698	$1e^{-64}$	yes	156	16.0	2	4.00
153	SR05055	VF13D12L.3	*C. elegans*	NP_496500	$2e^{-59}$	no	189	47.1	3	7.40
154	SR01321	Hypothetical protein Bm1_36850	*B. malayi*	XP_001898817	$1e^{-12}$	no	176	43.2	5	10.00
155	SS01276	F55F3.3	*C. elegans*	NP_510300	$2e^{-104}$	no	317	12.0	3	9.17
156	SR00450	Y6B3B.5a	*C. elegans*	NP_001021801	$5e^{-15}$	yes	136	19.1	2	4.99
157	SR02530	Hypothetical protein CBG03344	*C. briggsae*	NP_001670753	$2e^{-31}$	no	125	24.8	2	4.01
158	SR03285	Hypothetical protein CBG04457	*C. briggsae*	XP_001671529	$1e^{-77}$	no	236	10.2	2	4.00
159	SR00182	Hypothetical protein LOC100127627	*Xenopus tropicalis*	NP_001106450	$4e^{-42}$	no	180	16.7	2	4.04
160	SS00742	Temporarily assigned gene name tag-253	*C. elegans*	NP_741571	$9e^{-53}$	yes	188	17.6	2	4.00
161	SS01477	Hypothetical protein Bm1_23005	*B. malayi*	XP_001896058	$2e^{-14}$	yes	241	8.7	2	6.09
162	SR00244	Y53H1B.1	*C. elegans*	NP_492900	$1e^{-58}$	yes	284	8.5	2	4.00
163	SS01439	ZK1307.1a	*C. elegans*	NP_001022509	$2e^{-79}$	no	237	18.6		6.91
164	SR01140	Hypothetical protein CBG23403	*C. briggsae*	XP_001673594	$6e^{-15}$	no	104	31.7	2	4.21
165	SR01943	Novel protein similar to COG3	*Danio rerio*	CAQ14213	0.76	no	168	29.2	3	7.75
166	SS01523	Y54G2A.2a	*C. elegans*	NP_001023492	0.0	no	544	6.4	3	6.22
167	SR02095	Hypothetical protein CBG10437	*C. briggsae*	NP_001672867	$5e^{-36}$	no	119	24.4	2	4.10
168	SR00123	Unnamed protein product	*Tetraodon nigroviridis*	CAG11397	$3e^{-27}$	no	138	25.3	2	4.00
169	SR00366	hypothetical protein DDBD-RAFT_0217849	*Dictyostelium discoideum AX4*	XP_642992	$5e^{-08}$	no	190	40.5	6	13.15
170	SR02793	RO5H10.7	*C. elegans*	NP_001022271	$1e^{-15}$	no	212	12.7	2	5.17

Novel proteins that are not listed in one of the *Strongyloides ssp.* EST databases

N°	Acc. Number	BLAST Alignment	Species	SP	Fragment Length	% Cov.	Pep. #	UPS
171	gi|71987720 *see SR02558*	Lethal family member (let-805)	*C. elegans*	yes	4450	0.7	2	5.46
172	gi|17569483	Spectrin family member (sps-1)	*C. elegans*	no	2427	7.4	15	34.98
173	gi|17535441	R05F9.6	*C. elegans*	no	568	6.0	3	6.08
174	gi|17543050	Y37A1B.5	*C. elegans*	no	471	6.8	2	5.40
175	gi|17534675	G-protein, beta subunit (gpb-1)	*C. elegans*	no	340	7.4	2	4.05
176	gi|25151898	Dense body family member (deb-1)	*C. elegans*	no	999	2.5	2	6.09
177	gi|159893	Major body wall myosin	*O. volvulus*	no	1957	2.6	3	6.42
178	gi|72003683	Lin-5 interacting protein family member (lfi-1)	*C. elegans*	no	2350	0.8	2	4.58
179	gi|17534447	Aldehyde dehydrogenase family member (alh-6)	*C. elegans*	no	563	6.9	3	6.17
180	gi|25146553	C37H5.6a	*C. elegans*	no	457	4.2	2	4.08
181	gi|17507969	Homogentisate oxidase family member (hgo-1)	*C. elegans*	no	437	6.9	2	4.03
182	gi|71981209	C32F10.8a	*C. elegans*	no	504	5.8	2	4.13
183	gi|17568413	GPD family member	*C. elegans*	no	341	10.9	3	5.74
184	gi|17560440	F32D1.5	*C. elegans*	no	358	7.5	2	4.10
185	gi|74763811	Tubulin beta chain	*Trichuris trichiura*	no	444	52.9	24	51.84
186	gi|32566457	Filamin (flna-1)	*C. elegans*	no	2747	0.8	2	5.95
187	gi|392788	Intermediate filament protein	*B. malayi*	no	506	6.1	4	8.13
188	gi|17570289	W07E11.1	*C. elegans*	no	2207	1.4	2	7.38
189	gi|17555418	Uncoordinated family member (unc-116)	*C. elegans*	no	815	2.9	2	4.97
190	gi|17541896	Isoleucyl t-RNA synthetase family member (irs-1)	*C. elegans*	no	1141	1.8	2	4.02
191	gi|38016557	UNC-18	*H. contortus*	no	588	3.9	2	7.65
192	gi|17554896	T04A8.7a	*C. elegans*	no	681	3.5	2	4.00
193	gi|17556182	Y54F10AR.1	*C. elegans*	no	336	10.7	2	4.00

N°	**Acc. Number**	**BLAST Alignment**	**Species**	**SP**	**Fragment Length**	**% Cov.**	**Pep. #**	**UPS**
194	gi|17508491	Proteasome Alpha subunit family member (pas-4)	*C. elegans*	no	153	25.5	2	5.17
195	gi|17508451	Neuronal calcium sensor family member (ncs-2)	*C. elegans*	no	190	57.3	7	14.02
196	gi|25153953	Ubiquitin conjugating enzyme family member (ubc-13)	*C. elegans*	no	151	16.6	2	4.57

E, expectation value; SP, signal peptide; EST Lgt., EST length; % Cov., percentage coverage; Pep. # number of peptides (#); UPS, unused protein scores