

Table S1. Nano-LC MS/MS analysis of SDH activity stained band from HrCNE.

	Protein	MW	Score	Peptide	Coverage	Accession	Note*
1	Microneme protein Etmic-1	74,778	993	33	41	O43981	gi/2707733
2	Microneme protein 3	105,644	555	18	23	B6VCV4	gi/211905276
3	Mitochondrial-processing peptidase beta subunit, putative	57,496	389	22	52	U6KT33	gi/557144991
4	Mitochondrial-processing peptidase alpha subunit, putative	62,775	311	16	30	U6KH88	gi/557137520
5	Microneme protein Etmic-2	35,087	281	11	42	U6KXC3	gi/4164596
	Microneme protein-2						
	Ubiquinol-cytochrome <i>c</i> reductase domain-containing protein, putative (Fe2S2 subunit)	43,429	215	8	32	U6KR99	gi/557141998
7	Putative rhoptry neck protein	232,935	196	9	5	A7DZP6	gi/153581935
	Ubiquinol-cytochrome <i>c</i> reductase complex 14 kDa protein, putative	25,480	158	6	23	U6KKV7	gi/557139144
9	Uncharacterized protein (one transmembrane region)	23,144	147	4	31	U6KQV1	gi/557139998
10	Uncharacterized protein	33,398	140	9	36	U6KXU8	gi/557147873
11	Cytochrome <i>c</i> oxidase subunit Vb	25,120	133	36	38	C8TDR9	gi/118490698
12	Cytochrome <i>c</i> 1, putative	46,055	116	4	14	U6L5K5	gi/557147988

13	Nucleoside-triphosphatase, putative	100,043	91	2	3	U6KZA4	gi/557148408
14	Uncharacterized protein (3 transmembrane region) <i>[Eimeria necatrix]</i>	27,173	88	5	16	U6N036	gi/557233254
15	Transhydrogenase	108,380	88	3	3	Q07600	gi/305062
16	Superoxide dismutase	24,925	87	6	37	U6KZ13	gi/557146360
17	Sporozoite antigen	22,369	86	2	12	P15744	gi/113933
18	Uncharacterized protein (one transmembrane region)	15,581	80	2	15	U6KIX2	gi/557138220
19	Uncharacterized protein (one transmembrane region)	8,488	72	1	18	U6KUQ3	gi/557146721
20	Quinol Cytochrome <i>c</i> Reductase subunit 9	12,113	64	3	36	U6KG27	gi/557137182
21	Uncharacterized protein (two transmembrane region)	23,540	62	1	4	U6LB54	gi/557154558
22	Uncharacterized protein (Iron- sulfur cluster binding domain)	13,354	61	3	22	U6KZ96	gi/557146466
23	Cytochrome <i>c</i> oxidase subunit II, putative	22,720	59	2	12	H9BA62	gi/357017687
24	Cytochrome <i>c</i> oxidase IV	23,681	56	5	24	H9B966	gi/357016995

	Succinate dehydrogenase						
25	(Ubiquinone) flavoprotein subunit, mitochondrial, putative	71,427	55	1	2	U6KGY0	<i>gi/557137402</i>
26	Cytochrome c oxidase subunit 2	23,918	54	4	18	H9B9F9	<i>gi/357017181</i>
27	Uncharacterized protein (one transmembrane region)	13,843	52	4	50	U6L2Z0	<i>gi/557146997</i>
28	Zgc:110343, related (peroxyredoxin)	28,449	52	3	14	U6KYA3	<i>gi/557147835</i>

Yellow, orange and green cells are identified peptides related to complex II, III and IV, respectively.

Figure S1



Figure S1. Top: sequence alignment of amino acid sequences of NDH2 from *E. tenella* and other organisms. Residues were colored according to percentage identity by Jalview. The conserved GXGXXG motifs as potential NADH-binding residues and the ubiquinone binding residues according to the crystal structure of *S. cerevisiae* Ndi1 (PDB: 5YJW) are shown with “#” and “*” symbols, respectively. Bottom: Amino acid sequence identity. Abbreviations; *E. tenella*: *Eimeria tenella* (XP_013228441), *P. falciparum*: *Plasmodium falciparum* (XP_001352022), *N. caninum*: *Neospora caninum* (XP_003879906), *T. gondii*: *Toxoplasma gondii* (XP_002369675), *C. suis*: *Cystoisospora suis* (PHJ19914), *S. cerevisiae*: *Saccharomyces cerevisiae* (EDN64274), *M. tuberculosis*: *Mycobacterium tuberculosis* (L7N5D1_MYCTO), *C. soroki*: *Chlorella sorokiniana* (PRW59413), *O. sativa*: *Oryza sativa* (XP_015644788).

Figure S2

E. tenella 462 1 MMIAASLORHLS--SELAAAAYSSSSSSSSCSQHIA-C FSSAAAVATGFSVS-----KEGGYIESTHTIDAVVYAGGGAGLAKAANCFLAQSGLBLTRKICSLKLFPTFESHTVAAQGG 287
P.falciparum 452 1 I-----MIRNNKKYIEFMQSSFCRFSN-----IKTKAYDIDIHHDYDAVVYAGGGAGLAKAANCFLSNNKYKVAISKLFFPTFESHTVAAQGG 291
T.gondii 469 1 MHASASLTOALRPYARRPFLSSALSRSLSPLAAGVREGLNAAQPOATGPFSVQOKRFTTNVKKFAYBIDHEYDAVYAGGGAGLAKAANCFLASAIKTA CSLKLFPTFESHTVAAQGG 295
P.murinus 427 1 -----MSKLAVGVRSWGRBAVIVSTTIRG-----NISGHTVVEHTIDAVVYAGGGAGLAKAANCFLSNTTETACVSKLFFPTFESHTVAAQGG 312
M.soleimani 464 1 -----MSKLAVGVRSWGRBAVIVSTTIRG-----IISAOYFVDIFIDAVVYAGGGAGLAKAANCFLSNTTETACVSKLFFPTFESHTVAAQGG 316
M.soleimani 446 1 -----MSKLAVGVRSWGRBAVIVSTTIRG-----MVYTHRHSDYENVYAGGGAGLAKAANCFLSNTTETACVSKLFFPTFESHTVAAQGG 307
S.aureus 358 1 -----MSKLAVGVRSWGRBAVIVSTTIRG-----MAEKLHLVYSGCAGLAMSTKIAAKAFAHVDFLVYPVPERHSXCAQGG 49
E.coli 388 1 -----MSKLAVGVRSWGRBAVIVSTTIRG-----MLPVBFEDAVYAGGGAGLAKAANCFLSNTTETACVSKLFFPTFESHTVAAQGG 53

E. tenella 462 186 NAAALGNNMT-EDDWREWHADTIVVKGSDWLGDDQAIHYMCCKAPQVILEENLYGLPFSRTEIGKLYQR-AFGGOSLKFKGGGQATCRAAADETGHANIELHTLGOSLAKK-----241
P.falciparum 452 186 NAAALGNNMT-EDDWREWHADTIVVKGSDWLGDDQAIHYMCCKAPQVILEENLYGLPFSRTEIGKLYQR-AFGGOSLKFKGGGQATCRAAADETGHANIELHTLGOSLAKK-----241
T.gondii 469 186 NAAALGNNMT-EDDWREWHADTIVVKGSDWLGDDQAIHYMCCKAPQVILEENLYGLPFSRTEIGKLYQR-AFGGOSLKFKGGGQATCRAAADETGHANIELHTLGOSLAKK-----241
P.murinus 427 186 NAAALGNNMT-EDDWREWHADTIVVKGSDWLGDDQAIHYMCCKAPQVILEENLYGLPFSRTEIGKLYQR-AFGGOSLKFKGGGQATCRAAADETGHANIELHTLGOSLAKK-----241
M.soleimani 464 186 NAAALGNNMT-EDDWREWHADTIVVKGSDWLGDDQAIHYMCCKAPQVILEENLYGLPFSRTEIGKLYQR-AFGGOSLKFKGGGQATCRAAADETGHANIELHTLGOSLAKK-----241
M.soleimani 446 186 NAAALGNNMT-EDDWREWHADTIVVKGSDWLGDDQAIHYMCCKAPQVILEENLYGLPFSRTEIGKLYQR-AFGGOSLKFKGGGQATCRAAADETGHANIELHTLGOSLAKK-----241
S.aureus 358 186 NAAALGNNMT-EDDWREWHADTIVVKGSDWLGDDQAIHYMCCKAPQVILEENLYGLPFSRTEIGKLYQR-AFGGOSLKFKGGGQATCRAAADETGHANIELHTLGOSLAKK-----241
E.coli 388 186 NAAALGNNMT-EDDWREWHADTIVVKGSDWLGDDQAIHYMCCKAPQVILEENLYGLPFSRTEIGKLYQR-AFGGOSLKFKGGGQATCRAAADETGHANIELHTLGOSLAKK-----241

E. tenella 462 203 + CNT ETVYFADOLEMIAFGAFPGPPRCREVNLKATNTVLTGGYGRANQCESAHITGGGAMMAAVALQDLEEVDFHTTGF----AGC1 TEGCBEGEGGI 297
P.falciparum 452 203 - CTF ETVYFADOLEMILMNS-----NICEVCIINIAKDHHTFPHTVLTGGYGRANQCESAHITGGGAMMAAVALQDLEEVDFHTTGF----AGC1 TEGCBEGEGGI 291
T.gondii 469 203 - CTF ETVYFADOLEMILMNS-----NICEVCIINIAKDHHTFPHTVLTGGYGRANQCESAHITGGGAMMAAVALQDLEEVDFHTTGF----AGC1 TEGCBEGEGGI 291
P.murinus 427 203 - CTF ETVYFADOLEMILMNS-----NICEVCIINIAKDHHTFPHTVLTGGYGRANQCESAHITGGGAMMAAVALQDLEEVDFHTTGF----AGC1 TEGCBEGEGGI 291
M.soleimani 464 203 - CTF ETVYFADOLEMILMNS-----NICEVCIINIAKDHHTFPHTVLTGGYGRANQCESAHITGGGAMMAAVALQDLEEVDFHTTGF----AGC1 TEGCBEGEGGI 291
M.soleimani 446 203 - CTF ETVYFADOLEMILMNS-----NICEVCIINIAKDHHTFPHTVLTGGYGRANQCESAHITGGGAMMAAVALQDLEEVDFHTTGF----AGC1 TEGCBEGEGGI 291
S.aureus 358 203 - CTF ETVYFADOLEMILMNS-----NICEVCIINIAKDHHTFPHTVLTGGYGRANQCESAHITGGGAMMAAVALQDLEEVDFHTTGF----AGC1 TEGCBEGEGGI 291
E.coli 388 203 - CTF ETVYFADOLEMILMNS-----NICEVCIINIAKDHHTFPHTVLTGGYGRANQCESAHITGGGAMMAAVALQDLEEVDFHTTGF----AGC1 TEGCBEGEGGI 291

E. tenella 462 223 + CTF ETVYFADOLEMIAFGAFPGPPRCREVNLKATNTVLTGGYGRANQCESAHITGGGAMMAAVALQDLEEVDFHTTGF----AGC1 TEGCBEGEGGI 297
P.falciparum 452 223 - CTF ETVYFADOLEMILMNS-----NICEVCIINIAKDHHTFPHTVLTGGYGRANQCESAHITGGGAMMAAVALQDLEEVDFHTTGF----AGC1 TEGCBEGEGGI 291
T.gondii 469 223 - CTF ETVYFADOLEMILMNS-----NICEVCIINIAKDHHTFPHTVLTGGYGRANQCESAHITGGGAMMAAVALQDLEEVDFHTTGF----AGC1 TEGCBEGEGGI 291
P.murinus 427 223 - CTF ETVYFADOLEMILMNS-----NICEVCIINIAKDHHTFPHTVLTGGYGRANQCESAHITGGGAMMAAVALQDLEEVDFHTTGF----AGC1 TEGCBEGEGGI 291
M.soleimani 464 223 - CTF ETVYFADOLEMILMNS-----NICEVCIINIAKDHHTFPHTVLTGGYGRANQCESAHITGGGAMMAAVALQDLEEVDFHTTGF----AGC1 TEGCBEGEGGI 291
M.soleimani 446 223 - CTF ETVYFADOLEMILMNS-----NICEVCIINIAKDHHTFPHTVLTGGYGRANQCESAHITGGGAMMAAVALQDLEEVDFHTTGF----AGC1 TEGCBEGEGGI 291
S.aureus 358 223 - CTF ETVYFADOLEMILMNS-----NICEVCIINIAKDHHTFPHTVLTGGYGRANQCESAHITGGGAMMAAVALQDLEEVDFHTTGF----AGC1 TEGCBEGEGGI 291
E.coli 388 223 - CTF ETVYFADOLEMILMNS-----NICEVCIINIAKDHHTFPHTVLTGGYGRANQCESAHITGGGAMMAAVALQDLEEVDFHTTGF----AGC1 TEGCBEGEGGI 291

E. tenella 462 243 ENLEGEA---EMIEEAT-----TAKDLASRDVSWSMITEIIREGEGG-FKDNDHILYDIT-HIFPLTLATELGEMETAKAFAGNNAKTIEIPFLTVH 416
P.falciparum 452 243 ENLEGEA---EMIEEAT-----TAKDLASRDVSWSMITEIIREGEGG-FKDNDHILYDIT-HIFPLTLATELGEMETAKAFAGNNAKTIEIPFLTVH 420
T.gondii 469 243 ENLEGEA---EMIEEAT-----TAKDLASRDVSWSMITEIIREGEGG-FKDNDHILYDIT-HIFPLTLATELGEMETAKAFAGNNAKTIEIPFLTVH 423
P.murinus 427 243 ENLEGEA---EMIEEAT-----TAKDLASRDVSWSMITEIIREGEGG-FKDNDHILYDIT-HIFPLTLATELGEMETAKAFAGNNAKTIEIPFLTVH 423
M.soleimani 464 243 ENLEGEA---EMIEEAT-----TAKDLASRDVSWSMITEIIREGEGG-FKDNDHILYDIT-HIFPLTLATELGEMETAKAFAGNNAKTIEIPFLTVH 423
M.soleimani 446 243 ENLEGEA---EMIEEAT-----TAKDLASRDVSWSMITEIIREGEGG-FKDNDHILYDIT-HIFPLTLATELGEMETAKAFAGNNAKTIEIPFLTVH 423
S.aureus 358 243 ENLEGEA---EMIEEAT-----TAKDLASRDVSWSMITEIIREGEGG-FKDNDHILYDIT-HIFPLTLATELGEMETAKAFAGNNAKTIEIPFLTVH 423
E.coli 388 243 ENLEGEA---EMIEEAT-----TAKDLASRDVSWSMITEIIREGEGG-FKDNDHILYDIT-HIFPLTLATELGEMETAKAFAGNNAKTIEIPFLTVH 423

E. tenella 462 263 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
P.falciparum 452 263 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
T.gondii 469 263 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
P.murinus 427 263 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
M.soleimani 464 263 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
M.soleimani 446 263 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
S.aureus 358 263 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
E.coli 388 263 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524

E. tenella 462 283 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
P.falciparum 452 283 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
T.gondii 469 283 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
P.murinus 427 283 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
M.soleimani 464 283 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
M.soleimani 446 283 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
S.aureus 358 283 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
E.coli 388 283 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524

E. tenella 462 303 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
P.falciparum 452 303 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
T.gondii 469 303 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
P.murinus 427 303 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
M.soleimani 464 303 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
M.soleimani 446 303 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
S.aureus 358 303 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
E.coli 388 303 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524

E. tenella 462 323 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
P.falciparum 452 323 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
T.gondii 469 323 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
P.murinus 427 323 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
M.soleimani 464 323 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
M.soleimani 446 323 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
S.aureus 358 323 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
E.coli 388 323 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524

E. tenella 462 343 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
P.falciparum 452 343 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
T.gondii 469 343 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
P.murinus 427 343 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
M.soleimani 464 343 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
M.soleimani 446 343 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
S.aureus 358 343 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
E.coli 388 343 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524

E. tenella 462 363 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
P.falciparum 452 363 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
T.gondii 469 363 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
P.murinus 427 363 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
M.soleimani 464 363 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
M.soleimani 446 363 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
S.aureus 358 363 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524
E.coli 388 363 ENNGG1PTNWRSLVHIC---VKGKGRMAREECVLCGTVAGAAKACASVHGANEELGANSSLIDOLVFGKQLOADVISAKVKA-----SNPKSFSLFDGAEETLARIDKEK-NNSHSHAAE 524

	<i>E. tenella</i>	<i>P. falciparum</i>	<i>T. gondii</i>	<i>B. bovis</i>	<i>P. marinus</i>	<i>H. sapiens</i>	<i>M. tuberculosis</i>	<i>S. aureus</i>	<i>E. coli</i>
<i>E. tenella</i>	64.59	71.41	63.33	68.54	60.56	31.76	30.58	52.37	
<i>P. falciparum</i>		66.56	64.47	67.19	60.09	30.75	31.94	49.67	
<i>T. gondii</i>			63.54	70.56	62.19	31.78	31.16	51.82	
<i>B. bovis</i>				64.08	61.30	32.09	31.57	51.41	
<i>P. marinus</i>					62.02	32.87	31.48	52.28	
<i>H. sapiens</i>						30.51	30.29	51.22	
<i>M. tuberculosis</i>							26.58	34.02	
<i>S. aureus</i>								31.33	
<i>E. coli</i>									52.37

Sequence alignment of SDH1 (flavoprotein subunit) from *E. tenella* and other organisms. Residues were colored according to percentage identity by Jalview. Conserved residues involved in the dicarboxylate-binding, according to the crystal structure of *E. coli* succinate dehydrogenase SDH (PDB: 1NEK), are shown with "#" symbol.

Amino acid sequence identity. Abbreviations; *E. tenella*: *Eimeria tenella* (XP_013228047), *P. falciparum*: *Plasmodium falciparum* (CZT98601), *T. gondii*: *Toxoplasma gondii* (KYF42821), *B. bovis*: *Babesia bovis* (XP_001610645), *P. marinus*: *Perkinsus marinus* (EER16513), *H. sapiens*: *Homo sapiens* (AAA20683), *M. tuberculosis*: *Mycobacterium tuberculosis* (BAX25882), *S. aureus*: *Staphylococcus aureus* (EWC66604), *E. coli*: *Escherichia coli* (KGM73400).

Figure S3



Figure S3. Top: sequence alignment of amino acid sequences of SDH2 (iron-sulfur cluster subunit) from *E. tenella* and other organisms. Residues were colored according to percentage identity by Jalview. Conserved residues involved in the coordination of the iron-sulfur clusters, and interactions with cytochrome *b* and ubiquinone, according to the crystal structure of *E. coli* succinate dehydrogenase SDH (PDB: 1NEK), are shown with "#", "‡" and "*" symbols, respectively. Bottom: Amino acid sequence identity. Abbreviations; *E. tenella*: *Eimeria tenella* (XP_013233141), *P. falciparum*: *Plasmodium falciparum* (CZT99291), *T. gondii*: *Toxoplasma gondii* (CEL77101), *B. bovis*: *Babesia bovis* (EDO06889), *P. marinus*: *Perkinsus marinus* (EEQ98108), *H. sapiens*: *Homo sapiens* (AAA81167), *M. tuberculosis*: *Mycobacterium tuberculosis* (KLL09309), *S. aureus*: *Staphylococcus aureus* (AKJ17007), *E. coli*: *Escherichia coli* (KIH34397).

Figure S4



	<i>E. tenella</i>	<i>P. falciparum</i>	<i>T. gondii</i>	<i>N. caninum</i>	<i>B. ovata</i>	<i>E. coli</i>	<i>S. aureus</i>	<i>M. tuberculosis</i>	<i>H. pylori</i>
<i>E. tenella</i>	48.85	59.19	58.88	48.89	20.04	20.16	22.79	42.95	
<i>P. falciparum</i>		50.38	49.52	50.91	21.55	21.60	22.81	42.73	
<i>T. gondii</i>			87.64	49.80	22.54	21.27	23.87	42.73	
<i>N. caninum</i>				49.80	19.65	20.45	24.80	42.51	
<i>B. ovata</i>					22.61	22.13	23.55	44.25	
<i>E. coli</i>						45.40	47.78	22.84	
<i>S. aureus</i>							41.53	21.81	
<i>M. tuberculosis</i>								22.29	
<i>H. pylori</i>									42.95

Figure S4. Top: sequence alignment of amino acid sequences of MQO from *E. tenella* and other organisms. Residues were colored according to percentage identity by Jalview. Bottom: Amino acid sequence identity. Abbreviations; *E. tenella*: *Eimeria tenella* (CAK51433), *P. falciparum*: *Plasmodium falciparum* (CAG25406), *T. gondii*: *Toxoplasma gondii* (ABE76504), *N. caninum*: *Neospora caninum* (XP_003881055), *B. ovata*: *Babesia ovata* (GBE62760), *E. coli*: *Escherichia coli* (OAF94253), *S. aureus*: *Staphylococcus aureus* (ABR53505), *M. tuberculosis*: *Mycobacterium tuberculosis* (KXN95083), *H. pylori*: *Helicobacter pylori* (HP_0086).

Figure S5



Figure S5. Top: sequence alignment of amino acid sequences of G3PDH from *E. tenella* and other organisms. Residues were colored according to percentage identity by Jalview. Conserved residues possibly involved in the binding of glycerol-3-phosphate and ubiquinone, according to the crystal structure of *E. coli* G3PDH (PDB: 2R46), are shown with “#” and “*” symbols, respectively. Bottom: Amino acid sequence identity. Abbreviations; *E. tenella*: *Eimeria tenella* (XP_013232618), *P. falciparum*: *Plasmodium falciparum* (PKC45437), *T. gondii*: *Toxoplasma gondii* (EPR62522), *N. caninum*: *Neospora caninum* (CEL66611), *P. marinus*: *Perkinsus marinus* (XP_002774011), *H. sapiens*: *Homo sapiens* (XP_011509280), *M. tuberculosis*: *Mycobacterium tuberculosis* (CKM72788), *S. aureus*: *Staphylococcus aureus* (KII21235), *E. coli*: *Escherichia coli* (WP_021514332).

Figure S6

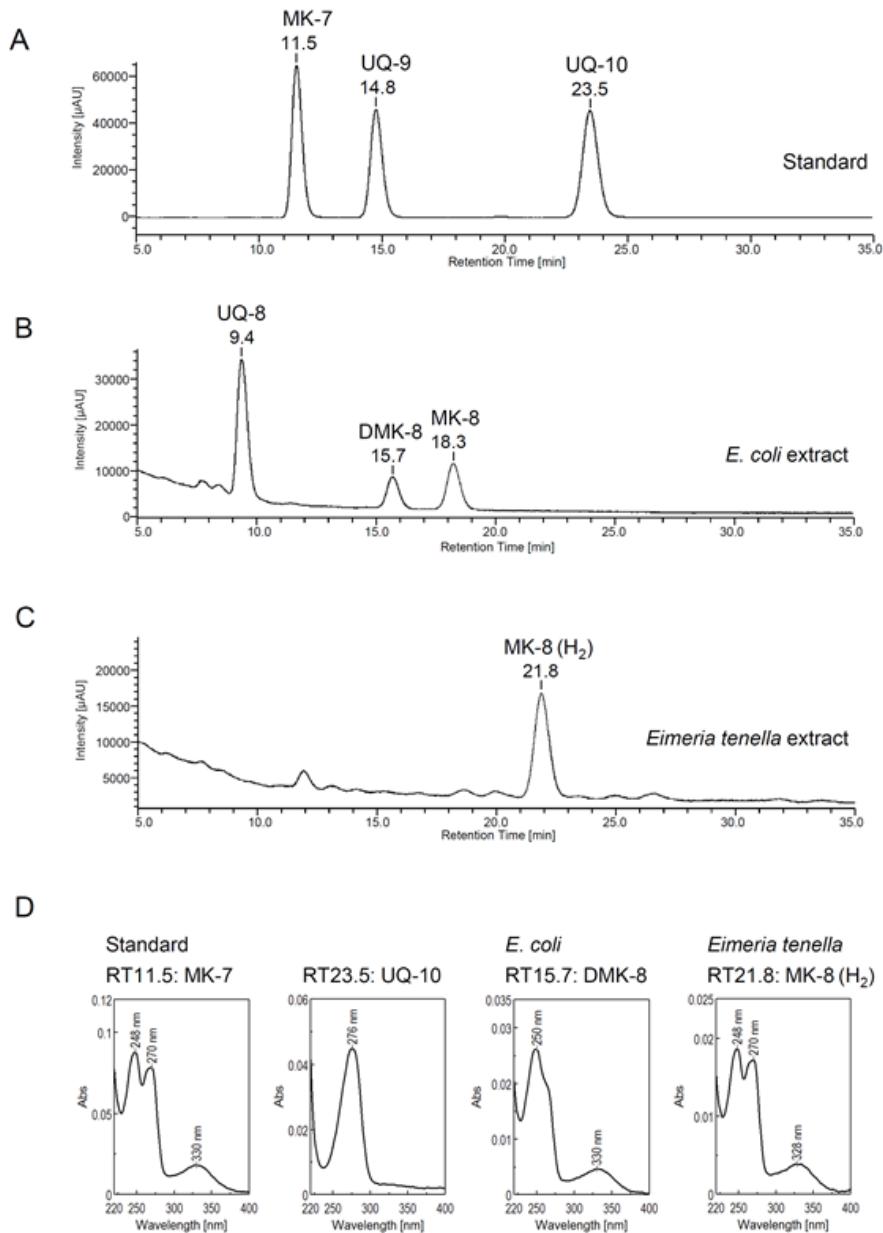


Figure S6. Quinone composition of *E. tenella* extract analysed by HPLC-PDA. **(a)**, mixture of standard quinones, MK-7, UQ-9 and UQ-10. **(b)**, *E. coli* extract containing UQ-8, DMK-8 and MK-8. **(c)**, *E. tenella* extract. **(d)**, UV-spectra of MK-7, UQ-10, DMK-8 and MK-8(H_2).

Figure S7

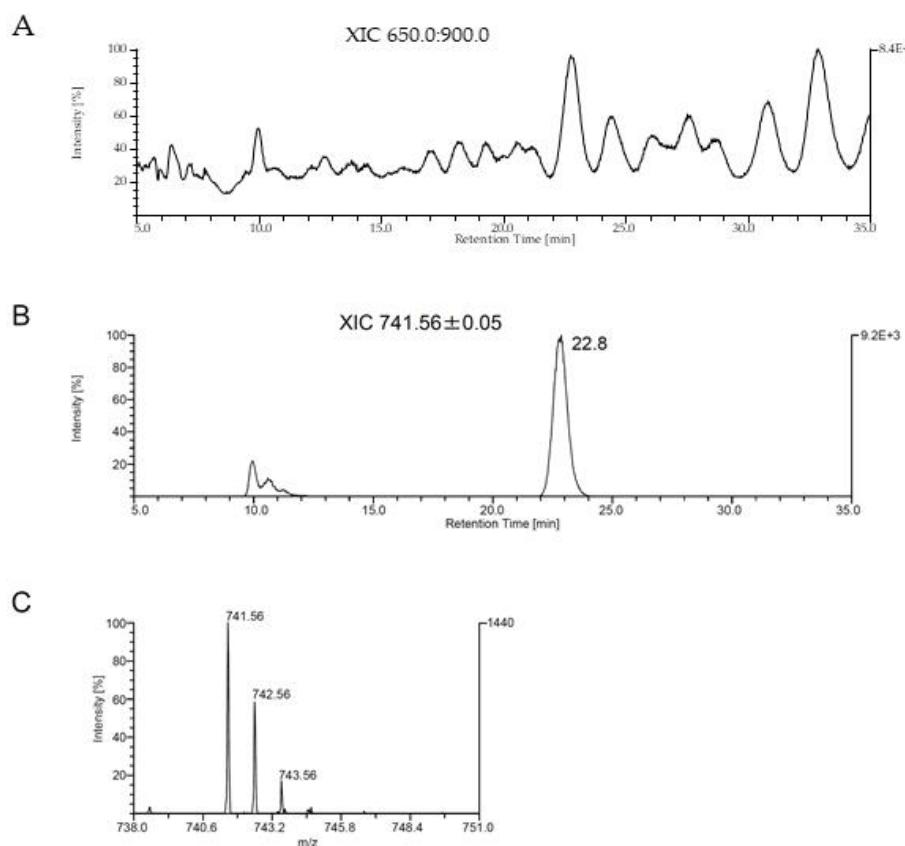


Figure S7. LC-MS analysis of *E. tenella* extract. **(a)**, extracted ion chromatogram (XIC) of m/z range 650-900. **(b)**, XIC of m/z 741.56 ± 0.05 corresponding to $[M + Na]^+$ from MK-8(H₂). **(c)**, Mass spectrum of the component eluted at retention time 22.8 minutes.