

Table S1. Proteins identified in *H. taeniaeformis* metacestodes.

ID	Molecular (kDa)	Percent (%)	Unique peptide	Unique Spectra	Description	COG Functional-Categories	NCBI nr Accession
1	225	1.30	115	187	myosin heavy chain	Structural/cytoskeletal proteins	gi 674572847 emb CDS41550.1
2	108	0.42	46	64	paramyosin	-	gi 42560539 sp P35418.2
3	882	0.27	39	46	basement membrane specific heparan sulfate	-	gi 674562108 emb CDS23619.1
4	71	0.44	35	55	heat shock 70 protein 4	Post-translational modification	gi 674571132 emb CDS43123.1
5	110	0.2	33	42	spectrin alpha actinin	-	gi 674561275 emb CDS24366.1
6	112	0.2	33	38	sodium/potassium-transporting ATPase subunit alpha	Metabolism	gi 576693508 gb EUB57119.1
7	70	0.46	30	51	phosphoenolpyruvate carboxykinase	Energy production and conversion	gi 283466482 emb CBH36496.1
8	42	0.87	27	58	actin	Structural/cytoskeletal proteins	gi 576695773 gb EUB59337.1
9	190	0.13	26	30	hemicentin 1	-	gi 674576561 emb CDS36997.1
10	127	0.27	26	33	type II collagen B	-	gi 674572459 emb CDS42884.1
11	325	0.12	25	29	titin	-	gi 674567709 emb CDS16820.1
12	117	0.15	25	30	spectrin beta chain brain 3	-	gi 674573973 emb CDS40896.1
13	72	0.23	24	34	succinate dehydrogenase flavoprotein subunit	Energy production and conversion	gi 576699397 gb EUB62925.1
14	37	0.67	24	43	cytosolic malate dehydrogenase	Energy production and conversion	gi 323361126 gb ADX42057.1
15	154	0.12	23	28	Spectrin beta chain brain 3	Structural/cytoskeletal proteins	gi 576699919 gb EUB63443.1
16	73	0.15	22	28	glycogen phosphorylase	Metabolism	gi 674566587 emb CDS19687.1
17	97	0.16	21	28	major vault protein	-	gi 674561667 emb CDS23982.1
18	42	0.18	21	26	L-threonine 3-dehydrogenase	Metabolism	gi 576693761 gb EUB57365.1
19	166	0.19	20	27	collagen alpha 1V chain	-	gi 674265696 emb CDI98199.1
20	184	0.082	20	21	clathrin heavy chain	-	gi 674267057 emb CDI97445.1
21	47	0.38	20	30	enolase	Metabolism	gi 563425937 gb AHB59732.1
22	40	0.24	20	32	fructose 16 bisphosphate aldolase	Metabolism	gi 674574479 emb CDS41408.1
23	28	0.16	19	27	putative growth regulator 14-3-3	Signal transduction	gi 563425939 gb AHB59733.1
24	166	0.086	19	21	titin	-	gi 576699428 gb EUB62955.1
25	79	0.12	19	24	molecular chaperone HtpG	Post-translational modification	gi 358339046 dbj GAA47176.1
26	60	0.1	19	19	ATP synthase subunit alpha mitochondrial	Energy production and conversion	gi 674562214 emb CDS23514.1
27	69	0.13	19	27	phosphoglucomutase 2	Metabolism	gi 674571151 emb CDS43145.1
28	183	0.12	18	20	filamin	Structural/cytoskeletal proteins	gi 674570113 emb CDS16181.1
29	33	0.1	18	21	tropomyosin 2 high molecular weight isoform	-	gi 29337029 sp Q95PU1.1

30	56	0.1	18	22	ATP synthase subunit beta	Energy production and conversion	gi 576697808 gb EUB61347.1
31	93	0.17	18	25	calpain-A	-	gi 576700942 gb EUB64462.1
32	28	0.18	18	29	14-3-3 protein zeta	Signal transduction	gi 576698574 gb EUB62107.1
33	57	0.1	17	21	UTP glucose 1 phosphate uridylyltransferase	Metabolism	gi 674569954 emb CDS16022.1
34	69	0.1	17	21	four and A half lim domains	-	gi 961439404 emb CUT98901.1
35	232	0.12	17	22	collagen alpha 1(IV) chain	-	gi 674561688 emb CDS24003.1
36	65	0.15	17	26	NADP dependent malic enzyme	Energy production and conversion	gi 674565192 emb CDS20746.1
37	62	0.15	16	22	phosphoglucose isomerase	Metabolism	gi 154369446 gb ABS81352.1
38	131	0.15	16	21	fibrillar collagen chain FAp1 alpha	-	gi 674568718 emb CDS17836.1
39	50	0.097	16	21	Rab GDP dissociation inhibitor alpha	Post-translational modification	gi 576694030 gb EUB57627.1
40	162	0.097	16	18	titin	Signal transduction	gi 674567709 emb CDS16820.1
41	22	0.13	16	20	myosin regulatory light chain	Structural/cytoskeletal proteins	gi 124783553 gb ABN14929.1
42	190	0.063	15	15	glycogen debranching enzyme	Metabolism	gi 576699668 gb EUB63194.1
43	80	0.063	15	16	glucan 14 alpha branching enzyme 1	Metabolism	gi 674565637 emb CDS20187.1
44	27	0.56	14	22	P29	-	gi 558698068 gb AHA85391.1
45	115	0.078	14	16	Filamin-A	Structural/cytoskeletal proteins	gi 576697079 gb EUB60625.1
46	65	0.13	14	21	Phosphoglucomutase	Metabolism	gi 576695399 gb EUB58969.1
47	118	0.074	13	13	calcium transporting atpase	Metabolism	gi 674568220 emb CDS17335.1
48	93	0.097	13	18	Basement membrane-specific heparan sulfate proteoglycan core protein	-	gi 576697991 gb EUB61528.1
49	50	0.093	13	17	tubulin alpha chain	Structural/cytoskeletal proteins	gi 674570366 emb CDS16437.1
50	176	0.093	13	16	abnormal embryogenesis family member emb 9	-	gi 674561689 emb CDS24004.1
51	61	0.074	13	15	heat shock protein 60	Post-translational modification	gi 674580112 emb CDS35950.1
52	127	0.13	13	20	Collagen alpha-2(I) chain	-	gi 576700155 gb EUB63678.1
53	34	0.089	13	17	atp:adp antiporter	-	gi 961439544 emb CUT99040.1
54	71	0.089	13	16	Transketolase	Metabolism	gi 576691476 gb EUB55174.1
55	83	0.082	13	15	Threonyl tRNA synthetase C	Transcription	gi 674577779 emb CDS36622.1
56	34	0.11	13	15	aldo keto reductase family 1 member B4	Function unknown	gi 674266307 emb CDI97754.1
57	89	0.071	13	14	6-phosphofructokinase	Metabolism	gi 576694014 gb EUB57612.1
58	17	0.25	12	19	Myosin essential light chain, striated adductor muscle	Structural/cytoskeletal proteins	gi 576700259 gb EUB63782.1
59	114	0.067	12	13	Ubiquitin-like modifier-activating enzyme	Metabolism	gi 576696184 gb EUB59741.1
60	66	0.063	12	14	NADP-dependent malic enzyme	Energy production and conversion	gi 576699687 gb EUB63213.1
61	42	0.11	12	16	Phosphoglycerate kinase	Metabolism	gi 576695835 gb EUB59398.1

62	99	0.12	12	16	elongation factor 2	Transcription	gi 674570164 emb CDS16232.1
63	130	0.082	12	15	filamin	-	gi 961440428 emb CDS40988.2
64	60	0.067	12	15	glucose 6 phosphate 1 dehydrogenase	Metabolism	gi 674564077 emb CDS21761.1
65	42	0.089	12	17	actin modulator protein [Taenia asiatica]	-	gi 124783834 gb ABN14949.1
66	123	0.12	11	16	collagen type i ii iii v xi alpha	-	gi 674563099 emb CDS22734.1
67	54	0.15	11	16	trypsin-like protein	Post-translational modification	gi 311335041 gb ADP89566.1
68	111	0.063	11	13	hemicentin 1	-	gi 674576560 emb CDS36996.1
69	343	0.052	11	12	WD repeat-containing protein	Function unknown	gi 576693505 gb EUB57116.1
70	48	0.063	11	13	Adenylosuccinate synthetase isozyme	Metabolism	gi 576698414 gb EUB61948.1
71	46	0.063	11	15	2 amino 3 ketobutyrate coenzyme A ligase	Metabolism	gi 674266918 emb CDI97306.1
72	95	0.14	11	19	fasciclin-1	-	gi 576902497 gb AHH45014.1
73	33	0.067	11	12	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit	Energy production and conversion	gi 576692886 gb EUB56517.1
74	36	0.17	11	17	glyceraldehyde-3-phosphate dehydrogenase	Metabolism	gi 149364041 gb ABR24229.1
75	85	0.059	11	12	calpain	-	gi 674574770 emb CDS39654.1
76	50	0.074	11	13	Tubulin beta-2 chain	Structural/cytoskeletal proteins	gi 29337144 sp Q9NFZ6.1
77	52	0.074	11	12	adenosylhomocysteinase	Metabolism	gi 674563544 emb CDS21893.1
78	50	0.082	11	15	cat eye syndrome critical region protein 5	Metabolism	gi 674569255 emb CDS15318.1
79	80	0.067	11	14	glycogen synthase	Structural/cytoskeletal proteins	gi 674572158 emb CDS42583.1
80	18	0.26	10	21	cyclophilin	Post-translational modification	gi 589812132 gb AHL20246.1
81	39	0.071	10	14	Pyruvate dehydrogenase E1 component subunit beta	Energy production and conversion	gi 576699464 gb EUB62991.1
82	13	0.093	10	12	transforming growth factor beta 1 induced	-	gi 961440199 emb CDI97591.2
83	22	0.2	10	15	2-cys peroxiredoxin	Post-translational modification	gi 223403612 gb ACM89281.1
84	62	0.093	10	12	fumarate hydratase class I	Energy production and conversion	gi 674565797 emb CDS20347.1
85	21	0.11	10	13	Myophilin	Structural/cytoskeletal proteins	gi 576693412 gb EUB57026.1
86	45	0.082	10	14	Ndr	-	gi 674572505 emb CDS42931.1
87	75	0.067	10	11	Arginyl-tRNA synthetase, cytoplasmic	Transcription	gi 576694953 gb EUB58531.1
88	32	0.052	10	11	tropomyosin 2 high molecular weight isoform	-	gi 311992220 gb ADQ26722.1
89	88	0.033	9	9	transitional endoplasmic reticulum atpase	Post-translational modification	gi 674566315 emb CDS19413.1
90	69	0.048	9	11	actin interacting protein 1	Function unknown	gi 674571818 emb CDS42236.1
91	39	0.063	9	14	guanine nucleotide binding protein subunit	Function unknown	gi 674265669 emb CDI98172.1
92	46	0.086	9	12	hypothetical transcript [Hymenolepis microstoma]	-	gi 961496852 emb CUU99433.1
93	17	0.067	9	11	Cofilin/actin-depolymerizing factor	-	gi 576697710 gb EUB61250.1

94	152	0.063	9	11	Peroxidasin	Function unknown	gi 576695249 gb EUB58822.1
95	67	0.059	9	10	glycogen phosphorylase	Metabolism	gi 674566586 emb CDS19686.1
96	31	0.041	9	11	Four and a half LIM domains-containing nrotein	-	gi 576696870 gb EUB60419.1
97	26	0.071	9	12	Triosephosphate isomerase	Metabolism	gi 38258647 sp Q9GTX8.1
98	14	0.063	9	12	Four and a half LIM domains-containing protein	-	gi 576697637 gb EUB61178.1
99	29	0.074	9	13	phosphoglycerate mutase	Metabolism	gi 674573499 emb CDS40416.1
100	70	0.048	9	10	heat shock protein 70	Post-translational modification	gi 674568757 emb CDS17875.1
101	192	0.052	9	11	putative ankyrin 2,3/unc44 Schistosoma mansoni]	Function unknown	gi 353232760 emb CCD80115.1
102	31	0.052	8	10	Actin-1	Structural/cytoskeletal proteins	gi 576692431 gb EUB56079.1
103	50	0.063	8	11	calponin-like protein	Structural/cytoskeletal proteins	gi 124784064 gb ABN14962.1
104	35	0.11	8	12	lactate dehydrogenase A	Energy production and conversion	gi 318054471 gb ADV35656.1
105	232	0.033	8	8	myosin heavy chain non muscle	Structural/cytoskeletal proteins	gi 674566383 emb CDS19483.1
106	43	0.033	8	9	Pyruvate dehydrogenase E1 component subunit alpha type I	Energy production and conversion	gi 576694194 gb EUB57787.1
107	29	0.037	8	8	14-3-3 protein zeta	Signal transduction	gi 576698383 gb EUB61917.1
108	12	0.13	8	16	tegumental protein	-	gi 60459970 gb AAX20156.1
109	50	0.052	8	10	dihydrolipoamide dehydrogenase	Energy production and conversion	gi 674570213 emb CDS16281.1
110	165	0.074	8	11	collagen type XI alpha 2	-	gi 674564565 emb CDS20882.1
111	38	0.063	8	10	Annexin A8	-	gi 576701205 gb EUB64725.1
112	58	0.052	8	10	glutamate dehydrogenase	Metabolism	gi 961439347 emb CUT98844.1
113	35	0.037	8	8	mitochondrial phosphate carrier protein precursor	-	gi 124782844 gb ABN14885.1
114	104	0.037	7	8	Alpha-actinin, sarcomeric	Structural/cytoskeletal proteins	gi 576699978 gb EUB63502.1
115	42	0.089	7	11	Beta-ureidopropionase	Function unknown	gi 576700488 gb EUB64010.1
116	135	0.026	7	7	importin 5	-	gi 674267405 emb CDI96909.1
117	128	0.026	7	7	Tetracycline resistance leader peptide TetL	Metabolism	gi 674580117 emb CDS35955.1
118	32	0.041	7	8	prohibitin	Post-translational modification	gi 674576684 emb CDS37121.1
119	49	0.059	7	9	elongation factor 1 alpha	Transcription	gi 815798391 gb AKE48498.1
120	29	0.048	7	8	14-3-3 protein zeta	Signal transduction	gi 576699818 gb EUB63343.1
121	42	0.074	7	11	Actin, cytoplasmic 2	Structural/cytoskeletal proteins	gi 576693212 gb EUB56832.1
122	63	0.041	7	8	NADP dependent malic enzyme	Energy production and conversion	gi 674562690 emb CDS22946.1
123	37	0.052	7	8	hemicentin 1	-	gi 674576560 emb CDS36996.1

124	42	0.033	7	8	cAMP-dependent protein kinase type II regulatory subunit	Signal transduction	gi 576701554 gb EUB65073.1
125	48	0.048	7	7	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase	Energy production and conversion	gi 576691716 gb EUB55398.1
126	66	0.086	6	11	fasciclin-2	-	gi 576902499 gb AHH45015.1
127	60	0.022	6	6	T complex protein 1 subunit alpha	Post-translational modification	gi 674573749 emb CDS40669.1
128	97	0.03	6	6	dynamain	Function unknown	gi 674266904 emb CDI97292.1
129	35	0.03	6	7	SH2 motif	-	gi 674563259 emb CDS22222.1
130	57	0.022	6	6	T-complex protein 1 subunit delta	Post-translational modification	gi 576700958 gb EUB64478.1
131	26	0.12	6	10	glutathione S-transferase	Post-translational modification	gi 21591409 gb AAM64045.1
132	16	0.033	6	6	Actin-depolymerizing factor 2	-	gi 576697711 gb EUB61251.1
133	30	0.033	6	8	thymidine phosphorylase	Metabolism	gi 961440116 emb CUT99611.1
134	11	0.093	6	12	dynein light chain	-	gi 29467010 dbj BAC66949.1
135	33	0.052	6	9	Calcium binding protein	Structural/cytoskeletal proteins	gi 674562291 emb CDS23332.1
136	36	0.056	6	8	small heat-shock protein	-	gi 21665905 emb CAD36617.1
137	32	0.03	6	7	Mitochondrial dicarboxylate carrier	-	gi 576692289 gb EUB55943.1
138	62	0.037	6	7	Asparaginyl-tRNA synthetase, cytoplasmic	Transcription	gi 576690884 gb EUB54629.1
139	18	0.033	6	7	Ubiquitin-conjugating enzyme E2 N	Post-translational modification	gi 576696369 gb EUB59924.1
140	20	0.041	6	7	glycogen phosphorylase	Metabolism	gi 674566587 emb CDS19687.1
141	30	0.074	6	9	purine nucleoside phosphorylase	Metabolism	gi 674567224 emb CDS18572.1
142	27	0.03	6	6	subfamily T1A non peptidase ue	Post-translational modification	gi 674563031 emb CDS22665.1
143	42	0.022	6	6	casein kinase ii subunit alpha	Signal transduction	gi 674576896 emb CDS37336.1
144	26	0.03	6	7	thioredoxin dependent peroxide reductase	Post-translational modification	gi 674561357 emb CDS24295.1
145	11	0.041	6	7	histone H3	Transcription	gi 602727727 ref XP_007449308.1
146	22	0.041	6	8	adenylate kinase	Metabolism	gi 674563965 emb CDS21649.1
147	58	0.033	6	8	chaperonin containing TCP1 subunit 2 beta	Post-translational modification	gi 674574995 emb CDS39497.1
148	65	0.033	6	6	dihydropyrimidinase	Metabolism	gi 674567717 emb CDS16828.1
149	28	0.045	6	8	3 oxoacyl acyl carrier protein reductase	Metabolism	gi 674573436 emb CDS40352.1
150	28	0.03	6	7	Proteasome subunit alpha type-3	Post-translational modification	gi 576697420 gb EUB60963.1
151	44	0.03	5	6	DnaJ subfamily A member	Post-translational modification	gi 576693390 gb EUB57005.1
152	80	0.045	5	7	Titin	-	gi 576695343 gb EUB58914.1
153	82	0.019	5	5	FERM domain-containing protein 3	-	gi 576701126 gb EUB64646.1
154	68	0.041	5	6	H17g protein, tegumental antigen	-	gi 34368418 emb CAE46111.1
155	35	0.033	5	6	Putative deoxyribose-phosphate aldolase	Metabolism	gi 576695900 gb EUB59462.1
156	75	0.022	5	5	thioredoxin glutathione reductase	Energy production and conversion	gi 29825896 gb AAN63052.1

157	59	0.026	5	6	T-complex protein 1 subunit gamma	Post-translational modification	gi 674570231 emb CDS16299.1
158	355	0.019	5	5	Titin	-	gi 576698310 gb EUB61845.1
159	37	0.03	5	6	Calumenin-B	-	gi 576701509 gb EUB65028.1
160	115	0.03	5	5	alpha actinin sarcomeric	Structural/cytoskeletal proteins	gi 674562490 emb CDS23200.1
161	57	0.019	5	5	aminopeptidase N	Metabolism	gi 674572490 emb CDS42915.1
162	40	0.033	5	6	Succinyl-CoA ligase GDP-formingJ subunit alpha	Energy production and conversion	gi 576693072 gb EUB56696.1
163	45	0.033	5	6	Aspartate aminotransferase	Metabolism	gi 576693792 gb EUB57395.1
164	14	0.048	5	7	histone H2B	-	gi 674577890 emb CDS36286.1
165	60	0.022	5	5	T-complex protein 1 subunit theta	Post-translational modification	gi 576696899 gb EUB60447.1
166	30	0.026	5	5	phosphatase 2a inhibitor i2pp2a	-	gi 674566256 emb CDS19354.1
167	26	0.033	5	6	Proteasome subunit alpha type-2	Post-translational modification	gi 576695969 gb EUB59529.1
168	42	0.033	5	7	heat shock protein 71 protein	Post-translational modification	gi 674560532 emb CDS25069.1
169	35	0.037	5	6	GDP L fucose synthase	Metabolism	gi 674577076 emb CDS37519.1
170	309	0.019	5	5	Titin	Signal transduction	gi 576698310 gb EUB61845.1
171	51	0.033	5	7	Innexin unc-9	-	gi 576699141 gb EUB62670.1
172	72	0.026	5	6	glucose-regulated protein mitochondrial processing peptidase beta	Post-translational modification	gi 576694898 gb EUB58477.1
173	53	0.019	5	5	subunit	Function unknown	gi 674266979 emb CDI97367.1
174	36	0.022	5	5	lactate dehydrogenase B	Energy production and conversion	gi 318054473 gb ADV35657.1
175	21	0.037	5	7	PDZ and LIM domain protein	-	gi 576695629 gb EUB59195.1
176	41	0.041	5	6	annexin B2	-	gi 62868630 gb AA17503.1
177	11	0.086	5	8	Dynein light chain 2	-	gi 576691998 gb EUB55665.1
178	342	0.03	5	5	Lipid transport protein N terminal	-	gi 674562598 emb CDS22854.1
179	15	0.022	5	5	cytosolic fatty acid binding protein	-	gi 82412213 gb ABB76135.1
180	163	0.022	5	5	Lethal(2) giant larvae protein	-	gi 576692591 gb EUB56232.1
181	57	0.026	5	6	lysyl oxidase	-	gi 674265829 emb CDI98333.1
182	88	0.03	5	6	n acetylated alpha linked acidic dipeptidase 2	-	gi 674574508 emb CDS41437.1
183	21	0.026	5	5	ADP-ribosylation factor	Function unknown	gi 576696292 gb EUB59848.1
184	13	0.048	5	7	transforming growth factor beta 1 induced	-	gi 961440199 emb CDI97591.2
185	29	0.019	5	5	peptidase inhibitor 16	-	gi 674573188 emb CDS40101.1
186	45	0.019	4	4	eukaryotic initiation factor 4A	Transcription	gi 674561290 emb CDS24381.1
187	31	0.033	4	5	carbonyl reductase 1	Metabolism	gi 674266977 emb CDI97365.1
188	14	0.026	4	4	histone H2A	Transcription	gi 674577655 emb CDS36693.1
189	11	0.026	4	7	Dynein light chain LC6, flagellar outer arm	-	gi 576691990 gb EUB55657.1

190	40	0.041	4	7	calponin-like protein <i>Taenia asiatica</i>]	Structural/cytoskeletal proteins	gi 124783983 gb ABN14959.1
191	48	0.019	4	5	hypothetical protein EGR_01765	-	gi 576699749 gb EUB63274.1
192	41	0.037	4	7	Serpin B9	Post-translational modification	gi 576696703 gb EUB60253.1
193	19	0.022	4	5	titin	-	gi 674566990 emb CDS18337.1
194	50	0.019	4	4	Tubulin beta-1 chain	Structural/cytoskeletal proteins	gi 576697601 gb EUB61142.1
195	16	0.03	4	5	Chain A	Metabolism	gi 347948498 pdb 3MND A
196	41	0.022	4	5	Calcium-binding protein 39-like protein	-	gi 576697595 gb EUB61136.1
197	36	0.037	4	5	transaldolase	Metabolism	gi 674560699 emb CDS24943.1
198	42	0.067	4	7	Severin	-	gi 576693443 gb EUB57056.1
199	36	0.022	4	5	Annexin A13	-	gi 576701204 gb EUB64724.1
200	179	0.015	4	4	Ankyrin-2	Function unknown	gi 576699604 gb EUB63130.1
201	31	0.022	4	4	prohibitin protein WPH	Post-translational modification	gi 674574612 emb CDS39840.1
202	36	0.026	4	5	serine:threonine protein phosphatase 2A	Signal transduction	gi 674570693 emb CDS43313.1
203	195	0.015	4	4	Muscle M-line assembly protein unc-89	-	gi 576698306 gb EUB61841.1
204	20	0.045	4	5	protein DJ 1	Function unknown	gi 674266694 emb CDI97572.1
205	15	0.022	4	5	Ubiquitin	Post-translational modification	gi 576701155 gb EUB64675.1
206	11	0.063	4	9	expressed protein	-	gi 674574827 emb CDS39329.1
207	27	0.037	4	5	ornithine aminotransferase	Metabolism	gi 674572180 emb CDS42605.1
208	36	0.033	4	6	NADH-cytochrome b5 reductase 3	Metabolism	gi 576700067 gb EUB63591.1
209	29	0.026	4	6	sj ts4 protein	-	gi 674577718 emb CDS36766.1
210	31	0.019	4	4	Microtubule associated protein RP:EB family	Structural/cytoskeletal proteins	gi 961439806 emb CUT99302.1
211	54	0.015	4	4	tubulin alpha 1C chain	Structural/cytoskeletal proteins	gi 674577457 emb CDS36904.1
212	29	0.019	4	5	putative cyclin-H	Post-translational modification	gi 576697794 gb EUB61333.1
213	30	0.022	4	5	Proteasome subunit alpha type-7-like protein	Post-translational modification	gi 576696890 gb EUB60438.1
214	104	0.015	4	4	multivalent antigen sj tpi	-	gi 674565534 emb CDS20084.1
215	218	0.019	4	4	ankyrin 23:unc44	Function unknown	gi 674566273 emb CDS19371.1
216	25	0.052	4	7	glutathione transferase	Post-translational modification	gi 1004227 emb CAA59739.1
217	9	0.026	4	5	LIM zinc bindingdomain containing protein	-	gi 674576398 emb CDS38102.1
218	15	0.026	4	4	histone	Transcription	gi 674569431 emb CDS15495.1
219	12	0.033	4	5	thioredoxin-1	Post-translational modification	gi 724471034 gb AIY26017.1
220	18	0.03	4	4	Tubulin polymerization-promoting protein	-	gi 576692624 gb EUB56264.1
221	32	0.015	4	4	GDP-mannose 4,6 dehydratase	Structural/cytoskeletal proteins	gi 576691516 gb EUB55210.1
222	52	0.019	4	4	Aldehyde dehydrogenase family 1 member A3	Energy production and conversion	gi 576693855 gb EUB57457.1

223	52	0.015	4	4	NADH dehydrogenase ubiquinone flavoprotein 1	Energy production and conversion	gi 674578154 emb CDS36554.1
224	20	0.03	4	7	cysteine and glycine rich protein 1	-	gi 674574369 emb CDS41298.1
225	52	0.019	4	5	hexokinase	Metabolism	gi 674576035 emb CDS38325.1
226	66	0.019	4	4	Phosphoacetylglucosamine mutase	Metabolism	gi 576698281 gb EUB61816.1
227	42	0.011	3	3	beta centractin	Structural/cytoskeletal proteins	gi 674568090 emb CDS17204.1
228	38	0.015	3	4	26S proteasome non ATPase regulatory subunit 7	Function unknown	gi 674574868 emb CDS39370.1
229	19	0.015	3	4	Calmodulin	Structural/cytoskeletal proteins	gi 576691891 gb EUB55563.1
230	21	0.015	3	3	ribosomal protein L11	Transcription	gi 674266506 emb CDI97959.1
231	39	0.015	3	3	Guanine nucleotide-binding protein subunit beta	Function unknown	gi 576698293 gb EUB61828.1
232	25	0.011	3	3	fascin 2	-	gi 674564399 emb CDS21401.1
233	34	0.019	3	4	2-oxoglutarate/malate carrier protein	-	gi 576692217 gb EUB55875.1
234	49	0.011	3	3	spliceosome rna helicase bat1	Transcription	gi 674564743 emb CDS21061.1
235	19	0.026	3	4	aldo keto reductase family 1 member B4	Function unknown	gi 674564193 emb CDS21191.1
236	56	0.019	3	3	alanine aminotransferase 2	Metabolism	gi 674566348 emb CDS19447.1
237	25	0.011	3	3	platelet activating factor acetylhydrolase IB	-	gi 674267045 emb CDI97433.1
238	33	0.019	3	4	inorganic pyrophosphatase	Energy production and conversion	gi 674577167 emb CDS37611.1
239	10	0.026	3	5	Dynein light chain LC6, flagellar outer arm	-	gi 576695376 gb EUB58946.1
240	47	0.015	3	3	NADH dehydrogenase ubiquinone re 3 protein 1	Energy production and conversion	gi 674568845 emb CDS17967.1
241	31	0.015	3	3	adenylate cyclase 9	-	gi 674571922 emb CDS42344.1
242	21	0.011	3	3	ras protein Rab 7a	Function unknown	gi 674266074 emb CDI98578.1
243	51	0.019	3	4	Tubulin beta-3 chain	Structural/cytoskeletal proteins	gi 576697602 gb EUB61143.1
244	122	0.011	3	3	Anoctamin-1	-	gi 576691278 gb EUB54990.1
245	42	0.011	3	3	NAD(P) transhydrogenase subunit alpha	Energy production and conversion	gi 576694192 gb EUB57785.1
246	50	0.019	3	3	Non-lysosomal glucosylceramidase	Metabolism	gi 576694850 gb EUB58430.1
247	74	0.015	3	4	hypothetical protein EGR_00474	-	gi 576701004 gb EUB64524.1
248	28	0.011	3	3	NADH dehydrogenase ubiquinone iron sulfur	Energy production and conversion	gi 961440051 emb CUT99546.1
249	57	0.011	3	3	coronin 1C	Function unknown	gi 674266210 emb CDI98717.1
250	61	0.019	3	5	pyruvate kinase	Metabolism	gi 674572621 emb CDS43052.1
251	53	0.011	3	3	4-hydroxybutyrate coenzyme A transferase	Energy production and conversion	gi 576692646 gb EUB56285.1
252	53	0.015	3	3	Cytochrome b c1 complex subunit 2	Function unknown	gi 674562375 emb CDS23417.1
253	22	0.019	3	4	rho gdp dissociation inhibitor	-	gi 674571096 emb CDS43731.1
254	24	0.03	3	3	sigma-type glutathione S-transferase	-	gi 225355240 gb ACN88552.1
255	20	0.015	3	4	translationally controlled tumor protein	-	gi 674267348 emb CDI96852.1
256	62	0.011	3	3	glycerol kinase	Energy production and conversion	gi 674266527 emb CDI97981.1

257	40	0.011	3	3	stomatin protein 2	Post-translational modification	gi 674571420 emb CDS41834.1
258	21	0.011	3	3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit	-	gi 576695550 gb EUB59117.1
259	26	0.015	3	3	Synaptic vesicle membrane protein VAT-1-like protein	Energy production and conversion	gi 576698237 gb EUB61772.1
260	38	0.011	3	3	alpha tocopherol transfer protein	-	gi 674562106 emb CDS23617.1
261	102	0.019	3	3	Lysosomal alpha-glucosidase	Metabolism	gi 576693012 gb EUB56638.1
262	10	0.045	3	6	Dynein light chain 1	-	gi 576698380 gb EUB61914.1
263	54	0.011	3	3	6-phosphogluconate dehydrogenase	Metabolism	gi 576699896 gb EUB63420.1
264	63	0.011	3	3	non lysosomal glucosylceramidase	Metabolism	gi 674570277 emb CDS16346.1
265	31	0.011	3	3	fructose-1,6-phosphatase	Metabolism	gi 338827796 gb AEJ15818.1
266	75	0.011	3	3	ubiquitin protein ligase BRE1	Structural/cytoskeletal proteins	gi 674569884 emb CDS15952.1
267	58	0.015	3	3	Aspartyl-tRNA synthetase, cytoplasmic	Transcription	gi 576701543 gb EUB65062.1
268	27	0.011	3	3	Proteasome subunit alpha type-6	Post-translational modification	gi 576694857 gb EUB58437.1
269	26	0.015	3	3	60S ribosomal protein L10a	Transcription	gi 674569308 emb CDS15371.1
270	38	0.011	3	3	aldo keto reductase family 1 member B4	Function unknown	gi 674576243 emb CDS37943.1
271	24	0.015	3	3	ras protein rab 8b	Function unknown	gi 674571909 emb CDS42331.1
272	59	0.015	3	3	Synaptotagmin-14	-	gi 576700387 gb EUB63909.1
273	36	0.015	3	3	malate dehydrogenase	Energy production and conversion	gi 674563046 emb CDS22680.1
274	9	0.022	3	4	acyl coenzyme A binding protein	Metabolism	gi 674573492 emb CDS40408.1
275	323	0.011	3	3	talin	-	gi 674561411 emb CDS24246.1
276	26	0.015	3	3	Metallo-beta-lactamase domain-containing protein	-	gi 576694466 gb EUB58053.1
277	61	0.011	3	3	protein phosphatase 2a regulatory subunit	-	gi 674565771 emb CDS20321.1
278	31	0.015	3	3	aldo keto reductase family 1 member B4	Function unknown	gi 674564192 emb CDS21190.1
279	33	0.022	3	4	ATP synthase subunit gamma	Energy production and conversion	gi 576697467 gb EUB61009.1
280	97	0.015	3	3	Cysteinyl-tRNA synthetase, cytoplasmic	Transcription	gi 576701405 gb EUB64924.1
281	21	0.026	3	4	tegumental protein	-	gi 576695787 gb EUB59351.1
282	29	0.019	3	4	SCO cytochrome oxidase deficient protein 1	Function unknown	gi 674565543 emb CDS20093.1
283	68	0.015	3	3	nadp transhydrogenase	Energy production and conversion	gi 674566810 emb CDS18157.1
284	59	0.011	3	3	cytosolic purine 5' nucleotidase	-	gi 674562874 emb CDS22508.1
285	14	0.041	3	5	Profilin allergen	-	gi 674267056 emb CDI97444.1
286	83	0.015	3	3	Dipeptidyl peptidase 3	-	gi 576698676 gb EUB62208.1
287	30	0.015	3	3	N(G),N(G)-dimethylarginine dimethylaminohydrolase	Metabolism	gi 576699391 gb EUB62919.1

288	68	0.011	3	3	lamin dm0	-	gi 674567902 emb CDS17015.1
289	42	0.011	3	3	annexin	-	gi 674266071 emb CDI98575.1
290	17	0.022	3	5	ubiquitin conjugating enzyme	Post-translational modification	gi 532576613 gb AGT98656.1
291	24	0.0074	2	2	60S ribosomal protein L13a	Transcription	gi 576699387 gb EUB62915.1
292	48	0.015	2	2	Elongation factor 1-gamma	Post-translational modification	gi 576697550 gb EUB61092.1
293	42	0.0074	2	2	Alpha-tocopherol transfer protein-like protein	-	gi 576695576 gb EUB59143.1
294	44	0.0074	2	2	nardilysin, partial	Post-translational modification	gi 674561072 emb CDS24623.1
295	23	0.0074	2	2	60S ribosomal protein L13	Transcription	gi 576694227 gb EUB57819.1
296	35	0.0074	2	2	mitochondrial glutamate carrier protein	-	gi 555232805 emb CDI70107.1
297	29	0.0074	2	2	tegumental protein	-	gi 576693059 gb EUB56683.1
298	27	0.0074	2	2	aminoacylase 1	Metabolism	gi 674567544 emb CDS18900.1
299	75	0.0074	2	2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	-	gi 576692720 gb EUB56357.1
300	49	0.011	2	2	galactokinase	Metabolism	gi 674565167 emb CDS20721.1
301	20	0.011	2	3	FAD linked sulfhydryl oxidase ALR	Post-translational modification	gi 674570875 emb CDS43499.1
302	60	0.0074	2	2	puromycin sensitive aminopeptidase	Metabolism	gi 674560979 emb CDS24674.1
303	45	0.011	2	2	actin protein 3B	Structural/cytoskeletal proteins	gi 674580528 emb CDS35468.1
304	47	0.011	2	3	succinyl coenzyme A ligase ADP forming subunit beta	Energy production and conversion	gi 674576203 emb CDS37901.1
305	38	0.0074	2	2	vesicle associated membrane protein vamp	Signal transduction	gi 674564989 emb CDS20538.1
306	47	0.0074	2	2	Lysosomal aspartic protease	-	gi 576694392 gb EUB57981.1
307	22	0.0074	2	2	nascent polypeptide associated complex subunit	Transcription	gi 674571946 emb CDS42368.1
308	55	0.015	2	3	Protein disulfide-isomerase	Post-translational modification	gi 576692553 gb EUB56196.1
309	82	0.0074	2	2	procollagen lysine2 oxoglutarate 5 dioxygenase	-	gi 674576758 emb CDS37197.1
310	32	0.0074	2	2	Transcriptional activator protein Pur-alpha	-	gi 576701516 gb EUB65035.1
311	41	0.011	2	3	ribosomal protein L7-like protein Taenia asiatica]	Transcription	gi 124782929 gb ABN14890.1
312	17	0.011	2	2	60S ribosomal protein L27	Transcription	gi 576692810 gb EUB56444.1
313	18	0.019	2	3	Nucleoside diphosphate kinase A 2	Metabolism	gi 576695995 gb EUB59555.1
314	193	0.0074	2	2	intron binding protein aquarius	Transcription	gi 674570162 emb CDS16230.1
315	180	0.0074	2	2	collagen alpha 1(IV) chain Hymenolepis microstoma]	-	gi 674591161 emb CDS29935.1
316	13	0.011	2	3	Calmodulin	Structural/cytoskeletal proteins	gi 576700576 gb EUB64098.1

317	94	0.0074	2	2	Integrin beta-7	-	gi 576697707 gb EUB61247.1
318	51	0.0074	2	2	dihydrolipoyllysine residue acetyltransferase	Energy production and conversion	gi 674566907 emb CDS18254.1
319	30	0.011	2	3	hemicentin 1	-	gi 674576561 emb CDS36997.1
320	88	0.0074	2	2	Protein transport protein Sec23A	Signal transduction	gi 576697713 gb EUB61253.1
321	14	0.011	2	2	Four and a half LIM domains protein 3	-	gi 674266711 emb CDI97590.1
322	49	0.0074	2	2	expressed protein	-	gi 674561116 emb CDS24544.1
323	22	0.0074	2	2	Proteasome subunit beta type-2	Post-translational modification	gi 576700475 gb EUB63997.1
324	35	0.0074	2	2	actin related protein 2.3 complex subunit 1A.1B	Function unknown	gi 961439601 emb CUT99097.1
325	53	0.0074	2	2	succinate semialdehyde dehydrogenase	Energy production and conversion	gi 674561217 emb CDS24488.1
326	32	0.0074	2	2	Protein phosphatase 1 regulatory subunit	Function unknown	gi 576699343 gb EUB62871.1
327	10	0.011	2	2	Antigen B	-	gi 576692423 gb EUB56071.1
328	29	0.0074	2	2	Immunoglobulin domain containing protein	-	gi 674561326 emb CDS24349.1
329	67	0.0074	2	2	Leukotriene A-4 hydrolase	Metabolism	gi 576698893 gb EUB62423.1
330	16	0.015	2	2	Thioredoxin	Post-translational modification	gi 576693344 gb EUB56960.1
331	38	0.0074	2	2	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	Signal transduction	gi 576701522 gb EUB65041.1
332	531	0.011	2	2	dynein heavy chain	Structural/cytoskeletal proteins	gi 674569847 emb CDS15915.1
333	59	0.0074	2	2	pleckstrin y domain containing family A	-	gi 674560993 emb CDS24688.1
334	22	0.0074	2	2	expressed protein	Transcription	gi 674562273 emb CDS23314.1
335	31	0.011	2	2	Chloride intracellular channel protein 5	-	gi 576697068 gb EUB60614.1
336	19	0.0074	2	2	Ubiquitin-conjugating enzyme E2	Post-translational modification	gi 576695523 gb EUB59091.1
337	33	0.0074	2	2	LIN 24 Twenty four Like family member	-	gi 674266446 emb CDI97898.1
338	28	0.0074	2	2	Ndr	-	gi 674571386 emb CDS41800.1
339	20	0.011	2	3	glycogen phosphorylase	Metabolism	gi 674577298 emb CDS37742.1
340	12	0.011	2	2	FK506-binding protein-like protein	Post-translational modification	gi 194324935 gb ACF49124.1
341	11	0.0074	2	2	Dynein light chain 2, cytoplasmic	-	gi 576691997 gb EUB55664.1
342	70	0.0074	2	2	lamin	-	gi 674571622 emb CDS42039.1
343	16	0.011	2	2	Calcium binding protein	Structural/cytoskeletal proteins	gi 674576918 emb CDS37358.1
344	34	0.0074	2	2	Fascin-2	-	gi 576691449 gb EUB55148.1
345	69	0.0074	2	2	fimbrin <i>Taenia asiatica</i>]	Structural/cytoskeletal proteins	gi 124783291 gb ABN14919.1
346	44	0.011	2	2	GTP binding protein CG1354	Transcription	gi 674567571 emb CDS18927.1
347	80	0.0074	2	2	Armadillo type fold	-	gi 674265874 emb CDI98378.1
348	121	0.0074	2	2	dihydropyrimidine dehydrogenase NADP	Metabolism	gi 674568815 emb CDS17936.1

349	110	0.0074	2	2	SNase domain containing protein	Transcription	gi 674568828 emb CDS17949.1
350	42	0.0074	2	2	Erlin-1	Post-translational modification	gi 576691975 gb EUB55643.1
351	74	0.011	2	2	von Willebrand factor A domain-containing protein 5A	Function unknown	gi 576695423 gb EUB58992.1
352	40	0.0074	2	2	mitochondrial trans 2 enoyl coenzyme A reductase	Energy production and conversion	gi 674561473 emb CDS24193.1
353	8	0.011	2	3	immunogenic protein Ts76	-	gi 7339853 gb AAF60976.1
354	38	0.0074	2	2	dnaJ subfamily B	Post-translational modification	gi 961439579 emb CUT99075.1
355	17	0.011	2	3	spectrin alpha actinin Hymenolepis microstomal	Structural/cytoskeletal proteins	gi 674591524 emb CDS29622.1
356	39	0.015	2	3	annexin	-	gi 674565627 emb CDS20177.1
357	50	0.011	2	2	NADH ubiquinone oxidoreductase 42 subunit	-	gi 674577975 emb CDS36372.1
358	51	0.0074	2	2	plastin 2	Structural/cytoskeletal proteins	gi 674573167 emb CDS40079.1
359	24	0.0074	2	2	60S ribosomal protein L15	Transcription	gi 576696309 gb EUB59865.1
360	75	0.0074	2	2	Metallophosphoesterase	Post-translational modification	gi 576694196 gb EUB57789.1
361	13	0.0074	2	2	60S ribosomal protein L23	Transcription	gi 576699448 gb EUB62975.1
362	25	0.011	2	3	Myophilin	Structural/cytoskeletal proteins	gi 961439407 emb CUT98904.1
363	26	0.011	2	3	proteasome prosome macropain subunit beta	Post-translational modification	gi 674565758 emb CDS20308.1
364	73	0.0074	2	2	alpha adducin	Metabolism	gi 674266887 emb CDI97275.1
365	17	0.015	2	2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit	-	gi 576697957 gb EUB61494.1
366	8	0.0074	2	2	40S ribosomal protein S28	Transcription	gi 576698176 gb EUB61712.1
367	34	0.015	2	2	mitochondrial carrier 2	-	gi 674566620 emb CDS19720.1
368	38	0.0074	2	2	Dehydrogenase:reductase SDR family	Metabolism	gi 674577428 emb CDS36875.1
369	12	0.015	2	2	expressed conserved protein	-	gi 674577450 emb CDS36897.1
370	46	0.015	2	4	calcium binding protein calreticulin precursor	-	gi 14029538 gb AAK52725.1
371	26	0.019	2	3	ES1 protein mitochondrial	Metabolism	gi 674568144 emb CDS17259.1
372	25	0.0074	2	2	NADH dehydrogenase ubiquinone iron sulfur	Energy production and conversion	gi 674561353 emb CDS24291.1
373	56	0.0074	2	2	protein disulfide isomerase A3	Post-translational modification	gi 674572082 emb CDS42507.1
374	48	0.0074	2	2	mitogen activated protein kinase	Signal transduction	gi 674574349 emb CDS41278.1
375	47	0.011	2	2	Enolase	Metabolism	gi 576691849 gb EUB55524.1
376	20	0.0074	2	2	ATP synthase subunit d	-	gi 674575042 emb CDS39544.1
377	79	0.0074	2	2	Long-chain-fatty-acid--CoA ligase 5	Metabolism	gi 576699113 gb EUB62642.1
378	97	0.0074	2	2	Lon protease	Post-translational modification	gi 576696096 gb EUB59654.1

379	84	0.019	2	4	hypothetical protein	Function unknown	gi 21912588 emb CAD21549.1
380	13	0.0074	2	2	expressed protein	-	gi 674571192 emb CDS43186.1
381	86	0.0074	2	2	hypothetical transcript	-	gi 961440318 emb CDS37307.2
382	10	0.015	2	2	immunogenic protein	-	gi 674577101 emb CDS37545.1
383	28	0.0074	2	2	EF-1, partial	Transcription	gi 7578954 gb AAF64192.1
384	17	0.0074	2	2	60S ribosomal protein L14	Transcription	gi 576698217 gb EUB61752.1
385	337	0.0074	2	2	twitchin	Signal transduction	gi 674566777 emb CDS18123.1
386	239	0.0074	2	2	otoferlin	-	gi 674565985 emb CDS19081.1
387	63	0.0074	2	2	T-complex protein 1 subunit epsilon	Post-translational modification	gi 576697091 gb EUB60637.1
388	26	0.011	2	2	ATP synthase subunit O	Energy production and conversion	gi 576698231 gb EUB61766.1
389	92	0.0074	2	2	U6 snRNA-associated Sm-like protein LSm8	-	gi 576695080 gb EUB58655.1
390	43	0.0074	2	2	WD40 repeat and tyve domain containing protein	-	gi 674561477 emb CDS24197.1
391	19	0.0074	2	2	hypothetical protein EGR_00893	-	gi 576700828 gb EUB64349.1
392	36	0.0074	2	2	Nuclear migration protein nudC	-	gi 576696811 gb EUB60360.1
393	35	0.0074	2	2	Ts5 protein	Transcription	gi 170783723 gb ACB37346.1
394	58	0.0074	2	2	Calnexin	-	gi 576694840 gb EUB58420.1
395	73	0.0074	2	2	cationic amino acid transporter 4	Metabolism	gi 674568117 emb CDS17231.1
396	11	0.011	2	2	heat shock protein	Post-translational modification	gi 576691723 gb EUB55405.1
397	21	0.011	2	2	MACRO domain containing protein 2	Function unknown	gi 674571215 emb CDS43209.1
398	19	0.015	2	4	titin	-	gi 961439545 emb CUT99041.1
399	14	0.0074	2	2	NADH dehydrogenase ubiquinone 1 beta	-	gi 674561702 emb CDS24017.1
400	88	0.0074	2	2	microtubule associated protein 1A	-	gi 674561041 emb CDS24648.1
401	54	0.0074	2	2	titin	-	gi 674567709 emb CDS16820.1
402	26	0.0074	2	2	Ras-related protein Rab-2A	Function unknown	gi 576699325 gb EUB62853.1
403	29	0.0074	2	2	Endophilin-B1	-	gi 576695776 gb EUB59340.1
404	59	0.011	2	2	T complex protein 1 subunit eta	Post-translational modification	gi 674562117 emb CDS23628.1
405	33	0.011	2	2	aldo keto reductase family 1 member B4	Function unknown	gi 674266305 emb CDI97752.1
406	50	0.022	2	2	Tubulin beta chain	Structural/cytoskeletal proteins	gi 576695709 gb EUB59274.1
407	65	0.0074	2	2	Fatty-acid amide hydrolase	Transcription	gi 576697203 gb EUB60748.1
408	22	0.0074	2	2	Protein archease	Function unknown	gi 674266531 emb CDI97985.1