Supplemental TABLE 2. List of *Strongyloides* proteins found in E/S products from all stages: in infective larvae, parasitic females and free-living stages

N°	Cluster	BLAST Alignment	Species	Accession Number	E	SP	EST Lgt.	% Cov.	Pep. #	UPS
Oxydative metabolism										
1	SS01309	Peroxiredoxin	*Ascaris suum*	Q9NL98	$1e^{-70}$	no	196	49.1	4	12.45
2	SS01223	Superoxide dismutase	*Caenorhabditis elegans*	NP_492290	$8e^{-69}$	no	173	52.5	7	14.00
3	SS01344	Superoxide dismutase	*Brugia pahangi*	P41962	$1e^{-58}$	no	157	34.1	5	11.70
4	SR04901	Thioredoxin	*Caenorhabditis brenneri*	ACD86930	$7e^{-31}$	truncated	129	46.0	6	12.01
5	SR04239	Thioredoxin	*A. suum*	AAS78778	$1e^{-48}$	no	147	32.7	4	8.55
6	SR00374	Thioredoxin peroxidase 1	*Brugia malayi*	P48822	$2e^{-73}$	yes	179	17.2	2	5.79
7	SR03061	Glutathione peroxidase	*B. malayi*	XP_001897517	$1e^{-39}$	no	144	33.9	4	8.00
8	SR04471	FAD dependent oxidoreductase	*B. malayi*	XP_001892448	$3e^{-47}$	yes	195	25.6	4	8.05
Carbohydrate Metabolism										
9	SR00792	Probable citrate synthase	*C. elegans*	P34575	$1e^{-166}$	no	339	46.0	11	24.50
10	SR05207	Transaldolase	*Nasonia vitripennis*	XP_001602166	$2e^{-72}$	no	193	45.9	6	14.59
11	SR05258	Citrate synthase	*C. elegans*	NP_499264	$2e^{-88}$	no	196	40.3	4	4.01
12	SR03532	Triose phosphate Isomerase	*C. elegans*	1MO0_A	$2e^{-45}$	no	129	34.3	3	4.00
13	SR02487	Carbohydrate phosphorylase	*B. malayi*	XP_001804669	$3e^{-81}$	no	171	49.5	7	7.44
14	SR00093	UDP-glucose pyrophosphorylase	*B. malayi*	XP_001899721	$1e^{-80}$	no	182	31.3	3	9.44
15	SR01173	Fructose biphosphate aldolase 1	*C. elegans*	P54216	$1e^{-12}$	no	69	71.0	4	16.03
16	SR01890	Aldolase	*Globodera rostochiensis*	AAN78210	$2e^{-54}$	no	185	15.1	3	6.12
17	SR02615	Transketolase	*B. malayi*	XP_001893528	$8e^{-75}$	no	193	51.3	9	16.00
18	SR03215	Transaldolase	*C. elegans*	NP_741369	$1e^{-68}$	no	178	36.5	5	12.76
19	SR01273	Aldehyde dehydrogenase (alh-12)	*C. elegans*	NP_001022931	$1e^{-36}$	no	171	13.5	2	5.78
20	SS00861	Aldehyde dehydrogenase (alh-8)	*C. elegans*	NP_001022078	$4e^{-123}$	no	272	22.4	4	9.54
21	SR00739	Aldehyde dehydrogenase (alh-8)	*C. elegans*	NP_001022078	$2e^{-124}$	no	274	15.7	3	8.26
22	SS00910	GDP-L-fucose synthetase	*B. malayi*	XP_001893725	$1e^{-62}$	no	154	42.9	3	6.92
23	SR01995	Aldo/keto reductase family protein	*B. malayi*	XP_001897743	$2e^{-35}$	no	159	43.4	5	16.21

N°	Cluster	BLAST Alignment	Species	Accession Number	E	SP	EST Lgt.	% Cov.	Pep. #	UPS
Cytosol energy metabolism										
24	SR00185	Enolase (enol-1)	*C. elegans*	NP_001022349	$2e^{-77}$	no	184	40.8	5	10.05
25	SR00704	Cytochrome C family member	*C. elegans*	NP_500629	$1e^{-46}$	no	106	45.2	4	8.09
26	SR02190	Enolase (enol-1)	*C. elegans*	NP_001022349	$2e^{-78}$	no	167	57.5	5	8.35
27	SR01215	Fumarase	*B. malayi*	XP_001900957	$2e^{-70}$	no	168	39.9	4	10.16
28	SR00949	ATP synthase subunit	*C. elegans*	NP_498111	0.0	no	473	34.5	10	21.70
29	SR00265	Lyase	*A. suum*	AAP51177	$2e^{-117}$	no	241	49.4	6	13.42
30	SR00941	Aconitase family member	*C. elegans*	NP_498738	$1e^{-123}$	no	280	42.1	8	18.18
31	SR02997	Isocitrate dehydrogenase	*Tribolium castaneum*	XP_968850	$1e^{-84}$	no	179	23.5	3	6.00
32	SR00966	Arginine kinase	*Heterodera glycines*	AAO49799	$2e^{-165}$	no	346	61.8	19	41.48
Protein biosynthesis										
33	SR00985	Elongation factor family member	*C. elegans*	NP_492457	$1e^{-162}$	no	321	28.9	7	15.60
34	SR00885	Eukaryotic translation initiation factor 5A-2	*B. malayi*	XP_001902971	$8e^{-68}$	no	155	17.4	3	6.41
35	SR03540	TPR domain containing protein	*B. malayi*	XP_001892919	$3e^{-30}$	no	251	33.5	7	15.15
36	SR00180	Cyclophylin	*C. elegans*	NP_497297	$4e^{-51}$	yes	152	25.7	4	11.93
Protein digestion and folding										
37	SR00990	Peptidyl-prolyl cis-trans isomerase	*Dirofilaria immitis*	Q23955	$1e^{-59}$	no	162	56.2	8	17.14
38	SR01407	Protein disulfide isomerase	*Teladorsagia circumcinata*	Q2HZY3	0.0	yes	287	35.9	10	23.95
39	SR00881	W07G4.4 Peptidase M17	*C. elegans*	NP_506260	$1e^{-111}$	no	356	31.5	11	25.77
40	SR01037	Protein disulfide isomerase	*A. suum*	CAK18211	0.0	yes	499	62.7	27	62.56
41	SS00975	Protein disulfide isomerase (pdi-3)	*C. elegans*	NP_491995	$5e^{-63}$	yes	152	27.6	3	6.00
42	SR02132	Serpin	*B. malayi*	XP_001896649	$1e^{-17}$	yes	162	45.1	7	15.36
43	SR02845	Serpin	*B. malayi*	XP_001892287	$2e^{-26}$	yes	173	28.3	4	9.87
44	SR02150	Serpin	*Mus musculus*	AAR89288	$5e^{-24}$	no	184	51.9	7	14.00
45	SR01375	Cyclophylin-type peptidyl-prolyl cis-trans isomerase 15	*B. malayi*	XP_001896264	$8e^{-70}$	no	186	49.5	8	16.74
46	SR01148	FKBP-peptidyl-prolyl cis-trans isomerase	*B. malayi*	XP_001901266	$7e^{-39}$	no	143	58.0	7	17.23

N°	Cluster	BLAST Alignment	Species	Accession Number	E	SP	EST Lgt.	% Cov.	Pep. #	UPS
47	SR01041	Calreticulin	*Necator americanus*	CAA07254	$1e^{-153}$	yes	410	34.6	8	17.37
48	SR02163	Peptidase family M1 containing protein	*B. malayi*	XP_001897028	$4e^{-36}$	no	178	51.7	8	18.51
49	SR00921	Serine carboxypeptidase	*B. malayi*	XP_001900088	$9e^{-101}$	yes	303	13.5	2	5.71
50	SR01946	Proteasome subunit beta type 1	*B. malayi*	XP_001894290	$3e^{-78}$	no	188	35.1	4	8.92
51	SR00682	BmFKBP59	*B. malayi*	XP_001902831	$3e^{-57}$	no	173	37.0	4	10.30
52	SR03139	Proteasome subunit alpha type 3	*B. malayi*	XP_001894710	$2e^{-51}$	no	166	73.5	9	18.00
53	SR01985	Proteasome subunit alpha type 1	*B. malayi*	XP_001895018	$3e^{-74}$	no	151	41.1	5	10.00
54	SS03222	20S proteasome alpha 5 subunit	*B. malayi*	XP_001898928	$2e^{-74}$	no	167	30.5	4	9.70
55	SR00809	Proteasome subunit beta type 2	*B. malayi*	XP_001897296	$1e^{-71}$	no	202	15.8	2	7.43
56	SR00774	Ubiquitin	*C. elegans*	NP_741157	0.0	no	439	84.1	6	18.68
Nucleic acid metabolism										
57	SR01051	Nucleoside diphosphate kinase	*B. malayi*	XP_001901495	$9e^{-70}$	no	194	47.4	7	15.53
Structural proteins										
58	SS01554	Actin 1	*B. malayi*	XP_001895795	$3e^{-55}$	no	376	38.6	11	24.80
59	SR01247	Profilin	*B. malayi*	XP_001895778	$8e^{-47}$	no	132	81.8	7	17.28
60	SR00329	Yeast Actin interacting protein 1	*B. malayi*	XP_001899636	$2e^{-66}$	no	210	38.1	7	15.45
61	SR00358	Actin depolymerizing factor 1	*B. malayi*	XP_001896055	$7e^{-64}$	no	164	17.7	2	4.89
62	SS01430	Tropomyosin	*Trichinella pseudospiralis*	Q8WR63	$4e^{-124}$	no	284	34.9	10	24.18
Sugar binding										
63	SR00857	Galectin protein 5	*C. elegans*	NP_495163	$7e^{-60}$	yes	183	28.4	4	9.54
64	SS00840	Galectin-1	*Teladorsagia circumcinata*	AAD39095	$4e^{-127}$	no	278	55.8	14	32.70
65	SR00900	Galectin	*B. malayi*	XP_001896448	$2e^{-68}$	no	163	54.6	6	17.50
66	SR00627	Galectin-2	*Haemonchus contortus*	AAF63405	$7e^{-139}$	no	276	38.0	10	25.56
Fatty acid binding										
67	SR00858	Fatty acid binding protein	*A. suum*	P55776	$7e^{-60}$	yes	165	60.0	12	25.00
68	SR00605	S1 protein	*Onchocerca volvulus*	CAA59101	$2e^{-32}$	no	180	31.7	6	13.81
69	SR00229	Lipid binding protein family	*C. elegans*	NP_491928	$7e^{-18}$	no	116	38.8	5	14.10

N°	Cluster	BLAST Alignment	Species	Accession Number	E	SP	EST Lgt.	% Cov.	Pep. #	UPS
Developmental processes										
70	SR00876	Calponin protein 3	*C. elegans*	O01542	$3e^{-55}$	no	144	76.4	13	31.21
71	SR01042	Elongation factor 2	*C. elegans*	P29691	0.0	no	531	29.2	12	33.34
72	SR00371	Nucleosome assembly protein 1	*B. malayi*	A8PJH0	$2e^{-29}$	no	247	42.1	8	16.00
73	SR02807	Elongation factor 1-beta/1-delta	*B. malayi*	XP_001897113	$2e^{-55}$	no	214	8.9	2	4.00
74	SS01391	Small subunit ribosomal protein 28	*Pristionchus maupasi*	ABR87582	$2e^{-25}$	no	68	33.8	2	5.70
Heat shock proteins										
75	SR01060	Heat shock protein 70	*Parastrongyloides trichosuri*	AAF87583	0.0	no	644	25.8	10	21.39
76	SR00952	Heat shock protein 90	*B. pahangi*	CAA06694	$3e^{-137}$	no	338	26.0	7	16.59
77	SR00728	Heat shock protein 60	*Strongyloides ratti*	ABY65231	0.0	no	563	64.1	33	71.01
78	SS01752	Chaperonin 10	*S. ratti*	ABN49241	$6e^{-51}$	no	109	33.9	3	6.17
79	SR00065	Heat shock protein 70-C	*H. glycines*	AAM93256	$9e^{-89}$	yes	185	11.9	2	4.00
Cytoplasmatic										
80	SS01336	Calexitin family member (CEX-1)	*C. elegans*	NP_495034	$4e^{-62}$	no	196	29.6	5	10.00
81	SR02058	Iron regulatory protein 1A	*Drosophila melanogaster*	NP_477371	$9e^{-59}$	no	183	29.5	3	7.76
82	SS02442	Aconitase family member	*C. elegans*	NP_509898	$7e^{-72}$	no	166	17.5	2	6.79
83	SR02277	4-Hydroxy-phenylpyruvate dioxygenase	*C. elegans*	NP_499324	$1e^{-86}$	no	199	58.8	6	16.14
84	SR00922	14-3-3 family member	*C. elegans*	NP_509939	$4e^{-110}$	no	250	59.2	12	32.14
Other functions										
85	SR04614	Probable Aspartate aminotransferase	*C. elegans*	Q22067	$5e^{-81}$	no	187	63.6	10	22.78
86	SR00060	Rab GDP dissociation inhibitor alpha, putative	*B. malayi*	EDP37909	$2e^{-66}$	truncated	196	16.3	3	7.70
87	SS03041	Conserved Cysteine/Glycine domain protein	*C. elegans*	NP_502842	$4e^{-33}$	yes	170	22.4	4	8.01
88	SS01143	Transthyretin-like protein	*C. brenneri*	ACD88894	$3e^{-48}$	truncated	141	48.9	5	12.51
89	SR00146	Transthyretin-related domain family member	*C. elegans*	NP_498657	$6e^{-33}$	yes	146	58.2	7	14.54
90	SR00027	Elongation factor 1-alpha	*B. malayi*	XP_001896880	0.0	no	455	29.5	9	22.79

N°	Cluster	BLAST Alignment	Species	Accession Number	E	SP	EST Lgt.	% Cov.	Pep. #	UPS
91	SR00743	Glutathione S-transferase	*A. suum*	P46436	$3e^{-40}$	no	205	42.4	6	12.03
92	SR02533	Elongation factor 1	*B. malayi*	XP_001901841	$2e^{-33}$	no	183	42.1	5	10.00
93	SR01119	Nuclear transport factor 2	*B. malayi*	XP_001894897	$3e^{-47}$	no	132	48.5	5	10.01
94	SR01065	Glutamate dehydrogenase	*B. malayi*	XP_001893113	0.0	no	383	25.1	8	16.24
95	SR02773	LEThal family member	*C. elegans*	NP_498730	$2e^{-86}$	no	207	25.1	3	6.50
96	SR00950	Activated protein kinase C receptor	*B. malayi*	XP_001898740	$2e^{-131}$	no	326	30.1	6	13.80
97	SR02588	Inorganic pyrophosphatase	*A. suum*	BAC66617	$2e^{-57}$	yes	190	13.2	2	5.74
98	SS00743	Transthyretin-related domain family member	*C. elegans*	NP_871961	$5e^{-42}$	yes	146	32.9	3	8.64
99	SR00387	Cyanate hydratase family protein	*B. malayi*	XP_001897006	$4e^{-32}$	no	171	37.4	5	11.08
100	SR00957	SEC-2 protein	*Globodera pallida*	CAA70477	$4e^{-35}$	yes	181	28.2	3	6.25
101	SS00219	Glutamate dehydrogenase	*H. contortus*	AAC19750	$6e^{-68}$	no	154	16.9	2	4.59
102	SS00999	GABA transaminase family member	*C. elegans*	NP_501862	$1e^{-64}$	no	199	10.6	2	5.57
103	SR00756	ADP ribosylation factor 79F	*D. melanogaster*	NP_476955	$2e^{-100}$	no	181	43.6	5	11.79
104	SS00738	Ov-16 antigen precursor	*B. malayi*	XP_001899662	$1e^{-61}$	no	173	21.4	2	7.88
105	SR02238	Submergence induced protein 2A	*Arabidopsis thaliana*	AAM63708	$1e^{-20}$	no	120	33.3	3	7.44
106	SR02779	DVA-1 polyprotein precursor	*Dictyocaulus viviparus*	Q24702	$3e^{-07}$	yes	133	24.8	2	4.05
107	SS02521	Transthyretin-related domain family member	*C. elegans*	NP_499054	$6e^{-43}$	yes	143	21.7	2	4.77
108	SR00623	Lysozyme family member (ilys-3)	*C. elegans*	NP_500206	$3e^{-47}$	yes	137	24.8	3	9.72
109	SR00930	Translationally controlled tumor protein-like protein	*S. ratti*	ABF69532	$2e^{-74}$	no	170	28.2	5	15.81
110	SS01532	Gaba	*B. malayi*	XP_001900805	$6e^{-52}$	no	117	39.3	2	5.00
111	SR02279	Aldehyde dehydrogenase (alh-8)	*C. elegans*	NP_001022078	$2e^{-68}$	no	183	25	2	4.21
112	SR00351	Major sperm protein (msp-78)	*C. elegans*	NP_501742	$2e^{-64}$	no	127	21.3	2	4.03
113	SR00903	SXP-1 protein	*Loa loa*	AAG09181	$4e^{-06}$	truncated	320	13.8	3	6.93
114	SS03457	Eukaryotic initiation factor	*C. elegans*	NP_493272	$3e^{-31}$	no	85	57.6	3	6.49

Cluster	BLAST Alignment	Species	Accession Number	E	SP	EST Lgt.	% Cov.	Pep. #	UPS
Not assigned									
115 SR00866	Hypothetical protein CBG18957	*C. briggsae*	XP_001674360	7e^{-139}	yes	338	51.5	21	46.19
116 SR01871	L3NieAg.01	*Strongyloides stercoralis*	AAD46493	4e^{-21}	truncated	169	71.0	18	46.28
117 SR00795	LL20 15 kDa ladder antigen	*B. malayi*	XP_001901667	2e^{-32}	no	250	41.2	8	16.14
118 SS00892	Immunogenic protein 3	*B. malayi*	Q6S5M8	2e^{-20}	yes	127	22.0	3	8.18
119 SR00488	Allergen polyprotein homolog	*S. stercoralis*	AAB97360	1e^{-31}	truncated	205	22.4	4	11.09
120 SR00403	Similar to dj-1	*Apis mellifera*	XP_624271	1e^{-30}	no	147	35.4	4	8.00
121 SR00753	T19B10.2	*C. elegans*	NP_505848	1e^{-63}	yes	191	37.7	5	10.00
122 SR02634	Hypothetical protein	*Aedes aegypti*	XP_001649379	1.3	no	172	24.4	3	7.32
123 SR00205	Hypothetical protein	*C. elegans*	XP_001667775	8e^{-66}	no	168	21.4	3	7.75
124 SR00281	F59A2.3	*C. elegans*	NP_497701	5e^{-68}	no	226	19.5	3	6.08
125 SR00872	Hpothetical protein	*C. briggsae*	XP_001676876	1e^{-134}	no	307	38.8	9	22.47
126 SR00768	UPF0587	*C. elegans*	Q9BI88	1e^{-43}	no	169	18.9	3	7.22
127 SR00250	Hypothetical protein CBG03400	*C. briggsae*	XP_001670800	5e^{-53}	no	170	21.2	3	7.98
128 SR02918	Hypothetical protein CBG04059	*C. elegans*	XP_001668188	6e^{-78}	no	188	32.4	4	11.38
129 SR00573	Hypothetical protein CBG21098	*C. briggsae*	XP_001666425	3e^{-34}	yes	181	14.4	2	4.95
130 SR02535	Hypothetical 19.4 kDa protein ZC395.10	*B. malayi*	XP_001897485	5e^{-05}	no	119	29.4	2	4.04
131 SS01194	K02F2.2	*C. elegans*	NP_491955	3e^{-134}	no	260	26.5	5	10.14
132 SR00840	Putative uncharacterized protein	C. briggsae	XP_001668392	5e^{-49}	yes	204	40.2	7	15.37
133 SR01280	Hypothetical protein CBG03385	C. briggsae	CAP24286	2e^{-59}	no	168	48.2	5	10.39
134 SR00428	Hypothetical protein F01G10.1	*C. elegans*	NP_501878	1e^{-88}	no	190	60.0	6	12.04

New 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**
135	gi|71996708	Glucose 6 phosphate iso-merase (gpi-1)	*C. elegans*	no	586	26.6	11	25.00
136	gi|71995829	Enolase family member (enol-1)	*C. elegans*	no	465	14.4	6	15.44
137	gi|17535107	Lactate dehydrogenase family member (ldh-1)	*C. elegans*	no	333	7.8	3	8.66
138	gi|71983429	C46F11.2b	*C. elegans*	no	473	9.1	3	6.00
139	gi|159183	Phosphoenolpyruvate carboxykinase	*H. contortus*	no	619	12.6	5	11.01
140	gi|17554310	Malate dehydrogenase family member (mdh-1)	*C. elegans*	no	341	20.2	4	9.16

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