	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 Microneme protein-2	35,087	281	11	42	U6KXC3	gi/4164596
6	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
8	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 c oxidase subunit Vb	25,120	133	36	38	C8TDR9	gi/118490698
12	Cytochrome $c1$, putative	46,055	116	4	14	U6L5K5	gi/557147988

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

13	Nucleoside-triphosphatase, putative	100,043	91	2	3	U6KZA4	gi/557148408
14	Uncharacterized protein (3 transmembrane region) [Eimeria necatrix]	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 c oxidase IV	23,681	56	5	24	H9B966	gi/357016995

	Succinate dehydrogenase										
25	(Ubiquinone) flavoprotein	71,427	55	1	2	U6KGY0	gi/557137402				
	subunit, mitochondrial, putative										
26	Cytochrome c oxidase subunit 2	23,918	54	4	18	H9B9F9	gi/357017181				
77	Uncharacterized protein (one	12 9/2	50	4	50	1141 270	ai/557146007				
21	transmembrane region)	15,645	52	4	50	00L2Z0	gi ₁ 557140997				
28	Zgc:110343, related	28 440	50	2	14		~;/5571 <i>4</i> 7925				
	(peroxyredoxin)	28,449	52	3	14	UOKIAS	gi 33/14/835				

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

C. sus S. cerevisiae sais

C. sorokiniana

O. sativa M. tuberculosis

teutla/2-836 folgeneuer/2-833 annauer/2-833 gendt/2-833 neu/32-724 services/2-832 services/2-832 services/2-842 anna/2-362 abbrodies/2-862	1	MV RMRAL MTASWL MAGQWL MSTRSFL	RYLGRALAGSTP- RFLAGASVPLL- RLLAGASVPMLS- RLLGGVSVLPAVS 	LATSSSSSPFSS	ALA APAR SSSRSSPPAR SSSRSSPPAR AAYAL	AAVGFFAQ CDSFQSF- CDSFASFS CDDKVHFS N- ENAAALGQ	CKERVSSSBDDS PRTPKEQVAAL SPSSPKERVSAL SNRSSPSSSSS BSRAC RASSASASSSPSS	SLVDSPPPVLGEGA AQPPRPFSFA AQPPRPFSFA SSINPKAFSSIA MLSKNI VALRASSAIFSVAR IALAGLADKTAAGA	S L RWQL RNAL MLVK P P LSSWMASKW P VSTWMSTKW P VTNYASLKP VSNRRLLTST AARLQCBATA AGRLQPSRGI	TSLOVELHLLELPSVAC RKCGQANIFESISNURKI TNRLWGLLSAAKVSP- TSBELRIGLLSAKVSP- TSBELRIGLLSAAVAS STICLELCLVDIFVFSS NILVEFASTRSTCVENSG VFTIKSTLPPPPPGAFTA
tendlar/2-688 (olganismi): 323 anetaeni/2-628 genith/2-628 neta/2-724 seretaeni/2-813 constraines/2-813 netaeni/2-863 mbereal/aca/2-663	56 EG		PGSRGPRGPREK NLENNEDIERKEK APGAAAPGORROK SPAAREAFARROK DEESGKTKKKROR MKVIDPOHSDKPN LDETAFKGGKKK LGPTRFGEKPR QOEFTAOPPERHR	V V V A GG V A A A S I I I K S SUNGGEN V I V S SUN SA S V V V V S SUN A A S V V V V S SUN A V S V V V V S SUN A V S V V V C S GWA A V S V V V C S GWA A V S V V V C S GWA A C S V V I G T GWA A C R V V I I S S FGG LN	F V S K L D F + + + F L L N I D F + + + F L A G L D M + F L A D L D M + F L T R L D L - + - F V K A F D E S MK E L K D V D T + + + A A K K E K R + + +	RRFEVVW KKYDYTLI TKYEPVV TRYEPVV TRYEPIVI KKYNYSI DKYELVLL RAYDVVC ADVDIKL	SFODHFSY FFLL SFRNYFTFTFLL SFRDYFTFTFLL SFRDYFTFTFLL SFRDYFTFTFLL SFRNYFTFL SFRNYFYTFLL SFRNYFYTFLL SFRNYFYTFLL	SACGOSIPVAACTS CLCSGTISVNVCTS SVCVGTIPASACMT SVCVGTIPASACMT SVSVGTIPASACMT SAPVGTVDIKSIII AMCACTVEIRSIVI STCVGTUEFRSVV SVCGTISIGEIAP	KLEDLLCFGG SIENFLEKKN SMEELLWRGG GVELLVRGG SIEELLRGG FIVNFALKKK FVEAVLGSKG FVSEIOSALA FTEVVLEKOR	L PAARGE YHEA I VISV DL G1 CG - NY LOLICTOV IV VFCG - 0 YI A EVII C VFCG - 0 YI A EVII C VFCG - 0 YI A EVII C VFCG - 0 YI A EATS MVT YI A EATS NF K
tendiari2-684 falopananri2-523 contramri2-628 gendir2-628 netri3-728 serviceari2-522 constramri2-626 constramri2-682 autouri2-582 tuberculaeuri2-682	185 A R K T Y T 123 EDK T I N 176 E T K T Y R 181 T Z K K Y R 135 D R N T Y T 166 E Z K T R 177 G R H E VN 15 A GQC Y Y 2 2 2	CRPAAVPEGPP CIDIEN CRATQASLKDA QSTHGKAQDA CRASSSASSS IKSLSAVSQLT ACFPEDAGPPE TAADGDGLPA SELLGHT	GGRGG PFHGKTGCLRELA QPENHLG- A- NP-	SSSSSSSARDHL LHQA	APWEEPPDIM NKVKLFYDIE HEWDEPFDIE REWEESTDIE HYWEEPTDIE PAEIKYDYE CFKIPYDIE TNFKYSYDKE - YQTPYDSE	V LAVGS DY IIAVGAKT VVTAGALV VVAAGADV VLAAGAEV ISAVGAEP VLGVGSIN VIAGAGO	NT F NT F GVK EHAT NT F NT NGVDK F A NT F NT P GVK ENAT NT F GT P GVK ENAT NT F GT P GVK EHAT NT F GT P GVT D Y GF NT ST F GT C GVO F HT N T ST F GT G K GVA F NAT ST F G GT K GVA F NAT ST F G GT K GVA F NAT	Y LETAODA LEVY AH Y VOIDDA LEUX KA Y VELLDA RELKAA Y VELLDA RELYAA I LEVY DA CEITR I LEUY DA CEITR I LEUY DA ALL LE I LEVSHAOII RE GMESIDDA LEL GE	LGACLTAAAN FLDILTKCTL LFDVVIAAAV LFDVITTASV LFDLIFKASL TAANLTKANL ISECFFRAAL LUTNLMLSEN ILSAFFOATR	PSWT
wella/2-686 (alepanum/2-533 ambain/2-628 gmlb/2-628 mat/2-724 servosae/2-512 ams/amar2-626 anna/2-562 habera/ams/2-463	279 ¥ ¥ ¥ G G G 284 Å ¥ ¥ G G G 282 ¥ ¥ ¥ G G G 287 ¥ ¥ ¥ G G G 287 ¥ ¥ ¥ G G G 289 ¥ I ¥ G G G 299 ¥ I ¥ G G G 295 ¥ ¥ ¥ G G G 274 T ¥ ¥ G G G	SGVIAAA IR TGVIVAA ID TGVIVAA ID TGVIVAA ID TGVIVAA ID TGVIVAA IC TGVIVAA IC TGVIVAA IC TGVIVAA IC TGVIVAA IC TGVIVAA IC TGVIVAA IC TGVIVAA IC	DY LNTT GARLY PO DFINK VKINKD OFFOLEGALHFPH DFFOLGATHFPO DFLOMEGKRYFPH OYVHODLRKFLFA OLITEDLVKLYP DFITROVRERYAH LATHTLKGAFRH	LQQ - HFK V L L L IFN-FISISII LMF - FVR T LV LRF - LVR T LV LTK - YFK V T LV LAF - LVQ I HV QIQ - DVS RVI VKD - TVK V T LI IDSTKARVI L LD	NGAAPLPMYD GGNNLLPTFT MLPTVLAAYN MLPTVLAAYN MLPTVLAAYN ALPIVLNMFE LMDHYLSMYD AN-EILSSFD AAPAYLPPMG	QQV QQA AK QN I SD F T K GSV QA F AK NDV QA F AK K E I QK F A L K L SSY A L RA I GQY T A VGL RQY A T AK L GQR A A	ATFOK - SGVELH ENFHN - LNINVI RL EENFRYDEC KK QSNFNMDVO SHLEN-TSIKVH ERFAR - SGINLV DH SK - 1 GVNLV ARLOK - LGVEIO	NT Q TR CFDAY TY NT Y ID DKHS FHI OT Q YG KFNSYKY OSQ YG GFDSYKY QAR YR DIDFYTI TA AK FEKQLA NSR KA QDGYTY GAW TD DINGITY	R R L O F R A A A OS S L N R T R R R T K R OS K K K V L K R T K T K H E D V D K E G N S D K D S D G T	ATAAAAATTAAAAGGGAA QPMVISPSPSSINLDKON
undlar2-686 (Algarund:2-823 sattanir:2-828 politi:2-828 nos:12-724 sensoss(2-823 sattani:2-862 sattani:2-862 https://2-862	992 K EGAPAC 294	GAGGT SAGAGA AQ AD KRT	AAAAAAAGAAAAT - KNEKKK GAAGQUHVEENE G- QVIEKE GRKRGEEDDEET - GK	PAADT 1 ETNFVL 	KAS GVRPTEL ASGLAQTTE KASGLAQTTE KASGLKSPKI KASGLKSPKV KASGVKSPKL KATGNKARPV KATGVAMHPV KSTGVGPSEP KSAGVSASRE	ATAVAR IQKFLK CLDLAG - K CLDLAR - K CLKFCKEN ITDLFK VRILQEKE VRSLFLFK GRDLAE	GLPAQSEPOF TIPYQANNAI TAELEEAQKSTPY TAELEEAQKSTPY EGMLIKAQQSPY EGMLIKAQQSPY - KIPEQNSSER PAGTQNHFES - SPGGE QSRYELDEAGF	LLVDFALBYLGTDC LKVDFKLRVILTFS LVVDQMKVRCCEG LLVDQCMKVRCCEG LLVDQCKVQCEF LANDFLVQCKVQCEF LANDFLVQCKVKSNN AVTBFHLRVRSNG IGVDVKRSFSVE IQVQLFDLSIF	- LTAAGDCC NNTTAIGDCC - ITALGDCC - VYALGDCC - ITALGDCA - ITALGDA - ITALGDA - TIFALGDA - VYALGDCA	T I EFFK LAOHROOLFORA KIOPK LIMENTNEI IKI I RLIPFILVOHADT LFFAA RLIPFILVOHADT LFFAA RIXFFALVOYADVLFDAA AGLFFIAQV MORAETI T I BOAKAYTKATOLFDKY GFLEG AVEGVFGVAQGA1QGAKT
teutla/2-688 (alcpenum/1-838 antro-2-838 penthi/2-638 nat/1-726 servicine/3-832 neroficine/3-812 neroficine/3-882 nation/2-582 nation/2-582	360 Q.R.E	NPTSGAGTEN GAGTASTDN GAGTASTDN ANGASTDN SKRHTVSSDN SKRHTVSSDN NPDGRLTLPE - TGRAVLPAL - TIKAELA	LANGEN LSTV FPO KLKOSE ITKT FPO EKEAFKLSTI FPO EQEAKSLSTV FPO FDEMAQI FNFOKN QQLMAFASQF FPH AQVÄHEGRYLAR GANPA HEEP FQY F	LHPKENKLDTLA LSISKWDTEKN- LASSKYDPSKKP LSPRKFDPSQKP LSPRKFDPSQKP LSPRKFDPSQKP LSPRKFLDF LSPRKFLDF LSPRKFFF LSPRFF LSPRFFFF LSPRFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	F R S N L D K K G E M T R Q T E M T R Q T O M T E I A E M T E L N N F K G M Q E F G G L A F A G R A Y G A Y A K I G	KA FQEANK	DKAAIYREVGVVE	LKOFTELL POOPHDIL KDOTVKL KEOFVKL KEOFVKL FISTLNHDOFVSL	OF IDKRYVSF FEIDKNYKSF AEIDLAYRAF ADIDAAYRAF KEIDAAYRSF NGIDAGLEAL	AFTAONA BOIGNY LA LL TFIAQNAS DEATY LSN'T AFTAQNAS DEATY LSN'T AFTAQNAS QAGIY LA UT AFTAQNAS QAGIY LA UT PATAQNAS QGIF LA LA
Institut 446 (departum/1-533 antener/2-628 pmht7-633 mitr2-754 services/1-633 constantion(1-634 antener/1-634 itaberealines(1-643	581 NATLGS 451 NNTIHTT 522 NATATP 521 NATPSVI 530 NSTASPI 438 NSTASPI 438	GDAPKGAPGAP 	QAAPVLEA VUDNW QKEN-IPSTEKW IKTL-AAVVGN IKTL-AAVVGN IKTL-AAVVGT IKTL-AAVVGT IKTL-AAVVGT ISTLANG IKTLAN	KÖSLCPLÖPGTA. KÖSLATI ENNOV RALYTLOGOA. RALYTLOGOA. RALYTLOGOA. LALATLOGTR. LALATLOSTRA SMASY BRA. JMASY BRA.	ALOLF - VGTY VADLF - VJFL AADIEGWRIF AADLEGWRIF AADLEFFGSL IATIRSGRT VMDVFKVGFL LVDLRENKDA KITTLLSWIV	V GG F K GG R L GG A L GG A L GG A H GG A H GG A H	PFTEV KKNV LOU FSSTPKVV LOU FSSTPKVV LOU ATCL LVKAA LOM ATCL LVKAA LOM ATCL LVKAA LOM ATCL LVKAA LOM ATCL LVKA LVV ATCL LVKAA LVVV NTFVLVRL LVVV NTFVLVRL LVVV SVK LMRASA LTT LSTERGOL TITOC	OLNA BATWRCCIGW LLŚWISECHIFIDT OFTFYNAFACLGGW HLTUNAVACLGW HLTWNELLCIGW GISFROILVANDW VYSWENELCIG	LOTAIFCEDI INTKWYCEPF LETHFYGRAY LRTSLYGRAY MRISLEGEDY MRISLEGEDY ARTKIFGEDY ARTKIFGEDY AATAQGSAAS	QCAASSFKDFKITO
		E. tenella	P. falciparon	N. санітон	T. gondii	C. suis	S. cerevisiae	C. sorokiniana	O. sativa	M. tuberculosis
E. ton	tella		25.45	36.03	33.96	34.06	23.67	29.51	26.10	24.05
P. fal	cipanon			33.39	31.57	31.34	28.37	27.01	25.05	20.25
N. ca	mimon				76.92	48.79	29.26	30.09	26.45	23.41
Tam	ndii			8		50.28	27.44	28.95	28.08	22.92

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).

26.38

27.45

22.86

23.30

28.66



	E. tenella	P. fakiparum	T. gondii	B. bovis	P. marinus	H. sapiens	M. tuberculosis	S. aureus	E. coli
E. tenella		64.59	71.41	63.33	68.54	60.56	31.76	30.58	52.37
P. fakiparum			66.56	64.47	67.19	60.09	30.75	31.94	49.67
T. gondii	8 23	0	52 	63.54	70.56	62.19	31.78	31.16	51.82
B. bovis		í.	8	i i	64.08	61.30	32.09	31.57	51.41
P. marinus		<u>0</u>		2		62.02	32.37	31.48	52.28
H. sapiens	J. J.						30.51	30.29	51.22
M. tuberculosis								26.58	34.02
S. aureus									31.33
E. coli			3	i					

Figure S2. Top: sequence alignment of amino acid sequences 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. Bottom: 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).

E.tesulla/2-386	I MHAGD SGAV CT LS EAOP SEWFVNS LIFMEMERE TSSLSPAGV SAACELLFPEASPVLSGLV SOORASF SSNAGG ····· TNLTER THEY DE LKG ··· GR	91
P Saleparan/2-322	I · · · · · · · · · · · · · · · · · · ·	\$2
T.genda/1-342	1 · · · · · · · · · · · · · · · · · · ·	87
8.boom/1-281	1	38
P.marma/1-280	1	37
Haminal1-280	1 · · · · · · · · · · · · · · · · · · ·	55
Mitaberedenu/1-263	1	39
8.mmma/1-271	1 · · · · · · · · · · · · · · · · · · ·	40
E. 46/0/1-238	1	17
	1 1 1 1	
E.tmalla/2-386	2 FHMOLYTLDTSTCG - FMVEDALEATKDRODPTLTFRESCREGICGSCAMNEDGINCEACLTPTOKTHRSTNRSFKIOGGTLGAAFGALEKSLEAODHMK	159
P.falconarum/2-322	ST POMET FEVEL DALES - PMVEDVEIX INDEL DISTUSTES CREGICGS CAMPINGENCLACLTEVNEDK	145
Teendu/1-342	8 PYNOKFELDVSTCG PNI LDALIA IKORODYSLVFRESCEEGICGSCAMNVDGKNCLACLTFIKRGDRENEAMELMPGODIKHDRHEELVVSRVTDKIN	155
B.bern/1-181	36 FRMOSYKYDTAACG - FMILDALIKIN NODSTLSFERSCREGICGSCAMNYNGENCLACURSIESCTNOGN	105
P marinau/1-250	N FHMOLENIDLACCG - FMILDALIKINDTODSTLAFEDSCREGICGSCANNINGKNGLACLOVIEFG.	102
Hanning/1-280	% PHMOTYKYDLNKCG PNYEDALIK INNEYDSTLT FRESCREGICGSCANNINGGNTLACTREDTN	120
Mithberealana/2-263	# AATGGWOSTEVPCLFSDELENLEY INGVLOGTET FEESCAHEVCGSDAMEINGVNELACKVLMEDLLPK	109
8.mmma/1-271	41 T F E I PYREN LNY I A CLME I REN FYN I NG FR TT FYWWDMN CLE EV CGACSMY I NG RAROSE SALVDOL	107
E.colu.2.2.14	IS FRMODY TITAFFORD, MMILEDALTOINES, BEST STRESCRED VCCS DGINMAGENGIACITETSALNO.	\$1
K.tmalla (1.336	199 GPST FEYHDHFEKDDDGAPVELVELFYLMULKDEVFDLTNEYTOVKSTOPWEORKTEPKE-GST LDSIEDBAKLDGLYFCLLCACCSTSCFSYWWNPOS	255
# falrmanan(1.31)	149	232
T.cond0/1-343	16 HA LFREANPEVELLELEHMMVLEBLVFDMTNEVADVRSVEPVLKRKTPKKDENVENLOSTEDERKLDGMVFCLLCACCSTSCENWNPOA	246
8. horn/1-282	106 · · · · · · · · · · · · · · · · · · ·	155
2 marma/1-7.63	103 · · · · · · · · · · · · · · · · · · ·	156
Hamina/1-280	121 · · · · · · · · · · · · · · · · · ·	205
Mahbredowil-263	119 ···································	194
8.mmma/1-271	105	199
E.relv1-2.54	55 · · · · · · · · · · · · · · · · · ·	165
a 11110 A 10		
E.truella/1-346	29 VIGTAVIMOA FEWISDSBDEFT, STELAOINDTMKLY BCHGIMNCSISC FROUDFAGA TERMIKELEFFFGTDFVKLAAGAAESESAFLAKELKIDSOF	386
# Kalvinimum11.371	23 Y LO PATEMOAY BWIVD SEDEXT . K TELMEVNDTMELY BCHGIMNCTMC CPEGID PAKAIKDMENLVOENESEDTIKEHSOYIK SEMEKTE	321
7 eenda/1-343	28 VICEAVINGATEWIADSHDIFT - III LAAINDTMKLY CHGIMNCTYSCPEGINFAGA JOKMEDOVIARTSPAWKSLOADOALTESOKLAKDIGLAA	342
#.becu/1.281	15 VICEAALMOAY EWITE STORY T. VERWYDYNDSMKLY CHGILLNOT RAC FROLD PAKALSKI KAKVEASADD TWRSTAASEYAKNNOT FLOGODKO	251
P marma/1-740	157 V LOAY BWI AD SEDIET - TERMAWI ND SMELY BONG INC TSC PEGID PAKA LAKME AFT FAAV FPGWTE I VAOFSLANKE ESGMYA	250
Harrison T. 740	THE ALL PAY I MORY PRIMITINES HOUSE . FEELAN LOD FEELAN CONFERENCE FEELINE CALLAR LANDAT.	250
Mitaberruland 3:553	195 VECTAALVNAHEET POSTOFAA, AT LOLLNEVDGYWECHTTENCTESCERGLEVTKA OFVERALMETE.	263
5 mmmal1.771	199 FV AGAISOVELENLINFTCSMENDE INALMETICIO COSCINEVIAL PROTECTELITS AAMNEETTENMESSFEGSDHEVE	221
K. aply 1-2.24	100 FICEAGULAAYEFLIDSHUTTE, DSEUDGLSDAFSVFECHSIMNCVSVCFKGUNETEALCHIESMLLORNA	235

	E. tenella	P. fakiparum	T. gondii	B. bovis	P. marinus	H. sapiens	M. tuberculosis	S. aureus	E. coli
E. tenella		46.34	58.12	50.15	52.28	48.17	32.47	19.64	42.11
P. fakiparum	÷		50.29	58.70	59.42	53.19	34.83	22.63	49.38
T. gondii	÷			54.06	54.06	49.23	33.11	19.17	46.57
B. bouis		57		P	59.79	54.92	36.40	19.42	48.54
P. marinus	0	3	-	8		62.26	34.59	20.44	49.17
H. sapiens		4					35.58	23.51	53.11
M. tuberculosis								23.68	41.39
S. aureus									24.39
E. coli	Ť.	÷			19			S	

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).

E tenella/2-518 P falceparson/1-521 T gendhi1-549 N coninan/1-553 8 con/2-549 8 con/2-548 8 mmen/2-438 M tuberculoria/2-493 H gylori/2-450	IMQL MILYNQL L	8 101 102
E. tenella?-518 P. faloparon/1-521 T.gendu?1-540 M. common?1-551 B. costa?-632 E. colu?1-545 S. costa?-645 M. tuberculosia?1-693 M. pylor/2-450	09 VI I GGGVGGTLUTT L VI GATTNIKK GLUT FØGJGLUG MPENNOT I GDDI TIN G	61 64 95 10 112 12
E.tenril/47-518 P.falesparson/1-521 T.gondis/1-540 M.coninam/1-551 B.con/1-545 E.colu7-545 S.aureu/1-428 M.tuberculosu/1-428 H.pylers/1-450	HE FP MALLANGOT COPARK TOT KET FEELQUYG TE CCLETEVEMICS SEPTODYCCLETYN HEADNIS ALA VEAA WOAAAGAQODFS CT VLETEEL IS TORWIGY GERECOFLET YPY FOLFNSMRLYN OD H VITEVALKOSHTLEFEQLSALMMFTLEFEQLSALMMFTLEFEQUSALMANA, SESTON AND AN UN AN EVOAN HAANAGAQODFSIN LETEN IS TORWIGY TE SETTON AND HEAL TEMOFTORKE AND HEVITEVALKOSHTLEFEQLSALMMFTLEFEQUSALMANA, SESTON AND AN WOAAAGAQODFSIN LETEN IS MOKAALANGOTECT MER YMY KULTEMOFTORKE AND TE GAMNSISLEFOFTORIE TO HEAVNYT HAAS FVOAN HAANAGQODFSILLDLEHD IS MOKAALANGOTECT MER YMY KULTEMOFTORKE AND TE GAMNSISLEFOFTORIE TO HEAVNYT HAAS FVOAN HAANAGQODFSILLDLEHD IS MOKAALANGOTECT MER YMY KULTEMOFTORKE AND TE GAMNSISLEFOFTORIE TO HEAVNYT HAAS FVOAN HAANAGQODFSILLDLEHD IS GAMNIG GOREOVER YN FALLEFTULLDE AND YN TE GAMNSISLEFOFTORIE TO HEAVNYT HAAS FVOAN HAANAGQODFSILLDLEHD IS CHINTER YN STANNA EN YN ALOOSSLEFROM YN STAHAAD YN TE GAMNSISLEFOFTORIA STAN AN HAAN STAN ANHOL. KHNOFTNI H IS LPHISTYME SNNNYLER YN ALOOSSLEFROM YN STAHAAD YN TE MER FON FOLMAAT HE IS GOVYNGE IT GULAS LOKEN - FSLOLSS VAAR HAAN HOU. KHNOFTNI H IS LPHISTYME SNNYLER KAN YN FRANT HAAL FFERMIN FLANKAFWY FLANKAFWYFLANKAAD SON YN AL AN STAN YN AN TY YN YN AN FYNYN AN AN TY YN YN AN TY TE STAN YN THAF IS LPHISTYME SNNYL ER YN ALOOSSLEFROM YN STAHAAN HYN FLANKAFWYFLANKAAD SON YN AL AN STAN YN AN TY YN YN YN AN TY YN YN AN TY YN YN AN TY YN YN YN AN TY YN AN TY YN YN AN TY YN YN YN AN TY YN YN AN TY YN YN YN AN TY YN THAFYN THAFYN THAFYN TY YN AN TY YN YN YN AN TY YN YN AN TY YN YN YN YN YN YN AN TY YN YN YN AN TY YN YN YN AN TY YN	67 69 60 81 344 39 35 39
E tenella/1-518 P falceparam/1-521 T gendu/1-549 M canimam/1-551 8 evat/1-645 8 eva/1-648 8 am eva/1-648 M tuberculoria/1-649 H pylor/2-650	MEDNIFSLITDGIKKET NVVGGGHS LIFAGILEYGLYGUVAGYTFADKMINDKVIYUDDAT.FFAAYMD TGILLGKTTGPTALFLFLL 200 NBLYKITYKGIINET VVGGGHS MIANNYGLYGUVAGYTFADKMINDKVIYUDDAT.FFAAYMD TGILLGKTTGPTALFLFLL 200 NBLYKITSKGIINET VVGGGHS MIANNYGLYGUVAGYTFADKMINDKVIYUDDAT.FFAAYMD TGILLGKTTGPTALFLFLL 200 NBLYKITSKGIINET VVGGGHS MIANNYGLYGUVAGYTFADKMINDKVIYUDDAT.FFAAYMD TGILLGKTTGPTALFLFLL 200 NBLYKITSKGIINET VVGGGHS MIANNYGKYFULMAGYTFADKMINDKVIYUDDAT.FFAAYMD TGILLGKTTGPTALFLFLL 200 NBLYKITSKGIINET VVGGGHS MIANNYGKYFULMAGYTFADKMINDKVIYUDDAT.FFAAYMD TGILLGKTTGPTALFLFLL 200 NBLYNYNYN NCGILSK VVGGGHS MIANNYGKYFULMAGYTFADKMINDKVIYUDDAT.FFAAYMD TGILLGKTTGPTALFLFLL 200 NBLYTYNNN NGGILSK VVGGGHS MIANNYG VGGGLAAKSUL NGGGHS VGGGUNAGYTFADAT. 200 NBLYTYNNN NGGGTFADNINGKTGGGAGALSL NGGGTFALKTSINGKTYGGGAGALSL NGGGUNAGYTTGPTALFAD TGIGANDAT. 200 NBLYTYNNN NGGGAGYTTANNYGYGGGAALSL NGGGTFALKSTN NGGGUNAGYTGGGAGAAATAATAANAD TGIGANDAT. 200 NBLYTYNNN NGGGAGYTTANNYGYGGGAALSL NGGGUNAGYTTGANGAYTGGAGAAATAATAANAD TGIGANDATAATAANAD TGIGANDATAATAANAD TGIGANTAATAANAD TGIGANTAATAANAD TGIGANTAANAD TGIGANTAATAANAD TGIGANTAANAD TGIGAANANAD TGIGAANANAD TGIGANTAANAD TGIGANTAANAD TGIGANTAANAD TGIGAANAD TGIGANTAANAD TGIGAANANAD TGIGAANAD TGIGAANANAD TGIGAANANAD TGIGAANAD TGIG	65 67 FF FE 44 42 15 16 77
E. tenella (?-518 P. faloparan/1-521 T. gredu/1-549 M. common/1-551 B. costa/1-492 E. colu?1-548 S. anaraa/1-498 M. tuberculosia/1-493 M. pylor/2-450	Me BNILET FDTAKCVETWE - LAOVYVOLLTANMEA VFKNLT FVALNEN LAVELEK I STOVELTAGGGE FOLINTEK - SLUG GE VTETM ME DNILET FDTAKCVETWE - LAOVYVOLLTANMEA VFKNLT FLYNALNEN LANDKEI STOVETTE LTAGGGE FOLINKES - SLUG GE VTETM ME DNIETLDTEKVEN FLS LOVYVOL GESMMEN VIENT FLYNENVLL KELLEN KENNE VSERFELTAGG GENFOLINKES - SLUG EN FOL ME DNIETDTEKVEN ME DNIETDTEKVEN ME DNIETDTEKVEN ME DNIETTEN ME DNIETTEN ME DNIETTEN ME DNIETTEN ME DNIETTEN ME DNIETEN ME	67 69 199 143 147 121
E toniTa/2-518 P faleparam/1-521 T.gradul/1-540 M.aminam/2-551 E.orata/1-492 E.orb/7-548 S.marna/1-493 M.niberalani/1-493 H.pyleri/2-450	465 I I FNIT F - SEGT C L GTA	15 21 49 31 92 45 95 95 95

	E. tenella	P. fakiparum	T. gondii	N. caninum	B. ovata	E. coli	S. aureus	M. tuberculosis	H. pylari
E. tenella		48.85	59.19	58.38	48.89	20.04	20.16	22.79	42.95
P. fakiparum			50.38	49.52	50.91	21.55	21.60	22.81	42.73
T. gondii				87.64	49.80	22.54	21.27	23.87	42.73
N. caninum					49.80	19.65	20.45	24.80	42.51
B. ovata						22.61	22.13	23.55	44.25
E. coli							45.40	47.78	22.84
S. aureus								41.53	21.81
M. tuberculosis									22.29
H. pylari									

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).

E analla/3-653 7-563parane/3-653 7-pm8/0/3-653 7-mm9/ae/7-643 7-mm9/ae/7-mm9/ae/7-643 7-mm9/ae/7-643 7-m	ALL FTAAPE AND FRELPA ADD FRELPA ADD FRELPA ADD FRELPA ADD ATTGEG SM ATTGEG SM ADMGNN R6 SQWLYE	IIRPIRP	DV P V NMS E L L P S D I D R K K R P H K F C	DAĐQKGFITIVD	VQRVLES I NVQMDEN	TLHEILNEVDINKN	GOVELNEFLOLMS	IQ4GRVSCSELAILMKTA	EENLDERVFIFV	433 433 433 441 0 R S C G G 402 441 9 R S C G G 402 457 581
2. tentlor 3-453 P. Johnson 2-453 T. genetics 453 N. enteren 2-452 P. enteren 2-452 M. bornslear 5-452 S. entro 3-857 E. ob/1-301	548 L P Y 577 T K P Y 549 A F P T 549 A F P T 549 A F P T 849 Y S L F P Y 849 Y S L F P Y 849 G Y L K 677 T	LKATYLYACBY ITATIIYACBY LKATYLYGVBY LKATYYGVBH LBTLLWAYDB ITATYKYGIK- YIAYAAPPBAP - YYLYYSIQOP TIALKYLYDH	QARSYSDILA ANIS SUIG ANIS SUUGA ARSYSDYLA ARSYSDYLA ARSYSDYLA ARSYSDYLA ARSYSDYLA ARSYSDYLA ARSYSD A	IRTGASTAFGRW	PRWSEPCSGGPPQTS	TARSET I WRAWRPR	LPIL LDHKI FELG IDSQ MEMA FVDAPS TENA FVDPV TENA FVDPV TELA LNVQ CSP PSPTTFRET SGKMYFNIKE ADDALWERTS	GVEALDTVCSMAARTC SNEVIDELAQLLENIL AFACIDEVARINGTIK AFACVDEVARINGTIK AFACVDEVARINGTIK AFACVDEVARINGTIK GUARTAN (GAAPTANYESSBACL) VEDYKDSTIDINADMLDT QG	SAATANKEKQIA NTIQVNKNVKIA SSAKLIKKIIA DSAQVAKEKQIA DKKERAAIMEKA DDYEKQEQLITA IEGYAKRVCRAV SPAQIIAYTEIV LN	KKYAFT 448 KDYINS 644 AAFLKT 642 KOFLKT 642 KOFLKT 643 KKFLYY 547 FPWSMM 642 EQAIKE 545 DOQORV 845
E tendin/3-633 P (departur/2-633 T product 453 N conserve?-643 P morthuar(3-642 N copress?-642 M colorend/cop?-643 E colo?-363 E colo?-363	48 LYDHES 56 LIDDN- 48 YYDEK 48 YYDEK 51 YIDKK 51 YIDKK 52 MEGKS- 52 MEGKS- 50 DINDED		NTT T R NO O NO T L NO NO D L L NO	EV HK DK VA A SMP RK TP NILKT KYN AA HED KYA TT RS I AHED KYA A TE P HHEGE YSA KYG (THNLK A GP S OF I P A ZYA S I - (ELKK DYGLT F S TT T QG - I GP AW -	CRIKGMEVOGAVD-P CRIKFELIGGAVD-P CRIKFELIGGAVD-P CRIKAMLIGGAVD-P CRIFREALIGGAVD- RIFREALIGGAVD- RIFREALIGGAVD- - IERVSLEADG - IERVSLEADG - IERVSLEGADG - IERVSLEGADG - IERVSLEGADG	LGTLQFIDCBFCSG YGIINIDDLTFGCS SGALFFKICIFASG TGALSSKICIFASG FSVGGGTDFDVLAD 	KLERLESTSPFEL KLSKTZVNKYPOI MLEVIEKENPFE VETLEKENPFE RMAMIENESYG-V TEYIREVQDYG-U VNQAENVGALQGE VEQKVDVAKGFGII GDEDDTAARERER	TEORENEY AN TETATON TOTANITYSI ETESIN I SOARNIYISI ETESIN I SOARNIYISI ETEARS I SOURNIYISI ETEARS I SOURNIYISI ETARTI SEVAONLAATI GOKAFIY IPTAVANI EDRIYSEANYOEL IPTITYSIA ASKI MSNYOEL	VELAK - KESLMEI CELAK ELNMENK COLAK ERPDESO CELAK ERPESO EFGONTNTESP AKMAS VIGKEWP LAMA SDPSELS FNI AQISQYHDSI SELLLGNAGAISI	VEG- 50
E analis/3-651 P. folgarism/3-653 T. pindt/3-653 N. commen/3-653 P. maptima/3-663 P. maptima/3-663 N. agrees/3-667 M. tuberralions/3-619 S. martup/3-807 E. colt/3-903	30 G V L L L 30 D V L L L 38 G V L V L M 38 G V L M 39 G V L M 39 G V L M 30 G V L M	LPW E - GRTVAGI LPW C - KATIAGI LPW O - GATIAGI LPW O - GATVAGI LPW O - GATVAGI LPW O - KMIIAGI LPW O - SHWIIGT LPW S - SHWIIGT LPW - SHWIIGT	TO A PANKA - A F R PG Y DIK R IMO - DD K I O T DA PC FLS - DA PO AT I DA PC FLS - DS PO AT I DY KSDET - FL K PT I DY KSDET - FL K PT I D T DYN LD LAH A A T KA D T Y YON KSS L L T O DV Y K GD FK A Y K I L S S	EVDFLVNT ISA DIFLINTUSK IIVAWYTNT LAN VILDFIVIISVK DINFILNEVRN VILDFIVIISVK DINFILNEVRN VILDFIVIISVK	YERMDPOOMICOTOS YIHVSAEEIKNDITA TEKMDIKREEDOVRS YEKLDERGIFGDITA YESENKEDIRGDITA YESENKEDIRGDITA YESENKEDIRGOVEN YEATFET-HADTOG MFPSVNVTDEDIES HFFKQLN-FDDIVW	VWA CM TTI I SOTSI ANC OF TTI I SOTSI ANC OF TTI I SOTO VWK CO TTI I SOTO TMA CO TTI I SOTO SOTO	A K D K K S K F S S NK K K NN P N F T A V T A D A D D T D P S P	INN I NSNSSSNSNN FDD I Q	NNNNNN I G HE I A TK DA QVS I A NV A AK DGHV S I SNV TSKM TOS I SKL SL SL QAI	V I S H T V 448 S S H E 1 455 V S H Y I 477 S C H Y V 477 S C H V 247 S C H V
5 and/a/3-601 P. folgearun/2-603 T. profit/2-603 N. angener/2-603 P. norma/2-602 P. norma/2-603 M. hobers/ans/2-603 S. angene/2-603	2H QMND S 25 OHD D S 25 OMND S 29 QMND S 20 QMND S 20 QMND S 18 QHND A 18 QHND A 18 V V DD A 16 T DD A 16 T DD A 16 Z Z Z	MCESLALSPTVP MNENLIETSAID MNEOLALTASLD MNEOLALTASLD VCENIAMTAXE NNEAIALTAAR NNEAIALTAAR TITTVARTAAR LTIEVMERAAEK LVEANAOMVVR	G F V E GNO F NA A KNHVA NYY F GO I GAT V C NHAIX G V E GMK G A V C NH I M G V E GMK G A V A NH I N Y I DGWVG A V A NH I N Y GAA T A NY I N Y GAA T A NY M Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y	KEFTENTINGO KNFTEDINGK- VDILKDINGK- LEUTIGK- LEVTEDIGGL- VBLLEKTDFQT VALLEGDEVI HEFTIDENOQV TSARBE-NGLW		DETETINCK V VY NC DETETISKVI I NA GETEDISKT VY NC GETENVTGKVI NA GOTEDISKT VY NC GETENVTGKVI NA GOTEDVEAKVI NA AVALVEGHVVNA NENTTIKAKKI VNA GEKTENVA BGLVNA	T C F L T D S Y F KMDHI F C F Y G D I I F K L AD A C F F S D A Y F MA D A C F F S D A Y R MA D A C F F S D I I F KDANI T C F F T D S Y F KMDD T C F F T D S Y F KMDD T C F F T D S Y F KMDD T C F F T D S Y F KMDD T C F Y W F C T A L S K A C F W V F C F T D G M	D-AASEY I PAAG THE L N-REFNIQVSVGCIFIL T-QPKLVFAAG LIFL T-QPKLVFAAG LIFL N-REFLVAAAGAALLM D-AAAICQPSAGVIIM R-GRQVFASKGVVVVI R-SRFQVFASKGVVVVI LFSFYGIELIKGSIVV	HWYTHKTPFGLL KWYTSASPYGLL HWYTSASPYGLL KSYSSPA-CGME GYSSPS-MGLL BDRIVSD-SMGLL BDRIVSD-ACMY RVHTOKO-AT	EPQTSD 382 IFKTSD 382 LFKTTD 387 LFKTTD 387 IFKTAD 388 DFATSD 380 MILETF 280 FDTEKD 277 ILQNED 252
E Analisi'i 403 P folgarowi 2 453 T gosta'i 453 N nanoseri 2 453 P marmar'i 463 N nanoseri 2 453 N nanoseri 2 453 S nenosi 3 457 E nebri 2 459 E nebri 2 452	122 S G T S S K 40 S G T S S K 140 D G T S S S 140 G G T S S S 71 S G T S S 71 S G T S S 30 G T S S S S 30 G T S S S S 30 G T S S S 30 G T S S S 3	NTK UV NGG I NYL STK UL NGG I RYL STK UL NGG V NYL STK UL NGG V NYL STK UL NGG V NYL STK UL NGG V NYL STK UNGG UNYL STK UNGG UNYL	0 A C E T F DWGQLS LYC ENVNNLDFTLYFW KAFFILDESCLYFW KAFFILDESCLYFW KAFFILDESCHYK KAFFILDESCHYK CHAFFILDESCHYK	ALTE AHLER- ALTE AHTME- ALTE SEMES- ALTE SEMES- ALTE AHMLH- ALTE AHMLH- TGE CALVE- ALTE ALSET TGE CALVE-	A A P H I A E V LA T LM F I I A P Y LS B V S I LM F I A P Y MNH I A I LM F V A A P Y MNH I A I LM F V A B P MT G LA I LM F V C S P MT G LA I LM F V LA P H L S A T P MT F T L B P H L S A T P F F F F B G F H T T C VML F M I A P H I A F MR F F L F	1	VKAYGFLANLVCCC IKIYOL ADLVCY VKYGL 25KLVCCI VKYGL 25KLVCCI LKMTIFCGNVATL IKLTOVAGSNCIJ IKLTOVAGSNCIJ IFLTOR G LGMTORAG	DTQ1 F FTS1 LSARTSRFT DKQVFN CL1 RKSNT LDN TGVF FS1 FFAATSATS QTQVFFK FFFAATSATS SPGL PN TWVSKSNS LMN SSARTSACHTSKSSALLA AKSYFAQRHFTKAGATL AKSYFAQRHFTKAGATL KKS1 FGGTGLRFGANSVL	L F L L P R EG L KG S F F L L P A G L KG S F F L L P A G L KG S F F L L P A G L KG S F F L L KN EG L L S F F L L KN EG L L S F F L K K EG L KG G K E L K R	L V F DG 243 L V F DG 214 L V F DG 225 L V F DG 225 V V Y DG 225 L V Y DG 259 L V Y DG 157 L R V V C Y 144 G V V V V V V V V V V V 144 G V V V V V V V 144 G V V V V V V V V V V V V V V V V V V V
N campung 5432 P merinar(2442 K oppens(2442 M hobersilvein/242) S mereo/1437 Z obl(2402	1 MG 1 MS FATB 1	RFGRVFACSAGE RFSRFASCSAGV LLGKTVKYGTVV	VGLGGAAAYGGLYYNH LGLGGVAAYAGLYYNH GGSAVGISCGIVYFFTT MNLAYVEAADCISFFY MSNFIQAFDGGOGWFAA MALSTFER	CKSMYPKITRYY RKSMIPKITRYY PTIPPSGYENP KALGPAQR	SSLAGEAEGR ASLPVGQGGA TPRTNE	LAHL	PPSETAMIERMEL PTSETEMIERMEL + DOMERLEN - AVAWERLET - AVAWERLET - HIKENLEN	REDLLY CGGATGSGYAL REDVLY CGGATGSGYAL Y DIVY CGGATGSYAL SEDILY CGGATGSGAGA OF DVY CGGGYGSGAGA Y DLY I CGG Y GSGAGAA TKDLIY CGG F NGAGIAA	DAAT GESCEV DAAT GESCEV DAAT GESCEV DAVT GEKTAEV DAYT GEKTAEV DAST GEKTAEV DAST GEKTAEV	EGDEA IN REDES % REDES % ARDES % ARDEA % MODEA %

E. tenella	37.35	52.69	52.91	37.42	39.90	29.04	30.22	28.10
P. fakiparum	2	40.27	39.85	35.42	35.20	25.71	29.01	25.73
T. gondii			83.44	39.45	41.15	30.23	28.78	30.74
N. caninum				41.64	41.60	30.69	27.60	28.98
P. marinus					40.00	29.66	28.50	27.55
H. sapiens	÷.					31.29	31.26	29.96
M. tuberculosis							30.07	31.01
S. aureus		6				- 2		30.90
E. coli								

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. 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(H₂).





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 \pm 0.05 corresponding to [M + Na]⁺ from MK-8(H₂). (c), Mass spectrum of the component eluted at retention time 22.8 minutes.