

**SD Table 1: Sequences of N-terminal leader peptides for *Blastocystis* putative mitochondrial proteins**

protein	MitoProt	probability
Cystein desulfurase (IscS)	MLSRFSSVIARAPAVLSLSCRALPNGIHMM	0.9688
Mitochondrial metal transporter (Mmt1)	MSFVVLRCSLARSPFQTAAIIRVASNRGLEACGKVR	0.9784
Pyruvate dehydrogenase (PDH E1alpha)	MISRIAVKGIPIRQFVRAFSSRTFTVELPEF	0.9866
Dihydrolipoyl dehydrogenase (PDH E3)	MLSLSRASVIAQRSLYAARFFSAAAAADK	0.9398
Dihydrolipoyl transacetylase (PDH E2)	MLASKLARSVVNPKGAALLRHYSYDYTKHFLMPSAARLVALNHLDASNIVGTGLGGRIMRY	0.6775
Fumarase	MFALAKSAPKFAAASKVAVRGVATRT	0.9515
Succinyl-CoA synthetase subunit beta (SCS beta)	MLRMAPKTGVAVRNLIHEWQSKQLIQKYGGRA	0.6301
Alanine transaminase	MLRLTKNVALPTLRCFSSRITID	0.9736
P-protein	MQSLLRQTLRRSSNAGMAIRCFTAARPFAPCFKVV	0.9963
T-protein	MLARFAQTLAKPTARAFSSGAIA	0.9839
L-protein	MLSLSRASVIAQRSLYAARFFSAAAAADK	0.9398
Serine dehydrogenase	MKRTSSHIRIISKGNH	0.8505
Branched chain amino acid transaminase	MMMSKSSVLARSFSAAKTNI	0.5349
Isovaleryl-CoA dehydratase	MLHSLCKQVGRCALSRVLPVHNPCFATLSKRAFSTDNECE	0.9559
Carbamoyl phosphate synthetase (CPS)	MFGRSFGAGISSVRIARSFATEAELP	0.9753
Methylmalonyl-CoA mutase	MLAVSRQLTKSSVRFAVTPYPE	0.9697
mt Hsp70	MRSSLATLARTHMT	0.6131
Glyoxalase I	MFANVAKRAFATGPKPYRILGVQIIAI	0.9588
Acetyl-CoA carboxylase	MLSKRAVAMTRSFAGAVDLT	0.7623
Mitochondrial elongation factor Tu (EF-Tu)	MRLVAGKQMVPAFTSVRNATYERK	0.2431
Mitochondrial Ribosomal protein (MRP-L4)	MLSRCFGACKTVACSWIKTPRV	0.9786
Mitochondrial ribosomal protein (MRP-L22)	MSLLCRLGASVSIGRGISTASRVFSQNSLLGLPALMEMTNSPACMCCTQFIRSFHSHTKKY	0.7917
Mitochondrial ribosomal protein (MRP-L54/L37)	MQSLLKLASIPRAALRSGAILAPQWHAASVYASTLSPFTRSFASDKKKG	0.9866
Mitochondrial ADP/ATP carrier (AAC)	MGKKQDRRLTFMQNFIAAGGIAGVGSRTFTSPLDVVKIIAQVGSKQHSFGIFTKNIYKQEGRLGFWKGNVACLRLFPYSAINF	0.7188
ETF:ubiquinone oxidoreductase	MFRSLQRAVKQSFPSLLFLRGRGYPSSLFFTRVLSTESTET	0.9945
Thioredoxin peroxidase	MLPKIAKTVASASKRFGVSAFTQVARFSQITYGPSQAFVRQ	0.9559
Thioredoxin	MVLPVSVASRAGSMVFRGFASAQDKV	0.8934
Pyruvate:ferredoxin oxidoreductase (PFO)	MFNTLVKRAMTSAARYNSVCAATLPKAVIARN	0.988
[FeFe] hydrogenase	MLSRLSRIATTKSMVMNAARSFAAEAQGK	0.9304
Complex I, subunit NDUF2	MLRCSKQSRMRPRAEFGTRI	0.843
Complex I, subunit NDUF5	MFATKALLATVKRT	0.4043
Complex I, subunit NDUF7	MRRYTLTEGNMQRVISSAAKAA	0.8712
Complex I, subunit NDUF9	MLARFANKPSVRVLARSITSDVFPGLGLGGRMSQAPQKVITIFGASTGNLGRSVVYELASRGVTCMIPYRG	0.993
Succinate dehydrogenase flavoprotein A (SDH-A)	MLPSFRIMGKSAPALTRAFRATACRS	0.9627
Succinate dehydrogenase iron sulphur protein (SDH-ip)	MFARSLSSLSKVAVRGSVVLQISAMNFSTGFKIGPDGKIPSYKLFSLFRY	0.9801

SP: secretory pathway

mtSP: mitochondrial targeting peptide

NO: no targeting peptide predicted

**SD Table 1 continued**

<b>protein</b>	<b>TargetP</b>	<b>probability</b>	<b>SignalP</b>	<b>probability</b>	<b>iPSORT</b>
Cystein desulfurase (IscS)	MLSRF	0.787	MLSRFSSVIARAPAVLSLSCRA	0.915	SP
Mitochondrial metal transporter (Mmt1)	MSFVVLRCSLARSPFQTAAIIRVASNRGLEACGKVRFM	0.905	MSFVVLRCSLARSPFQTAA	0.301	mtSP
Pyruvate dehydrogenase (PDH E1alpha)	MISRIVKGIPIRQFVRAFFSRTFTV	0.805	MISRIVKGIPIRQFVRAFF		mtSP
Dihydrolipoyl dehydrogenase (PDH E3)	MLSLSRASVIAQRSLYAARFF	0.879	MLSLSRASVIAQRSLYAARFFSAAAA	0.462	NO
Dihydrolipoyl transacetylase (PDH E2)	MLASKLARSVVNPKGAALLRHV	0.875	NO		mtSP
Fumarase	MFALAKSAPKFAAASKVAVRG	0.612	MFALAKSAPKFAAASKVAVRGVAT	0.15	NO
Succinyl-CoA synthetase subunit beta (SCS beta)	MLRMAPKTVGAVRN	0.524	NO		mtSP
Alanine transaminase	MLRLTKNVALPTLRFC	0.743	NO		mtSP
P-protein	MQSLLRQTLRRSSNAGMAIRCF	0.952	NO		mtSP
T-protein	MLARFAQTLAKPTARAFSSGAAIA	0.677	MLARFAQTLAKPTARAFSSGAAIAHTPL	0.107	NO
L-protein	MLSLSRASVIAQRSLYAARFF	0.879	MLSLSRASVIAQRSLYAARFFSAAAA	0.462	NO
Serine dehydrogenase	NO		NO		mtSP
Branched chain amino acid transaminase	MMMSKSSVLARSFSAAKTNI	0.506	NO		mtSP
Isovaleryl-CoA dehydratase	MLHSLCKQVGRCALSRYLPCVLHNPCFATLSKRAF	0.756	NO		mtSP
Carbamoyl phosphate synthetase (CPS)	MFGRSFAGISSVSRARSFA	0.796	MFGRSFAGISSVSRARSFA	0.467	mtSP
Methylmalonyl-CoA mutase	MLAVSRQLTKSSVRAFAVTYPPE	0.663	NO		mtSP
mt Hsp70	MRSSLATLARTHMRMTM	0.498	MRSSLATLARTHMRMTATA	0.297	NO
Glyoxalase I	MFANVAKRAF	0.694	NO		mtSP
Acetyl-CoA carboxylase	MLSKRA	0.707	NO		NO
Mitochondrial elongation factor Tu (EF-Tu)	MRLVAGKQMVPAFTSVRN	0.566	NO		NO
Mitochondrial Ribosomal protein (MRP-L4)	MLSRFC	0.683	NO		mtSP
Mitochondrial ribosomal protein (MRP-L22)	MSLLCRLGSVASIGRGISTASRVFSQNSLLGLPALMEMTNSPACMCCTQFIRSF	0.917	MSLLCRLGSVASIGR	0.517	mtSP
Mitochondrial ribosomal protein (MRP-L54/L37)	MQSLLKLASIPRAALRSGAILAPQWHAASVYASTLSPFTRSF	0.804	MQSLLKLASIPRAALRSGAILAPQWHAASVY	0.874	mtSP
Mitochondrial ADP/ATP carrier (AAC)	MGKKQDRRLTFMQNFIAGGIAGVGSRTF	0.587	NO		NO
ETF:ubiquinone oxidoreductase	MFRSLQRA	0.955	probability for signal anchor	0.723	mtSP
Thioredoxin peroxidase	MLPKIAKTVASASKRFGGVSAFTQVARFSQITYGP	0.881	MLPKIAKTVASASKRFGGVSAFTQVARFSF	0.342	mtSP
Thioredoxin	MVLPSVASRAGSMVFQRF	0.561	MVLPSVASRAGSMVFGGFASA	0.116	NO
Pyruvate:ferredoxin oxidoreductase (PFO)	MFNTLVKRAMTSAARYNSVCAATLPKAVIARN	0.863	MFNTLVKRAMTSAARYNSVCAATLPKAVIARN	0.111	NO
[FeFe] hydrogenase	MLSRLSRIATTKSMLVMNAARSF	0.831	MLSRLSRIATTKSMLVMNAARSFA	0.434	mtSP
Complex I, subunit NDUF2	MLRCS	0.71	NO		mtSP
Complex I, subunit NDUF5	MFATKALLATVKRTGMVGLPVIPNARA	0.356	MFATKALLATVKRTGMVGLPVIPNARA	0.492	NO
Complex I, subunit NDUF7	MRRYTLTEGNMQRVIVISSAAKAASKNAIQTY	0.702	NO		mtSP
Complex I, subunit NDUF9	MLARFANKPSVRVLRARSITSDVFPGLTGLGGRMSQAPQVKTIIFGASTGNLGRSVVYELASRG	0.731	NO		mtSP
Succinate dehydrogenase flavoprotein A (SDH-A)	MLPSFRIMGKSAPALTRAFRATACRS	0.882	MLPSFRIMGKSAPALTRAFRATACRS	0.546	mtSP
Succinate dehydrogenase iron sulphur protein (SDH-ip)	MFARS	0.778	MFARSLSSLSKVAVRGSVVLPQISA	0.449	SP

SP: secretory pathway  
mtSP: mitochondrial targeting peptide  
NO: no targeting peptide predicted