

# Using Sequence Data to Identify Potential Cryptic Sequences Unique to Plasmodium falciparum Malate Dehydrogenase but not present in Human Cytosolic or Mitochondrial Malate Dehydrogenases

Human Cytosolic MDH  
Human Mitochondrial MDH  
P. falciparum MDH  
P. falciparum MDH

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NP_005908.1  -----HSEPIRVLVGTGAAGQIAYSLLYSIGNGSVFGKDQPI 36
pdb | 2DFD | D  MHHHHHSSGVDLGTENLYFQSHSAQNNAKVAVLGASGGIGQPLSLLKNSPLV-----S 55
pdb | 5NFR | P  -----MTKTALIG-SGQIGAIVGELCL-LLENL-----G 26
AAQ23154.1  -----MTKTALIG-SGQIGAIVGELCL-LLENL-----G 26
                : : * : * : :

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Aligning Sequences using Clustal Omega  
The four indicated sequences were obtained in FASTA format and aligned using Clustal Omega

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NP_005908.1  ILLVLDITPMGVLDGVLMEIQDC--ALPLKDVIAQKEDVAFKDLVDAILVGSMPRR 94
pdb | 2DFD | D  RLTLYDIAH---TPGVAADLSHIETKAAVK-GYLGPEQLPDLKGCDDVVIPAGVPRPK 110
pdb | 5NFR | P  DLILYDVVP--GIPQGKALDLKHFSTILGNRNILGTNQL-EDTKDADIIVITAGVQRKE 83
AAQ23154.1  DLILYDVVP--GIPQGKALDLKHFSTILGNRNILGTNQL-EDTKDADIIVITAGVQRKE 83
                * * * : : * : : : : : : : : : : : : : : : : : : : : : : : :

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NP_005908.1  GMERKDLLKANVKTIFKSQGAALDKYAKKSVKIVVGNPANTNCLTA---SKSAPSIPE 150
pdb | 2DFD | D  GMTRDDLFTNATIVATLTAACAQHCPEA-MICVIANPVNSTITAEVFKKHGVYVNPVK 169
pdb | 5NFR | P  GMTREDLIGVNGKTMKSAESVKLHCCKA-FVICVSNPLDIMV---NVFHKFSNLPHEK 138
AAQ23154.1  GMTREDLIGVNGKTMKSAESVKLHCCKA-FVICVSNPLDIMV---NVFHKFSNLPHEK 138
                * * * : : * : : : : : : : : : : : * : : : : : : : : : : :

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NP_005908.1  NFSCLTRLDHNRAKAQIALKLGVTANDVKNVIITWGHSSSTQYPDVNHAKVKLQGEVGVY 210
pdb | 2DFD | D  IFGVTT-LDIVRANTFVAELKGLDPARVNVVPTGGHAGKTIPLISQC-----TP---KV 220
pdb | 5NFR | P  ICGMAGILDTSRYCSLIADKLVSAEDVNAVILGGED-IVNPLQRYTSVNGVP-----LS 193
AAQ23154.1  ICGMAGILDTSRYCSLIADKLVSAEDVNAVILGGED-IVNPLQRYTSVNGVP-----LS 193
                . * * * : : * : : : : : : : : : : : : : : : : : : : : : : : :

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Creating Web Logo Plots:  
<https://weblogo.berkeley.edu/logo.cgi>

The P. falciparum amino acid sequence was used in a BLAST search to find 100 closely related sequences (data below) to establish that the identified Cryptic sequences were highly conserved. The sequences of the appropriate regions were used to construct the Web Logo plot shown in the poster.

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NP_005908.1  NP_005908.1  EALKDSSNL---KGEFVTTVQQRGAAVIKARKLS-----SAMSAAKICDHVRDINFGT 261
pdb | 2DFD | D  DF-----PQDQALTGRTOEAGTEVVKAKAGAGSATLSMAYAGARFVSLV-DAMNGK 273
pdb | 5NFR | P  EFVKKNMISQNEIQEITOKTRNMIAEIIKLAKAS-----AAFAPAAAITKMIKSYLYNE 247
AAQ23154.1  EFVKKNMISQNEIQEITOKTRNMIAEIIKLAKAS-----AAFAPAAAITKMIKSYLYNE 247
                : : : : : * : : : : : : : : : : : : : : : : : : : : : : : : :

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Cryptic Sequence 1

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NP_005908.1  PEGEFVSHGVISDGNLS--YGVPPDLLYSFPVVIKKNKTKWKFVEGLPINDFSRKMDLTAKE 319
pdb | 2DFD | D  E-GVVEC-SFVKSQTECTYFSTPLLLGKKGIEKNLIGIKV-S---SFEKMSIDAPE 326
pdb | 5NFR | P  N-NLFTC-AVYLNGHYNCS---NLFVSGTAKINNKGAHPV-EFPLTKKEEQDLYTESIAS 300
AAQ23154.1  N-NLFTC-AVYLNGHYNCS---NLFVSGTAKINNKGAHPV-EFPLTKKEEQDLYTESIAS 300
                . . . . . * : : * : * : : . . . . . : :

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NP_005908.1  LTEEKESAFELSSA----- 334
pdb | 2DFD | D  LKASIKKGEDFVKTLK----- 342
pdb | 5NFR | P  VQSNTOKAFDLIKGHHHHH 320
AAQ23154.1  VQSNTOKAFDLIK----- 313
                : . . . . : : :

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**COVID-19 Information**[Public health information \(CDC\)](#)[Research information \(NIH\)](#)[SARS-CoV-2 data \(NCBI\)](#)[Prevention and treatment information \(HHS\)](#)[Español](#)**BLAST**® » [blastp suite](#) » results for RID-7PB8BBYK016

Job Title [pdb|5NFR|P...](#)  
 RID [7PB8BBYK016](#) Search expires on 04-19 02:46 am  
 Program BLASTP  
 Database nr  
 Query ID [5NFR\\_P](#)  
 Description [Crystal structure of malate dehydrogenase from Plasmodium falciparum \(PfMDH\)\[Plasmodium falciparum 3D7\]...](#)  
 Molecule type amino acid  
 Query Length 320

**Descriptions**

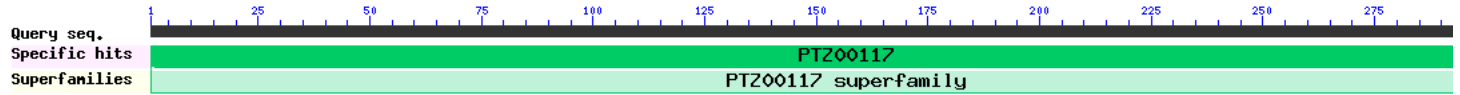
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium falciparum (PfMDH)[Plasmodium falciparum 3D7]</a>	<a href="#">Plasmodium falciparum 3D7</a>	655	655	100%	0.0	100.00%	320	<a href="#">5NFR_A</a>
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium Falciparum in complex with 4-(3,4-difluorophenyl)thiazol-2-amine [Plasmodium falciparum]</a>	<a href="#">Plasmodium falciparum</a>	648	648	100%	0.0	98.46%	324	<a href="#">6R8G_A</a>
<a href="#">malate dehydrogenase [Plasmodium falciparum 3D7]</a>	<a href="#">Plasmodium falciparum 3D7</a>	638	638	97%	0.0	100.00%	313	<a href="#">XP_966170.1</a>
<a href="#">malate dehydrogenase [Plasmodium reichenowi]</a>	<a href="#">Plasmodium reichenowi</a>	630	630	97%	0.0	98.08%	313	<a href="#">XP_012761998.1</a>
<a href="#">malate dehydrogenase [Plasmodium sp. DRC-Itaito]</a>	<a href="#">Plasmodium sp. DRC-Itaito</a>	623	623	97%	0.0	96.81%	313	<a href="#">CAC9696262.1</a>
<a href="#">hypothetical protein PFMALIP_01469 [Plasmodium falciparum MaliPS096_E11]</a>	<a href="#">Plasmodium falciparum MaliPS096_E11</a>	622	622	95%	0.0	99.67%	309	<a href="#">ETW50453.1</a>
<a href="#">malate dehydrogenase [Plasmodium sp. gorilla clade G3]</a>	<a href="#">Plasmodium sp. gorilla clade G3</a>	615	615	97%	0.0	96.17%	313	<a href="#">SOV74725.1</a>
<a href="#">malate dehydrogenase [Plasmodium sp. DRC-Itaito]</a>	<a href="#">Plasmodium sp. DRC-Itaito</a>	580	580	97%	0.0	94.23%	313	<a href="#">SOV21691.1</a>
<a href="#">malate dehydrogenase [Plasmodium gaboni]</a>	<a href="#">Plasmodium gaboni</a>	580	580	97%	0.0	94.23%	313	<a href="#">XP_018642816.1</a>
<a href="#">malate dehydrogenase [Plasmodium sp. gorilla clade G2]</a>	<a href="#">Plasmodium sp. gorilla clade G2</a>	579	579	97%	0.0	93.29%	313	<a href="#">XP_028537330.1</a>
<a href="#">malate dehydrogenase, putative [Plasmodium relictum]</a>	<a href="#">Plasmodium relictum</a>	503	503	97%	1e-177	79.55%	313	<a href="#">XP_028533952.1</a>
<a href="#">Malate dehydrogenase [Plasmodium coatneyi]</a>	<a href="#">Plasmodium coatneyi</a>	503	503	97%	2e-177	76.92%	313	<a href="#">XP_019915696.1</a>
<a href="#">malate dehydrogenase, putative (MDH)[Plasmodium ovale wallikeri]</a>	<a href="#">Plasmodium ovale wallikeri</a>	501	501	97%	1e-176	79.81%	313	<a href="#">SBT38197.1</a>
<a href="#">malate dehydrogenase, putative (MDH)[Plasmodium ovale curtisi]</a>	<a href="#">Plasmodium ovale curtisi</a>	499	499	97%	8e-176	79.81%	313	<a href="#">SBS85361.1</a>
<a href="#">malate dehydrogenase, NAD-dependent [Plasmodium fragile]</a>	<a href="#">Plasmodium fragile</a>	497	497	97%	5e-175	75.32%	313	<a href="#">XP_012335265.1</a>
<a href="#">malate dehydrogenase [Plasmodium gonderi]</a>	<a href="#">Plasmodium gonderi</a>	496	496	97%	9e-175	74.04%	313	<a href="#">XP_028544431.1</a>
<a href="#">malate dehydrogenase [Plasmodium inui San Antonio 1]</a>	<a href="#">Plasmodium inui San Antonio 1</a>	494	494	97%	6e-174	74.36%	313	<a href="#">XP_008814730.1</a>
<a href="#">malate dehydrogenase, putative [Plasmodium vivax]</a>	<a href="#">Plasmodium vivax</a>	493	493	97%	1e-173	73.08%	313	<a href="#">XP_001616198.1</a>
<a href="#">malate dehydrogenase [Plasmodium vivax India VII]</a>	<a href="#">Plasmodium vivax India VII</a>	493	493	97%	2e-173	72.76%	313	<a href="#">KMZ79541.1</a>
<a href="#">malate dehydrogenase, putative [Plasmodium gallinaceum]</a>	<a href="#">Plasmodium gallinaceum</a>	493	493	97%	2e-173	78.85%	313	<a href="#">XP_028526585.1</a>
<a href="#">malate dehydrogenase, putative [Plasmodium knowlesi strain H]</a>	<a href="#">Plasmodium knowlesi strain H</a>	489	489	97%	4e-172	73.72%	313	<a href="#">XP_002261491.1</a>
<a href="#">malate dehydrogenase [Plasmodium cynomolgi strain B]</a>	<a href="#">Plasmodium cynomolgi strain B</a>	486	486	97%	1e-170	72.76%	313	<a href="#">XP_004223317.1</a>

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<a href="#">malate dehydrogenase, putative [Plasmodium vinckei brucechwatti]</a>	<a href="#">Plasmodium vinckei brucechwatti</a>	479	479	97%	4e-168	71.79%	313	<a href="#">CAD2095064.1</a>
<a href="#">malate dehydrogenase, NAD-dependent [Plasmodium yoelii 17X]</a>	<a href="#">Plasmodium yoelii 17X</a>	475	475	97%	1e-166	71.15%	313	<a href="#">ETB56770.1</a>
<a href="#">hypothetical protein PFDG_04373 [Plasmodium falciparum Dd2]</a>	<a href="#">Plasmodium falciparum Dd2</a>	471	471	71%	2e-166	100.00%	229	<a href="#">KOB87837.1</a>
<a href="#">malate dehydrogenase, putative [Plasmodium malariae]</a>	<a href="#">Plasmodium malariae</a>	475	475	97%	2e-166	76.28%	313	<a href="#">SBT79735.1</a>
<a href="#">malate dehydrogenase, putative [Plasmodium malariae]</a>	<a href="#">Plasmodium malariae</a>	474	474	97%	4e-166	75.96%	313	<a href="#">XP_028862636.1</a>
<a href="#">malate dehydrogenase, putative [Plasmodium yoelii]</a>	<a href="#">Plasmodium yoelii</a>	474	474	97%	6e-166	70.83%	313	<a href="#">XP_022812395.1</a>
<a href="#">malate dehydrogenase, putative [Plasmodium chabaudi chabaudi]</a>	<a href="#">Plasmodium chabaudi chabaudi</a>	473	473	97%	2e-165	70.51%	313	<a href="#">XP_737386.2</a>
<a href="#">malate dehydrogenase [Hepaticocystis sp. ex Piliocolobus tephrosceles]</a>	<a href="#">Hepaticocystis sp. ex Piliocolobus tephrosceles</a>	472	472	97%	4e-165	70.19%	313	<a href="#">VWU52414.1</a>
<a href="#">malate dehydrogenase, putative [Plasmodium vinckei]</a>	<a href="#">Plasmodium vinckei</a>	471	471	97%	4e-165	70.51%	313	<a href="#">CAD2108495.1</a>
<a href="#">malate dehydrogenase, putative [Plasmodium vinckei lentum]</a>	<a href="#">Plasmodium vinckei lentum</a>	452	452	97%	3e-157	71.47%	313	<a href="#">CAD2095098.1</a>
<a href="#">malate dehydrogenase, putative [Plasmodium chabaudi adami]</a>	<a href="#">Plasmodium chabaudi adami</a>	450	450	97%	2e-156	70.83%	313	<a href="#">SCN61096.1</a>
<a href="#">malate dehydrogenase [Plasmodium vinckei petteri]</a>	<a href="#">Plasmodium vinckei petteri</a>	449	449	97%	5e-156	70.83%	313	<a href="#">EUD73291.1</a>
<a href="#">malate dehydrogenase, putative [Plasmodium vinckei vinckei]</a>	<a href="#">Plasmodium vinckei vinckei</a>	447	447	97%	2e-155	70.19%	313	<a href="#">XP_008624410.2</a>
<a href="#">malate dehydrogenase [Plasmodium vinckei vinckei]</a>	<a href="#">Plasmodium vinckei vinckei</a>	446	446	97%	5e-155	69.87%	313	<a href="#">KEG02700.1</a>
<a href="#">malate dehydrogenase, putative [Plasmodium berghei ANKA]</a>	<a href="#">Plasmodium berghei ANKA</a>	444	444	97%	5e-154	70.19%	313	<a href="#">XP_034422383.1</a>
<a href="#">malate dehydrogenase [Plasmodium yoelii yoelii]</a>	<a href="#">Plasmodium yoelii yoelii</a>	420	420	97%	1e-144	65.38%	323	<a href="#">EAA22943.1</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with oxamate [Apicomplexa]</a>	<a href="#">Apicomplexa</a>	322	322	87%	5e-106	53.02%	326	<a href="#">4PLH_A</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with oxamate [Apicomplexa]</a>	<a href="#">Apicomplexa</a>	315	315	87%	7e-103	51.75%	331	<a href="#">4PLT_A</a>
<a href="#">Crystal structure of ancestral apicomplexan lactate dehydrogenase with malate [Apicomplexa]</a>	<a href="#">Apicomplexa</a>	311	311	95%	2e-101	48.41%	334	<a href="#">4PLC_A</a>
<a href="#">malate dehydrogenase [Devosia sp. FKR38]</a>	<a href="#">Devosia sp. FKR38</a>	310	310	93%	4e-101	48.84%	320	<a href="#">WP_137152966.1</a>
<a href="#">malate dehydrogenase [Devosia sp. S02]</a>	<a href="#">Devosia sp. S02</a>	309	309	93%	5e-101	48.01%	320	<a href="#">WP_193334840.1</a>
<a href="#">malate dehydrogenase [Oceanibium sediminis]</a>	<a href="#">Oceanibium sediminis</a>	309	309	94%	7e-101	47.52%	320	<a href="#">WP_112321891.1</a>
<a href="#">malate dehydrogenase [Candidatus Fonsibacter lacus]</a>	<a href="#">Candidatus Fonsibacter lacus</a>	308	308	96%	3e-100	45.66%	328	<a href="#">NCU49226.1</a>
<a href="#">malate dehydrogenase [Devosia epidermidihirudinis]</a>	<a href="#">Devosia epidermidihirudinis</a>	307	307	93%	3e-100	47.68%	320	<a href="#">WP_046140904.1</a>
<a href="#">malate dehydrogenase [Pelagibacteriales bacterium]</a>	<a href="#">Pelagibacteriales bacterium</a>	307	307	96%	5e-100	45.34%	328	<a href="#">GDX35174.1</a>
<a href="#">malate dehydrogenase [Candidatus Fonsibacter lacus]</a>	<a href="#">Candidatus Fonsibacter lacus</a>	307	307	96%	6e-100	45.66%	328	<a href="#">NCU53456.1</a>
<a href="#">malate dehydrogenase [Candidatus Fonsibacter lacus]</a>	<a href="#">Candidatus Fonsibacter lacus</a>	307	307	96%	6e-100	45.66%	328	<a href="#">NCU63045.1</a>
<a href="#">malate dehydrogenase [Devosia limi]</a>	<a href="#">Devosia limi</a>	306	306	93%	7e-100	47.68%	320	<a href="#">WP_046135361.1</a>
<a href="#">malate dehydrogenase [Oceanomicrobium pacificus]</a>	<a href="#">Oceanomicrobium pacificus</a>	306	306	94%	1e-99	47.19%	320	<a href="#">WP_160851963.1</a>
<a href="#">malate dehydrogenase [Rhodospirillales bacterium]</a>	<a href="#">Rhodospirillales bacterium</a>	305	305	94%	2e-99	47.19%	316	<a href="#">MBK8210760.1</a>
<a href="#">malate dehydrogenase, putative [Eimeria maxima]</a>	<a href="#">Eimeria maxima</a>	305	305	94%	2e-99	46.20%	317	<a href="#">XP_013336105.1</a>
<a href="#">malate dehydrogenase [Proteobacteria bacterium]</a>	<a href="#">Proteobacteria bacterium</a>	305	305	96%	3e-99	45.02%	323	<a href="#">NBY89657.1</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium]</a>	<a href="#">Alphaproteobacteria bacterium</a>	305	305	94%	3e-99	47.85%	320	<a href="#">PCJ41639.1</a>
<a href="#">malate dehydrogenase [Candidatus Fonsibacter lacus]</a>	<a href="#">Candidatus Fonsibacter lacus</a>	305	305	96%	3e-99	45.02%	325	<a href="#">NCU49057.1</a>
<a href="#">malate dehydrogenase [Candidatus Fonsibacter lacus]</a>	<a href="#">Candidatus Fonsibacter lacus</a>	305	305	96%	3e-99	45.02%	328	<a href="#">NCU69999.1</a>
<a href="#">malate dehydrogenase [Proteobacteria bacterium]</a>	<a href="#">Proteobacteria bacterium</a>	305	305	96%	3e-99	45.02%	329	<a href="#">NBQ46335.1</a>
<a href="#">malate dehydrogenase, putative [Eimeria acervulina]</a>	<a href="#">Eimeria acervulina</a>	305	305	94%	3e-99	46.20%	317	<a href="#">XP_013246728.1</a>
<a href="#">TPA: malate dehydrogenase [Sphingomonadales bacterium]</a>	<a href="#">Sphingomonadales bacterium</a>	305	305	96%	3e-99	47.44%	320	<a href="#">HEC00426.1</a>
<a href="#">malate dehydrogenase [Eilatimonas milleporae]</a>	<a href="#">Eilatimonas milleporae</a>	305	305	94%	4e-99	47.19%	320	<a href="#">WP_121938586.1</a>
<a href="#">malate dehydrogenase [Candidatus Fonsibacter lacus]</a>	<a href="#">Candidatus Fonsibacter lacus</a>	305	305	96%	4e-99	45.02%	328	<a href="#">NCU46848.1</a>

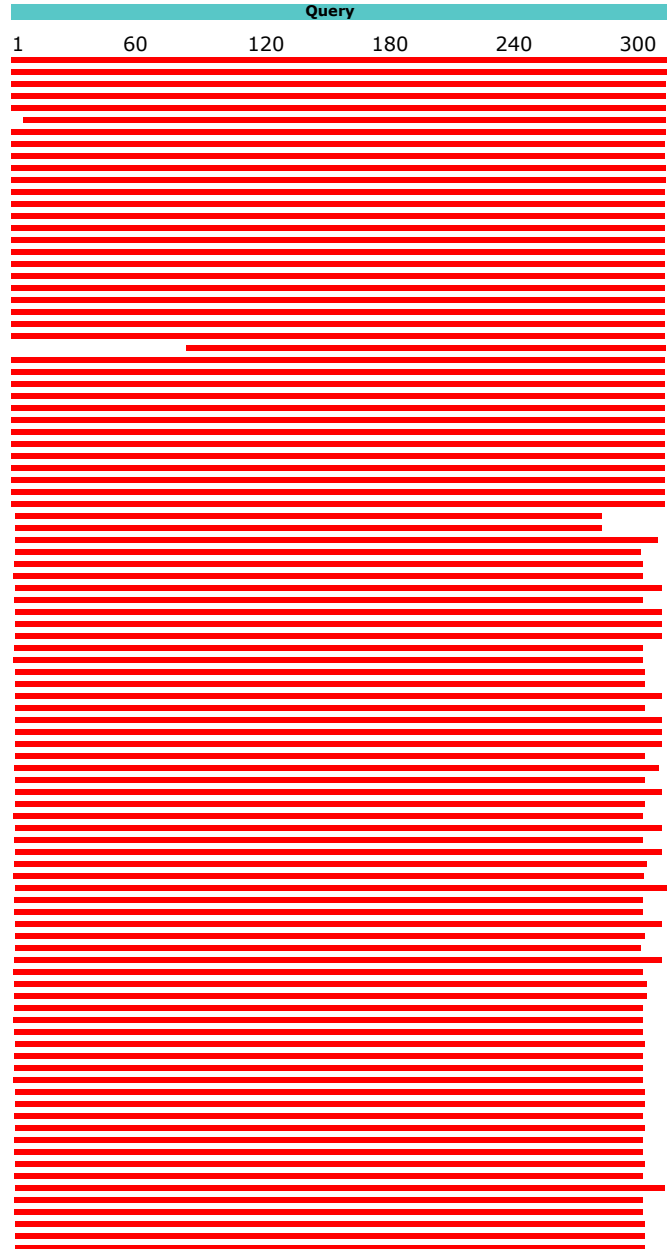
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium]</a>	<a href="#">Alphaproteobacteria bacterium</a>	305	305	94%	4e-99	47.19%	320	<a href="#">MBI1328659.1</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium]</a>	<a href="#">Alphaproteobacteria bacterium</a>	305	305	94%	4e-99	47.19%	322	<a href="#">RCL75573.1</a>
<a href="#">malate dehydrogenase [Candidatus Fonsibacter ubiquis]</a>	<a href="#">Candidatus Fonsibacter ubiquis</a>	305	305	96%	4e-99	45.02%	328	<a href="#">WP_099340841.1</a>
<a href="#">malate dehydrogenase [Devosia sp. Root635]</a>	<a href="#">Devosia sp. Root635</a>	304	304	93%	5e-99	47.35%	320	<a href="#">WP_056229719.1</a>
<a href="#">malate dehydrogenase [Pelagibacteriales bacterium]</a>	<a href="#">Pelagibacteriales bacterium</a>	305	305	96%	6e-99	45.02%	328	<a href="#">MBM5787331.1</a>
<a href="#">TPA: malate dehydrogenase [Alphaproteobacteria bacterium]</a>	<a href="#">Alphaproteobacteria bacterium</a>	304	304	94%	6e-99	46.71%	323	<a href="#">HIB19697.1</a>
<a href="#">malate dehydrogenase [Limibacillus halophilus]</a>	<a href="#">Limibacillus halophilus</a>	304	304	94%	6e-99	46.71%	321	<a href="#">WP_183417264.1</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium]</a>	<a href="#">Alphaproteobacteria bacterium</a>	304	304	99%	6e-99	44.86%	325	<a href="#">MQA65584.1</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium MarineAlpha9_Bin7]</a>	<a href="#">Alphaproteobacteria bacterium MarineAlpha9_Bin7</a>	304	304	93%	7e-99	47.68%	323	<a href="#">PPR17482.1</a>
<a href="#">malate dehydrogenase [Devosia naphthalenivorans]</a>	<a href="#">Devosia naphthalenivorans</a>	303	303	93%	1e-98	47.02%	320	<a href="#">WP_108459774.1</a>
<a href="#">malate dehydrogenase [Proteobacteria bacterium]</a>	<a href="#">Proteobacteria bacterium</a>	304	304	96%	1e-98	45.02%	328	<a href="#">NBT38276.1</a>
<a href="#">malate dehydrogenase [Oceanibaculum indicum]</a>	<a href="#">Oceanibaculum indicum</a>	303	303	94%	1e-98	45.54%	320	<a href="#">WP_008943063.1</a>
<a href="#">malate dehydrogenase [Rhizobiales bacterium]</a>	<a href="#">Rhizobiales bacterium</a>	303	303	93%	1e-98	48.50%	320	<a href="#">RYE11063.1</a>
<a href="#">malate dehydrogenase [Brevundimonas sp.]</a>	<a href="#">Brevundimonas sp.</a>	303	303	96%	1e-98	45.83%	320	<a href="#">MAL87662.1</a>
<a href="#">malate dehydrogenase [Rhodobacteraceae bacterium]</a>	<a href="#">Rhodobacteraceae bacterium</a>	303	303	94%	1e-98	47.19%	322	<a href="#">MAP00672.1</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium MarineAlpha9_Bin5]</a>	<a href="#">Alphaproteobacteria bacterium MarineAlpha9_Bin5</a>	303	303	94%	1e-98	47.04%	323	<a href="#">PPR37875.1</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium MarineAlpha9_Bin6]</a>	<a href="#">Alphaproteobacteria bacterium MarineAlpha9_Bin6</a>	303	303	94%	2e-98	46.71%	323	<a href="#">PPR36537.1</a>
<a href="#">malate dehydrogenase [Devosia sp. Root436]</a>	<a href="#">Devosia sp. Root436</a>	302	302	93%	3e-98	47.02%	320	<a href="#">WP_056254967.1</a>
<a href="#">malate dehydrogenase [Rhodobacterales bacterium TMED271]</a>	<a href="#">Rhodobacterales bacterium TMED271</a>	302	302	94%	4e-98	46.86%	322	<a href="#">OUX44185.1</a>
<a href="#">malate dehydrogenase [Rhodovibrio sodomensis]</a>	<a href="#">Rhodovibrio sodomensis</a>	302	302	93%	5e-98	45.70%	318	<a href="#">WP_200339844.1</a>
<a href="#">uncharacterized protein LOC34621309 [Cyclospora cayetanensis]</a>	<a href="#">Cyclospora cayetanensis</a>	301	301	94%	6e-98	46.20%	317	<a href="#">XP_022589240.1</a>
<a href="#">MULTISPECIES: malate dehydrogenase [unclassified Bradyrhizobium]</a>	<a href="#">unclassified Bradyrhizobium</a>	301	301	93%	7e-98	47.35%	322	<a href="#">WP_166213281.1</a>
<a href="#">Crystal structure of ancestral apicomplexan lactate dehydrogenase in alternate dimer configuration with sulfate [Apicomplexa sp.]</a>	<a href="#">Apicomplexa sp.</a>	302	302	93%	7e-98	48.86%	330	<a href="#">6VDH_A</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium]</a>	<a href="#">Alphaproteobacteria bacterium</a>	301	301	94%	7e-98	46.20%	322	<a href="#">TAH36160.1</a>
<a href="#">malate dehydrogenase [Oceanibaculum pacificum]</a>	<a href="#">Oceanibaculum pacificum</a>	301	301	94%	8e-98	45.21%	320	<a href="#">WP_067555953.1</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium]</a>	<a href="#">Alphaproteobacteria bacterium</a>	301	301	94%	1e-97	47.52%	320	<a href="#">MBA2590478.1</a>
<a href="#">malate dehydrogenase [Kordiimonadaceae bacterium]</a>	<a href="#">Kordiimonadaceae bacterium</a>	301	301	93%	1e-97	46.36%	320	<a href="#">MBO6506542.1</a>
<a href="#">malate dehydrogenase [Kordiimonadales bacterium]</a>	<a href="#">Kordiimonadales bacterium</a>	300	300	94%	2e-97	47.19%	321	<a href="#">PCI63361.1</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium MarineAlpha2_Bin1]</a>	<a href="#">Alphaproteobacteria bacterium MarineAlpha2_Bin1</a>	300	300	93%	2e-97	46.36%	324	<a href="#">PPR79434.1</a>
<a href="#">malate dehydrogenase [Bradyrhizobium sp. 2S1]</a>	<a href="#">Bradyrhizobium sp. 2S1</a>	300	300	93%	2e-97	47.02%	322	<a href="#">WP_166300597.1</a>
<a href="#">malate dehydrogenase [Proteobacteria bacterium]</a>	<a href="#">Proteobacteria bacterium</a>	300	300	94%	2e-97	47.52%	320	<a href="#">MBI3675661.1</a>
<a href="#">malate dehydrogenase [Rhodospirillaceae bacterium]</a>	<a href="#">Rhodospirillaceae bacterium</a>	300	300	93%	2e-97	45.70%	324	<a href="#">MBT05681.1</a>
<a href="#">malate dehydrogenase [Rhodospirillales bacterium]</a>	<a href="#">Rhodospirillales bacterium</a>	300	300	96%	2e-97	45.19%	316	<a href="#">MBK8174980.1</a>
<a href="#">MULTISPECIES: malate dehydrogenase [unclassified Bradyrhizobium]</a>	<a href="#">unclassified Bradyrhizobium</a>	300	300	93%	3e-97	47.02%	322	<a href="#">WP_029081325.1</a>
<a href="#">malate dehydrogenase [Rhodovibrio salinarum]</a>	<a href="#">Rhodovibrio salinarum</a>	300	300	93%	3e-97	45.70%	318	<a href="#">WP_027287413.1</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium]</a>	<a href="#">Alphaproteobacteria bacterium</a>	300	300	94%	3e-97	47.52%	320	<a href="#">MBN9587800.1</a>

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<a href="#">malate dehydrogenase [Oceanibaculum nanhaiense]</a>	<a href="#">Oceanibaculum nanhaiense</a>	300	300	94%	3e-97	45.21%	320	<a href="#">MBC7134210.1</a>
<a href="#">malate dehydrogenase [Oceanibaculum nanhaiense]</a>	<a href="#">Oceanibaculum nanhaiense</a>	300	300	94%	4e-97	45.21%	320	<a href="#">WP_086463724.1</a>

**Graphic Summary**



**Distribution of the top 100 Blast Hits on 100 subject sequences**



**Alignments**

Alignment view   CDS feature

Crystal structure of malate dehydrogenase from Plasmodium falciparum (PfMDH) [Plasmodium falciparum 3D7]  
 Sequence ID: **5NFR\_A** Length: 320 Number of Matches: 1  
 Range 1: 1 to 320

Score	Expect	Method	Identities	Positives	Gaps	Frame
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655 bits(1690) 0.0() Compositional matrix adjust. 320/320(100%) 320/320(100%) 0/320(0%)

Query	1	MTKIALIGSGQIGAIVGELCLLENLGDILYDVVPGIPQGGKALDLKHFSTILGVRNRLG	60
Sbjct	1	MTKIALIGSGQIGAIVGELCLLENLGDILYDVVPGIPQGGKALDLKHFSTILGVRNRLG	60
Query	61	TNQIEDIKDADIIVITAGVQRKEGMDRELDIGVNGKIMKSVAESVKLHCSKAFVICVSNP	120
Sbjct	61	TNQIEDIKDADIIVITAGVQRKEGMDRELDIGVNGKIMKSVAESVKLHCSKAFVICVSNP	120
Query	121	LDIMVNVFHKFNSLPHEKICGMAGILDTSRYCSLIADKLKVAEDVNAVILGGHGLMVP	180
Sbjct	121	LDIMVNVFHKFNSLPHEKICGMAGILDTSRYCSLIADKLKVAEDVNAVILGGHGLMVP	180
Query	181	LQRYTSVNGVPLSEFVKKNMISQNEIQEIIQKTRNMGAEIIKLAKASAAFAPAAAITKMI	240
Sbjct	181	LQRYTSVNGVPLSEFVKKNMISQNEIQEIIQKTRNMGAEIIKLAKASAAFAPAAAITKMI	240
Query	241	KSYYLNENLFTCAVYLNHYNCNSL FVGSTAKINNKAHPVEFPLTKEEQDLYTESIAS	300
Sbjct	241	KSYYLNENLFTCAVYLNHYNCNSL FVGSTAKINNKAHPVEFPLTKEEQDLYTESIAS	300
Query	301	VQSNTQKAFDLIKGHHHHHH 320	
Sbjct	301	VQSNTQKAFDLIKGHHHHHH 320	

Crystal structure of malate dehydrogenase from Plasmodium Falciparum in complex with 4-(3,4-difluorophenyl)thiazol-2-amine [Plasmodium falciparum]

Sequence ID: **6R8G\_A** Length: 324 Number of Matches: 1  
Range 1: 1 to 324

Score	Expect	Method	Identities	Positives	Gaps	Frame
648 bits(1672) 0.0() Compositional matrix adjust. 319/324(98%) 319/324(98%) 4/324(1%)						
Query	1	MTKIALIGSGQIGAIVGELCLLENLGDILYDVVPGIPQGGKALDLKHFSTILGVRNRLG	60			
Sbjct	1	MTKIALIGSGQIGAIVGELCLLENLGDILYDVVPGIPQGGKALDLKHFSTILGVRNRLG	60			
Query	61	TNQIEDIKDADIIVITAGVQRKEGMDRELDIGVNGKIMKSVAESVKLHCSKAFVICVSNP	120			
Sbjct	61	TNQIEDIKDADIIVITAGVQRKEGMDRELDIGVNGKIMKSVAESVKLHCSKAFVICVSNP	120			
Query	121	LDIMVNVFHKFNSLPHEKICGMAGILDTSRYCSLIADKLKVAEDVNAVILGGHGLMVP	180			
Sbjct	121	LDIMVNVFHKFNSLPHEKICGMAGILDTSRYCSLIADKLKVAEDVNAVILGGHGLMVP	180			
Query	181	LQRYTSVNGVPLSEFVKKNMISQNEIQEIIQKTRNMGAEIIKLAKASAAFAPAAAITKMI	240			
Sbjct	181	LQRYTSVNGVPLSEFVKKNMISQNEIQEIIQKTRNMGAEIIKLAKASAAFAPAAAITKMI	240			
Query	241	KSYYLNENLFTCAVYLNHYNCNSL FVGSTAKINNKAHPVEFPLTKEEQDLYTESIAS	300			
Sbjct	241	KSYYLNENLFTCAVYLNHYNCNSL FVGSTAKINNKAHPVEFPLTKEEQDLYTESIAS	300			
Query	301	VQSNTQKAFDLIKG---HHHHHH 320				
Sbjct	301	VQSNTQKAFDLIKAAAALEHHHHHH 324				

malate dehydrogenase [Plasmodium falciparum 3D7]

Sequence ID: **XP\_966170.1** Length: 313 Number of Matches: 1  
Range 1: 1 to 313

Score	Expect	Method	Identities	Positives	Gaps	Frame
638 bits(1646) 0.0() Compositional matrix adjust. 313/313(100%) 313/313(100%) 0/313(0%)						
Query	1	MTKIALIGSGQIGAIVGELCLLENLGDILYDVVPGIPQGGKALDLKHFSTILGVRNRLG	60			
Sbjct	1	MTKIALIGSGQIGAIVGELCLLENLGDILYDVVPGIPQGGKALDLKHFSTILGVRNRLG	60			
Query	61	TNQIEDIKDADIIVITAGVQRKEGMDRELDIGVNGKIMKSVAESVKLHCSKAFVICVSNP	120			
Sbjct	61	TNQIEDIKDADIIVITAGVQRKEGMDRELDIGVNGKIMKSVAESVKLHCSKAFVICVSNP	120			
Query	121	LDIMVNVFHKFNSLPHEKICGMAGILDTSRYCSLIADKLKVAEDVNAVILGGHGLMVP	180			
Sbjct	121	LDIMVNVFHKFNSLPHEKICGMAGILDTSRYCSLIADKLKVAEDVNAVILGGHGLMVP	180			
Query	181	LQRYTSVNGVPLSEFVKKNMISQNEIQEIIQKTRNMGAEIIKLAKASAAFAPAAAITKMI	240			
Sbjct	181	LQRYTSVNGVPLSEFVKKNMISQNEIQEIIQKTRNMGAEIIKLAKASAAFAPAAAITKMI	240			
Query	241	KSYYLNENLFTCAVYLNHYNCNSL FVGSTAKINNKAHPVEFPLTKEEQDLYTESIAS	300			
Sbjct	241	KSYYLNENLFTCAVYLNHYNCNSL FVGSTAKINNKAHPVEFPLTKEEQDLYTESIAS	300			
Query	301	VQSNTQKAFDLIK 313				
Sbjct	301	VQSNTQKAFDLIK 313				

malate dehydrogenase [Plasmodium reichenowi]

Sequence ID: **XP\_012761998.1** Length: 313 Number of Matches: 1  
Range 1: 1 to 313

Score	Expect	Method	Identities	Positives	Gaps	Frame
630 bits(1625) 0.0() Compositional matrix adjust. 307/313(98%) 312/313(99%) 0/313(0%)						
Query	1	MTKIALIGSGQIGAIVGELCLLENLGDILYDVVPGIPQGGKALDLKHFSTILGVRNRLG	60			
Sbjct	1	MTKIALIGSGQIGAIVGELCL+ENLGDILYDVVPGIPQGGKALDLKHFSTILGVRNRI+G	60			
Query	61	TNQIEDIKDADIIVITAGVQRKEGMDRELDIGVNGKIMKSVAESVKLHCSKAFVICVSNP	120			
Sbjct	61	TNQIEDIKDADIIVITAGVQRKEGMDRELDIGVNGKIMKSVAESVKLHCSKAFVICVSNP	120			

Sbjct 61 TNQIEDIKDADIIVITAGVQRKEGMDRETLIGVNGKIMKVAESVKLHCSKAFVICVSNP 120  
 Query 121 LDIMVNVFHKFNSLPHEKICGMAGILDTSRYCSLIADKLVSAEDVNAVILGGHGLMVP 180  
 LDIMVNVFHKFNSLPHEKICGMAGILDTSRYCSLIADKLVSAEDVNAVILGGHGLMVP  
 Sbjct 121 LDIMVNVFHKFNSLPHEKICGMAGILDTSRYCSLIADKLVSAEDVNAVILGGHGLMVP 180  
 Query 181 LQRYTSVNGVPLSEFVKKNMISQNEIQEIIQKTRNMGAEIILAKASAAFAPAAAITKMI 240  
 LQRYTSVNGVPLSEFVKKNMISQNEIQEIIQKTRNMGAEIILAKASAAFAPAAAITKMI  
 Sbjct 181 LQRYTSVNGVPLSEFVKKNMISQNEIQEIIQKTRNMGAEIILAKASAAFAPAAAITKMI 240  
 Query 241 KSYLYNENLFTCAVYLNHYNCNSLFGVSTAKINNKGAHPVEFPLTKEEQDLYTESIAS 300  
 KSYLYNENLFTCAVYLNHYNCNSLFGVSTAKINNKGA+PVEFPLTKEEQDLY ESIA+  
 Sbjct 241 KSYLYNENLFTCAVYLNHYNCNSLFGVSTAKINNKGAHPVEFPLTKEEQDLYMESIAN 300  
 Query 301 VQSNTQKAFDLIK 313  
 VQSNTQKAFDLIK  
 Sbjct 301 VQSNTQKAFDLIK 313

malate dehydrogenase [Plasmodium sp. DRC-Itaito]

Sequence ID: **CAC9696262.1** Length: 313 Number of Matches: 1  
 Range 1: 1 to 313

Score	Expect	Method	Identities	Positives	Gaps	Frame
623 bits(1607) 0.0() Compositional matrix adjust. 303/313(97%) 311/313(99%) 0/313(0%)						
Query 1	MTKIALIGSGQIGAI	VGELCLLENLGD	LILYDVVPGIPQ	GKALDLKHFST	ILGVNRN	ILG 60
Sbjct 1	MTKIALIGSGQIGAI	VGELCLLENLGD	LILYDVVPGIPQ	GKALDLKHFST	ILGVNRN	ILG 60
Query 61	TNQIEDIKDADIIV	ITAGVQRKEGMD	RETLIGVNGKIM	KVAESVKLHCS	KAFVICVSNP	120
Sbjct 61	TNQIEDIKDADIIV	ITAGVQRKEGMD	RETLIGVNGKIM	KVAESVKLHCS	KAFVICVSNP	120
Query 121	LDIMVNVFHKFNS	LPHEKICGMAGI	LDSRYCSLIAD	KLKVAEDVNA	VILGGHGLMVP	180
Sbjct 121	LDIMVNVFHKFNS	LPHEKICGMAGI	LDSRYCSLIAD	KLKVAEDVNA	VILGGHGLMVP	180
Query 181	LQRYTSVNGVPLS	EFVKKNMISQNE	IQEIIQKTRNMG	AEIILAKASAA	FAPAAAITKMI	240
Sbjct 181	LQRYTSVNGVPLS	EFVKKNMISQNE	IQEIIQKTRNMG	AEIILAKASAA	FAPAAAITKMI	240
Query 241	KSYLYNENLFTCA	VYLNHYNCNSL	FGVSTAKINNK	GAHPVEFPLT	KEEQDLYTESIAS	300
Sbjct 241	KSYLYNENLFTCA	VYLNHYNCNSL	FGVSTAKINNK	GAHPVEFPLT	KEEQDLYTESIAS	300
Query 301	VQSNTQKAFDLIK					313
Sbjct 301	VQSNTQKAFDLIK					313

hypothetical protein PFMALIP\_01469 [Plasmodium falciparum MaliPS096\_E11]

Sequence ID: **ETW50453.1** Length: 309 Number of Matches: 1  
 Range 1: 3 to 309

Score	Expect	Method	Identities	Positives	Gaps	Frame
622 bits(1605) 0.0() Compositional matrix adjust. 306/307(99%) 306/307(99%) 0/307(0%)						
Query 7	IGSGQIGAI	VGELCLLENLGD	LILYDVVPGIPQ	GKALDLKHFST	ILGVNRN	ILG 66
Sbjct 3	IGSGQIGAI	VGELCLLENLGD	LILYDVVPGIPQ	GKALDLKHFST	ILGVNRN	ILG 62
Query 67	IKDADIIVITAGV	QRKEGMDRETL	IGVNGKIMKVA	ESVKLHCSKAF	VICVSNPLDIMN	126
Sbjct 63	IKDADIIVITAGV	QRKEGMDRETL	IGVNGKIMKVA	ESVKLHCSKAF	VICVSNPLDIMN	122
Query 127	VFHKFNSLPHEK	ICGMAGILDTS	RYCSLIADKLV	SAEDVNAVIL	GGHGLMVP	186
Sbjct 123	VFHKFNSLPHEK	ICGMAGILDTS	RYCSLIADKLV	SAEDVNAVIL	GGHGLMVP	182
Query 187	VNGVPLSEFVKK	NMISQNEIQEII	QKTRNMGAEI	ILAKASAAF	FAPAAAITKMI	246
Sbjct 183	VNGVPLSEFVKK	NMISQNEIQEII	QKTRNMGAEI	ILAKASAAF	FAPAAAITKMI	242
Query 247	ENLFTCAVYLN	HYNCNSLFGV	STAKINNKGA	HPVEFPLTKEE	QDLYTESIASV	306
Sbjct 243	ENLFTCAVYLN	HYNCNSLFGV	STAKINNKGA	HPVEFPLTKEE	QDLYTESIASV	302
Query 307	KAFDLIK					313
Sbjct 303	KAFDLIK					309

malate dehydrogenase [Plasmodium sp. gorilla clade G3]

Sequence ID: **SOV74725.1** Length: 313 Number of Matches: 1  
 Range 1: 1 to 313

Score	Expect	Method	Identities	Positives	Gaps	Frame
615 bits(1587) 0.0() Compositional matrix adjust. 301/313(96%) 309/313(98%) 0/313(0%)						
Query 1	MTKIALIGSGQIGAI	VGELCLLENLGD	LILYDVVPGIPQ	GKALDLKHFST	ILGVNRN	ILG 60
Sbjct 1	MTKIALIGSGQIGAI	VGELCLLENLGD	LILYDVVPGIPQ	GKALDLKHFST	ILGVNRN	ILG 60
Query 61	TNQIEDIKDADIIV	ITAGVQRKEGMD	RETLIGVNGKIM	KVAESVKLHCS	KAFVICVSNP	120
Sbjct 61	TNQIEDIKDADIIV	ITAGVQRKEGMD	RETLIGVNGKIM	KVAESVKLHCS	KAFVICVSNP	120
Query 121	LDIMVNVFHKFNS	LPHEKICGMAGI	LDSRYCSLIAD	KLKVAEDVNA	VILGGHGLMVP	180
Sbjct 121	LDIMVNVFHKFNS	LPHEKICGMAGI	LDSRYCSLIAD	KLKVAEDVNA	VILGGHGLMVP	180
Query 181	LQRYTSVNGVPLS	EFVKKNMISQNE	IQEIIQKTRNMG	AEIILAKASAA	FAPAAAITKMI	240
Sbjct 181	LQRYTSVNGVPLS	EFVKKNMISQNE	IQEIIQKTRNMG	AEIILAKASAA	FAPAAAITKMI	240

Query 241 KSYLYNENNLFTCAVYLNHYNCSNLFVVGSTAKINNKGAVHVEFPLTKEEQDLYTESIAS 300  
 KSYLYN+NLFTCAVYLNHYNCSNLFVVGSTAKI+KNGAVHVEFPLTKEEQDLYTESIAS  
 Sbjct 241 KSYLYNQNNLFTCAVYLNHYNCSNLFVVGSTAKIDNKGAVHVEFPLTKEEQDLYTESIAS 300

Query 301 VQSNTQKAFDLIK 313  
 V+SNTQKAF+LIK  
 Sbjct 301 VKSNTQKAFNLIK 313

malate dehydrogenase [Plasmodium sp. DRC-Itaito]

Sequence ID: **SOV21691.1** Length: 313 Number of Matches: 1  
 Range 1: 1 to 312

Score	Expect	Method	Identities	Positives	Gaps	Frame
580 bits(1494) 0.0() Compositional matrix adjust. 294/312(94%) 306/312(98%) 0/312(0%)						
Query 1		MTKIALIGSGQIGAI	VGELCLLENLGD	LILYDVVPGIPQ	GKALDLKHFSTI	LGVNRNII
Sbjct 1		MTKIALIGSGQIG	VGELCL+EN	GDL+LYDVV	GIPOGKALDLK	HVFSTILGVRNI+G
Query 61		TNQIEDIKDADI	IIVITAGVQRKE	GMTREDLIGVNG	KIMKVAESVKL	HCSKAFVICSNP
Sbjct 61		TNQIEDIKD+DII	IIVITAGVQRKE	GMTREDLIGVNG	KIMKVAESVKL	HCSKAFVICSNP
Query 121		LDIMVNVFHKF	SNLPHEKICMAG	ILDTSRYCSLI	ADKLVSAEDVNA	ILGGHGLMVP
Sbjct 121		LDIMVNVFHKF	SNLPHEKICMAG	ILDTSRY +LIA	+KLVSAEDVNA	ILGGHGLMVP
Query 181		LQRYTSVNGVPL	SEFVKKNMISQ	NEIQEIIQKTR	NMGAEIILKAKA	SAFAPAAAITKMI
Sbjct 181		LQRYTSVNGVPL	SEFVKKNMISQ	NEIQEIIQKTR	NMGAEIILKAKA	SAFAPAAAITKMI
Query 241		KSYLYNENNLFT	CAVYLNHYNCS	NLFVVGSTAKI	NNKGAVHVEFPL	TKEEQDLYTESIAS
Sbjct 241		KSYLYNQSNLFT	CAVYLNHYNCS	NLFVVGSTAKI	DNKGVHVEFPL	TKEEQDLYTESIAS
Query 301		VQSNTQKAFDLI				312
Sbjct 301		V+SNTQKAFDLI				312

malate dehydrogenase [Plasmodium gaboni]

Sequence ID: **XP\_018642816.1** Length: 313 Number of Matches: 1  
 Range 1: 1 to 312

Score	Expect	Method	Identities	Positives	Gaps	Frame
580 bits(1494) 0.0() Compositional matrix adjust. 294/312(94%) 306/312(98%) 0/312(0%)						
Query 1		MTKIALIGSGQIGAI	VGELCLLENLGD	LILYDVVPGIPQ	GKALDLKHFSTI	LGVNRNII
Sbjct 1		MTKIALIGSGQIG	VGELCL+EN	GDL+LYDVV	GIPOGKALDLK	HVFSTILGVRNI+G
Query 61		TNQIEDIKDADI	IIVITAGVQRKE	GMTREDLIGVNG	KIMKVAESVKL	HCSKAFVICSNP
Sbjct 61		TNQIEDIKD+DII	IIVITAGVQRKE	GMTREDLIGVNG	KIMKVAESVKL	HCSKAFVICSNP
Query 121		LDIMVNVFHKF	SNLPHEKICMAG	ILDTSRYCSLI	ADKLVSAEDVNA	ILGGHGLMVP
Sbjct 121		LDIMVNVFHKF	SNLPHEKICMAG	ILDTSRY +LIA	+KLVSAEDVNA	ILGGHGLMVP
Query 181		LQRYTSVNGVPL	SEFVKKNMISQ	NEIQEIIQKTR	NMGAEIILKAKA	SAFAPAAAITKMI
Sbjct 181		LQRYTSVNGVPL	SEFVKKNMISQ	NEIQEIIQKTR	NMGAEIILKAKA	SAFAPAAAITKMI
Query 241		KSYLYNENNLFT	CAVYLNHYNCS	NLFVVGSTAKI	NNKGAVHVEFPL	TKEEQDLYTESIAS
Sbjct 241		KSYLYNQSNLFT	CAVYLNHYNCS	NLFVVGSTAKI	DNKGVHVEFPL	TKEEQDLYTESIAS
Query 301		VQSNTQKAFDLI				312
Sbjct 301		V+SNTQKAFDLI				312

malate dehydrogenase [Plasmodium sp. gorilla clade G2]

Sequence ID: **XP\_028537330.1** Length: 313 Number of Matches: 1  
 Range 1: 1 to 313

Score	Expect	Method	Identities	Positives	Gaps	Frame
579 bits(1493) 0.0() Compositional matrix adjust. 292/313(93%) 307/313(98%) 0/313(0%)						
Query 1		MTKIALIGSGQIGAI	VGELCLLENLGD	LILYDVVPGIPQ	GKALDLKHFSTI	LGVNRNII
Sbjct 1		MTKIALIGSGQIG	VGELCL+EN	GDL+LYDVV	GIPOGKALDLK	HVFSTILGVRNI+G
Query 61		TNQIEDIKDADI	IIVITAGVQRKE	GMTREDLIGVNG	KIMKVAESVKL	HCSKAFVICSNP
Sbjct 61		TNQIEDIKD+DII	IIVITAGVQRKE	GMTREDLIGVNG	KIMKVAESVKL	HCSKAFVICSNP
Query 121		LDIMVNVFHKF	SNLPHEKICMAG	ILDTSRYCSLI	ADKLVSAEDVNA	ILGGHGLMVP
Sbjct 121		LDIMVNVFHKF	SNLPHEKICMAG	ILDTSRY +LIA	+KLVSAEDVNA	ILGGHGLMVP
Query 181		LQRYTSVNGVPL	SEFVKKNMISQ	NEIQEIIQKTR	NMGAEIILKAKA	SAFAPAAAITKMI
Sbjct 181		LQRYTSVNGVPL	SEFVKKNMISQ	NEIQEIIQKTR	NMGAEIILKAKA	SAFAPAAAITKMI
Query 241		KSYLYNENNLFT	CAVYLNHYNCS	NLFVVGSTAKI	NNKGAVHVEFPL	TKEEQDLYTESIAS
Sbjct 241		KSYLYNQSNLFT	CAVYLNHYNCS	NLFVVGSTAKI	DNKGVHVEFPL	TKEEQDLYTESIAS
Query 301		VQSNTQKAFDLIK				313
Sbjct 301		V+SNT+KAFDLIK				313



malate dehydrogenase, putative [Plasmodium relictum]

Sequence ID: **XP\_028533952.1** Length: 313 Number of Matches: 1  
 Range 1: 1 to 313

Score	Expect	Method	Identities	Positives	Gaps	Frame
503 bits(1296) 1e-177() Compositional matrix adjust. 249/313(80%) 290/313(92%) 0/313(0%)						
Query 1		MTKIALIGSGQIGAI	VGELCCLLENLGD	LILYDVVPGIPQ	GKALDLKHFSTIL	GVNRNILG 60
Sbjct 1		MTKISLIGSGQIGAI	VGELCCLLENLGD	IVLYDVVQGIPO	GKCLDLKHFSTIL	GVNRNILG 60
Query 61		TNQIEDIKDADI	IIVITAGVQRKE	GMTREDLIGVNG	KIMKSVAESV	LHCSKAFVICVSNP 120
Sbjct 61		+N IEDIKD+D+I	VITAG+QRKEGM	TREDLIG+NGK	IMK+VAESV	KL+ AFVICVSNP 120
Query 121		LDIMVNVFHK	FNSLPHEKICM	GAGILDTSRYC	SLIADKLK	VSAEDVNAVILGGHGLMVP 180
Sbjct 121		LDIMVNVF K+S	N+PHEK+CGM	AGILDTSR+ +L	+A+KL VS E	+VNAVILGGHGLMVP 180
Query 181		LQRYTSVNGV	PLSEFVKNMIS	QNEIQEIIQK	TRNMGAEI	IKLAKASAAFAPAAAITKMI 240
Sbjct 181		++RY SV+G+P	L+SV+FNKN	IISQKEINE	IVEKTRDGG	AEIIKLAKASACFAPAAAITKMI 240
Query 241		KSYYLNENL	LFTCAVYLN	GHYNCNLFV	GVSTAKINN	KAHPVEFPLTKKEEQDLYTESIAS 300
Sbjct 241		KSFLFNQQL	LFTCAVYLN	GIYNCNDL	YVGVSTAT	INSKGAFPVEFPLTKQEQELYDKSIAH 300
Query 301		VQSNTQKAF	DLIK 313			
Sbjct 301		V+ NTQKAF	+IK 313			

Malate dehydrogenase [Plasmodium coatneyi]

Sequence ID: **XP\_019915696.1** Length: 313 Number of Matches: 1  
 Range 1: 1 to 312

Score	Expect	Method	Identities	Positives	Gaps	Frame
503 bits(1295) 2e-177() Compositional matrix adjust. 240/312(77%) 281/312(90%) 0/312(0%)						
Query 1		MTKIALIGSGQIGAI	VGELCCLLENLGD	LILYDVVPGIPQ	GKALDLKHFSTIL	GVNRNILG 60
Sbjct 1		M KI++IGSGQIGAI	VGELCCLLENLGD	++LYDVV G+PQ	GK+LDLKHFS	TIVGNK+ I+G 60
Query 61		TNQIEDIKDADI	IIVITAGVQRKE	GMTREDLIGVNG	KIMKSVAESV	LHCSKAFVICVSNP 120
Sbjct 61		TN +EDIK +D+I	VITAGVQRKE	GMTREDLIG+NG	KIMKSVAESV	KL+C AFVICVSNP 120
Query 121		LDIMVNVFHK	FNSLPHEKICM	GAGILDTSRYC	SLIADKLK	VSAEDVNAVILGGHGLMVP 180
Sbjct 121		LDIMVNVFHK+S	LPHEKICM	AGILDTSR+ SL	+DKL V+ E+V	N+V+LGGHGLMVP 180
Query 181		LQRYTSVNGV	PLSEFVKNMIS	QNEIQEIIQK	TRNMGAEI	IKLAKASAAFAPAAAITKMI 240
Sbjct 181		L+RYTSVNGV	PLSEFVKN	+IS EI II++	TR+MGAEI	IKLAKASAAFAPAAAITKMI 240
Query 241		KSYYLNENL	LFTCAVYLN	GHYNCNLFV	GVSTAKINN	KAHPVEFPLTKKEEQDLYTESIAS 300
Sbjct 241		KSYYLNE+S	L+TCVYLN	GHYNCN	+VGSTA IN+ GA	PVEF LTKKEEQ+LY +SIA 300
Query 301		VQSNTQKAF	DLI 312			
Sbjct 301		VQ +TQKAF	LI 312			

malate dehydrogenase, putative (MDH) [Plasmodium ovale wallikeri]

Sequence ID: **SBT38197.1** Length: 313 Number of Matches: 1  
 Range 1: 1 to 312

Score	Expect	Method	Identities	Positives	Gaps	Frame
501 bits(1289) 1e-176() Compositional matrix adjust. 249/312(80%) 290/312(92%) 0/312(0%)						
Query 1		MTKIALIGSGQIGAI	VGELCCLLENLGD	LILYDVVPGIPQ	GKALDLKHFSTIL	GVNRNILG 60
Sbjct 1		MTKI+LIGSGQIGAI	VGELCCLLENLGD	IVLYDVVQGIPO	GKSLDLKHFSA	ILGNR I+G 60
Query 61		TNQIEDIKDADI	IIVITAGVQRKE	GMTREDLIGVNG	KIMKSVAESV	LHCSKAFVICVSNP 120
Sbjct 61		TN +EDIK +D+I	VITAGVQRKE	GMTREDLIG+NG	KIMKSVAESV	KL+ AFVICVSNP 120
Query 121		LDIMVNVFHK	FNSLPHEKICM	GAGILDTSRYC	SLIADKLK	VSAEDVNAVILGGHGLMVP 180
Sbjct 121		LDIMVNVFHK+S	NLP+EKICM	AG+LDT+R+ +L	+A+KL VS E+V	N+V+LGGHGLMVP 180
Query 181		LQRYTSVNGV	PLSEFVKNMIS	QNEIQEIIQK	TRNMGAEI	IKLAKASAAFAPAAAITKMI 240
Sbjct 181		L+RYTSVNGV	PLSEFVKN	+I++ EI EI++	KTR+MGAEI	IKLAKASAAFAPAAAITKMI 240
Query 241		KSYYLNENL	LFTCAVYLN	GHYNCNLFV	GVSTAKINN	KAHPVEFPLTKKEEQDLYTESIAS 300
Sbjct 241		KSYYLNE+S	L+TCVYLN	GHYNCN	+VGSTA IN+KG	HPVEFPLTKKEEQDLY +SIA 300
Query 301		VQSNTQKAF	DLI 312			
Sbjct 301		V+ NTQKAF	+I 312			

malate dehydrogenase, putative (MDH) [Plasmodium ovale curtisi]

Sequence ID: **SBS85361.1** Length: 313 Number of Matches: 1  
 Range 1: 1 to 312

Score	Expect	Method	Identities	Positives	Gaps	Frame
499 bits(1284) 8e-176() Compositional matrix adjust. 249/312(80%) 288/312(92%) 0/312(0%)						

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Query 1  MTKIALIGSGQIGAI VGE LCLLENLGD LILYDVVPGIPQ GKALDLKHFSTILGVNRN ILG 60
Sbjct 1  MTKI+LIGSGQIGAI VGE LCL+ENLGD++LYDVV G+PQ GK+LDLKHFS ILGVNR I+G 60
MTKISLIGSGQIGAI VGE LCLVENLGDIVLYDVVQGVPGKSLDLKHFSAITLGVNRKIITG

Query 61  TNQIEDIKDADIIVITAGVQRKEG MTR EDLIGVNGKIMKSVAESV KLHCSKAFVICSNP 120
Sbjct 61  TN+EDIKD+DIIVITAG+QRKEG MTR EDLIG+NGKIMKSVAESV KL+ AFVICSNP 120
TNNVEDIKDSDIIVITAGIQRKEG MTR EDLIGINGKIMKSVAESV KLYSPNAFVICSNP

Query 121  LDIMVNVFHKFSNLPHEKICGMAGIL DTSRYCSLIADKLKVS AEDVNAVILGGHGLMVP 180
Sbjct 121  LDIMVNVFHK+SNLP+EKICGMAG+LDT+R+ +L+A KL VS E+VNA+ILGGHGLMVP 180
LDIMVNVFHKYSNLPYEKICGMAGVLDTARFRTLAVLKNVSPENVNAIILGGHGLMVP

Query 181  LQRYTSVNGVPLSEFVKKNMISQNEIQEIIQKTRNMGAEI IKLAKASAAFAPAAAITKMI 240
Sbjct 181  L+RYTS++G+PLSEFVKKN+I++ EI EI++KTR+MGAEI IKLAKASAAFAPAAAI KM+ 240
LERYTSVSGIPLSEFVKKNVINKTEINEILEKTRDMGAEI IKLAKASAAFAPAAAIKMM

Query 241  KSYLYNENNLFTCAVYLN GHYNCNL FVGSTAKINNKGAHPVEFPLTKEEQDLYTESIAS 300
Sbjct 241  KSYLHNQNLFTCAVY LKGEYNCKDLYVGSTAVINAKGAHPVEFPLTKEEQDLYDKSIAH 300

Query 301  VQSNTQKAFDLI 312
Sbjct 301  V+ NTQKAF+ I 312
VKENTQKAFNQI 312
    
```

malate dehydrogenase, NAD-dependent [Plasmodium fragile]

Sequence ID: **XP\_012335265.1** Length: 313 Number of Matches: 1  
 Range 1: 1 to 312

Score	Expect	Method	Identities	Positives	Gaps	Frame
497 bits(1279) 5e-175() Compositional matrix adjust. 235/312(75%) 280/312(89%) 0/312(0%)						
Query 1		MTKIALIGSGQIGAI VGE LCLLENLGD LILYDVVPGIPQ GKALDLKHFSTILGVNRN ILG	60			
Sbjct 1		M KI+++GSGQIGAI VGL L L+EN+GD++LYDV+ G+PQ GK+LDLKHFS TI+GVN+ ILG	60			
Query 61		TNQIEDIKDADIIVITAGVQRKEG MTR EDLIGVNGKIMKSVAESV KLHCSKAFVICSNP	120			
Sbjct 61		TN+EDIKD+DIIVITAG+QRKEG MTR EDLIG+NGKIMKSVAESV KL+ AFVICSNP	120			
Query 121		LDIMVNVFHKFSNLPHEKICGMAGIL DTSRYCSLIADKLKVS AEDVNAVILGGHGLMVP	180			
Sbjct 121		LDIMVNVFHK+S LPHEKICGMAGIL DTSR+ SL+ +KL V+ E+VN V+LGGHGLMVP	180			
Query 181		LQRYTSVNGVPLSEFVKKNMISQNEIQEIIQKTRNMGAEI IKLAKASAAFAPAAAITKMI	240			
Sbjct 181		L+RY SV+G+PLSEFVKK +IS +I +II++TR+MGA+I IKL+K+SA F+PAAAI KMI	240			
Query 241		KSYLYNENNLFTCAVYLN GHYNCNL FVGSTAKINNKGAHPVEFPLTKEEQDLYTESIAS	300			
Sbjct 241		KSYLYNE+ L+TCAVYLN GHYNCNL+VGSTA IN+ GA PVEF LTKEEQ+LY +SIA	300			
Query 301		VQSNTQKAFDLI 312				
Sbjct 301		V +TQKAF LI 312				
Query 301		VHEHTQKAFALI 312				

## Taxonomy

### Reports

- Lineage

Organism	Blast Name	Score	Number of Hits	Description
<a href="#">cellular organisms</a>			<u>254</u>	
<a href="#">.Alveolata</a>	<a href="#">eukaryotes</a>		<u>162</u>	
<a href="#">..Apicomplexa</a>	<a href="#">apicomplexans</a>		<u>32</u>	
<a href="#">...Plasmodiidae</a>	<a href="#">apicomplexans</a>		<u>118</u>	
<a href="#">....Plasmodium</a>	<a href="#">apicomplexans</a>		<u>117</u>	
<a href="#">.....Plasmodium (Laverania)</a>	<a href="#">apicomplexans</a>		<u>52</u>	
<a href="#">.....Plasmodium falciparum</a>	<a href="#">apicomplexans</a>		<u>9</u>	
<a href="#">.....Plasmodium falciparum 3D7</a>	<a href="#">apicomplexans</a>	655	<u>17</u>	<a href="#">Plasmodium falciparum 3D7 hits</a>
<a href="#">.....Plasmodium falciparum Vietnam Oak-Knoll (FVO)</a>	<a href="#">apicomplexans</a>	638	<u>1</u>	<a href="#">Plasmodium falciparum Vietnam Oak-Knoll (FVO) hits</a>
<a href="#">.....Plasmodium falciparum FCH/4</a>	<a href="#">apicomplexans</a>	638	<u>1</u>	<a href="#">Plasmodium falciparum FCH/4 hits</a>
<a href="#">.....Plasmodium falciparum Tanzania (2000708)</a>	<a href="#">apicomplexans</a>	638	<u>1</u>	<a href="#">Plasmodium falciparum Tanzania (2000708) hits</a>
<a href="#">.....Plasmodium falciparum NF135/5.C10</a>	<a href="#">apicomplexans</a>	638	<u>1</u>	<a href="#">Plasmodium falciparum NF135/5.C10 hits</a>
<a href="#">.....Plasmodium falciparum Palo Alto/Uganda</a>	<a href="#">apicomplexans</a>	638	<u>1</u>	<a href="#">Plasmodium falciparum Palo Alto/Uganda hits</a>
<a href="#">.....Plasmodium falciparum CAMP/Malaysia</a>	<a href="#">apicomplexans</a>	638	<u>1</u>	<a href="#">Plasmodium falciparum CAMP/Malaysia hits</a>
<a href="#">.....Plasmodium falciparum 7G8</a>	<a href="#">apicomplexans</a>	638	<u>1</u>	<a href="#">Plasmodium falciparum 7G8 hits</a>
<a href="#">.....Plasmodium falciparum Santa Lucia</a>	<a href="#">apicomplexans</a>	638	<u>1</u>	<a href="#">Plasmodium falciparum Santa Lucia hits</a>
<a href="#">.....Plasmodium falciparum UGT5.1</a>	<a href="#">apicomplexans</a>	638	<u>1</u>	<a href="#">Plasmodium falciparum UGT5.1 hits</a>
<a href="#">.....Plasmodium falciparum NF54</a>	<a href="#">apicomplexans</a>	638	<u>1</u>	<a href="#">Plasmodium falciparum NF54 hits</a>
<a href="#">.....Plasmodium falciparum HB3</a>	<a href="#">apicomplexans</a>	638	<u>1</u>	<a href="#">Plasmodium falciparum HB3 hits</a>
<a href="#">.....Plasmodium falciparum MaliPS096_E11</a>	<a href="#">apicomplexans</a>	622	<u>1</u>	<a href="#">Plasmodium falciparum MaliPS096_E11 hits</a>
<a href="#">.....Plasmodium falciparum Dd2</a>	<a href="#">apicomplexans</a>	471	<u>1</u>	<a href="#">Plasmodium falciparum Dd2 hits</a>
<a href="#">.....Plasmodium falciparum</a>	<a href="#">apicomplexans</a>	648	<u>9</u>	<a href="#">Plasmodium falciparum hits</a>
<a href="#">.....Plasmodium sp. gorilla clade G1</a>	<a href="#">apicomplexans</a>	638	<u>1</u>	<a href="#">Plasmodium sp. gorilla clade G1 hits</a>

..... <a href="#">Plasmodium reichenowi</a>	<a href="#">apicomplexans</a>	630	4	<a href="#">Plasmodium reichenowi hits</a>
..... <a href="#">Plasmodium sp. DRC-Itaito</a>	<a href="#">apicomplexans</a>	623	2	<a href="#">Plasmodium sp. DRC-Itaito hits</a>
..... <a href="#">Plasmodium sp. gorilla clade G3</a>	<a href="#">apicomplexans</a>	615	1	<a href="#">Plasmodium sp. gorilla clade G3 hits</a>
..... <a href="#">Plasmodium gaboni</a>	<a href="#">apicomplexans</a>	580	3	<a href="#">Plasmodium gaboni hits</a>
..... <a href="#">Plasmodium sp. gorilla clade G2</a>	<a href="#">apicomplexans</a>	579	2	<a href="#">Plasmodium sp. gorilla clade G2 hits</a>
..... <a href="#">Plasmodium relictum</a>	<a href="#">apicomplexans</a>	503	2	<a href="#">Plasmodium relictum hits</a>
..... <a href="#">Plasmodium coatneyi</a>	<a href="#">apicomplexans</a>	503	2	<a href="#">Plasmodium coatneyi hits</a>
..... <a href="#">Plasmodium ovale wallikeri</a>	<a href="#">apicomplexans</a>	501	2	<a href="#">Plasmodium ovale wallikeri hits</a>
..... <a href="#">Plasmodium ovale</a>	<a href="#">apicomplexans</a>	501	2	<a href="#">Plasmodium ovale hits</a>
..... <a href="#">Plasmodium ovale curtisi</a>	<a href="#">apicomplexans</a>	499	2	<a href="#">Plasmodium ovale curtisi hits</a>
..... <a href="#">Plasmodium fragile</a>	<a href="#">apicomplexans</a>	497	2	<a href="#">Plasmodium fragile hits</a>
..... <a href="#">Plasmodium gonderi</a>	<a href="#">apicomplexans</a>	496	2	<a href="#">Plasmodium gonderi hits</a>
..... <a href="#">Plasmodium inui San Antonio 1</a>	<a href="#">apicomplexans</a>	494	2	<a href="#">Plasmodium inui San Antonio 1 hits</a>
..... <a href="#">Plasmodium vivax</a>	<a href="#">apicomplexans</a>	493	5	<a href="#">Plasmodium vivax hits</a>
..... <a href="#">Plasmodium vivax North Korean</a>	<a href="#">apicomplexans</a>	493	1	<a href="#">Plasmodium vivax North Korean hits</a>
..... <a href="#">Plasmodium vivax India VII</a>	<a href="#">apicomplexans</a>	493	1	<a href="#">Plasmodium vivax India VII hits</a>
..... <a href="#">Plasmodium vivax Brazil I</a>	<a href="#">apicomplexans</a>	493	1	<a href="#">Plasmodium vivax Brazil I hits</a>
..... <a href="#">Plasmodium vivax Mauritania I</a>	<a href="#">apicomplexans</a>	493	1	<a href="#">Plasmodium vivax Mauritania I hits</a>
..... <a href="#">Plasmodium gallinaceum</a>	<a href="#">apicomplexans</a>	493	3	<a href="#">Plasmodium gallinaceum hits</a>
..... <a href="#">Plasmodium knowlesi strain H</a>	<a href="#">apicomplexans</a>	489	5	<a href="#">Plasmodium knowlesi strain H hits</a>
..... <a href="#">Plasmodium knowlesi</a>	<a href="#">apicomplexans</a>	489	1	<a href="#">Plasmodium knowlesi hits</a>
..... <a href="#">Plasmodium cynomolgi strain B</a>	<a href="#">apicomplexans</a>	486	2	<a href="#">Plasmodium cynomolgi strain B hits</a>
..... <a href="#">Plasmodium vinckei brucechwatti</a>	<a href="#">apicomplexans</a>	479	1	<a href="#">Plasmodium vinckei brucechwatti hits</a>
..... <a href="#">Plasmodium yoelii 17X</a>	<a href="#">apicomplexans</a>	475	1	<a href="#">Plasmodium yoelii 17X hits</a>
..... <a href="#">Plasmodium malariae</a>	<a href="#">apicomplexans</a>	475	4	<a href="#">Plasmodium malariae hits</a>
..... <a href="#">Plasmodium yoelii</a>	<a href="#">apicomplexans</a>	474	3	<a href="#">Plasmodium yoelii hits</a>
..... <a href="#">Plasmodium chabaudi chabaudi</a>	<a href="#">apicomplexans</a>	473	4	<a href="#">Plasmodium chabaudi chabaudi hits</a>
..... <a href="#">Plasmodium chabaudi adami</a>	<a href="#">apicomplexans</a>	473	2	<a href="#">Plasmodium chabaudi adami hits</a>
..... <a href="#">Plasmodium vinckei</a>	<a href="#">apicomplexans</a>	471	1	<a href="#">Plasmodium vinckei hits</a>
..... <a href="#">Plasmodium vinckei lentum</a>	<a href="#">apicomplexans</a>	452	1	<a href="#">Plasmodium vinckei lentum hits</a>
..... <a href="#">Plasmodium vinckei petteri</a>	<a href="#">apicomplexans</a>	449	2	<a href="#">Plasmodium vinckei petteri hits</a>
..... <a href="#">Plasmodium vinckei vinckei</a>	<a href="#">apicomplexans</a>	447	3	<a href="#">Plasmodium vinckei vinckei hits</a>
..... <a href="#">Plasmodium berghei ANKA</a>	<a href="#">apicomplexans</a>	444	1	<a href="#">Plasmodium berghei ANKA hits</a>
..... <a href="#">Plasmodium berghei</a>	<a href="#">apicomplexans</a>	444	5	<a href="#">Plasmodium berghei hits</a>
..... <a href="#">Plasmodium yoelii yoelii</a>	<a href="#">apicomplexans</a>	420	1	<a href="#">Plasmodium yoelii yoelii hits</a>
..... <a href="#">Hepatocystis sp. ex Piliocolobus tephrosceles</a>	<a href="#">apicomplexans</a>	472	1	<a href="#">Hepatocystis sp. ex Piliocolobus tephrosceles hits</a>
..... <a href="#">Eimeria maxima</a>	<a href="#">apicomplexans</a>	305	2	<a href="#">Eimeria maxima hits</a>
..... <a href="#">Eimeria acervulina</a>	<a href="#">apicomplexans</a>	305	2	<a href="#">Eimeria acervulina hits</a>
..... <a href="#">Cyclospora cayetanensis</a>	<a href="#">apicomplexans</a>	301	2	<a href="#">Cyclospora cayetanensis hits</a>
..... <a href="#">Apicomplexa sp.</a>	<a href="#">apicomplexans</a>	302	6	<a href="#">Apicomplexa sp. hits</a>
..... <a href="#">Apicomplexa</a>	<a href="#">apicomplexans</a>	322	32	<a href="#">Apicomplexa hits</a>
..... <a href="#">Devosia sp. FKR38</a>	<a href="#">a-proteobacteria</a>	310	1	<a href="#">Devosia sp. FKR38 hits</a>
..... <a href="#">Devosia sp. S02</a>	<a href="#">a-proteobacteria</a>	309	1	<a href="#">Devosia sp. S02 hits</a>
..... <a href="#">Oceanibium sediminis</a>	<a href="#">a-proteobacteria</a>	309	1	<a href="#">Oceanibium sediminis hits</a>
..... <a href="#">Candidatus Fonsibacter lacus</a>	<a href="#">a-proteobacteria</a>	308	9	<a href="#">Candidatus Fonsibacter lacus hits</a>
..... <a href="#">Devosia epidermidihirudinis</a>	<a href="#">a-proteobacteria</a>	307	2	<a href="#">Devosia epidermidihirudinis hits</a>
..... <a href="#">Pelagibacteriales bacterium</a>	<a href="#">a-proteobacteria</a>	307	3	<a href="#">Pelagibacteriales bacterium hits</a>
..... <a href="#">Devosia limi</a>	<a href="#">a-proteobacteria</a>	306	1	<a href="#">Devosia limi hits</a>
..... <a href="#">Devosia limi DSM 17137</a>	<a href="#">a-proteobacteria</a>	306	3	<a href="#">Devosia limi DSM 17137 hits</a>
..... <a href="#">Oceanomicrobium pacificus</a>	<a href="#">a-proteobacteria</a>	306	2	<a href="#">Oceanomicrobium pacificus hits</a>
..... <a href="#">Rhodospirillales bacterium</a>	<a href="#">a-proteobacteria</a>	305	2	<a href="#">Rhodospirillales bacterium hits</a>
..... <a href="#">Proteobacteria bacterium</a>	<a href="#">proteobacteria</a>	305	8	<a href="#">Proteobacteria bacterium hits</a>
..... <a href="#">Alphaproteobacteria bacterium</a>	<a href="#">a-proteobacteria</a>	305	12	<a href="#">Alphaproteobacteria bacterium hits</a>
..... <a href="#">Sphingomonadales bacterium</a>	<a href="#">a-proteobacteria</a>	305	1	<a href="#">Sphingomonadales bacterium hits</a>
..... <a href="#">Eilatimonas milleporae</a>	<a href="#">a-proteobacteria</a>	305	2	<a href="#">Eilatimonas milleporae hits</a>
..... <a href="#">Candidatus Fonsibacter ubiquis</a>	<a href="#">a-proteobacteria</a>	305	4	<a href="#">Candidatus Fonsibacter ubiquis hits</a>
..... <a href="#">Devosia sp. Root635</a>	<a href="#">a-proteobacteria</a>	304	2	<a href="#">Devosia sp. Root635 hits</a>
..... <a href="#">Limibacillus halophilus</a>	<a href="#">a-proteobacteria</a>	304	2	<a href="#">Limibacillus halophilus hits</a>
..... <a href="#">Alphaproteobacteria bacterium MarineAlpha9_Bin7</a>	<a href="#">a-proteobacteria</a>	304	1	<a href="#">Alphaproteobacteria bacterium MarineAlpha9_Bin7 hits</a>
..... <a href="#">Devosia naphthalenivorans</a>	<a href="#">a-proteobacteria</a>	303	1	<a href="#">Devosia naphthalenivorans hits</a>
..... <a href="#">Oceanibaculum indicum</a>	<a href="#">a-proteobacteria</a>	303	2	<a href="#">Oceanibaculum indicum hits</a>

<a href="#">.Oceanibaculum indicum P24</a>	<a href="#">a-proteobacteria</a>	303	1	<a href="#">Oceanibaculum indicum P24 hits</a>
<a href="#">.Rhizobiales bacterium</a>	<a href="#">a-proteobacteria</a>	303	1	<a href="#">Rhizobiales bacterium hits</a>
<a href="#">.Brevundimonas sp.</a>	<a href="#">a-proteobacteria</a>	303	3	<a href="#">Brevundimonas sp. hits</a>
<a href="#">.Rhodobacteraceae bacterium</a>	<a href="#">a-proteobacteria</a>	303	1	<a href="#">Rhodobacteraceae bacterium hits</a>
<a href="#">.Alphaproteobacteria bacterium MarineAlpha9_Bin5</a>	<a href="#">a-proteobacteria</a>	303	1	<a href="#">Alphaproteobacteria bacterium MarineAlpha9_Bin5 hits</a>
<a href="#">.Alphaproteobacteria bacterium MarineAlpha9_Bin6</a>	<a href="#">a-proteobacteria</a>	303	1	<a href="#">Alphaproteobacteria bacterium MarineAlpha9_Bin6 hits</a>
<a href="#">.Devosia sp. Root436</a>	<a href="#">a-proteobacteria</a>	302	2	<a href="#">Devosia sp. Root436 hits</a>
<a href="#">.Rhodobacterales bacterium TMED271</a>	<a href="#">a-proteobacteria</a>	302	1	<a href="#">Rhodobacterales bacterium TMED271 hits</a>
<a href="#">.Rhodovibrio sodomensis</a>	<a href="#">a-proteobacteria</a>	302	2	<a href="#">Rhodovibrio sodomensis hits</a>
<a href="#">.unclassified Bradyrhizobium</a>	<a href="#">a-proteobacteria</a>	301	2	<a href="#">unclassified Bradyrhizobium hits</a>
<a href="#">.Bradyrhizobium sp. 1S1</a>	<a href="#">a-proteobacteria</a>	301	1	<a href="#">Bradyrhizobium sp. 1S1 hits</a>
<a href="#">.Bradyrhizobium sp. 162S2</a>	<a href="#">a-proteobacteria</a>	301	1	<a href="#">Bradyrhizobium sp. 162S2 hits</a>
<a href="#">.Oceanibaculum pacificum</a>	<a href="#">a-proteobacteria</a>	301	2	<a href="#">Oceanibaculum pacificum hits</a>
<a href="#">.Kordiimonadaceae bacterium</a>	<a href="#">a-proteobacteria</a>	301	3	<a href="#">Kordiimonadaceae bacterium hits</a>
<a href="#">.Kordiimonadales bacterium</a>	<a href="#">a-proteobacteria</a>	300	1	<a href="#">Kordiimonadales bacterium hits</a>
<a href="#">.Alphaproteobacteria bacterium MarineAlpha2_Bin1</a>	<a href="#">a-proteobacteria</a>	300	1	<a href="#">Alphaproteobacteria bacterium MarineAlpha2_Bin1 hits</a>
<a href="#">.Bradyrhizobium sp. 2S1</a>	<a href="#">a-proteobacteria</a>	300	2	<a href="#">Bradyrhizobium sp. 2S1 hits</a>
<a href="#">.Rhodospirillaceae bacterium</a>	<a href="#">a-proteobacteria</a>	300	1	<a href="#">Rhodospirillaceae bacterium hits</a>
<a href="#">.Bradyrhizobium sp. 6(2017)</a>	<a href="#">a-proteobacteria</a>	300	1	<a href="#">Bradyrhizobium sp. 6(2017) hits</a>
<a href="#">.Rhodovibrio salinarum</a>	<a href="#">a-proteobacteria</a>	300	2	<a href="#">Rhodovibrio salinarum hits</a>
<a href="#">.Oceanibaculum nanhaiense</a>	<a href="#">a-proteobacteria</a>	300	2	<a href="#">Oceanibaculum nanhaiense hits</a>

## o Organism

Description	Score	E value	Accession
Plasmodium falciparum 3D7 [apicomplexans ]			
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium falciparum (PfMDH) [Plasmodium falciparum 3D7]</a>	655	0.0	<a href="#">5NFR_A</a>
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium falciparum (PfMDH) [Plasmodium falciparum 3D7]</a>	655	0.0	<a href="#">5NFR_B</a>
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium falciparum (PfMDH) [Plasmodium falciparum 3D7]</a>	655	0.0	<a href="#">5NFR_C</a>
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium falciparum (PfMDH) [Plasmodium falciparum 3D7]</a>	655	0.0	<a href="#">5NFR_D</a>
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium falciparum (PfMDH) [Plasmodium falciparum 3D7]</a>	655	0.0	<a href="#">5NFR_E</a>
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium falciparum (PfMDH) [Plasmodium falciparum 3D7]</a>	655	0.0	<a href="#">5NFR_F</a>
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium falciparum (PfMDH) [Plasmodium falciparum 3D7]</a>	655	0.0	<a href="#">5NFR_G</a>
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium falciparum (PfMDH) [Plasmodium falciparum 3D7]</a>	655	0.0	<a href="#">5NFR_H</a>
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium falciparum (PfMDH) [Plasmodium falciparum 3D7]</a>	655	0.0	<a href="#">5NFR_I</a>
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium falciparum (PfMDH) [Plasmodium falciparum 3D7]</a>	655	0.0	<a href="#">5NFR_J</a>
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium falciparum (PfMDH) [Plasmodium falciparum 3D7]</a>	655	0.0	<a href="#">5NFR_K</a>
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium falciparum (PfMDH) [Plasmodium falciparum 3D7]</a>	655	0.0	<a href="#">5NFR_L</a>
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium falciparum (PfMDH) [Plasmodium falciparum 3D7]</a>	655	0.0	<a href="#">5NFR_M</a>
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium falciparum (PfMDH) [Plasmodium falciparum 3D7]</a>	655	0.0	<a href="#">5NFR_N</a>
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium falciparum (PfMDH) [Plasmodium falciparum 3D7]</a>	655	0.0	<a href="#">5NFR_O</a>
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium falciparum (PfMDH) [Plasmodium falciparum 3D7]</a>	655	0.0	<a href="#">5NFR_P</a>
<a href="#">malate dehydrogenase [Plasmodium falciparum 3D7]</a>	638	0.0	<a href="#">XP_966170</a>
Plasmodium falciparum (malaria parasite P. falciparum) [apicomplexans ]			
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium Falciparum in complex with 4-(3,4-difluorophenyl)thiazol-2-amine [Plasmodium falciparum]</a>	648	0.0	<a href="#">6R8G_A</a>
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium Falciparum in complex with 4-(3,4-difluorophenyl)thiazol-2-amine [Plasmodium falciparum]</a>	648	0.0	<a href="#">6R8G_B</a>
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium Falciparum in complex with 4-(3,4-difluorophenyl)thiazol-2-amine [Plasmodium falciparum]</a>	648	0.0	<a href="#">6R8G_C</a>
<a href="#">Crystal structure of malate dehydrogenase from Plasmodium Falciparum in complex with 4-(3,4-difluorophenyl)thiazol-2-amine [Plasmodium falciparum]</a>	648	0.0	<a href="#">6R8G_D</a>
<a href="#">Chain A, Malate dehydrogenase [Plasmodium falciparum]</a>	648	0.0	<a href="#">6Y91_A</a>
<a href="#">Chain B, Malate dehydrogenase [Plasmodium falciparum]</a>	648	0.0	<a href="#">6Y91_B</a>
<a href="#">Chain C, Malate dehydrogenase [Plasmodium falciparum]</a>	648	0.0	<a href="#">6Y91_C</a>
<a href="#">Chain D, Malate dehydrogenase [Plasmodium falciparum]</a>	648	0.0	<a href="#">6Y91_D</a>
<a href="#">malate dehydrogenase [Plasmodium falciparum]</a>	638	0.0	<a href="#">AAQ23154</a>
Plasmodium falciparum Vietnam Oak-Knoll (FVO) [apicomplexans ]			
<a href="#">malate dehydrogenase, NAD-dependent [Plasmodium falciparum Vietnam Oak-Knoll (FVO)]</a>	638	0.0	<a href="#">ETW19634</a>
Plasmodium falciparum FCH/4 [apicomplexans ]			
<a href="#">malate dehydrogenase, NAD-dependent [Plasmodium falciparum FCH/4]</a>	638	0.0	<a href="#">ETW27831</a>

Description	Score	E value	Accession
Plasmodium falciparum Tanzania (2000708) [apicomplexans ]			
<a href="#">malate dehydrogenase, NAD-dependent [Plasmodium falciparum Tanzania (2000708)]</a>	638	0.0	<a href="#">ETW37742</a>
Plasmodium falciparum NF135/5.C10 [apicomplexans ]			
<a href="#">malate dehydrogenase, NAD-dependent [Plasmodium falciparum NF135/5.C10]</a>	638	0.0	<a href="#">ETW43957</a>
Plasmodium falciparum Palo Alto/Uganda [apicomplexans ]			
<a href="#">malate dehydrogenase, NAD-dependent [Plasmodium falciparum Palo Alto/Uganda]</a>	638	0.0	<a href="#">ETW53159</a>
Plasmodium falciparum CAMP/Malaysia [apicomplexans ]			
<a href="#">malate dehydrogenase, NAD-dependent [Plasmodium falciparum CAMP/Malaysia]</a>	638	0.0	<a href="#">ETW62616</a>
Plasmodium falciparum 7G8 [apicomplexans ]			
<a href="#">malate dehydrogenase, NAD-dependent [Plasmodium falciparum 7G8]</a>	638	0.0	<a href="#">EUR75006</a>
Plasmodium falciparum Santa Lucia [apicomplexans ]			
<a href="#">malate dehydrogenase, NAD-dependent [Plasmodium falciparum Santa Lucia]</a>	638	0.0	<a href="#">EUT89255</a>
Plasmodium falciparum UGT5.1 [apicomplexans ]			
<a href="#">malate dehydrogenase, NAD-dependent [Plasmodium falciparum UGT5.1]</a>	638	0.0	<a href="#">EWC77752</a>
Plasmodium falciparum NF54 [apicomplexans ]			
<a href="#">malate dehydrogenase, NAD-dependent [Plasmodium falciparum NF54]</a>	638	0.0	<a href="#">EWC89726</a>
Plasmodium falciparum HB3 [apicomplexans ]			
<a href="#">hypothetical protein PFHG_04607 [Plasmodium falciparum HB3]</a>	638	0.0	<a href="#">KOB62875</a>
Plasmodium sp. gorilla clade G1 [apicomplexans ]			
<a href="#">malate dehydrogenase [Plasmodium sp. gorilla clade G1]</a>	638	0.0	<a href="#">SOS77447</a>
Plasmodium reichenowi [apicomplexans ]			
<a href="#">malate dehydrogenase [Plasmodium reichenowi]</a>	630	0.0	<a href="#">XP_012761998</a>
<a href="#">malate dehydrogenase [Plasmodium reichenowi]</a>	630	0.0	<a href="#">KYO01065</a>
<a href="#">malate dehydrogenase [Plasmodium reichenowi]</a>	630	0.0	<a href="#">CDO63371</a>
<a href="#">malate dehydrogenase [Plasmodium reichenowi]</a>	630	0.0	<a href="#">SOV77526</a>
Plasmodium sp. DRC-Itaito [apicomplexans ]			
<a href="#">malate dehydrogenase [Plasmodium sp. DRC-Itaito]</a>	623	0.0	<a href="#">CAC9696262</a>
<a href="#">malate dehydrogenase [Plasmodium sp. DRC-Itaito]</a>	580	0.0	<a href="#">SOV21691</a>
Plasmodium falciparum MaliPS096_E11 [apicomplexans ]			
<a href="#">hypothetical protein PFMALIP_01469 [Plasmodium falciparum MaliPS096_E11]</a>	622	0.0	<a href="#">ETW50453</a>
Plasmodium sp. gorilla clade G3 [apicomplexans ]			
<a href="#">malate dehydrogenase [Plasmodium sp. gorilla clade G3]</a>	615	0.0	<a href="#">SOV74725</a>
Plasmodium gaboni [apicomplexans ]			
<a href="#">malate dehydrogenase [Plasmodium gaboni]</a>	580	0.0	<a href="#">XP_018642816</a>
<a href="#">malate dehydrogenase [Plasmodium gaboni]</a>	580	0.0	<a href="#">KYO01877</a>
<a href="#">malate dehydrogenase [Plasmodium gaboni]</a>	580	0.0	<a href="#">SOV12323</a>
Plasmodium sp. gorilla clade G2 [apicomplexans ]			
<a href="#">malate dehydrogenase [Plasmodium sp. gorilla clade G2]</a>	579	0.0	<a href="#">XP_028537330</a>
<a href="#">malate dehydrogenase [Plasmodium sp. gorilla clade G2]</a>	579	0.0	<a href="#">SOV12596</a>
Plasmodium relictum [apicomplexans ]			
<a href="#">malate dehydrogenase, putative [Plasmodium relictum]</a>	503	1e-177	<a href="#">XP_028533952</a>
<a href="#">malate dehydrogenase, putative [Plasmodium relictum]</a>	503	1e-177	<a href="#">CRH00951</a>
Plasmodium coatneyi [apicomplexans ]			
<a href="#">Malate dehydrogenase [Plasmodium coatneyi]</a>	503	2e-177	<a href="#">XP_019915696</a>
<a href="#">Malate dehydrogenase [Plasmodium coatneyi]</a>	503	2e-177	<a href="#">ANQ09001</a>
Plasmodium ovale wallikeri [apicomplexans ]			
<a href="#">malate dehydrogenase, putative (MDH) [Plasmodium ovale wallikeri]</a>	501	1e-176	<a href="#">SBT38197</a>
<a href="#">malate dehydrogenase, putative (MDH) [Plasmodium ovale wallikeri]</a>	501	1e-176	<a href="#">SBT38962</a>
Plasmodium ovale (malaria parasite P. ovale) [apicomplexans ]			
<a href="#">malate dehydrogenase, putative [Plasmodium ovale]</a>	501	1e-176	<a href="#">SBT77738</a>
<a href="#">malate dehydrogenase, putative [Plasmodium ovale]</a>	499	8e-176	<a href="#">SCP05083</a>
Plasmodium ovale curtisi [apicomplexans ]			
<a href="#">malate dehydrogenase, putative (MDH) [Plasmodium ovale curtisi]</a>	499	8e-176	<a href="#">SBS85361</a>
<a href="#">malate dehydrogenase, putative (MDH) [Plasmodium ovale curtisi]</a>	499	8e-176	<a href="#">SBS94489</a>
Plasmodium fragile [apicomplexans ]			
<a href="#">malate dehydrogenase, NAD-dependent [Plasmodium fragile]</a>	497	5e-175	<a href="#">XP_012335265</a>
<a href="#">malate dehydrogenase, NAD-dependent [Plasmodium fragile]</a>	497	5e-175	<a href="#">KJP88094</a>
Plasmodium gonderi [apicomplexans ]			
<a href="#">malate dehydrogenase [Plasmodium gonderi]</a>	496	9e-175	<a href="#">XP_028544431</a>

Description	Score	E value	Accession
<a href="#">malate dehydrogenase [Plasmodium gonderi]</a> Plasmodium inui San Antonio 1 [apicomplexans ]	496	9e-175	<a href="#">GAW81842</a>
<a href="#">malate dehydrogenase [Plasmodium inui San Antonio 1]</a>	494	6e-174	<a href="#">XP_008814730</a>
<a href="#">malate dehydrogenase [Plasmodium inui San Antonio 1]</a> Plasmodium vivax (malaria parasite P. vivax) [apicomplexans ]	494	6e-174	<a href="#">EUD68500</a>
<a href="#">malate dehydrogenase, putative [Plasmodium vivax]</a>	493	1e-173	<a href="#">XP_001616198</a>
<a href="#">malate dehydrogenase, putative [Plasmodium vivax]</a>	493	1e-173	<a href="#">EDL46471</a>
<a href="#">malate dehydrogenase, putative [Plasmodium vivax]</a>	493	1e-173	<a href="#">SCO68209</a>
<a href="#">malate dehydrogenase, putative [Plasmodium vivax]</a>	493	2e-173	<a href="#">SCO73674</a>
<a href="#">malate dehydrogenase, putative [Plasmodium vivax]</a> Plasmodium vivax North Korean [apicomplexans ]	493	2e-173	<a href="#">VUZ97056</a>
<a href="#">malate dehydrogenase [Plasmodium vivax North Korean]</a> Plasmodium vivax India VII [apicomplexans ]	493	1e-173	<a href="#">KMZ98651</a>
<a href="#">malate dehydrogenase [Plasmodium vivax India VII]</a> Plasmodium vivax Brazil I [apicomplexans ]	493	2e-173	<a href="#">KMZ79541</a>
<a href="#">malate dehydrogenase [Plasmodium vivax Brazil I]</a> Plasmodium vivax Mauritania I [apicomplexans ]	493	2e-173	<a href="#">KMZ85666</a>
<a href="#">malate dehydrogenase [Plasmodium vivax Mauritania I]</a> Plasmodium gallinaceum [apicomplexans ]	493	2e-173	<a href="#">KMZ92140</a>
<a href="#">malate dehydrogenase, putative [Plasmodium gallinaceum]</a>	493	2e-173	<a href="#">XP_028526585</a>
<a href="#">malate dehydrogenase [Plasmodium gallinaceum]</a>	493	2e-173	<a href="#">BAM15616</a>
<a href="#">malate dehydrogenase, putative [Plasmodium gallinaceum]</a> Plasmodium knowlesi strain H [apicomplexans ]	493	2e-173	<a href="#">CRG93763</a>
<a href="#">malate dehydrogenase, putative [Plasmodium knowlesi strain H]</a>	489	4e-172	<a href="#">XP_002261491</a>
<a href="#">malate dehydrogenase, putative [Plasmodium knowlesi strain H]</a>	489	4e-172	<a href="#">CAA9989144</a>
<a href="#">malate dehydrogenase, putative [Plasmodium knowlesi strain H]</a>	489	4e-172	<a href="#">SBO27363</a>
<a href="#">malate dehydrogenase, putative [Plasmodium knowlesi strain H]</a>	489	4e-172	<a href="#">SBO27524</a>
<a href="#">malate dehydrogenase, putative [Plasmodium knowlesi strain H]</a> Plasmodium knowlesi [apicomplexans ]	489	4e-172	<a href="#">VVS78618</a>
<a href="#">putative Malate dehydrogenase [Plasmodium knowlesi]</a> Plasmodium cynomolgi strain B [apicomplexans ]	489	4e-172	<a href="#">OTN64503</a>
<a href="#">malate dehydrogenase [Plasmodium cynomolgi strain B]</a>	486	1e-170	<a href="#">XP_004223317</a>
<a href="#">malate dehydrogenase [Plasmodium cynomolgi strain B]</a> Plasmodium vinckei brucechwatti [apicomplexans ]	486	1e-170	<a href="#">GAB67370</a>
<a href="#">malate dehydrogenase, putative [Plasmodium vinckei brucechwatti]</a> Plasmodium yoelii 17X [apicomplexans ]	479	4e-168	<a href="#">CAD2095064</a>
<a href="#">malate dehydrogenase, NAD-dependent [Plasmodium yoelii 17X]</a> Plasmodium falciparum Dd2 [apicomplexans ]	475	1e-166	<a href="#">ETB56770</a>
<a href="#">hypothetical protein PFDG_04373 [Plasmodium falciparum Dd2]</a> Plasmodium malariae [apicomplexans ]	471	2e-166	<a href="#">KOB87837</a>
<a href="#">malate dehydrogenase, putative [Plasmodium malariae]</a>	475	2e-166	<a href="#">SBT79735</a>
<a href="#">malate dehydrogenase, putative [Plasmodium malariae]</a>	474	4e-166	<a href="#">XP_028862636</a>
<a href="#">malate dehydrogenase, putative [Plasmodium malariae]</a>	474	4e-166	<a href="#">SBS87209</a>
<a href="#">malate dehydrogenase, putative [Plasmodium malariae]</a> Plasmodium yoelii [apicomplexans ]	474	4e-166	<a href="#">SCO93198</a>
<a href="#">malate dehydrogenase, putative [Plasmodium yoelii]</a>	474	6e-166	<a href="#">XP_022812395</a>
<a href="#">malate dehydrogenase, putative [Plasmodium yoelii]</a>	474	6e-166	<a href="#">CDU18879</a>
<a href="#">malate dehydrogenase, putative [Plasmodium yoelii]</a> Plasmodium chabaudi chabaudi [apicomplexans ]	474	6e-166	<a href="#">VTZ79464</a>
<a href="#">malate dehydrogenase, putative [Plasmodium chabaudi chabaudi]</a>	473	2e-165	<a href="#">XP_737386</a>
<a href="#">malate dehydrogenase, putative [Plasmodium chabaudi chabaudi]</a>	473	2e-165	<a href="#">SCM23634</a>
<a href="#">malate dehydrogenase, putative [Plasmodium chabaudi chabaudi]</a>	473	2e-165	<a href="#">SCN61099</a>
<a href="#">malate dehydrogenase, putative [Plasmodium chabaudi chabaudi]</a> Plasmodium chabaudi adami [apicomplexans ]	473	2e-165	<a href="#">VTZ69167</a>
<a href="#">malate dehydrogenase, putative [Plasmodium chabaudi adami]</a>	473	2e-165	<a href="#">SCM22369</a>
<a href="#">malate dehydrogenase, putative [Plasmodium chabaudi adami]</a> Hepaticystis sp. ex Piliocolobus tephrosceles [apicomplexans ]	450	2e-156	<a href="#">SCN61096</a>
<a href="#">malate dehydrogenase [Hepaticystis sp. ex Piliocolobus tephrosceles]</a> Plasmodium vinckei [apicomplexans ]	472	4e-165	<a href="#">VWU52414</a>

Description	Score	E value	Accession
<a href="#">malate dehydrogenase, putative [Plasmodium vinckei]</a> Plasmodium vinckei lentum [apicomplexans ]	471	4e-165	<a href="#">CAD2108495</a>
<a href="#">malate dehydrogenase, putative [Plasmodium vinckei lentum]</a> Plasmodium vinckei petteri [apicomplexans ]	452	3e-157	<a href="#">CAD2095098</a>
<a href="#">malate dehydrogenase [Plasmodium vinckei petteri]</a>	449	5e-156	<a href="#">EUD73291</a>
<a href="#">malate dehydrogenase, putative [Plasmodium vinckei petteri]</a> Plasmodium vinckei vinckei [apicomplexans ]	449	5e-156	<a href="#">CAD2108523</a>
<a href="#">malate dehydrogenase, putative [Plasmodium vinckei vinckei]</a>	447	2e-155	<a href="#">XP_008624410</a>
<a href="#">malate dehydrogenase, putative [Plasmodium vinckei vinckei]</a>	447	2e-155	<a href="#">VEV57303</a>
<a href="#">malate dehydrogenase [Plasmodium vinckei vinckei]</a> Plasmodium berghei ANKA [apicomplexans ]	446	5e-155	<a href="#">KEG02700</a>
<a href="#">malate dehydrogenase, putative [Plasmodium berghei ANKA]</a> Plasmodium berghei [apicomplexans ]	444	5e-154	<a href="#">XP_034422383</a>
<a href="#">malate dehydrogenase, putative [Plasmodium berghei]</a>	444	5e-154	<a href="#">CXI63152</a>
<a href="#">malate dehydrogenase, putative [Plasmodium berghei]</a>	444	5e-154	<a href="#">SCM23772</a>
<a href="#">malate dehydrogenase, putative [Plasmodium berghei]</a>	444	5e-154	<a href="#">SCN26767</a>
<a href="#">malate dehydrogenase, putative [Plasmodium berghei]</a>	444	5e-154	<a href="#">SCO61099</a>
<a href="#">malate dehydrogenase, putative [Plasmodium berghei]</a> Plasmodium yoelii yoelii [apicomplexans ]	444	5e-154	<a href="#">SCO63186</a>
<a href="#">malate dehydrogenase [Plasmodium yoelii yoelii]</a> Apicomplexa (apicomplexans) [apicomplexans ]	420	1e-144	<a href="#">EAA22943</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with oxamate. [Apicomplexa]</a>	322	5e-106	<a href="#">4PLH_A</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with oxamate. [Apicomplexa]</a>	322	5e-106	<a href="#">4PLH_B</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with oxamate. [Apicomplexa]</a>	322	5e-106	<a href="#">4PLH_C</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with oxamate. [Apicomplexa]</a>	322	5e-106	<a href="#">4PLH_D</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with lactate. [Apicomplexa]</a>	322	5e-106	<a href="#">4PLW_A</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with lactate. [Apicomplexa]</a>	322	5e-106	<a href="#">4PLW_B</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with lactate. [Apicomplexa]</a>	322	5e-106	<a href="#">4PLW_C</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with lactate. [Apicomplexa]</a>	322	5e-106	<a href="#">4PLW_D</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with oxamate. [Apicomplexa]</a>	315	7e-103	<a href="#">4PLT_A</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with oxamate. [Apicomplexa]</a>	315	7e-103	<a href="#">4PLT_B</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with oxamate. [Apicomplexa]</a>	315	7e-103	<a href="#">4PLT_C</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with oxamate. [Apicomplexa]</a>	315	7e-103	<a href="#">4PLT_D</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with lactate. [Apicomplexa]</a>	315	7e-103	<a href="#">4PLV_A</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with lactate. [Apicomplexa]</a>	315	7e-103	<a href="#">4PLV_B</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with lactate. [Apicomplexa]</a>	315	7e-103	<a href="#">4PLV_C</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with lactate. [Apicomplexa]</a>	315	7e-103	<a href="#">4PLV_D</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with malate. [Apicomplexa]</a>	315	7e-103	<a href="#">4PLY_A</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with malate. [Apicomplexa]</a>	315	7e-103	<a href="#">4PLY_B</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with malate. [Apicomplexa]</a>	315	7e-103	<a href="#">4PLY_C</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with malate. [Apicomplexa]</a>	315	7e-103	<a href="#">4PLY_D</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with malate. [Apicomplexa]</a>	315	7e-103	<a href="#">4PLY_E</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with malate. [Apicomplexa]</a>	315	7e-103	<a href="#">4PLY_F</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with malate. [Apicomplexa]</a>	315	7e-103	<a href="#">4PLY_G</a>
<a href="#">Crystal structure of ancestral apicomplexan malate dehydrogenase with malate. [Apicomplexa]</a>	315	7e-103	<a href="#">4PLY_H</a>
<a href="#">Crystal structure of ancestral apicomplexan lactate dehydrogenase with malate. [Apicomplexa]</a>	311	2e-101	<a href="#">4PLC_A</a>
<a href="#">Crystal structure of ancestral apicomplexan lactate dehydrogenase with malate. [Apicomplexa]</a>	311	2e-101	<a href="#">4PLC_B</a>
<a href="#">Crystal structure of ancestral apicomplexan lactate dehydrogenase with malate. [Apicomplexa]</a>	311	2e-101	<a href="#">4PLC_C</a>
<a href="#">Crystal structure of ancestral apicomplexan lactate dehydrogenase with malate. [Apicomplexa]</a>	311	2e-101	<a href="#">4PLC_D</a>
<a href="#">Crystal structure of ancestral apicomplexan lactate dehydrogenase with lactate. [Apicomplexa]</a>	311	2e-101	<a href="#">4PLF_A</a>
<a href="#">Crystal structure of ancestral apicomplexan lactate dehydrogenase with lactate. [Apicomplexa]</a>	311	2e-101	<a href="#">4PLF_B</a>
<a href="#">Crystal structure of ancestral apicomplexan lactate dehydrogenase with oxamate. [Apicomplexa]</a>	311	2e-101	<a href="#">4PLG_A</a>
<a href="#">Crystal structure of ancestral apicomplexan lactate dehydrogenase with oxamate. [Apicomplexa]</a> Devosia sp. FKR38 [a-proteobacteria ]	311	2e-101	<a href="#">4PLG_B</a>
<a href="#">malate dehydrogenase [Devosia sp. FKR38]</a> Devosia sp. S02 [a-proteobacteria ]	310	4e-101	<a href="#">WP_137152966</a>
<a href="#">malate dehydrogenase [Devosia sp. S02]</a> Oceanibium sediminis [a-proteobacteria ]	309	5e-101	<a href="#">WP_193334840</a>
<a href="#">malate dehydrogenase [Oceanibium sediminis]</a>	309	7e-101	<a href="#">WP_112321891</a>

Description	Score	E value	Accession
Candidatus Fonsibacter lacus [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Candidatus Fonsibacter lacus]</a>	308	3e-100	<a href="#">NCU49226</a>
<a href="#">malate dehydrogenase [Candidatus Fonsibacter lacus]</a>	307	6e-100	<a href="#">NCU53456</a>
<a href="#">malate dehydrogenase [Candidatus Fonsibacter lacus]</a>	307	6e-100	<a href="#">NCU63045</a>
<a href="#">malate dehydrogenase [Candidatus Fonsibacter lacus]</a>	305	3e-99	<a href="#">NCU49057</a>
<a href="#">malate dehydrogenase [Candidatus Fonsibacter lacus]</a>	305	3e-99	<a href="#">NCU69999</a>
<a href="#">malate dehydrogenase [Candidatus Fonsibacter lacus]</a>	305	4e-99	<a href="#">NCU46848</a>
<a href="#">malate dehydrogenase [Candidatus Fonsibacter lacus]</a>	305	4e-99	<a href="#">NCU53323</a>
<a href="#">malate dehydrogenase [Candidatus Fonsibacter lacus]</a>	305	4e-99	<a href="#">NCU71976</a>
<a href="#">malate dehydrogenase [Candidatus Fonsibacter lacus]</a>	305	4e-99	<a href="#">NCU73984</a>
Devosia epidermidihirudinis [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Devosia epidermidihirudinis]</a>	307	3e-100	<a href="#">WP_046140904</a>
<a href="#">malate dehydrogenase [Devosia epidermidihirudinis]</a>	307	3e-100	<a href="#">KKC40854</a>
Pelagibacterales bacterium [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Pelagibacterales bacterium]</a>	307	5e-100	<a href="#">GDY35174</a>
<a href="#">malate dehydrogenase [Pelagibacterales bacterium]</a>	305	4e-99	<a href="#">GBL33396</a>
<a href="#">malate dehydrogenase [Pelagibacterales bacterium]</a>	305	6e-99	<a href="#">MBM5787331</a>
Devosia limi [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Devosia limi]</a>	306	7e-100	<a href="#">WP_046135361</a>
Devosia limi DSM 17137 [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Devosia limi DSM 17137]</a>	306	7e-100	<a href="#">KKB84199</a>
<a href="#">malate dehydrogenase [Devosia limi DSM 17137]</a>	306	7e-100	<a href="#">KKB84316</a>
<a href="#">malate dehydrogenase (NAD) [Devosia limi DSM 17137]</a>	306	7e-100	<a href="#">SHE84169</a>
Oceanomicrobium pacificus [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Oceanomicrobium pacificus]</a>	306	1e-99	<a href="#">WP_160851963</a>
<a href="#">malate dehydrogenase [Oceanomicrobium pacificus]</a>	306	1e-99	<a href="#">MXU64513</a>
Rhodospirillales bacterium [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Rhodospirillales bacterium]</a>	305	2e-99	<a href="#">MBK8210760</a>
<a href="#">malate dehydrogenase [Rhodospirillales bacterium]</a>	300	2e-97	<a href="#">MBK8174980</a>
Eimeria maxima [apicomplexans ]			
<a href="#">malate dehydrogenase, putative [Eimeria maxima]</a>	305	2e-99	<a href="#">XP_013336105</a>
<a href="#">malate dehydrogenase, putative [Eimeria maxima]</a>	305	2e-99	<a href="#">CDJ59457</a>
Proteobacteria bacterium [proteobacteria ]			
<a href="#">malate dehydrogenase [Proteobacteria bacterium]</a>	305	3e-99	<a href="#">NBY89657</a>
<a href="#">malate dehydrogenase [Proteobacteria bacterium]</a>	305	3e-99	<a href="#">NDE64866</a>
<a href="#">malate dehydrogenase [Proteobacteria bacterium]</a>	305	3e-99	<a href="#">NBQ46335</a>
<a href="#">malate dehydrogenase [Proteobacteria bacterium]</a>	305	4e-99	<a href="#">NDE48906</a>
<a href="#">malate dehydrogenase [Proteobacteria bacterium]</a>	305	4e-99	<a href="#">NDB38016</a>
<a href="#">malate dehydrogenase [Proteobacteria bacterium]</a>	304	1e-98	<a href="#">NBT38276</a>
<a href="#">malate dehydrogenase [Proteobacteria bacterium]</a>	304	1e-98	<a href="#">NBU53834</a>
<a href="#">malate dehydrogenase [Proteobacteria bacterium]</a>	300	2e-97	<a href="#">MBI3675661</a>
Alphaproteobacteria bacterium [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium]</a>	305	3e-99	<a href="#">PCJ41639</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium]</a>	305	4e-99	<a href="#">MBI1328659</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium]</a>	305	4e-99	<a href="#">RCL75573</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium]</a>	304	6e-99	<a href="#">HIB19697</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium]</a>	304	6e-99	<a href="#">MQA65584</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium]</a>	303	1e-98	<a href="#">HIN91290</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium]</a>	303	2e-98	<a href="#">HHZ66959</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium]</a>	303	2e-98	<a href="#">HIB55980</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium]</a>	303	2e-98	<a href="#">HIO03488</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium]</a>	301	7e-98	<a href="#">TAH36160</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium]</a>	301	1e-97	<a href="#">MBA2590478</a>
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium]</a>	300	3e-97	<a href="#">MBN9587800</a>
Eimeria acervulina [apicomplexans ]			
<a href="#">malate dehydrogenase, putative [Eimeria acervulina]</a>	305	3e-99	<a href="#">XP_013246728</a>
<a href="#">malate dehydrogenase, putative [Eimeria acervulina]</a>	305	3e-99	<a href="#">CDI84253</a>
Sphingomonadales bacterium [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Sphingomonadales bacterium]</a>	305	3e-99	<a href="#">HEC00426</a>



Description	Score	E value	Accession
<i>Eilatimonas milleporae</i> [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Eilatimonas milleporae]</a>	305	4e-99	<a href="#">WP_121938586</a>
<a href="#">malate dehydrogenase (NAD) [Eilatimonas milleporae]</a>	305	4e-99	<a href="#">RMB07798</a>
<i>Candidatus Fonsibacter ubiqvis</i> [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Candidatus Fonsibacter ubiqvis]</a>	305	4e-99	<a href="#">WP_099340841</a>
<a href="#">malate dehydrogenase [Candidatus Fonsibacter ubiqvis]</a>	305	4e-99	<a href="#">NCU46030</a>
<a href="#">malate dehydrogenase [Candidatus Fonsibacter ubiqvis]</a>	305	4e-99	<a href="#">NCU47817</a>
<a href="#">malate dehydrogenase [Candidatus Fonsibacter ubiqvis]</a>	305	4e-99	<a href="#">NCU54133</a>
<i>Devosia sp. Root635</i> [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Devosia sp. Root635]</a>	304	5e-99	<a href="#">WP_056229719</a>
<a href="#">malate dehydrogenase [Devosia sp. Root635]</a>	304	5e-99	<a href="#">KRA50451</a>
<i>Limibacillus halophilus</i> [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Limibacillus halophilus]</a>	304	6e-99	<a href="#">WP_183417264</a>
<a href="#">malate dehydrogenase [Limibacillus halophilus]</a>	304	6e-99	<a href="#">MBB3066453</a>
<i>Alphaproteobacteria bacterium MarineAlpha9_Bin7</i> [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium MarineAlpha9_Bin7]</a>	304	7e-99	<a href="#">PPR17482</a>
<i>Devosia naphthalenivorans</i> [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Devosia naphthalenivorans]</a>	303	1e-98	<a href="#">WP_108459774</a>
<i>Oceanibaculum indicum</i> [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Oceanibaculum indicum]</a>	303	1e-98	<a href="#">WP_008943063</a>
<a href="#">malate dehydrogenase [Oceanibaculum indicum]</a>	303	1e-98	<a href="#">RKQ68736</a>
<i>Oceanibaculum indicum P24</i> [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Oceanibaculum indicum P24]</a>	303	1e-98	<a href="#">EKE78340</a>
<i>Rhizobiales bacterium</i> [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Rhizobiales bacterium]</a>	303	1e-98	<a href="#">RYE11063</a>
<i>Brevundimonas sp.</i> [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Brevundimonas sp.]</a>	303	1e-98	<a href="#">MAL87662</a>
<a href="#">malate dehydrogenase [Brevundimonas sp.]</a>	303	1e-98	<a href="#">HAJ03120</a>
<a href="#">malate dehydrogenase [Brevundimonas sp.]</a>	303	1e-98	<a href="#">HAV50294</a>
<i>Rhodobacteraceae bacterium</i> [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Rhodobacteraceae bacterium]</a>	303	1e-98	<a href="#">MAP00672</a>
<i>Alphaproteobacteria bacterium MarineAlpha9_Bin5</i> [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium MarineAlpha9_Bin5]</a>	303	1e-98	<a href="#">PPR37875</a>
<i>Alphaproteobacteria bacterium MarineAlpha9_Bin6</i> [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium MarineAlpha9_Bin6]</a>	303	2e-98	<a href="#">PPR36537</a>
<i>Devosia sp. Root436</i> [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Devosia sp. Root436]</a>	302	3e-98	<a href="#">WP_056254967</a>
<a href="#">malate dehydrogenase [Devosia sp. Root436]</a>	302	3e-98	<a href="#">KQX40310</a>
<i>Rhodobacterales bacterium TMED271</i> [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Rhodobacterales bacterium TMED271]</a>	302	4e-98	<a href="#">OUX44185</a>
<i>Rhodovibrio sodomensis</i> [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Rhodovibrio sodomensis]</a>	302	5e-98	<a href="#">WP_200339844</a>
<a href="#">malate dehydrogenase [Rhodovibrio sodomensis]</a>	302	5e-98	<a href="#">MBK1667685</a>
<i>Cyclospora cayetanensis</i> [apicomplexans ]			
<a href="#">uncharacterized protein LOC34621309 [Cyclospora cayetanensis]</a>	301	6e-98	<a href="#">XP_022589240</a>
<a href="#">putative malate dehydrogenase [Cyclospora cayetanensis]</a>	301	6e-98	<a href="#">OEH76447</a>
<i>unclassified Bradyrhizobium</i> [a-proteobacteria ]			
<a href="#">MULTISPECIES: malate dehydrogenase [unclassified Bradyrhizobium]</a>	301	7e-98	<a href="#">WP_166213281</a>
<a href="#">MULTISPECIES: malate dehydrogenase [unclassified Bradyrhizobium]</a>	300	3e-97	<a href="#">WP_029081325</a>
<i>Bradyrhizobium sp. 1S1</i> [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Bradyrhizobium sp. 1S1]</a>	301	7e-98	<a href="#">NVI49853</a>
<i>Bradyrhizobium sp. 162S2</i> [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Bradyrhizobium sp. 162S2]</a>	301	7e-98	<a href="#">NVL12414</a>
<i>Apicomplexa sp.</i> [apicomplexans ]			
<a href="#">Crystal structure of ancestral apicomplexan lactate dehydrogenase in alternate dimer configuration with sulfate. [Apicomplexa sp.]</a>	302	7e-98	<a href="#">6VDH_A</a>
<a href="#">Crystal structure of ancestral apicomplexan lactate dehydrogenase in alternate dimer configuration with sulfate. [Apicomplexa sp.]</a>	302	7e-98	<a href="#">6VDH_B</a>
<a href="#">Crystal structure of ancestral apicomplexan lactate dehydrogenase with sulfate. [Apicomplexa sp.]</a>	302	7e-98	<a href="#">6VDI_A</a>
<a href="#">Crystal structure of ancestral apicomplexan lactate dehydrogenase with sulfate. [Apicomplexa sp.]</a>	302	7e-98	<a href="#">6VDI_B</a>
<a href="#">Crystal structure of ancestral apicomplexan lactate dehydrogenase with sulfate and NADH4. [Apicomplexa sp.]</a>	302	7e-98	<a href="#">6VDJ_A</a>

Description	Score	E value	Accession
<a href="#">Crystal structure of ancestral apicomplexan lactate dehydrogenase with sulfate and NADH4. [Apicomplexa sp.]</a>	302	7e-98	<a href="#">6VDJ_B</a>
Oceanibaculum pacificum [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Oceanibaculum pacificum]</a>	301	8e-98	<a href="#">WP_067555953</a>
<a href="#">malate dehydrogenase [Oceanibaculum pacificum]</a>	301	8e-98	<a href="#">KZD08276</a>
Kordiimonadaceae bacterium [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Kordiimonadaceae bacterium]</a>	301	1e-97	<a href="#">MBO6506542</a>
<a href="#">malate dehydrogenase [Kordiimonadaceae bacterium]</a>	301	1e-97	<a href="#">MBO6567721</a>
<a href="#">malate dehydrogenase [Kordiimonadaceae bacterium]</a>	301	1e-97	<a href="#">MBO6963064</a>
Kordiimonadales bacterium [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Kordiimonadales bacterium]</a>	300	2e-97	<a href="#">PCI63361</a>
Alphaproteobacteria bacterium MarineAlpha2_Bin1 [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Alphaproteobacteria bacterium MarineAlpha2_Bin1]</a>	300	2e-97	<a href="#">PPR79434</a>
Bradyrhizobium sp. 2S1 [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Bradyrhizobium sp. 2S1]</a>	300	2e-97	<a href="#">WP_166300597</a>
<a href="#">malate dehydrogenase [Bradyrhizobium sp. 2S1]</a>	300	2e-97	<a href="#">NVI57972</a>
Rhodospirillaceae bacterium [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Rhodospirillaceae bacterium]</a>	300	2e-97	<a href="#">MBT05681</a>
Bradyrhizobium sp. 6(2017) [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Bradyrhizobium sp. 6(2017)]</a>	300	3e-97	<a href="#">QIG96430</a>
Rhodovibrio salinarum [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Rhodovibrio salinarum]</a>	300	3e-97	<a href="#">WP_027287413</a>
<a href="#">malate dehydrogenase [Rhodovibrio salinarum]</a>	300	3e-97	<a href="#">MBK1696980</a>
Oceanibaculum nanhaiense [a-proteobacteria ]			
<a href="#">malate dehydrogenase [Oceanibaculum nanhaiense]</a>	300	3e-97	<a href="#">MBC7134210</a>
<a href="#">malate dehydrogenase [Oceanibaculum nanhaiense]</a>	300	4e-97	<a href="#">WP_086463724</a>

## o Taxonomy


Taxonomy	Number of hits	Number of Organisms	Description
cellular organisms	254	98	
. Alveolata	162	57	
.. Apicomplexa	32	57	<a href="#">Apicomplexa hits</a>
... Plasmodiidae	118	52	
.... Plasmodium	117	51	
..... Plasmodium (Laverania)	52	21	
..... Plasmodium falciparum	9	15	<a href="#">Plasmodium falciparum hits</a>
..... Plasmodium falciparum 3D7	17	1	<a href="#">Plasmodium falciparum 3D7 hits</a>
..... Plasmodium falciparum Vietnam Oak-Knoll (FVO)	1	1	<a href="#">Plasmodium falciparum Vietnam Oak-Knoll (FVO) hits</a>
..... Plasmodium falciparum FCH/4	1	1	<a href="#">Plasmodium falciparum FCH/4 hits</a>
..... Plasmodium falciparum Tanzania (2000708)	1	1	<a href="#">Plasmodium falciparum Tanzania (2000708) hits</a>
..... Plasmodium falciparum NF135/5.C10	1	1	<a href="#">Plasmodium falciparum NF135/5.C10 hits</a>
..... Plasmodium falciparum Palo Alto/Uganda	1	1	<a href="#">Plasmodium falciparum Palo Alto/Uganda hits</a>
..... Plasmodium falciparum CAMP/Malaysia	1	1	<a href="#">Plasmodium falciparum CAMP/Malaysia hits</a>
..... Plasmodium falciparum 7G8	1	1	<a href="#">Plasmodium falciparum 7G8 hits</a>
..... Plasmodium falciparum Santa Lucia	1	1	<a href="#">Plasmodium falciparum Santa Lucia hits</a>
..... Plasmodium falciparum UGT5.1	1	1	<a href="#">Plasmodium falciparum UGT5.1 hits</a>
..... Plasmodium falciparum NF54	1	1	<a href="#">Plasmodium falciparum NF54 hits</a>
..... Plasmodium falciparum HB3	1	1	<a href="#">Plasmodium falciparum HB3 hits</a>
..... Plasmodium falciparum MaliPS096_E11	1	1	<a href="#">Plasmodium falciparum MaliPS096_E11 hits</a>
..... Plasmodium falciparum Dd2	1	1	<a href="#">Plasmodium falciparum Dd2 hits</a>
..... Plasmodium sp. gorilla clade G1	1	1	<a href="#">Plasmodium sp. gorilla clade G1 hits</a>
..... Plasmodium reichenowi	4	1	<a href="#">Plasmodium reichenowi hits</a>
..... Plasmodium sp. DRC-Itaito	2	1	<a href="#">Plasmodium sp. DRC-Itaito hits</a>
..... Plasmodium sp. gorilla clade G3	1	1	<a href="#">Plasmodium sp. gorilla clade G3 hits</a>
..... Plasmodium gaboni	3	1	<a href="#">Plasmodium gaboni hits</a>
..... Plasmodium sp. gorilla clade G2	2	1	<a href="#">Plasmodium sp. gorilla clade G2 hits</a>
..... Plasmodium (Haemamoeba)	5	2	
..... Plasmodium relictum	2	1	<a href="#">Plasmodium relictum hits</a>
..... Plasmodium gallinaceum	3	1	<a href="#">Plasmodium gallinaceum hits</a>

..... <a href="#">Plasmodium coatneyi</a>	<u>2</u>	1	<a href="#">Plasmodium coatneyi hits</a>
..... <a href="#">Plasmodium (Plasmodium)</a>	<u>33</u>	15	
..... <a href="#">Plasmodium ovale</a>	<u>2</u>	3	<a href="#">Plasmodium ovale hits</a>
..... <a href="#">Plasmodium ovale wallikeri</a>	<u>2</u>	1	<a href="#">Plasmodium ovale wallikeri hits</a>
..... <a href="#">Plasmodium ovale curtisi</a>	<u>2</u>	1	<a href="#">Plasmodium ovale curtisi hits</a>
..... <a href="#">Plasmodium fragile</a>	<u>2</u>	1	<a href="#">Plasmodium fragile hits</a>
..... <a href="#">Plasmodium gonderi</a>	<u>2</u>	1	<a href="#">Plasmodium gonderi hits</a>
..... <a href="#">Plasmodium inui San Antonio 1</a>	<u>2</u>	1	<a href="#">Plasmodium inui San Antonio 1 hits</a>
..... <a href="#">Plasmodium vivax</a>	<u>5</u>	5	<a href="#">Plasmodium vivax hits</a>
..... <a href="#">Plasmodium vivax North Korean</a>	<u>1</u>	1	<a href="#">Plasmodium vivax North Korean hits</a>
..... <a href="#">Plasmodium vivax India VII</a>	<u>1</u>	1	<a href="#">Plasmodium vivax India VII hits</a>
..... <a href="#">Plasmodium vivax Brazil I</a>	<u>1</u>	1	<a href="#">Plasmodium vivax Brazil I hits</a>
..... <a href="#">Plasmodium vivax Mauritania I</a>	<u>1</u>	1	<a href="#">Plasmodium vivax Mauritania I hits</a>
..... <a href="#">Plasmodium knowlesi</a>	<u>1</u>	2	<a href="#">Plasmodium knowlesi hits</a>
..... <a href="#">Plasmodium knowlesi strain H</a>	<u>5</u>	1	<a href="#">Plasmodium knowlesi strain H hits</a>
..... <a href="#">Plasmodium cynomolgi strain B</a>	<u>2</u>	1	<a href="#">Plasmodium cynomolgi strain B hits</a>
..... <a href="#">Plasmodium malariae</a>	<u>4</u>	1	<a href="#">Plasmodium malariae hits</a>
..... <a href="#">Plasmodium (Vinckeia)</a>	<u>25</u>	12	
..... <a href="#">Plasmodium vinckeii</a>	<u>1</u>	5	<a href="#">Plasmodium vinckeii hits</a>
..... <a href="#">Plasmodium vinckeii brucechwattii</a>	<u>1</u>	1	<a href="#">Plasmodium vinckeii brucechwattii hits</a>
..... <a href="#">Plasmodium vinckeii lentum</a>	<u>1</u>	1	<a href="#">Plasmodium vinckeii lentum hits</a>
..... <a href="#">Plasmodium vinckeii petteri</a>	<u>2</u>	1	<a href="#">Plasmodium vinckeii petteri hits</a>
..... <a href="#">Plasmodium vinckeii vinckeii</a>	<u>3</u>	1	<a href="#">Plasmodium vinckeii vinckeii hits</a>
..... <a href="#">Plasmodium yoelii</a>	<u>3</u>	3	<a href="#">Plasmodium yoelii hits</a>
..... <a href="#">Plasmodium yoelii 17X</a>	<u>1</u>	1	<a href="#">Plasmodium yoelii 17X hits</a>
..... <a href="#">Plasmodium yoelii yoelii</a>	<u>1</u>	1	<a href="#">Plasmodium yoelii yoelii hits</a>
..... <a href="#">Plasmodium chabaudi</a>	<u>6</u>	2	
..... <a href="#">Plasmodium chabaudi chabaudi</a>	<u>4</u>	1	<a href="#">Plasmodium chabaudi chabaudi hits</a>
..... <a href="#">Plasmodium chabaudi adami</a>	<u>2</u>	1	<a href="#">Plasmodium chabaudi adami hits</a>
..... <a href="#">Plasmodium berghei</a>	<u>5</u>	2	<a href="#">Plasmodium berghei hits</a>
..... <a href="#">Plasmodium berghei ANKA</a>	<u>1</u>	1	<a href="#">Plasmodium berghei ANKA hits</a>
.... <a href="#">Hepatocystis sp. ex Piliocolobus tephrosceles</a>	<u>1</u>	1	<a href="#">Hepatocystis sp. ex Piliocolobus tephrosceles hits</a>
... <a href="#">Eimeriidae</a>	<u>6</u>	3	
.... <a href="#">Eimeria</a>	<u>4</u>	2	
..... <a href="#">Eimeria maxima</a>	<u>2</u>	1	<a href="#">Eimeria maxima hits</a>
..... <a href="#">Eimeria acervulina</a>	<u>2</u>	1	<a href="#">Eimeria acervulina hits</a>
.... <a href="#">Cyclospora cayetanensis</a>	<u>2</u>	1	<a href="#">Cyclospora cayetanensis hits</a>
... <a href="#">Apicomplexa sp.</a>	<u>6</u>	1	<a href="#">Apicomplexa sp. hits</a>
. <a href="#">Proteobacteria</a>	<u>92</u>	41	
.. <a href="#">Alphaproteobacteria</a>	<u>84</u>	40	
... <a href="#">Hyphomicrobiales</a>	<u>21</u>	14	
.... <a href="#">Devosia</a>	<u>13</u>	8	
..... unclassified <a href="#">Devosia</a>	<u>6</u>	4	
..... <a href="#">Devosia sp. FKR38</a>	<u>1</u>	1	<a href="#">Devosia sp. FKR38 hits</a>
..... <a href="#">Devosia sp. S02</a>	<u>1</u>	1	<a href="#">Devosia sp. S02 hits</a>
..... <a href="#">Devosia sp. Root635</a>	<u>2</u>	1	<a href="#">Devosia sp. Root635 hits</a>
..... <a href="#">Devosia sp. Root436</a>	<u>2</u>	1	<a href="#">Devosia sp. Root436 hits</a>
..... <a href="#">Devosia epidermidihirudinis</a>	<u>2</u>	1	<a href="#">Devosia epidermidihirudinis hits</a>
..... <a href="#">Devosia limi</a>	<u>1</u>	2	<a href="#">Devosia limi hits</a>
..... <a href="#">Devosia limi DSM 17137</a>	<u>3</u>	1	<a href="#">Devosia limi DSM 17137 hits</a>
..... <a href="#">Devosia naphthalenivorans</a>	<u>1</u>	1	<a href="#">Devosia naphthalenivorans hits</a>
.... <a href="#">Rhizobiales bacterium</a>	<u>1</u>	1	<a href="#">Rhizobiales bacterium hits</a>
.... <a href="#">Bradyrhizobium</a>	<u>7</u>	5	
..... unclassified <a href="#">Bradyrhizobium</a>	<u>2</u>	5	<a href="#">unclassified Bradyrhizobium hits</a>
..... <a href="#">Bradyrhizobium sp. 1S1</a>	<u>1</u>	1	<a href="#">Bradyrhizobium sp. 1S1 hits</a>
..... <a href="#">Bradyrhizobium sp. 162S2</a>	<u>1</u>	1	<a href="#">Bradyrhizobium sp. 162S2 hits</a>
..... <a href="#">Bradyrhizobium sp. 2S1</a>	<u>2</u>	1	<a href="#">Bradyrhizobium sp. 2S1 hits</a>
..... <a href="#">Bradyrhizobium sp. 6(2017)</a>	<u>1</u>	1	<a href="#">Bradyrhizobium sp. 6(2017) hits</a>
... <a href="#">Rhodobacterales</a>	<u>5</u>	4	
.... <a href="#">Rhodobacteraceae</a>	<u>4</u>	3	
..... <a href="#">Oceanibium sediminis</a>	<u>1</u>	1	<a href="#">Oceanibium sediminis hits</a>

..... <a href="#">Oceanomicrobium pacificus</a>	2	1	<a href="#">Oceanomicrobium pacificus hits</a>
..... <a href="#">Rhodobacteraceae bacterium</a>	1	1	<a href="#">Rhodobacteraceae bacterium hits</a>
.... <a href="#">Rhodobacterales bacterium TMED271</a>	1	1	<a href="#">Rhodobacterales bacterium TMED271 hits</a>
... <a href="#">Pelagibacterales</a>	16	3	
..... <a href="#">Candidatus Fonsibacter</a>	13	2	
..... <a href="#">Candidatus Fonsibacter lacus</a>	9	1	<a href="#">Candidatus Fonsibacter lacus hits</a>
..... <a href="#">Candidatus Fonsibacter ubiqvis</a>	4	1	<a href="#">Candidatus Fonsibacter ubiqvis hits</a>
.... <a href="#">Pelagibacterales bacterium</a>	3	1	<a href="#">Pelagibacterales bacterium hits</a>
... <a href="#">Rhodospirillales</a>	16	9	
.... <a href="#">Rhodospirillales bacterium</a>	2	1	<a href="#">Rhodospirillales bacterium hits</a>
.... <a href="#">Rhodospirillaceae</a>	14	8	
..... <a href="#">Limibacillus halophilus</a>	2	1	<a href="#">Limibacillus halophilus hits</a>
..... <a href="#">Oceanibaculum</a>	7	4	
..... <a href="#">Oceanibaculum indicum</a>	2	2	<a href="#">Oceanibaculum indicum hits</a>
..... <a href="#">Oceanibaculum indicum P24</a>	1	1	<a href="#">Oceanibaculum indicum P24 hits</a>
..... <a href="#">Oceanibaculum pacificum</a>	2	1	<a href="#">Oceanibaculum pacificum hits</a>
..... <a href="#">Oceanibaculum nanhaiense</a>	2	1	<a href="#">Oceanibaculum nanhaiense hits</a>
.... <a href="#">Rhodovibrio</a>	4	2	
..... <a href="#">Rhodovibrio sodomensis</a>	2	1	<a href="#">Rhodovibrio sodomensis hits</a>
..... <a href="#">Rhodovibrio salinarum</a>	2	1	<a href="#">Rhodovibrio salinarum hits</a>
.... <a href="#">Rhodospirillaceae bacterium</a>	1	1	<a href="#">Rhodospirillaceae bacterium hits</a>
... <a href="#">unclassified Alphaproteobacteria</a>	16	5	
.... <a href="#">Alphaproteobacteria bacterium</a>	12	1	<a href="#">Alphaproteobacteria bacterium hits</a>
.... <a href="#">Alphaproteobacteria bacterium MarineAlpha9_Bin7</a>	1	1	<a href="#">Alphaproteobacteria bacterium MarineAlpha9_Bin7 hits</a>
.... <a href="#">Alphaproteobacteria bacterium MarineAlpha9_Bin5</a>	1	1	<a href="#">Alphaproteobacteria bacterium MarineAlpha9_Bin5 hits</a>
.... <a href="#">Alphaproteobacteria bacterium MarineAlpha9_Bin6</a>	1	1	<a href="#">Alphaproteobacteria bacterium MarineAlpha9_Bin6 hits</a>
.... <a href="#">Alphaproteobacteria bacterium MarineAlpha2_Bin1</a>	1	1	<a href="#">Alphaproteobacteria bacterium MarineAlpha2_Bin1 hits</a>
... <a href="#">Sphingomonadales bacterium</a>	1	1	<a href="#">Sphingomonadales bacterium hits</a>
... <a href="#">Kordiimonadales</a>	6	3	
.... <a href="#">Kordiimonadaceae</a>	5	2	
..... <a href="#">Eilatimonas milleporae</a>	2	1	<a href="#">Eilatimonas milleporae hits</a>
..... <a href="#">Kordiimonadaceae bacterium</a>	3	1	<a href="#">Kordiimonadaceae bacterium hits</a>
.... <a href="#">Kordiimonadales bacterium</a>	1	1	<a href="#">Kordiimonadales bacterium hits</a>
... <a href="#">Brevundimonas sp.</a>	3	1	<a href="#">Brevundimonas sp. hits</a>
.. <a href="#">Proteobacteria bacterium</a>	8	1	<a href="#">Proteobacteria bacterium hits</a>

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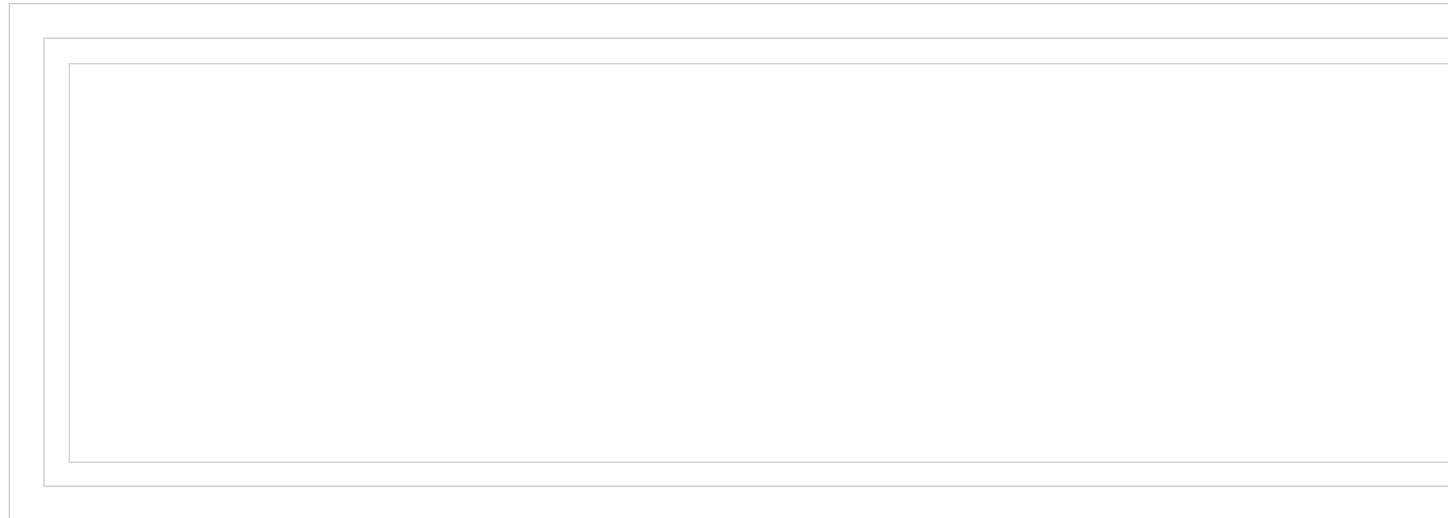
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**Multiple Alignment Results - pdb|5NFR|P - Cobalt RID 7PBDUR3F212 (100 seqs)**

**Graphical Overview**



**Descriptions**  Select All [Re-align](#) [Alignment parameters](#)

Accession	Description	Links
<input checked="" type="checkbox"/> <a href="#">5NFR_A</a>	Crystal structure of malate dehydrogenase from Plasmodium falciparum (PfMDH) [Plasmodium falciparum]	<a href="#">Related Information</a>
	Crystal structure of malate dehydrogenase from Plasmodium Falciparum in complex with 4-(3,4-dichlorophenyl)-N,N-dimethyl-2,6-pyridinedicarboximide	

<a href="#">6R8G_A</a>		<a href="#">Related Information</a>
<a href="#">XP_966170.1</a>	malate dehydrogenase [Plasmodium falciparum 3D7]	<a href="#">Related Information</a>
<a href="#">XP_012761998.1</a>	malate dehydrogenase [Plasmodium reichenowi]	<a href="#">Related Information</a>
<a href="#">CAC9696262.1</a>	malate dehydrogenase [Plasmodium sp. DRC-Itaito]	
<a href="#">ETW50453.1</a>	hypothetical protein PFMALIP_01469 [Plasmodium falciparum MaliPS096_E11]	
<a href="#">SOV74725.1</a>	malate dehydrogenase [Plasmodium sp. gorilla clade G3]	
<a href="#">SOV21691.1</a>	malate dehydrogenase [Plasmodium sp. DRC-Itaito]	
<a href="#">XP_018642816.1</a>	malate dehydrogenase [Plasmodium gaboni]	<a href="#">Related Information</a>
<a href="#">XP_028537330.1</a>	malate dehydrogenase [Plasmodium sp. gorilla clade G2]	<a href="#">Related Information</a>
<a href="#">XP_028533952.1</a>	malate dehydrogenase, putative [Plasmodium relictum]	<a href="#">Related Information</a>
<a href="#">XP_019915696.1</a>	Malate dehydrogenase [Plasmodium coatneyi]	<a href="#">Related Information</a>
<a href="#">SBT38197.1</a>	malate dehydrogenase, putative (MDH) [Plasmodium ovale wallikeri]	<a href="#">Related Information</a>
<a href="#">SBS85361.1</a>	malate dehydrogenase, putative (MDH) [Plasmodium ovale curtisii]	<a href="#">Related Information</a>
<a href="#">XP_012335265.1</a>	malate dehydrogenase, NAD-dependent [Plasmodium fragile]	<a href="#">Related Information</a>
<a href="#">XP_028544431.1</a>	malate dehydrogenase [Plasmodium gonderi]	<a href="#">Related Information</a>
<a href="#">XP_008814730.1</a>	malate dehydrogenase [Plasmodium inui San Antonio 1]	<a href="#">Related Information</a>
<a href="#">XP_001616198.1</a>	malate dehydrogenase, putative [Plasmodium vivax]	<a href="#">Related Information</a>
<a href="#">KMZ79541.1</a>	malate dehydrogenase [Plasmodium vivax India VII]	<a href="#">Related Information</a>
<a href="#">XP_028526585.1</a>	malate dehydrogenase, putative [Plasmodium gallinaceum]	<a href="#">Related Information</a>
<a href="#">XP_002261491.1</a>	malate dehydrogenase, putative [Plasmodium knowlesi strain H]	<a href="#">Related Information</a>
<a href="#">XP_004223317.1</a>	malate dehydrogenase [Plasmodium cynomolgi strain B]	<a href="#">Related Information</a>
<a href="#">CAD2095064.1</a>	malate dehydrogenase, putative [Plasmodium vinckeii brucechwattii]	
<a href="#">ETB56770.1</a>	malate dehydrogenase, NAD-dependent [Plasmodium yoelii 17X]	
<a href="#">KOB87837.1</a>	hypothetical protein PFDG_04373 [Plasmodium falciparum Dd2]	
<a href="#">SBT79735.1</a>	malate dehydrogenase, putative [Plasmodium malariae]	<a href="#">Related Information</a>
<a href="#">XP_028862636.1</a>	malate dehydrogenase, putative [Plasmodium malariae]	<a href="#">Related Information</a>
<a href="#">XP_022812395.1</a>	malate dehydrogenase, putative [Plasmodium yoelii]	<a href="#">Related Information</a>
<a href="#">XP_737386.2</a>	malate dehydrogenase, putative [Plasmodium chabaudi chabaudi]	<a href="#">Related Information</a>
<a href="#">VWU52414.1</a>	malate dehydrogenase [Hepatocystis sp. ex Piliocolobus tephrosceles]	
<a href="#">CAD2108495.1</a>	malate dehydrogenase, putative [Plasmodium vinckeii]	
<a href="#">CAD2095098.1</a>	malate dehydrogenase, putative [Plasmodium vinckeii lentum]	
<a href="#">SCN61096.1</a>	malate dehydrogenase, putative [Plasmodium chabaudi adami]	
<a href="#">EUD73291.1</a>	malate dehydrogenase [Plasmodium vinckeii petteri]	<a href="#">Related Information</a>
<a href="#">XP_008624410.2</a>	malate dehydrogenase, putative [Plasmodium vinckeii vinckeii]	<a href="#">Related Information</a>
<a href="#">KEG02700.1</a>	malate dehydrogenase [Plasmodium vinckeii vinckeii]	<a href="#">Related Information</a>
<a href="#">XP_034422383.1</a>	malate dehydrogenase, putative [Plasmodium berghei ANKA]	<a href="#">Related Information</a>
<a href="#">EAA22943.1</a>	malate dehydrogenase [Plasmodium yoelii yoelii]	
<a href="#">4PLH_A</a>	Crystal structure of ancestral apicomplexan malate dehydrogenase with oxamate [Apicomplexa]	<a href="#">Related Information</a>
<a href="#">4PLT_A</a>	Crystal structure of ancestral apicomplexan malate dehydrogenase with oxamate [Apicomplexa]	<a href="#">Related Information</a>
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<a href="#">WP_137152966.1</a>	malate dehydrogenase [Devosia sp. FKR38]	
<a href="#">WP_193334840.1</a>	malate dehydrogenase [Devosia sp. S02]	
<a href="#">WP_112321891.1</a>	malate dehydrogenase [Oceanibium sediminis]	
<a href="#">NCU49226.1</a>	malate dehydrogenase [Candidatus Fonsibacter lacus]	
<a href="#">WP_046140904.1</a>	malate dehydrogenase [Devosia epidermidihirudinis]	<a href="#">Related Information</a>
<a href="#">GDX35174.1</a>	malate dehydrogenase [Pelagibacteriales bacterium]	
<a href="#">NCU53456.1</a>	malate dehydrogenase [Candidatus Fonsibacter lacus]	
<a href="#">NCU63045.1</a>	malate dehydrogenase [Candidatus Fonsibacter lacus]	
<a href="#">WP_046135361.1</a>	malate dehydrogenase [Devosia limi]	<a href="#">Related Information</a>
<a href="#">WP_160851963.1</a>	malate dehydrogenase [Oceanomicrobium pacificus]	<a href="#">Related Information</a>
<a href="#">MBK8210760.1</a>	malate dehydrogenase [Rhodospirillales bacterium]	
<a href="#">XP_013336105.1</a>	malate dehydrogenase, putative [Eimeria maxima]	<a href="#">Related Information</a>
<a href="#">NBY89657.1</a>	malate dehydrogenase [Proteobacteria bacterium]	
<a href="#">PCJ41639.1</a>	malate dehydrogenase [Alphaproteobacteria bacterium]	
<a href="#">NCU49057.1</a>	malate dehydrogenase [Candidatus Fonsibacter lacus]	
<a href="#">NCU69999.1</a>	malate dehydrogenase [Candidatus Fonsibacter lacus]	<a href="#">Related Information</a>
<a href="#">NBQ46335.1</a>	malate dehydrogenase [Proteobacteria bacterium]	
<a href="#">XP_013246728.1</a>	malate dehydrogenase, putative [Eimeria acervulina]	<a href="#">Related Information</a>

<a href="#">✓ HEC00426.1</a>	TPA: malate dehydrogenase [Sphingomonadales bacterium]	
<a href="#">✓ WP_121938586.1</a>	malate dehydrogenase [Eilatimonas milleporae]	<a href="#">Related Information</a>
<a href="#">✓ NCU46848.1</a>	malate dehydrogenase [Candidatus Fonsibacter lacus]	<a href="#">Related Information</a>
<a href="#">✓ MBI1328659.1</a>	malate dehydrogenase [Alphaproteobacteria bacterium]	
<a href="#">✓ RCL75573.1</a>	malate dehydrogenase [Alphaproteobacteria bacterium]	
<a href="#">✓ WP_099340841.1</a>	malate dehydrogenase [Candidatus Fonsibacter ubiqvis]	<a href="#">Related Information</a>
<a href="#">✓ WP_056229719.1</a>	malate dehydrogenase [Devosia sp. Root635]	<a href="#">Related Information</a>
<a href="#">✓ MBM5787331.1</a>	malate dehydrogenase [Pelagibacterales bacterium]	
<a href="#">✓ HIB19697.1</a>	TPA: malate dehydrogenase [Alphaproteobacteria bacterium]	
<a href="#">✓ WP_183417264.1</a>	malate dehydrogenase [Limibacillus halophilus]	<a href="#">Related Information</a>
<a href="#">✓ MQA65584.1</a>	malate dehydrogenase [Alphaproteobacteria bacterium]	
<a href="#">✓ PPR17482.1</a>	malate dehydrogenase [Alphaproteobacteria bacterium MarineAlpha9_Bin7]	
<a href="#">✓ WP_108459774.1</a>	malate dehydrogenase [Devosia naphthalenivorans]	
<a href="#">✓ NBT38276.1</a>	malate dehydrogenase [Proteobacteria bacterium]	<a href="#">Related Information</a>
<a href="#">✓ WP_008943063.1</a>	malate dehydrogenase [Oceanibaculum indicum]	<a href="#">Related Information</a>
<a href="#">✓ RYE11063.1</a>	malate dehydrogenase [Rhizobiales bacterium]	
<a href="#">✓ MAL87662.1</a>	malate dehydrogenase [Brevundimonas sp.]	<a href="#">Related Information</a>
<a href="#">✓ MAP00672.1</a>	malate dehydrogenase [Rhodobacteraceae bacterium]	
<a href="#">✓ PPR37875.1</a>	malate dehydrogenase [Alphaproteobacteria bacterium MarineAlpha9_Bin5]	<a href="#">Related Information</a>
<a href="#">✓ PPR36537.1</a>	malate dehydrogenase [Alphaproteobacteria bacterium MarineAlpha9_Bin6]	<a href="#">Related Information</a>
<a href="#">✓ WP_056254967.1</a>	malate dehydrogenase [Devosia sp. Root436]	<a href="#">Related Information</a>
<a href="#">✓ OUX44185.1</a>	malate dehydrogenase [Rhodobacterales bacterium TMED271]	
<a href="#">✓ WP_200339844.1</a>	malate dehydrogenase [Rhodovibrio sodomensis]	<a href="#">Related Information</a>
<a href="#">✓ XP_022589240.1</a>	uncharacterized protein LOC34621309 [Cyclospora cayetanensis]	<a href="#">Related Information</a>
<a href="#">✓ WP_166213281.1</a>	MULTISPECIES: malate dehydrogenase [unclassified Bradyrhizobium]	<a href="#">Related Information</a>
<a href="#">✓ 6VDH_A</a>	Crystal structure of ancestral apicomplexan lactate dehydrogenase in alternate dimer configuration	<a href="#">Related Information</a>
<a href="#">✓ TAH36160.1</a>	malate dehydrogenase [Alphaproteobacteria bacterium]	
<a href="#">✓ WP_067555953.1</a>	malate dehydrogenase [Oceanibaculum pacificum]	<a href="#">Related Information</a>
<a href="#">✓ MBA2590478.1</a>	malate dehydrogenase [Alphaproteobacteria bacterium]	
<a href="#">✓ MBO6506542.1</a>	malate dehydrogenase [Kordiimonadaceae bacterium]	<a href="#">Related Information</a>
<a href="#">✓ PCI63361.1</a>	malate dehydrogenase [Kordiimonadales bacterium]	
<a href="#">✓ PPR79434.1</a>	malate dehydrogenase [Alphaproteobacteria bacterium MarineAlpha2_Bin1]	
<a href="#">✓ WP_166300597.1</a>	malate dehydrogenase [Bradyrhizobium sp. 2S1]	<a href="#">Related Information</a>
<a href="#">✓ MBI3675661.1</a>	malate dehydrogenase [Proteobacteria bacterium]	
<a href="#">✓ MBT05681.1</a>	malate dehydrogenase [Rhodospirillaceae bacterium]	
<a href="#">✓ MBK8174980.1</a>	malate dehydrogenase [Rhodospirillales bacterium]	
<a href="#">✓ WP_029081325.1</a>	MULTISPECIES: malate dehydrogenase [unclassified Bradyrhizobium]	<a href="#">Related Information</a>
<a href="#">✓ WP_027287413.1</a>	malate dehydrogenase [Rhodovibrio salinarum]	<a href="#">Related Information</a>
<a href="#">✓ MBN9587800.1</a>	malate dehydrogenase [Alphaproteobacteria bacterium]	
<a href="#">✓ MBC7134210.1</a>	malate dehydrogenase [Oceanibaculum nanhaiense]	
<a href="#">✓ WP_086463724.1</a>	malate dehydrogenase [Oceanibaculum nanhaiense]	

**Alignments**  Select All  Mouse over the sequence identifier for sequence title

View Format:  Conservation Setting:

<a href="#">✓ 5NFR_A</a>	1	--	-[ 1]TKIALIGSGQIGAIIVGELCLLENLGLDILYDVVPGIPQKALDLKHFSTILGVNRNIIIGTNQIEDIKDAD	71
<a href="#">✓ 6R8G_A</a>	1	--	-[ 1]TKIALIGSGQIGAIIVGELCLLENLGLDILYDVVPGIPQKALDLKHFSTILGVNRNIIIGTNQIEDIKDAD	71
<a href="#">✓ XP_966170.1</a>	1	--	-[ 1]TKIALIGSGQIGAIIVGELCLLENLGLDILYDVVPGIPQKALDLKHFSTILGVNRNIIIGTNQIEDIKDAD	71
<a href="#">✓ XP_012761998.1</a>	1	--	-[ 1]TKIALIGSGQIGAIIVGELCLMENLGLDVLVYDVVPGIPQKALDLKHFSTILGVNRNIIIGTNQIEDIKDAD	71
<a href="#">✓ CAC9696262.1</a>	1	--	-[ 1]TKIALIGSGQIGAIIVGELCLMENFGDLVLYDVVPGIPQKALDLKHFSTILGVNRNIIIGTNQIEDIKDAD	71
<a href="#">✓ ETW50453.1</a>	1	--	-[ 1]Y----ICSGQIGAIIVGELCLLENLGLDILYDVVPGIPQKALDLKHFSTILGVNRNIIIGTNQIEDIKDAD	67
<a href="#">✓ SOV74725.1</a>	1	--	-[ 1]TKIALIGSGQIGAIIVGELCLMENFGDLVLYDVVPGIPQKALDLKHFSTILGVNKNIIIGTNQIEDIKDAD	71
<a href="#">✓ SOV21691.1</a>	1	--	-[ 1]TKIALIGSGQIGTIVGELCLMENFGDLVLYDVVGGIPQKALDLKHFSTILGVNRNIIIGTNQIEDIKDSD	71
<a href="#">✓ XP_018642816.1</a>	1	--	-[ 1]TKIALIGSGQIGTIVGELCLMENFGDLVLYDVVGGIPQKALDLKHFSTILGVNRNIIIGTNQIEDIKDSD	71
<a href="#">✓ XP_028537330.1</a>	1	--	-[ 1]TKIALIGSGQIGTIVGELCLMENFGDLVLYDVVPGIPQKALDLKHFSTILGVNRNIIIGTNQIEDIKDSD	71
<a href="#">✓ XP_028533952.1</a>	1	--	-[ 1]TKISLIGSGQIGALVGECLLIENLGLDVLVYDVVQIPQKCLDLKHFSTILGVNRNIIIGSNNIIEDIKDSD	71

<a href="#">XP_019915696.1</a>	1	--	-	[ 1]PKISMIGSGQIGAIIVGQLILLENIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">SBT38197.1</a>	1	--	-	[ 1]TKISLIGSGQIGAIIVGELCLVENLGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">SBS85361.1</a>	1	--	-	[ 1]TKISLIGSGQIGAIIVGELCLVENLGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">XP_012335265.1</a>	1	--	-	[ 1]VKISMVSGSQIGAIIVGQLILMENIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">XP_028544431.1</a>	1	--	-	[ 1]TKISMIGSGQIGAIIVGQLVLMENIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">XP_008814730.1</a>	1	--	-	[ 1]PKISMVSGSQIGAIIVGQLILMENIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">XP_001616198.1</a>	1	--	-	[ 1]PKISMVSGSQIGAIIVGQLILMENIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">KMZ79541.1</a>	1	--	-	[ 1]PKISMVSGSQIGAIIVGQLILMENIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">XP_028526585.1</a>	1	--	-	[ 1]TKISLIGSGQIGALVGECLLENLGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">XP_002261491.1</a>	1	--	-	[ 1]TKISMIGSGQIGTIVGQLILMENIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">XP_004223317.1</a>	1	--	-	[ 1]PKISMVSGSQIGAIIVGQLILMENIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">CAD2095064.1</a>	1	--	-	[ 1]TKISLIGSGQIGAIIVGQLCLSENIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">ETB56770.1</a>	1	--	-	[ 1]TKISLIGSGQIGAIIVGQLCLSENIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">KOB87837.1</a>				-----	
<a href="#">SBT79735.1</a>	1	--	-	[ 1]PKISLIGSGYIGALVGLCLVDNLGDVLYDVMQGVVPQGKSLDLKHLSTILGVNRIITGTNNVEDIKGSD	71
<a href="#">XP_028862636.1</a>	1	--	-	[ 1]PKISLIGSGYIGALVGLCLVDNLGDVLYDVMQGVVPQGKSLDLKHLSTILGVNRIITGTNNVEDIKGSD	71
<a href="#">XP_022812395.1</a>	1	--	-	[ 1]TKISLIGSGQIGAIIVGQLCLSENIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">XP_737386.2</a>	1	--	-	[ 1]TKISLIGSGQIGAIIVGQLCLSENIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">VWU52414.1</a>	1	--	-	[ 1]PKISLIGSGQIGSIVGQLCLQANIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">CAD2108495.1</a>	1	--	-	[ 1]TKISLIGSGQIGAIIVGQLCLSENIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">CAD2095098.1</a>	1	--	-	[ 1]TKISLIGSGQIGAIIVGQLCLSENIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">SCN61096.1</a>	1	--	-	[ 1]TKISLIGSGQIGAIIVGQLCLSENIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">EUD73291.1</a>	1	--	-	[ 1]TKISLIGSGQIGAIIVGQLCLSENIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">XP_008624410.2</a>	1	--	-	[ 1]TKISLIGSGQIGAIIVGQLCLSENIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">KEG02700.1</a>	1	--	-	[ 1]TKISLIGSGQIGAIIVGQLCLSENIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">XP_034422383.1</a>	1	--	-	[ 1]PKISLIGSGQIGAIIVGQLCLSENIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	71
<a href="#">EAA22943.1</a>	1	MC	[6]F	[21]TKISLIGSGQIGAIIVGQLCLSENIGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	100
<a href="#">4PLH_A</a>	1	MT	[1]R	KKISLIGAGNIGGTLAHLIAQKELGDVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	74
<a href="#">4PLT_A</a>	1	MT	[1]R	KKISLIGAGNIGGTLAHLIAQKELGDVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	74
<a href="#">4PLC_A</a>	1	MT	[5]R	KKISLIGSGMIGGTMAYLCAQKELGDVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	78
<a href="#">WP_137152966.1</a>	1	MA	R	KKIALIGSGQIGGTLAHLAALKDLGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	73
<a href="#">WP_193334840.1</a>	1	MA	R	KKIALIGSGQIGGTLAHLAALKDLGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	73
<a href="#">WP_112321891.1</a>	1	MA	R	AKIALIGSGQIGGTLAHLAALKDLGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	73
<a href="#">NCU49226.1</a>	1	MR	-	KKISLIGSGQIGGTLAHLSLKLGDVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	72
<a href="#">WP_046140904.1</a>	1	MA	R	KKIALIGSGQIGGTLAHLAALKDLGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	73
<a href="#">GDX35174.1</a>	1	MR	-	KKISLIGSGQIGGTLAHLSLKLGDVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	72
<a href="#">NCU53456.1</a>	1	MR	-	KKISLIGSGQIGGTLAHLSLKLGDVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	72
<a href="#">NCU63045.1</a>	1	MR	-	KKISLIGSGQIGGTLAHLSLKLGDVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	72
<a href="#">WP_046135361.1</a>	1	MA	R	KKIALIGSGQIGGTLAHLAALKDLGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	73
<a href="#">WP_160851963.1</a>	1	MA	R	AKIALIGSGQIGGTLAHLAALKDLGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	73
<a href="#">MBK8210760.1</a>	1	MA	R	KKIALVGGNIGGTLAHLAALKDLGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	73
<a href="#">XP_013336105.1</a>	1	MR	R	PKIALVGGGQIGAVLAFSSLKLGDVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	73
<a href="#">NBY89657.1</a>	1	MR	-	KKISLIGSGQIGGTLAHLSLKLGDVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	72
<a href="#">PCJ41639.1</a>	1	MA	R	KKIALIGGGQIGGTLAHLAALKDLGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	73
<a href="#">NCU49057.1</a>	1	MR	-	KKISLIGSGQIGGTLAHLSLKLGDVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	72
<a href="#">NCU69999.1</a>	1	MR	-	KKISLIGSGQIGGTLAHLSLKLGDVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	72
<a href="#">NBQ46335.1</a>	1	MR	-	KKISLIGSGQIGGTLAHLSLKLGDVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	72
<a href="#">XP_013246728.1</a>	1	MR	R	PKIALVGGGQIGAVLAFSSLKLGDVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	73
<a href="#">HEC00426.1</a>	1	MA	R	KKIALIGGGQIGGTLAHLAALKDLGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	73
<a href="#">WP_121938586.1</a>	1	MS	R	KKIALIGGGQIGGTLAHLAALKDLGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	73
<a href="#">NCU46848.1</a>	1	MR	-	KKISLIGSGQIGGTLAHLSLKLGDVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	72
<a href="#">MBI1328659.1</a>	1	MA	R	KKIALIGGGQIGGTLAHLAALKDLGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	73
<a href="#">RCL75573.1</a>	1	MA	K	AKISLIGAGQIGGTLAHLVALKDLGDVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	73
<a href="#">WP_099340841.1</a>	1	MR	-	KKISLIGSGQIGGTLAHLSLKLGDVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	72
<a href="#">WP_056229719.1</a>	1	MA	R	KKIALIGSGQIGGTLAHLAALKDLGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	73
<a href="#">MBM5787331.1</a>	1	MR	-	KKISLIGSGQIGGTLAHLSLKLGDVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	72
<a href="#">HIB19697.1</a>	1	MA	R	NKIALIGAGNIGGTLAHLAALKDLGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	73
<a href="#">WP_183417264.1</a>	1	MA	R	TKIALIGSGQIGGTLAHLAALKDLGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	73
<a href="#">MQA65584.1</a>	1	MA	R	KKIALIGAGNIGGTLAHLAALKDLGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	73
<a href="#">PPR17482.1</a>	1	MT	R	NKIALIGAGSIGGTLAHLVGLKDLGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	73
<a href="#">WP_108459774.1</a>	1	MA	R	KKIALIGSGQIGGTLAHLAALKDLGDIVLYDVMQGVVPQGKSLDLKHFSTIVGVNKKIVGTNNVEDIKGSD	73



<a href="#">NBT38276.1</a>	1	MR	-	KKISLIGSGQIGGTLAHLISLKELDVWIFDIAAGLPDGKSLDIAQSGAVERFNANLKGTTSSYSDIVNSD	72
<a href="#">WP_008943063.1</a>	1	MA	R	NKIALVGAGNIGGTLALAGLKELDIVLFDIAEGMPQKALDIAQASPVDFDAAVSGTNDYADLKGAD	73
<a href="#">RYE11063.1</a>	1	MA	R	KKIALIGAGQIGGTLAHLAAMKELGDVILFDIVDGTTPQKALDLISQSAPVEGFNANIKGTSEYKDIAGAD	73
<a href="#">MAL87662.1</a>	1	MA	R	AKIALIGAGMIGGTLAHVAAREALGDVILFDIAEGMPQKALDIAEATAVIGTDVSLKGANAYEDIAGAD	73
<a href="#">MAP00672.1</a>	1	MA	K	AKISLIGAGQIGGTLAHLIALKNLGDVWIFDIAEGTPQKSLDLAEISGPVESFNMQLKGTNDYSDIAGSD	73
<a href="#">PPR37875.1</a>	1	MA	R	NKIALIGAGNIGGTLAHLAGLKELDVWVFDIVKGVPPQKALDIVEASPIEGFADKFLGVNSYRPIRGTD	73
<a href="#">PPR36537.1</a>	1	MA	R	NKIALIGAGNIGGTLAHLAGLKELDVWVFDIVKGVPPQKALDIVEASPIEGFADKFLGVNSYRPIRGTD	73
<a href="#">WP_056254967.1</a>	1	MA	R	KKIALIGSGQIGGTLAHLAALKDLGDIVLFDIVDGTTPQKALDLISQSAPVEGYDAKITGTSKYEDLKGSD	73
<a href="#">OUX44185.1</a>	1	MA	K	AKISLIGAGQIGGTLAHLVALKNLGDVWIFDIAEGTPQKALDLAEISGPVESFNMVCLKGTNDYSDIEGSD	73
<a href="#">WP_200339844.1</a>	1	MA	R	NKIALIGAGQIGGTLALSGLKQLGDVWVFDIQEGTPQKALDIAEAPVEGFDSRVQGTNSYADIKDAD	73
<a href="#">XP_022589240.1</a>	1	MP	R	PKIALVGGGQIGAVLAFSSLKELDVSI FDIIVEGMPQKALDISQVGP IEGFDAALSGANQFSALQGD	73
<a href="#">WP_166213281.1</a>	1	MA	R	DKIALIGSGQIGGTLAHLVGLKELDVWVFDIAEGVPPQKALDIAQSSPDVGFDSNLVANSYEAALDGA	73
<a href="#">6VDH_A</a>	1	MA[6]	R	PKISLIGSGMIGGTMAYLCAKKELDVWVFDVVKNMPQKALDLSHSTSVADTNVKTGTNSYEDIKGS	79
<a href="#">TAH36160.1</a>	1	MA[2]	R	AKISLIGAGQIGGTLALAGLKELDVWVFDVVEGTPQKGLDIAEAPVLFDAKFGSANGYEAIQDSD	75
<a href="#">WP_067555953.1</a>	1	MA	R	NKIALVGAGNIGGTLALAGLKDLDITLFDIAEGMPQKALDIAQASPVGFDAVLKGTNDYADLKGAD	73
<a href="#">MBA2590478.1</a>	1	MA	R	KKIALIGGGQIGGTLAHLAALKELDVWVFDIAEGLPQKALDLISQSGPVDGFNAKLSGTNSYADIKGAD	73
<a href="#">MBO6506542.1</a>	1	MA	R	NKIALIGAGQIGGTLAHLAALKEMGDIVVFDIVEGMPAGKALDLAQSAVEGFYASLKGANDYADIADAD	73
<a href="#">PC163361.1</a>	1	MA	R	KKIALIGGGQIGGTLAHLAALKELDIVLFDIVEGLPQKCLDLAQSAVEGFNAEMTGANDYEA IAGAD	73
<a href="#">PPR79434.1</a>	1	MT	R	RKIALIGAGNIGGTLAHLIGLQKLDVWVFDIADGLPQKALDMAESTPVEGVDISYQGTKSYSKIKGAD	73
<a href="#">WP_166300597.1</a>	1	MA	R	DKIALIGSGQIGGTLAHLVGLKELDVWVFDIAEGVPPQKALDIAQSSPDVGFDSNLVANSYEAALDGA	73
<a href="#">MBI3675661.1</a>	1	MP	R	RKIALIGGGQIGGTLAHLVGLKELDVWVFDIVEGLPQKCLDLIAQAGPVEGYDAKFRGTNSYADIAGAD	73
<a href="#">MBT05681.1</a>	1	MA	R	KKIALIGAGNIGGTLAHLAGLQELGDVWVFDIVKGVPPQKALDIVEASPVSGFADKYVGTNNYRAIRGAD	73
<a href="#">MBK8174980.1</a>	1	MA	R	KKIALIGGGNIGGTLAHLCAKKELDVWVFDIVEGLPQKSLDLQSTPVERISVSLKGANAYEDIAGAD	73
<a href="#">WP_029081325.1</a>	1	MA	R	DKIALIGSGQIGGTLAHLVGLKELDVWVFDIAEGVPPQKALDIAQSSPDVGFDSNLVANSYDALDGA	73
<a href="#">WP_027287413.1</a>	1	MA	R	NKIALIGAGQIGGTLALSGLKQLGDVWVFDIQEGTPQKALDIAEAPVEGFDSRLQGANSYADIKDAD	73
<a href="#">MBN9587800.1</a>	1	MA	R	KKIALIGGGQIGGTLAHLAVLKELDVWVFDIAEGLPQKALDLAQSGPVDGFNATLKGNTNAYSADIAGAD	73
<a href="#">MBC7134210.1</a>	1	MA	R	NKIALVGAGNIGGTLALAGLKELDIVLFDIAEGLPQKALDIAQASPVGFDAAVTGANDYSALKGAD	73
<a href="#">WP_086463724.1</a>	1	MA	R	NKIALVGAGNIGGTLALAGLKELDIVLFDIAEGLPQKALDIAQASPVGFDAAVTGANDYSALKGAD	73
<a href="#">5NFR_A</a>	72			IIVITAGVQRKEGMT REDLIGVNGKIMKSVAESVKLHCSKAFVICVSNPLDIMVNVFHKFSNLPHEKICGMAGILDT	148
<a href="#">6R8G_A</a>	72			IIVITAGVQRKEGMT REDLIGVNGKIMKSVAESVKLHCSKAFVICVSNPLDIMVNVFHKFSNLPHEKICGMAGILDT	148
<a href="#">XP_966170.1</a>	72			IIVITAGVQRKEGMT REDLIGVNGKIMKSVAESVKLHCSKAFVICVSNPLDIMVNVFHKFSNLPHEKICGMAGILDT	148
<a href="#">XP_012761998.1</a>	72			IIVITAGVQRKEGMT REDLIGVNGKIMKSVAESVKLHCSKAFVICVSNPLDIMVNVFHKFSNLPHEKICGMAGILDT	148
<a href="#">CAC9696262.1</a>	72			IIVITAGVQRKEGMT REDLIGVNGKIMKSVAESVKLYCSKAFVICVSNPLDIMVNVFHKFSNLPHEKICGMAGILDT	148
<a href="#">ETW50453.1</a>	68			IIVITAGVQRKEGMT REDLIGVNGKIMKSVAESVKLHCSKAFVICVSNPLDIMVNVFHKFSNLPHEKICGMAGILDT	144
<a href="#">SOV74725.1</a>	72			IIVITAGVQRKEGMT REDLIEVNGKIMKSVAESVKLHCSKAFVICVSNPLDIMVNVFHKFSNLPHEKICGMAGILDT	148
<a href="#">SOV21691.1</a>	72			IIVITAGVQRKEGMT REDLIGVNGKIMKDVESVKLHCSKAFVICVSNPLDIMVNVFHKFSNLPHEKICGMAGILDT	148
<a href="#">XP_018642816.1</a>	72			IIVITAGVQRKEGMT REDLIGVNGKIMKGVESVKLHCSKAFVICVSNPLDIMVNVFHKFSNLPHEKICGMAGILDT	148
<a href="#">XP_028537330.1</a>	72			IIVITAGVQRKEGMT REDLIGVNGKIMKGVESVKLHCSKAFVICVSNPLDIMVNVFHKFSNLPHEKICGMAGILDT	148
<a href="#">XP_028533952.1</a>	72			VIVITAGMQRKEGMT REDLIGINGKIMKNVAESVKLYSPNAFVICVSNPLDIMVNVFHKYSNIPHEKVCGMAGILDT	148
<a href="#">XP_019915696.1</a>	72			VIVITAGVQRKEGMT REDLIGINGKIMKSVAESVKLYCPNAFVICVSNPLDIMVNVFHKYSNLPYKICGMAGVLD	148
<a href="#">SBT38197.1</a>	72			IIVITAGIQRKEGMT REDLIGINGKIMKSVAESVKLYSPNAFVICVSNPLDIMVNVFHKYSNLPYKICGMAGVLD	148
<a href="#">SBS85361.1</a>	72			IIVITAGIQRKEGMT REDLIGINGKIMKSVAESVKLYSPNAFVICVSNPLDIMVNVFHKYSNLPYKICGMAGVLD	148
<a href="#">XP_012335265.1</a>	72			VIVITAGVQRKEGMT REDLIGINGKIMKSVAESVKLYSPNAFVICVSNPLDIMVNVFHKYSNLPYKICGMAGILDT	148
<a href="#">XP_028544431.1</a>	72			VIVITAGIQRKEGMT REDLIGINGKIMKSVAESVKLYSPNAFVICVSNPLDIMVNVFHKYSNLPYKICGMAGILDT	148
<a href="#">XP_008814730.1</a>	72			VLVITAGIQRKEGMT REDLIGINGKIMKSVAESVKLHSPNAFVICVSNPLDIMVNVFQKYSNLPYKICGMAGILDT	148
<a href="#">XP_001616198.1</a>	72			VIVITAGVQRKEGMT REDLIGINGKIMKSVAESVKVHSPNAFVICVSNPLDIMVNVFQKYSNLPYKICGMAGILDT	148
<a href="#">KMZ79541.1</a>	72			VIVITAGVQRKEGMT REDLIGINGKIMKSVAESVKVHSPNAFVICVSNPLDIMVNVFQKYSNLPYKICGMAGILDT	148
<a href="#">XP_028526585.1</a>	72			IIVITAGMQRKEGMT REDLIGINGKIMKSVAESVKLYSPNAFVICVSNPLDIMVNVFHKYSNLPHEKICGMAGILDT	148
<a href="#">XP_002261491.1</a>	72			VIVITAGVQRKEGMT REDLIGINGKIMKSVAESVKLYSPNAFVICVSNPLDIMVNVFHKYSNLPYKICGMAGILDT	148
<a href="#">XP_004223317.1</a>	72			VIVITAGVQRKEGMT REDLIGINGKIMKSVAESVKQYSPNAFVICVSNPLDIMVNVFQKYSNLPYKICGMAGILDT	148
<a href="#">CAD2095064.1</a>	72			VIVITAGVQRKEGMS REDLIGINGKIIKSVAESVKQHAPNAFVICVNTNLDVDMVNVFHKYSNLPYKICGMAGILDT	148
<a href="#">ETB56770.1</a>	72			VIVITAGVQRKEGMS REDLIGINGKIIKSVAESVKQYAPNAFVICVNTNLDVDMVNVFHKYSNLPYKICGMAGILDT	148
<a href="#">KOB87837.1</a>	1		-----MT	REDLIGVNGKIMKSVAESVKLHCSKAFVICVSNPLDIMVNVFHKFSNLPHEKICGMAGILDT	64
<a href="#">SBT79735.1</a>	72			VIVITAGVQRKEGMS REDLIGVNGKIMKSVAESVKTYSPNAFVICVSNPLDIMVNVFHKYSNLPHEKICGMAGILDT	148
<a href="#">XP_028862636.1</a>	72			VIVITAGVQRKEGMS REDLIGVNGKIMKSVAESVKTYSPNAFVICVSNPLDIMVNVFHKYSNLPHEKICGMAGILDT	148
<a href="#">XP_022812395.1</a>	72			VIVITAGVQRKEGMS REDLIGINGKIIKSVAESVKQYAPNAFVICVNTNLDVDMVNVFHKYSNLPYKICGMAGILDT	148
<a href="#">XP_737386.2</a>	72			VIVITAGVQRKEGMS REDLIGINGKIIKSVAESVKQYAPNAFVICVNTNLDVDMVNVFHKYSNLPYKICGMAGILDT	148
<a href="#">VWU52414.1</a>	72			VIVITAGMQRKEGMS REDLIGINGKIMKNVAESVKTYSPNAFVICVSNPLDIMVNVFHKYSNLPVHKICGMAGILDA	148
<a href="#">CAD2108495.1</a>	72			VIVITAGVQRKEGMS REDLIGINGKIIKSVAESVKQHAPNAFVICVNTNLDVDMVNVFHKYSNLPYKICGMAGILDT	148
<a href="#">CAD2095098.1</a>	72			VIVITAGVQRKEGMS REDLIGINGKIIKSVAESVKQHAPNAFVICVNTNLDVDMVNVFHKYSNLPYKICGMAGILDT	148

<a href="#">SCN61096.1</a>	72	VIVITAGVQRKEGMS	REDLIGINGKIIKSVAESVKQYAPNAFVICVTNPLDVMVNFHFKYSNLPYEKICGMAGILDT	148
<a href="#">EUD73291.1</a>	72	VIVITAGVQRKEGMS	REDLIGINGKIIKSVAESVKQHAPNAFVICVTNPLDVMVNFHFKYSNLPYEKICGMAGILDT	148
<a href="#">XP_008624410.2</a>	72	VIIITAGVQRKEGMS	REDLIGINGKIIKSVAESVKQHAPNAFVICVTNPLDVMVNFHFKYSNLPYEKICGMAGILDT	148
<a href="#">KEG02700.1</a>	72	VIIITAGVQRKEGMS	RDDLIGINGKIIKSVAESVKQHAPNAFVICVTNPLDVMVNFHFKYSNLPYEKICGMAGILDT	148
<a href="#">XP_034422383.1</a>	72	VIVITAGVQRKEGMS	REDLIGINGKIIKSVAESVKQYAPNAFVICVTNPLDVMVNFHFKYSNLPYEKICGMAGILDT	148
<a href="#">EAA22943.1</a>	101	VIVITAGVQRKEGMS	REDLIGINGKIIKSVAESVKQYAPNAFVICVTNPLDVMVNFHFKYSNLPYEKICGMAGILDT	177
<a href="#">4PLH_A</a>	75	VIIITAGIPRKP GMS	RDDL LSVNAKIMKDVAENIKKYCPNAFVIVVTNPLDVMVYVHLHKYSGLPHNKVCGMAGVLD	151
<a href="#">4PLT_A</a>	75	VIIITAGIPRKP GMS [5]	RDDL LSVNAKIMKDVAENIKKYCPNAFVIVVTNPLDVMVYVHLHKYSGLPHNKVCGMAGVLD	156
<a href="#">4PLC_A</a>	79	VIIITAGLTKAPGKS [5]	RDDL LFPNAKIMREVGENIKKYCPNAFVIVITNPLDVMVKVLEHESGLPKNKVCGMAGVLD	160
<a href="#">WP_137152966.1</a>	74	VVIVTAGVPRKPGMS	RDDL L E INLKVMEQVGGAGIAKYCPKAFVICITNPLDAMWALQKFSGLATNQVIGMAGVLD	150
<a href="#">WP_193334840.1</a>	74	VVIVTAGVPRKPGMS	RDDL L E INLKVMEQVGGAGIAKYAPKAFVICITNPLDAMWALQKFSGLPTNMVIGMAGVLD	150
<a href="#">WP_112321891.1</a>	74	VCIVTAGVARKPGMS	RDDL LGINLKVMSVGGEGIAHAPNAFVICITNPLDAMWALREFSGLPHEKVKCGMAGVLD	150
<a href="#">NCU49226.1</a>	73	VIVITAGVPRKEGMS	RDDL LGINSKVMKQVGGEGIKYSPNAFVICITNPLDVMVLAQKYSGLPAEKVVGMAGVLD	149
<a href="#">WP_046140904.1</a>	74	VVIVTAGVPRKPGMS	RDDL L E INLKVMEQVGGAGIAKYAPKAFVICITNPLDAMWALQKFSGLPTNQVIGMAGVLD	150
<a href="#">GDX35174.1</a>	73	VIVITAGVPRKEGMS	RDDL LGINSKVMKQVGGEGIKYSPKAFVICITNPLDVMVLAQKYSGLPAERVVGMAGVLD	149
<a href="#">NCU53456.1</a>	73	VIVITAGVPRKEGMS	RDDL LGINSKVMKQVGGEGIKYSPNAFVICITNPLDVMVLAQKYSGLPAEKVVGMAGVLD	149
<a href="#">NCU63045.1</a>	73	VIVITAGVPRKEGMS	RDDL LGINSKVMKQVGGEGIKYSPNAFVICITNPLDVMVLAQKYSGLPAEKVVGMAGVLD	149
<a href="#">WP_046135361.1</a>	74	VVIVTAGVPRKPGMS	RDDL L E INLKVMEQVGGAGIAKYAPKAFVICITNPLDAMWALQKFSGLPTSQVIGMAGVLD	150
<a href="#">WP_160851963.1</a>	74	VCIVTAGVARKPGMS	RDDL LGINLKVMSVGGEGIRDAPNAFVICITNPLDAMWALREFSGLPHHKVCGMAGILDS	150
<a href="#">MBK8210760.1</a>	74	VVIVTAGVARKPGMS	RDDL IGINTKVMKAVGGEGIAHCPKAFVICITNPLDVMVWVREFSGLPQYNMVCGMAGVLD	150
<a href="#">XP_013336105.1</a>	74	VVIVTAGVPRKPGMS	RDDL L S INSKIVSEVADNIKIHAPDAFVICITNPLDAMVQLMRERSGLPHAKVVGMAGVLD	150
<a href="#">NBY89657.1</a>	73	VIVITAGVPRKEGMS	RDDL LGINSKVMKQVGGEGIKYSPNAFVICITNPLDVMVLAQKYSGLPAEKVVGMAGVLD	149
<a href="#">PCJ41639.1</a>	74	VVIVTAGVPRKPGMS	RDDL LGINLKVMSVGGEGIRDAPDAFVICITNPLDVMWALQQFSGLPAKVVGMAGVLD	150
<a href="#">NCU49057.1</a>	73	VIVITAGVPRKEGMS	RDDL LGINSKVMKQVGGEGIKYSPNAFVICITNPLDVMVLAQKYSGLPAEKVVGMAGVLD	149
<a href="#">NCU69999.1</a>	73	VIVITAGVPRKEGMS	RDDL LGINSKVMKQVGGEGIKYSPNAFVICITNPLDVMVLAQKYSGLPAEKVVGMAGVLD	149
<a href="#">NBQ46335.1</a>	73	VIVITAGVPRKEGMS	RDDL LGINSKVMKQVGGEGIKYSPNAFVICITNPLDVMVLAQKYSGLPAEKVVGMAGVLD	149
<a href="#">XP_013246728.1</a>	74	VVIVTAGVPRKPGMS	RDDL L S INSKIVSEVAENIKIHAPDAFVICITNPLDAMVQLMRERSGLPHAKVVGMAGVLD	150
<a href="#">HEC00426.1</a>	74	VVIVTAGVPRKPGMS	RDDL LGINLKVMSVGGEGIRDAPDAFVICITNPLDVMWALQQFSGLPANKVVGMAGVLD	150
<a href="#">WP_121938586.1</a>	74	VVIVTAGVPRKPGMS	RDDL LGINLKVMSVGGEGIRQYAPNAFVICITNPLDAMWALQKFSGLPTEKVKCGMAGVLD	150
<a href="#">NCU46848.1</a>	73	VIVITAGVPRKEGMS	RDDL LGINSKVMKQVGGEGIKYSPNAFVICITNPLDVMVLAQKYSGLPAEKVVGMAGVLD	149
<a href="#">MBI1328659.1</a>	74	VVIVTAGVPRKPGMS	RDDL LGINLKVMAAVGGEGIKNHAPNAFVICITNPLDAMWALRQFSGLPHNKVVGMAGVLD	150
<a href="#">RCL75573.1</a>	74	VCIVTAGVARKPGMS	RDDL LGINLKVMSVAGGISTHAPNAFVICITNPLDAMWALKEYSGLPHEKVVGMAGVLD	150
<a href="#">WP_099340841.1</a>	73	VIVITAGVPRKEGMS	RDDL LGINSKVMKQVGGEGIKYSPKAFVICITNPLDVMVLAQKYSGLPAERVVGMAGVLD	149
<a href="#">WP_056229719.1</a>	74	VVIVTAGVPRKPGMS	RDDL L E INLKVMEQVGGAGIAKYAPKAFVICITNPLDAMWALQKFSGLPTNQVIGMAGVLD	150
<a href="#">MBM5787331.1</a>	73	VIVITAGVPRKEGMS	RDDL LGINSKVMKQVGGEGIKYSPKAFVICITNPLDVMVLAQKYSGLPAERVVGMAGVLD	149
<a href="#">HIB19697.1</a>	74	LIVITAGIPRKP GMS	RDDL IGINTGVMEAVGAGIANKCPGAFVICITNPLDAMWALREASGLPHHKVVGMAGILDS	150
<a href="#">WP_183417264.1</a>	74	VVIVTAGVPRKPGMS	RDDL LGINLKVMSVGGGIRENCPDAFVICITNPLDAMWALREASGLPHAKVVGMAGVLD	150
<a href="#">MQA65584.1</a>	74	VVIVTAGIARKPGMS	RDDL LGINSIGVQTVGKAIKYCPKAFVIVITNPLDVMVGMRDASGLPHNRVVGMAGVLD	150
<a href="#">PPR17482.1</a>	74	LVVVITAGIPRKP GMS	RDDL IGINTRVMEAVGAGIKTNCPKAFVICITNPLDAMWALREASGLAHSKVVGMAGILDS	150
<a href="#">WP_108459774.1</a>	74	VVIVTAGVPRKPGMS	RDDL L E INLKVMEQVGGAGIAKYAPDAFVICITNPLDAMWALQKFSGLPANKVIGMAGVLD	150
<a href="#">NBT38276.1</a>	73	VIVITAGVPRKEGMS	RDDL LGINSKVMKQVGGEGIKRSPNAFVICITNPLDVMVLAQKYSGLPAEKVVGMAGVLD	149
<a href="#">WP_008943063.1</a>	74	VVIVTAGVPRKPGMS	RDDL VGINTKVMRSVGGAGIAHCPDAFVICITNPLDVMVGLREACGLPHEKVVGMAGVLD	150
<a href="#">RYE11063.1</a>	74	VVIVTAGVPRKPGMS	RDDL L E INLKVMEQVGGAGIAKYAPDAFVICITNPLDAMWALQKFSGLPSSKVVIGMAGVLD	150
<a href="#">MAL87662.1</a>	74	VCIVTAGVPRKPGMS	RDDL LGINLKVMSVGGEGIAHAPNAFVICITNPLDAMWALQKFSGLPKEKVVGMAGVLD	150
<a href="#">MAP00672.1</a>	74	VCIVTAGVPRKPGMS	RDDL LGINLKVMSVAGGISTHAPNAFVICITNPLDAMWALKEFSGLPHEKVVGMAGVLD	150
<a href="#">PPR37875.1</a>	74	LIVITAGIPRKP GMS	RDDL IGINTGVMEAVGAGIANKCPGAFVICITNPLDAMWALREASGLPHHKVVGMAGILDS	150
<a href="#">PPR36537.1</a>	74	LIVITAGIPRKP GMS	RDDL IGINTGVMEAVGAGIANKCPGAFVICITNPLDAMWALREASGLPHHKVVGMAGILDS	150
<a href="#">WP_056254967.1</a>	74	VVIVTAGVPRKPGMS	RDDL L E INLKVMEQVGGAGIAKYAPKAFVICITNPLDAMWALQKFSGLPTNQVIGMAGVLD	150
<a href="#">OUX44185.1</a>	74	VCIVTAGVARKPGMS	RDDL LGINLKVMSVAGGISTHAPNAFVICITNPLDAMWALKEYSGLPHEKVVGMAGVLD	150
<a href="#">WP_200339844.1</a>	74	VVIVTAGVPRKPGMS	RDDL VETNAKVMHQVGGEGIKNNCPNAFVICITNPLDAMVYVQLQAAGLPPEKVCGMAGVLD	150
<a href="#">XP_022589240.1</a>	74	VVIVTAGVPRKPGMS	RDDL L S INSKIVTGVADSIKLYAPDAFVICITNPLDAMVQLMRERSGLPPQKVVGMAGVLD	150
<a href="#">WP_166213281.1</a>	74	VCIVTAGVPRKPGMS	RDDL L S INLKVMEQVGGAGIKKYAPDAFVICITNPLDAMWALQKASGLPHKVVGMAGVLD	150
<a href="#">6VDH_A</a>	80	VIIITAGLTKVPGKS [5]	RDDL LPINAKIMKEVGENIKKYCPNAFVICITNPLDVMVKVLEQASGLPHNKVCGMAGVLD	161
<a href="#">TAH36160.1</a>	76	VVIVTAGIPRKP GMS	RDDL IGINTKVMQAVGGEGIKKYCPGAFVICITNPLDAMVGLQEVSGLPKNKVVGMAGVLD	152
<a href="#">WP_067555953.1</a>	74	VVIVTAGVPRKPGMS	RDDL VGINTKVMRAVGGAGIANKCPDAFVICITNPLDVMVGLRDAAGLPYEKVVGMAGVLD	150
<a href="#">MBA2590478.1</a>	74	VVIVTAGVPRKPGMS	RDDL LGINLKVMAAVGGEGIANKCPNAFVICITNPLDAMWALQKFSGVPHDKIVGMAGVLD	150
<a href="#">MBO6506542.1</a>	74	VIVITAGVARKPGMS	RDDL LGINLKVMSVGGEGIAHAPNAFVICITNPLDAMWALQKFSGLPTNKVCGMAGVLD	150
<a href="#">PCI63361.1</a>	74	VVIVTAGVARKPGMS	RDDL LGINLKVMSVGGEGIANAPDAFVICITNPLDAMWALQKFSGLPAHKVCGMAGILDS	150
<a href="#">PPR79434.1</a>	74	VIVITAGIARKPGMS	RDDL IEINTQVMKSVGGEGIKRFAPEAFVICITNPLDAMWALRKYSGLNHKVVGMAGVLD	150
<a href="#">WP_166300597.1</a>	74	VCIVTAGVPRKPGMS	RDDL L S INLKVMEQVGGAGIKKYAPDAFVICITNPLDAMWALQKASGLPHKVVGMAGVLD	150
<a href="#">MBI3675661.1</a>	74	VVIVTAGVARKPGMS	RDDL LGINLKVMAAVGGEGIAHAPKAFVICITNPLDAMWALRQFSGLPHSHVIGMAGVLD	150

<a href="#">MBT05681.1</a>	74	VVIVTAGIPRKPMS	RDDLVSNTGVMEAVGAGIKANCPNAFVICITNPLDAMVVLVQKASGLPHNKVVMGAGILDS	150
<a href="#">MBK8174980.1</a>	74	VVIVTAGVARKPGMS	RDDLIGINTKVMKAVGEGIKAHCPNAFVICITNPLDVMVWVREFSQPHNMVCMGAGVLDS	150
<a href="#">WP_029081325.1</a>	74	VCIVTAGVPRKPMS	RDDL LSINLKVMEQVVGAGIKYAPDAFVICITNPLDAMVWALQKASGLPHKKVVMGAGVLDS	150
<a href="#">WP_027287413.1</a>	74	VVIVTAGVPRKPMS	RDDL VETNSKVMHQVGEIKNNCPNAFVICITNPLDAMVYVQLQAAGLPPEKVCVMGAGVLDS	150
<a href="#">MBN9587800.1</a>	74	VVIVTAGVPRKPMS	RDDL LGINLKVMAAVGEGIKANCPNAFVICITNPLDAMVWALQKFSVGPVHGKIVGMAGVLDS	150
<a href="#">MBC7134210.1</a>	74	VVIVTAGVARKPGMS	RDDL VGINTKVMRSVGEIKNNCPDAFVICITNPLDVMVGLREACGLPEYKVVGMAGVLDS	150
<a href="#">WP_086463724.1</a>	74	VVIVTAGVARKPGMS	RDDL VGINTKVMRSVGEIKNNCPDAFVICITNPLDVMVGLREACGLPEYKVVGMAGVLDS	150
<a href="#">5NFR_A</a>	149	SRYCSLIADKLVSAEDVNAVILGGHGDLMVPL	QRYTSVNGVPLSEFVKKNMISQNEIQEIIQKTRNMGAEI IKLAK-AS	227
<a href="#">6R8G_A</a>	149	SRYCSLIADKLVSAEDVNAVILGGHGDLMVPL	QRYTSVNGVPLSEFVKKNMISQNEIQEIIQKTRNMGAEI IKLAK-AS	227
<a href="#">XP_966170.1</a>	149	SRYCSLIADKLVSAEDVNAVILGGHGDLMVPL	QRYTSVNGVPLSEFVKKNMISQNEIQEIIQKTRNMGAEI IKLAK-AS	227
<a href="#">XP_012761998.1</a>	149	SRYCSLIADKLVSAEDVNAVILGGHGDLMVPL	QRYTSVNGVPLSEFVKKNMISQNEIQEIIQKTRNMGAEI IKLAK-AS	227
<a href="#">CAC9696262.1</a>	149	SRYCSLIADKLVSAEDVNAVILGGHGDLMVPL	QRYTSVNGVPLSEFVKKNMISQNEIQEIIQKTRNMGAEI IKLAK-AS	227
<a href="#">ETW50453.1</a>	145	SRYCSLIADKLVSAEDVNAVILGGHGDLMVPL	QRYTSVNGVPLSEFVKKNMISQNEIQEIIQKTRNMGAEI IKLAK-AS	223
<a href="#">SOV74725.1</a>	149	SRYSRLIADKLVSAEDVNAVILGGHGDLMVPL	QRYTSVNGVPLSEFVKKNMISQNEIQEIIHKTRNMGSEI IKLAK-AS	227
<a href="#">SOV21691.1</a>	149	SRYSRLIADKLVSAEDVNAVILGGHGDLMVPL	QRYTSVNGVPLSEFVKKNMISQNEIQEIIQRTRNMGSEI IKLAK-AS	227
<a href="#">XP_018642816.1</a>	149	SRYSRLIADKLVSAEDVNAVILGGHGDLMVPL	QRYTSVNGVPLSEFVKKNMISQNEIQEIIQRTRNMGSEI IKLAK-AS	227
<a href="#">XP_028537330.1</a>	149	SRYSRLIADKLVSAEDVNAVILGGHGDLMVPL	QRYTSVNGVPLSEFVKKNMISQNDIQEIIQRTRNMGSEI IKLAK-AS	227
<a href="#">XP_028533952.1</a>	149	SRFRLLAEKLVNSPENVNAILGGHGDLMVPL	ERYCSVSGIPLSDFVKNKNIISQKEINEIVEKTRDGGAEI IKLAK-AS	227
<a href="#">XP_019915696.1</a>	149	SRFRSLLGDKLVNAPENVNAILGGHGDLMVPL	KRYCSVSGIPLSDFVKNKNIISDEEINAIKQTRDGMGAEI IKLSK-SS	227
<a href="#">SBT38197.1</a>	149	ARFRLLANKLVNSPENVNAILGGHGDLMVPL	ERYTSISGIPLSEFVKKNVINKTEINEIEKTRDGMGAEI IKLAK-AS	227
<a href="#">SBS85361.1</a>	149	ARFRLLAVKLVNSPENVNAILGGHGDLMVPL	ERYTSISGIPLSEFVKKNVINKTEINEIEKTRDGMGAEI IKLAK-AS	227
<a href="#">XP_012335265.1</a>	149	SRFRSLLGDKLVNAPENVNAILGGHGDLMVPL	ERYCSVSGIPLSEFVKKLLISNQDINDIIEKTRDGMGAEI IKLSK-SS	227
<a href="#">XP_028544431.1</a>	149	SRFRLLAEKLVNSPNDVNSQVLLGGHGDLMVPL	ERYCSVSGIPLSEFVKQGLITKDEINEITQKTRGMGAEI IKLAK-SS	227
<a href="#">XP_008814730.1</a>	149	SRFRSLLAEKLVNAPENVSQVLLGGHGDLMVPL	ERFCSVSGIPLSEFVKKGLISNEEINHIIKTRDGMGAEI IKLSK-SS	227
<a href="#">XP_001616198.1</a>	149	SRFRLLAEKLVKAPQNVNSQVLLGGHGDLMVPL	ERYCSISGIPLSEFVKKLLISKEEINEIVKQTRDGMGSQI IKLAK-SS	227
<a href="#">KMZ79541.1</a>	149	SRFRLLAEKLVKAPQNVNSQVLLGGHGDLMVPL	ERYCSISGIPLSEFVKKLLISKEEINEIVKQTRDGMGSQI IKLAK-SS	227
<a href="#">XP_028526585.1</a>	149	SRFRLLAEKLVNSSENVNAILGGHGDLMVPL	VRYCSVSGIPLTDFVNQNFISQKDIINEIVEKTRDGGAEI IKLAK-AS	227
<a href="#">XP_002261491.1</a>	149	SRFRSLLGDKLVNAPENVNAILGGHGDLMVPL	KRYCSVSGIPLSDFIEKLLITNEEINDIIEKTRDGMGAEI IKLSK-SS	227
<a href="#">XP_004223317.1</a>	149	SRFRSLLAEKLVNAPENVSQVLLGGHGDLMVPL	VRYCSVSGIPLSEFVKKGLITNEEINDIIEKTRDGMGAEI IKLSK-SS	227
<a href="#">CAD2095064.1</a>	149	SRFRSLLGDKLVNSPENVNAILGGHGDLMVPL	PRYCSISGIPLLEIYKNNHISEKDIINDIIEKTRDGMGAEI IKLAK-SS	227
<a href="#">ETB56770.1</a>	149	SRFRYLLGDKLVNSPENINAILGGHGDLMVPL	PRYCSISGIPLLDYIKNNDMSEKDIINDIIEKTRNMGSEI IKLAK-SS	227
<a href="#">KOB87837.1</a>	65	SRYCSLIADKLVSAEDVNAVILGGHGDLMVPL	QRYTSVNGVPLSEFVKKNMISQNEIQEIIQKTRNMGAEI IKLAK-AS	143
<a href="#">SBT79735.1</a>	149	ARFRLLAEKLVNSPANINAILGGHGDLMVPL	ERYCSVSGIPLSEFVKKNLITSKDIINEIEKTRDGMGAEI IKLAK-SS	227
<a href="#">XP_028862636.1</a>	149	ARFRLLAEKLVNSPANINAILGGHGDLMVPL	ERYCSVSGIPLSEFVKKNLITSKDIINEVEIKTRDGMGAEI IKLAK-SS	227
<a href="#">XP_022812395.1</a>	149	SRFRYLLGDKLVNSPENINAILGGHGDLMVPL	PRYCSISGIPLLDYIKNNDMSEKDIINDIIEKTRNMGSEI IKLAK-SS	227
<a href="#">XP_737386.2</a>	149	SRFRSLLSEKLVNSPENINAILGGHGDLMVPL	PRYCSISGIPLLEIYKNNHISEKDIINDIIEKTRNMGSEI IKLAK-SS	227
<a href="#">VWU52414.1</a>	149	ARFRLLSEKLVKAPENINTILLGGHGDLMVPL	QSYTSISGIPLSEFVKKLNNDVNEIIEKTRDGMGAEI IKLCK-MS	227
<a href="#">CAD2108495.1</a>	149	SRFRSLLGDKLVNSPENVNAILGGHGDLMVPL	PRYCSISGIPLLEIYKNNHISEKDIINDIIEKTRDGMGAEI IKLAK-SS	227
<a href="#">CAD2095098.1</a>	149	SRFRSLLGDKLVNSPENVNAILGGHGDLMVPL	PRYCSISGIPLLEIYKNNHISEKDIINDIIEKTRDGMGAEI IKLAK-SS	227
<a href="#">SCN61096.1</a>	149	SRFRSLLSEKLVNSPENINAILGGHGDLMVPL	PRYCSISGIPLLEIYKNNHISEKDIINDIIEKTRNMGSEI IKLAK-SS	227
<a href="#">EUD73291.1</a>	149	SRFRSLLGDKLVNSPENVNAILGGHGDLMVPL	PRYCSISGIPLLEIYKNNHISEKDIINDIIEKTRDGMGAEI IKLAK-SS	227
<a href="#">XP_008624410.2</a>	149	SRFRSLLSEKLVNSPENINAILGGHGDLMVPL	PRYCSISGIPLLEIYKNNHISEKDIINDIIEKTRNMGSEI IKLAK-SS	227
<a href="#">KEG02700.1</a>	149	SRFRSLLSEKLVNSPENINAILGGHGDLMVPL	PRYCSISGIPLLEIYKNNHISEKDIINDIIEKTRDGMGAEI IKLAK-SS	227
<a href="#">XP_034422383.1</a>	149	SRFRYLLSEKLVNSPENINAILGGHGDLMVPL	PRYCSISGIPLLDYIKNNDMSEKDISDIIEKTRNMGSEI IKLAK-SS	227
<a href="#">EAA22943.1</a>	178	SRFRYLLGDKLVNSPENINAILGGXGDLMPPL	PRYCSISGIPLLDYIKNNDMSEKDIIXDIIEKTRNMGSEI IKLAK-SS	256
<a href="#">4PLH_A</a>	152	SRFRYLLAEKLVNSPNDVQAMVIGHGDTMVPL	TRYCTVGGIPLTEFIKQGWITQEEIDEIVERTRNAGGEIVNLLKTGS	231
<a href="#">4PLT_A</a>	157	SRFRYLLAEKLVNSPNDVQAMVIGHGDTMVPL	TRYCTVGGIPLTEFIKQGWITQEEIDEIVERTRNAGGEIVNLLKTGS	236
<a href="#">4PLC_A</a>	161	SRFRHFIADKLVNSPRDVQAMVIGAHGDKMVPL	TRYVTVNGIPLQEFIKKGRITQEEIDEIVERTKNAGGEIVNLLQGGS	240
<a href="#">WP_137152966.1</a>	151	SRFVHFIADELKVSVEDINAFVLLGGHGD TMVPL	ARYSTVAGIPLTDIVKMGWMSKEKLDIAIQRTRDGGAEIVGLLKTGS	230
<a href="#">WP_193334840.1</a>	151	SRFCHFIADELNVSVDVNAFVVMGGHDTMVPL	ARYSTVAGIPLTDIVKMGWMSKEKLEEIIQRTRDGGAEIVGLLKTGS	230
<a href="#">WP_112321891.1</a>	151	ARFRHFLADEFEVSVKDVSAFVLLGGHGD TMVPL	ARYSTVAGIPLPDLVDMGWTSDQKLDIAIQRTRDGGAEIVGLLKTGS	230
<a href="#">NCU49226.1</a>	150	SRFRLLFLSEEFKVSIEDVTAFAVLLGGHGD TMVPL	ARYSTVAGIPIPLDIDMKWSTKERIEKIIQRTRDGGAEIVKLLKTGS	229
<a href="#">WP_046140904.1</a>	151	SRFVHFIADELNVSVEDINAFVLLGGHGD TMVPL	ARYSTVAGIPLTDIVKMGWMSKERLEEIIQRTRDGGAEIVGLLKTGS	230
<a href="#">GDX35174.1</a>	150	SRFRLLFLSEEFKVSIEDVTAFAVLLGGHGD TMVPL	ARYSTVAGIPIPLDIDMKWSTKERIDKIIQRTRDGGAEIVKLLKTGS	229
<a href="#">NCU53456.1</a>	150	SRFRLLFLSEEFKVSIEDVTAFAVLLGGHGD TMVPL	ARYSTVAGIPIPLDIDMKWSTKERIDKIIQRTRDGGAEIVKLLKTGS	229
<a href="#">NCU63045.1</a>	150	SRFRLLFLSEEFKVSIEDVTAFAVLLGGHGD TMVPL	ARYSTVAGIPIPLDIDMKWSTKERIDKIIQRTRDGGAEIVKLLKTGS	229
<a href="#">WP_046135361.1</a>	151	SRFVHFIADELNVSVEDINAFVLLGGHGD TMVPL	ARYSTVAGIPLTDIVKMGWMSKEKLDIAIQRTRDGGAEIVGLLKTGS	230
<a href="#">WP_160851963.1</a>	151	ARFRHFLADEFEVSVKDVTAFAVLLGGHGD TMVPL	TRYSTVAGIPLPDLVDMGWTQDKLDIAIVQRTRDGGAEIVGLLKTGS	230
<a href="#">MBK8210760.1</a>	151	ARFRFLAEFEKVSIEDVTAFAVLLGGHGD TMVPL	ARYSTVAGIPLPDLVDMGWTQEKLDKIVQRTRDGGAEIVGLLKTGS	230
<a href="#">XP_013336105.1</a>	151	ARFRSFVAERLQVSVEDVQAMVVMGGHGDAMVPL	PRYCTVGGIPLPDLVAMGQLTKQDVDDIVQRTRNNGGGEIVNLLKAGS	230

<a href="#">✓NBY89657.1</a>	150	SRFRLFLSEEFKVSIEDVTAFLVGGHGD <sup>TMVPL</sup> ARYSTVAGIPI <sup>PDL</sup> IDM <sup>NW</sup> STKERIDKIIQ <sup>RT</sup> RDGGAEIVKLLKTGS	229
<a href="#">✓PCJ41639.1</a>	151	ARFKFLAEELNVSVEDVNAFVGGHGD <sup>TMVPL</sup> PRYSTVAGIPI <sup>PDL</sup> VKMGWITNDKLEQIIQ <sup>RT</sup> RDGGAEIVGLLKTGS	230
<a href="#">✓NCU49057.1</a>	150	SRFRLFLSEEFKVSIEDVTAFLVGGHGD <sup>TMVPL</sup> ARYSTVAGIPI <sup>PDL</sup> IDM <sup>NW</sup> STKERIDKIIQ <sup>RT</sup> RDGGAEIVKLLKTGS	229
<a href="#">✓NCU69999.1</a>	150	SRFRLFLSEEFKVSIEDVTAFLVGGHGD <sup>TMVPL</sup> ARYSTVAGIPI <sup>PDL</sup> IDM <sup>NW</sup> STKERIDKIIQ <sup>RT</sup> RDGGAEIVKLLKTGS	229
<a href="#">✓NBQ46335.1</a>	150	SRFRLFLSEEFKVSIEDVTAFLVGGHGD <sup>TMVPL</sup> ARYSTVAGIPI <sup>PDL</sup> IDM <sup>NW</sup> STKERIDKIIQ <sup>RT</sup> RDGGAEIVKLLKTGS	229
<a href="#">✓XP_013246728.1</a>	151	ARFRSFVAERLQVSVEDVQAMVMGGHGDAMVPLPRYCTVSGI <sup>PL</sup> PDLVAMG <sup>LAQKDVDD</sup> IVQRTRNGGGEIVD <sup>LL</sup> KAGS	230
<a href="#">✓HEC00426.1</a>	151	ARFKFLAEELNVSVEDVNAFVGGHGD <sup>TMVPL</sup> ARYSTVAGIPI <sup>PDL</sup> VEMGWITNEKLEQIIQ <sup>RT</sup> RDGGAEIVGLLKTGS	230
<a href="#">✓WP_121938586.1</a>	151	ARFRHFLAEEDFVSVEDVTAFLVGGHGD <sup>TMVPL</sup> TRYSAVAGI <sup>PV</sup> PDLVKMGWSTQE <sup>KID</sup> AIQ <sup>RT</sup> RDGGAEIVGLLKTGS	230
<a href="#">✓NCU46848.1</a>	150	SRFRLFLSEEFKVSIEDVTAFLVGGHGD <sup>TMVPL</sup> ARYSTVAGIPI <sup>PDL</sup> IDM <sup>NW</sup> STKERIDKIIQ <sup>RT</sup> RDGGAEIVKLLKTGS	229
<a href="#">✓MBI1328659.1</a>	151	ARFRHFLADEMGVSVEDVSAFVGGHGD <sup>TMVPM</sup> PRFSTVAGI <sup>SL</sup> PELVKMGWIKQ <sup>DR</sup> LQIVQRTRDGGAEIVGLLKTGS	230
<a href="#">✓RCL75573.1</a>	151	SRFRYFISEATGVSVDISAFVGGHGD <sup>TMVPL</sup> VRYSTVGGI <sup>PL</sup> PDIVEMG <sup>LSQDAL</sup> DNIVQRTRDGGAEIVGLLKTGS	230
<a href="#">✓WP_099340841.1</a>	150	SRFRLFLSEEFKVSIEDVTAFLVGGHGD <sup>TMVPL</sup> ARYSTVAGIPI <sup>PDL</sup> IDM <sup>KW</sup> STKERIDKIIQ <sup>RT</sup> RDGGAEIVKLLKTGS	229
<a href="#">✓WP_056229719.1</a>	151	SRFVHFIADELKVSVEDINAFVGGHGD <sup>TMVPL</sup> ARYSTVAGI <sup>PL</sup> TDIVKMGWMSK <sup>EKL</sup> DAIIQ <sup>RT</sup> RDGGAEIVGLLKTGS	230
<a href="#">✓MBM5787331.1</a>	150	SRFRLFLSEEFKVSIEDVTAFLVGGHGD <sup>TMVPL</sup> ARYSTVAGIPI <sup>PDL</sup> IDM <sup>KW</sup> STKERINKIIQ <sup>RT</sup> RDGGAEIVKLLKTGS	229
<a href="#">✓HIB19697.1</a>	151	ARFRYFLAEEMDISVRDVTAFVGGHGD <sup>TMVPL</sup> VRYSTVSGI <sup>PL</sup> PDLVKMGWISK <sup>SRL</sup> GEIVQRTRDGGAEIVGLLQ <sup>AGS</sup>	230
<a href="#">✓WP_183417264.1</a>	151	ARFRHFLADEMNVSVQDVSAFVGGHGD <sup>TMVPT</sup> VRYTTVAGI <sup>PL</sup> PDLVKMGWITQ <sup>ER</sup> VDAIVDRTRNGGAEIVGLLKTGS	230
<a href="#">✓MQA65584.1</a>	151	ARFRYFLAEEFKVSVEDVTAFLVGGHGD <sup>SMVPL</sup> PRYSAVGGI <sup>PL</sup> PDLVKMGWTTQ <sup>KR</sup> INDIVQRTRDGGAEIVALLKTGS	230
<a href="#">✓PPR17482.1</a>	151	ARFRFLAEEMGVSVRDVTAFVGGHGD <sup>TML</sup> PLARYSTVSGI <sup>PL</sup> PDLVKMGWISK <sup>HRL</sup> EQIIQ <sup>RT</sup> RDGGAEIVGLLKTGS	230
<a href="#">✓WP_108459774.1</a>	151	SRFVHFIADELNVSVEDINAFVGGHGD <sup>TMVPL</sup> PRYSTVAGI <sup>PL</sup> TDIVKMGWMSK <sup>EKL</sup> LESIIQ <sup>RT</sup> RDGGAEIVGLLKTGS	230
<a href="#">✓NBT38276.1</a>	150	SRFRLFLSEEFKVSIEDVTAFLVGGHGD <sup>TMVPL</sup> ARYSTVAGIPI <sup>PDL</sup> IEMK <sup>W</sup> STKERIEKIIQ <sup>RT</sup> RDGGAEIVKLLKTGS	229
<a href="#">✓WP_008943063.1</a>	151	ARFRYFLAEEFKVSVEDVNAFVGGHGD <sup>TMVPL</sup> VRYSAVAGI <sup>PV</sup> PDLIKMGWSTQE <sup>KID</sup> QIVQRTRDGGAEIVGLLKTGS	230
<a href="#">✓RYE11063.1</a>	151	SRFRHFLIADELKVSVEDVTAFLVGGHGD <sup>TMVPL</sup> ARYSTVAGI <sup>PL</sup> TDLVKMGWLSK <sup>EKL</sup> EAIQ <sup>RT</sup> RDGGAEIVGLLKTGS	230
<a href="#">✓MAL87662.1</a>	151	ARFAYFLAEKTGVSIQDIHAWTLGGHGD <sup>DMVPM</sup> VRHSTVGGI <sup>PL</sup> PDVAVSAG <sup>MSQ</sup> GELDAIVERTKGGGEIVALLKTGS	230
<a href="#">✓MAP00672.1</a>	151	SRFRYFISEATGVSVDISAFVGGHGD <sup>TMVPL</sup> VRYSTVGGI <sup>PL</sup> PDIVEMG <sup>LSQ</sup> EGLDKIVQRTRDGGAEIVGLLKTGS	230
<a href="#">✓PPR37875.1</a>	151	ARFRYFLAEEMDISVRDVTAFVGGHGD <sup>TMVPL</sup> VRYSTVSGI <sup>PL</sup> PDLVKMGWISK <sup>SRL</sup> GEIVQRTRDGGAEIVGLLQ <sup>AGS</sup>	230
<a href="#">✓PPR36537.1</a>	151	ARFRYFLAEEMDISVRDVTAFVGGHGD <sup>TMVPL</sup> VRYSTVSGI <sup>PL</sup> PDLVKMGWISK <sup>SRL</sup> GEIVQRTRDGGAEIVGLLQ <sup>AGS</sup>	230
<a href="#">✓WP_056254967.1</a>	151	SRFVHFIADELKVSVEDINAFVGGHGD <sup>TMVPL</sup> PRYSTVAGI <sup>PL</sup> TDIVKMGWMSK <sup>EKL</sup> DAIIQ <sup>RT</sup> RDGGAEIVGLLKTGS	230
<a href="#">✓OUX44185.1</a>	151	SRFRYFXSEATGVSVDISAFVGGHGD <sup>TMVPL</sup> VRYSTVGGI <sup>PL</sup> PDIVEMG <sup>LSQDAL</sup> DNIVQRTRDGGAEIVGLLKTGS	230
<a href="#">✓WP_200339844.1</a>	151	ARFRHFLAEAMDVSVEDVNAFVGGHGD <sup>TMVPI</sup> TRYSAVAGI <sup>PL</sup> PDLVQMGWITQ <sup>DKVDQ</sup> IVDRTRKGGGEIVNLLK <sup>SGS</sup>	230
<a href="#">✓XP_022589240.1</a>	151	ARFRTFVAERMQVSVEDVHAMVMGGHGDAMVPLPRYCTVGGI <sup>PL</sup> PDLVAMG <sup>LQTKD</sup> IDEMVERTRNGGGEIVSLLK <sup>TGS</sup>	230
<a href="#">✓WP_166213281.1</a>	151	ARFRYFLADEFNVSVEDVTAFLVGGHGD <sup>TMVPL</sup> TRYSVAGI <sup>PL</sup> PDLVKMGWTSQ <sup>AR</sup> IDEIVDRTRNGGAEIVNLLK <sup>TGS</sup>	230
<a href="#">✓6VDH_A</a>	162	SRFRYFIAEKLNVSPRDVQAMVIGAHGDNM <sup>VPL</sup> PRYVTVNGI <sup>PL</sup> QEFIKKGWITQ <sup>EE</sup> EIDEIVERTRNAGGEIVNLLG <sup>TGS</sup>	241
<a href="#">✓TAH36160.1</a>	153	ARFRHFLADEFNVSVEDVTAFLVGGHGD <sup>TMVPL</sup> VRYSTIAGI <sup>PL</sup> PDVMKMGWSTQ <sup>AK</sup> IDKIVDRTRNGGGEIVALLK <sup>TGS</sup>	232
<a href="#">✓WP_067555953.1</a>	151	ARFRYFLAEEFKVSVEDVNAFVGGHGD <sup>TMVPL</sup> VRYSAVAGI <sup>PV</sup> PDLIKMGWSTQE <sup>KID</sup> QIVQRTRDGGAEIVGLLKTGS	230
<a href="#">✓MBA2590478.1</a>	151	ARFRHFLAEEMGVSVEDVSAFVGGHGD <sup>TMVPM</sup> PRFSTVAGI <sup>AL</sup> PELVKMGWIKQ <sup>DR</sup> LQIITRTANGGAEIVGLLKTGS	230
<a href="#">✓MBO6506542.1</a>	151	SRFSCFLAEEFNVSVQDVTTFVGGHGD <sup>TMVPL</sup> TRYSVAGI <sup>PV</sup> PDLIKMGWSTQE <sup>KID</sup> EIVQRTRDGGAEIVGLLKTGS	230
<a href="#">✓PCI63361.1</a>	151	SRFRHFLADEFEVSIEDVTAFLVGGHGD <sup>TMVPL</sup> TRYSVAGI <sup>PI</sup> PDMIKMGWSTQE <sup>KID</sup> EIVQRTRDGGAEIVGLLKTGS	230
<a href="#">✓PPR79434.1</a>	151	ARFRYFLSQEFKVSVEDVSAFVGGHGD <sup>TMVPL</sup> VRYSTVAGI <sup>PI</sup> PDLVKMGWITD <sup>KKL</sup> DAIVQRTRDGGAEIVGLLKTGS	230
<a href="#">✓WP_166300597.1</a>	151	ARFRYFLADEFNVSVEDVTAFLVGGHGD <sup>TMVPL</sup> TRYSVAGI <sup>PL</sup> PDLVKMGWTSQ <sup>AR</sup> IDEIVDRTRNGGAEIVNLLK <sup>TGS</sup>	230
<a href="#">✓MBI3675661.1</a>	151	ARFRHFLAEELNVSVEDVSAFVGGHGD <sup>TMVPM</sup> PRFSTVAGI <sup>PL</sup> PELVKMGWIKQ <sup>ER</sup> LQIVQRTRDGGAEIVGLLKTGS	230
<a href="#">✓MBT05681.1</a>	151	ARFRYFLAEEMGVSVKDVTAFLVGGHGD <sup>TMVPL</sup> PRYSTVAGI <sup>PL</sup> PDLVKMGWISK <sup>TQL</sup> SEIVQRTRDGGAEIVKLLK <sup>AGS</sup>	230
<a href="#">✓MBK8174980.1</a>	151	ARFRTFLAEEFQVSVEDITAFVGGHGD <sup>TMVPL</sup> ARYSTVAGI <sup>PL</sup> PDLIKMGWTTQ <sup>EKL</sup> DKIIQ <sup>RT</sup> RDGGAEIVSLLK <sup>TGS</sup>	230
<a href="#">✓WP_029081325.1</a>	151	ARFRYFLADEFNVSVEDVTAFLVGGHGD <sup>TMVPL</sup> TRYSVAGI <sup>PL</sup> PDLVKMGWTSQ <sup>AR</sup> IDEIVDRTRNGGAEIVNLLK <sup>TGS</sup>	230
<a href="#">✓WP_027287413.1</a>	151	ARFRHFLAEAMDVSVEDVNAFVGGHGD <sup>TMVPT</sup> TRYSVAGI <sup>PL</sup> PDLVEMGWITQ <sup>DKVDQ</sup> IVERTKGGGEIVNLLK <sup>SGS</sup>	230
<a href="#">✓MBN9587800.1</a>	151	ARFRHFLAEELGVSVEDVSAFVGGHGD <sup>TMVPM</sup> PRFSTVAGI <sup>AL</sup> PELVKMGWISQ <sup>DR</sup> LQIVDRTRNGGAEIVGLLKTGS	230
<a href="#">✓MBC7134210.1</a>	151	ARFRYFLAEEFKVSVEDVNAFVGGHGD <sup>TMVPL</sup> VRYSAVAGI <sup>PV</sup> PDLIKMGWSTQE <sup>KID</sup> QIVQRTRDGGAEIVGLLKTGS	230
<a href="#">✓WP_086463724.1</a>	151	ARFRYFLAEEFKVSVEDVNAFVGGHGD <sup>TMVPL</sup> VRYSAVAGI <sup>PV</sup> PDLIKMGWSTQE <sup>KID</sup> QIVQRTRDGGAEIVGLLKTGS	230
<a href="#">✓5NFR_A</a>	228	AAFAPAAAITKMIKSYLYNENNLFTCAVYLN <sup>GHY</sup> NCNSL <sup>N</sup> LVG <sup>ST</sup> AKIN <sup>NK</sup> GA-HPVEF <sup>PL</sup> TKEEQ <sup>DL</sup> YTESIASV <sup>QSN</sup> -T	305
<a href="#">✓6R8G_A</a>	228	AAFAPAAAITKMIKSYLYNENNLFTCAVYLN <sup>GHY</sup> NCNSL <sup>N</sup> LVG <sup>ST</sup> AKIN <sup>NK</sup> GA-HPVEF <sup>PL</sup> TKEEQ <sup>DL</sup> YTESIASV <sup>QSN</sup> -T	305
<a href="#">✓XP_966170.1</a>	228	AAFAPAAAITKMIKSYLYNENNLFTCAVYLN <sup>GHY</sup> NCNSL <sup>N</sup> LVG <sup>ST</sup> AKIN <sup>NK</sup> GA-HPVEF <sup>PL</sup> TKEEQ <sup>DL</sup> YTESIASV <sup>QSN</sup> -T	305
<a href="#">✓XP_012761998.1</a>	228	AAFAPAAAITKMIKSYLYNENNLFTCAVYLN <sup>GHY</sup> NCNSL <sup>N</sup> LVG <sup>ST</sup> AKIN <sup>NK</sup> GA-YPVEF <sup>PL</sup> TKEEQ <sup>DL</sup> YTESIASV <sup>QSN</sup> -T	305
<a href="#">✓CAC9696262.1</a>	228	AAFAPAAAITKMIKSYLYNQ <sup>N</sup> NLFTCAVYLN <sup>GHY</sup> NCNSL <sup>N</sup> LVG <sup>ST</sup> AKIN <sup>NK</sup> GA-HPVEF <sup>PL</sup> TKEEQ <sup>DL</sup> YTESIASV <sup>QSN</sup> -T	305
<a href="#">✓ETW50453.1</a>	224	AAFAPAAAITKMIKSYLYNENNLFTCAVYLN <sup>GHY</sup> NCNSL <sup>N</sup> LVG <sup>ST</sup> AKIN <sup>NK</sup> GA-HPVEF <sup>PL</sup> TKEEQ <sup>DL</sup> YTESIASV <sup>QSN</sup> -T	301
<a href="#">✓SOV74725.1</a>	228	AAFAPAAAITKMIKSYLYNQ <sup>N</sup> NLFTCAVYLN <sup>GHY</sup> NCNSL <sup>N</sup> LVG <sup>ST</sup> AKIN <sup>NK</sup> GA-HPVEF <sup>PL</sup> TKEEQ <sup>DL</sup> YTESIASV <sup>QSN</sup> -T	305
<a href="#">✓SOV21691.1</a>	228	AAFAPAAAITKMIKSYLYNQ <sup>S</sup> NLFTCAVYLN <sup>GHY</sup> NCNSL <sup>N</sup> LVG <sup>ST</sup> AKIN <sup>NK</sup> GV-HPVEF <sup>PL</sup> TKEEQ <sup>DL</sup> YTESIASV <sup>QSN</sup> -T	305
<a href="#">✓XP_018642816.1</a>	228	AAFAPAAAITKMIKSYLYNQ <sup>S</sup> NLFTCAVYLN <sup>GHY</sup> NCNSL <sup>N</sup> LVG <sup>ST</sup> AKIN <sup>NK</sup> GV-HPVEF <sup>PL</sup> TKEEQ <sup>DL</sup> YTESIASV <sup>QSN</sup> -T	305
<a href="#">✓XP_028537330.1</a>	228	AAFAPAAAITKMIKSYLYNQ <sup>S</sup> NLFTCAVYLN <sup>GHY</sup> NCNSL <sup>N</sup> LVG <sup>ST</sup> AKIN <sup>NK</sup> GV-HPVEF <sup>PL</sup> TKEEQ <sup>DL</sup> YTESIASV <sup>QSN</sup> -T	305
<a href="#">✓XP_028533952.1</a>	228	ACFAPAAAITKMIKSYLYNQ <sup>S</sup> NLFTCAVYLN <sup>GI</sup> YNCNDL <sup>N</sup> LVG <sup>ST</sup> ATIN <sup>SK</sup> GA-FPVEF <sup>PL</sup> TKEEQ <sup>EL</sup> YDKSIAHV <sup>KEN</sup> -T	305
<a href="#">✓XP_019915696.1</a>	228	ATFSPAAAIVKMIKSYLYNESQLYTCAVYLN <sup>GL</sup> YNCNSL <sup>N</sup> LVG <sup>ST</sup> ATIN <sup>SS</sup> GA-KPVEF <sup>PL</sup> TKEEQ <sup>EL</sup> YDKSIAHV <sup>QEH</sup> -T	305
<a href="#">✓SBT38197.1</a>	228	AAFAPAAAITKMMKSYLHNQ <sup>S</sup> QLFTCAVYLN <sup>GE</sup> YNCNDL <sup>N</sup> LVG <sup>ST</sup> AVIN <sup>SK</sup> GV-HPVEF <sup>PL</sup> TKEEQ <sup>DL</sup> YDKSIAHV <sup>KEN</sup> -T	305

✓SBS85361.1	228	AAFAPAAAIIKMMKSYLHNQNLFTCAVYLKGEYNCKDLVVGSTAVINAKGA-HPVEFPLTKEEQDLYDKSIAHVKEN-T	305
✓XP_012335265.1	228	ATFSPAAAIVKMIKSYLYNESQLYTCVAVLNLGNLNCNSLVVGSTAIINSSGA-KPVEFVLTKEEQELYDKSIAFVHEH-T	305
✓XP_028544431.1	228	ATFSPAAAIVKMIKSYLYNESQLYTCVAVLNGVYNCSDLVVGSTAVINNSGV-KPVEFTLTQEEKELYDKSIAFVRDH-T	305
✓XP_008814730.1	228	AVFSPAAAIVKMIKSYLYNESQLYTCVAVLNLGNLNCNSLVVGSTAIINSRGA-RPLEFSLTQEEKELYDKSIAFVREH-T	305
✓XP_001616198.1	228	ATFAPAAAIVKMIKSYLNFNSQLYTCVAVLNLGNLNCNSLVVGTTAIINSSGA-KPIEFALTQEEQQLYDKSIAFVREH-T	305
✓KMZ79541.1	228	ATFAPAAAIVKMIKSYLNFNSQLYTCVAVLNLGNLNCNSLVVGTTAIINSSGA-KPIEFALTQEEQQLYDKSIAFVREH-T	305
✓XP_028526585.1	228	ACFAPAAAIVKMIKSYLNFNQQLFTCAVYLKGIYNCNDLVFGTTATINSKGA-FPVEFPLTKEEQELYDKSIQHVREN-T	305
✓XP_002261491.1	228	ATFSPAAAIVKMIKSYLYNESQLYTCVAVLNLGNLNCNSLVVGSTAIINSSGA-KAIEFALTKEEQELYDKSISFVHEH-T	305
✓XP_004223317.1	228	ATFSPAAAIVKMKVSYLYNESQLYTCVAVLNLGNLNCNSLVVGSTAIINSSGA-KPIEFALTQEEQELYDKSIAFVREH-T	305
✓CAD2095064.1	228	ATFAPAAIILKMKVSYLQDQSLFTCAVYLNLGNLNCNDLVFAGSTAIINKTGA-HPIEFVLTEEEQACVYQKINSIREN-T	305
✓ETB56770.1	228	AIFAPAAIILKMIKSYLQDQQLFTCAVYLNGQYNCNLVVGSTAIINKTGA-HPIEFILTEEEQASYQKINSIREN-T	305
✓KOB87837.1	144	AAFAPAAITKMIKSYLYNENLFTCAVYLNGHYNCNSLVFGSTAKINNKGA-HPVEFPLTKEEQDLYTESIASVQSN-T	221
✓SBT79735.1	228	AAFAPAAAIVNMIKSYLYNQNKLFCAVYLNLGNLYKCSDLVFGSTTFINNKGV-YPIEFPLTQEEQQLYDKSIEHVKN-V	305
✓XP_028862636.1	228	AAFAPAAAIVNMIKSYLYNQNKLFCAVYLNLGNLYKCSDLVFGSTTFINNKGV-YPIEFPLTQEEQQLYDKSIEHVKN-V	305
✓XP_022812395.1	228	AIFAPAAIILKMIKSYLQDQQLFTCAVYLNGQYNCNLVYAGSTAIINKTGA-HPIEFILTEEEQASYQKINSIREN-T	305
✓XP_737386.2	228	ATFAPAAIILKMIKSYLQDQSLFTCAVYLNLGNLNCNDLVYAGSTAFINKTGA-HPIEFVLTEEEQSCVYQKINSIREN-T	305
✓VWU52414.1	228	ATFAPAAAIVKMIKSYFYNNQLFTCAVYLNIIYKCNMFMVGTATAQINAEGI-KPVEFTLTKEEQDLFDKSIHVQKS-T	305
✓CAD2108495.1	228	AVFAPAAIILKMKVSYLQDQSLFTCAVYLNLGNLNCNDLVFAGSTAIINKTGV-HPIEFVLTEEEQACVYQKINSIREN-T	305
✓CAD2095098.1	228	AAFAPAAIILKMKVSYLQDQSLFTCAVYLNLGNLNCNDLVFAGSTAIINKTGA-HPIEFVLTEEEQACVYQKIDNIREN-T	305
✓SCN61096.1	228	AAFAPAAIILKMIKSYLQDQSLFTCAVYLNLGNLNCNDLVYAGSTAFINKTGA-HPIEFVLTEEEQSCVYQKINSIREN-T	305
✓EUD73291.1	228	AAFAPAAIILKMKVSYLQDQSLFTCAVYLNLGNLNCNDLVFAGSTAIINKTGV-HPIEFVLTEEEQACVYQKINSIREN-T	305
✓XP_008624410.2	228	AAFAPAAIILKMKVSYLQDQSLFTCAVYLNLGNLYDCKDLFAGSTAIINKSGA-HPIEFILTEEEQAFYQKINSIREN-T	305
✓KEG02700.1	228	AAFAPAAIILKMKVSYLQDQSLFTCAVYLNLGNLNCNDLVFAGSTAIINKSGA-HPIEFILTEEEQAFYQKINSIREN-T	305
✓XP_034422383.1	228	AAFAPAAIILKMIKSYLHDQQLFTCAVYLSGLYNCKDLVYAGSTAIINKTGA-HPIEFILTEEEQACVYQKINSIREN-T	305
✓EAA22943.1	257	AIFAPAAIILKMIKSYLQDQQLF-----TSIINKTGA-HPIEFILTXEEQASYQKSIKXBXREN-T	315
✓4PLH_A	232	AYFAPAAIAIEMAESYLKDKKRILPCSAYLEGQYGVKDLFVGVVPIIGKNGVEKIELELLETEEEQEMFDKSVESVREL-V	310
✓4PLT_A	237	AYFAPAAIAIEMAESYLKDKKRILPCSAYLEGQYGVKDLFVGVVPIIGKNGVEKIELELLETEEEQEMFDKSVESVREL-V	315
✓4PLC_A	241	AYFAPAAIAIEMAEAYLKDKKRVLVCSYCLEGQYGHKDMFVGVVPIIGNGVEKIELELLETEEEQEMFDKSVESVREL-V	319
✓WP_137152966.1	231	AFYAPATSAIEMAESYLKDKKRVLPAAYLDGQYGVKGTVYGVVPIIGAGGAERIVEISLNSAEQKAFDKSVAVDGL-I	309
✓WP_193334840.1	231	AFYAPATSAIEMAESFLKDKKRVLPAAYLNGEFGVKGTVYGVVPIIGAGGAERIVEITLNSAEQKAFDKSVAVDGL-I	309
✓WP_112321891.1	231	AFYAPAAIAIEMAEAYLKDKRLLPCAAYLDGAFGVDKMYGVPTIIGAGGIERIVEIKMTKDEKAMFDKSVSAVKGL-V	309
✓NCU49226.1	230	AYYAPASSAIEMAEAYLKDKKILPCAVYLDGEYGVDDL VYGVVPIIGAKGVEKIEIKFNPEEKDMFLRSVDSVKKL-T	308
✓WP_046140904.1	231	AFYAPATSAIEMAESYLKDKKRVLPAAYLDGQYGVKGTVYGVVPIIGAGGAERIVEISLNSAEQKAFDKSVAVDGL-I	309
✓GDX35174.1	230	AYYAPASSAIEMAEAYLKDKKILPCAVYLDGEYGVDDL VYGVVPIIGAKGVEKIEIKFNPEEKEMFLKSVDSVKKL-T	308
✓NCU53456.1	230	AYYAPASSAIEMAEAYLKDKKILPCAVYLDGEYGVDDL VYGVVPIIGAKGVEKIEIKFNPEEKDMFLKSVDSVKKL-T	308
✓NCU63045.1	230	AYYAPASSAIEMAEAYLKDKKILPCAVYLDGEYGVDDL VYGVVPIIGAKGVEKIEIKFNPEEKDMFLKSVDSVKKL-T	308
✓WP_046135361.1	231	AFYAPATSAIEMAESYLKDKKRVLPAAYLDGQYGVKGTVYGVVPIIGAGGAERIVEISLNSAEQKAFDKSVAVDGL-I	309
✓WP_160851963.1	231	AFYAPAAIAIEMAEAYLKDKRVLPCAAYLDGAYGQSDLVYGVPTIIGAGGIEKIVEIKLNKEEQAMFDKSVDAVKGL-V	309
✓MBK8210760.1	231	AFYAPATSAIEMAESFLKDKRLLPCAAYLDGAYGQSDLVYGVPTIIGAGGIEKIVEIKLNKEEQAMFDKSVDAVKGL-V	309
✓XP_013336105.1	231	AFYAPAAIILMAEAYLKDKRLLPCAAYLDGQYGVNGLVYGVPCIVGAGGVEKIELELQLTPEEKAMFAKSVAVRSL-V	309
✓NBY89657.1	230	AYYAPASSAIEMAEAYLKDKKILPCAVYLDGEYGVDDL VYGVVPIIGAKGVEKIEIKFNPEEKEMFLKSVDSVKKL-T	308
✓PCJ41639.1	231	AFYAPATAAISMAESYLKDKRLLPCAVELNGEYGVNGIYVGVVPIIGANGVEKIVEISLNDDEKAGFDHSAVAVQGL-I	309
✓NCU49057.1	230	AYYAPASSAIEMAEAYLKDKKILPCAVYLDGEYGVDDL VYGVVPIIGAKGVEKIEIKFNPEEKEMFLKSVDSVKKL-T	308
✓NCU69999.1	230	AYYAPASSAIEMAEAYLKDKKILPCAVYLDGEYGVDDL VYGVVPIIGAKGVEKIEIKFNPEEKEMFLKSVDSVKKL-T	308
✓NBQ46335.1	230	AYYAPASSAIEMAEAYLKDKKILPCAVYLDGEYGVDDL VYGVVPIIGAKGVEKIEIKFNPEEKEMFLKSVDSVKKL-T	308
✓XP_013246728.1	231	AFYAPAAIILMAEAYLKDKRVLPCAAYLDGQYGVNGLVYGVPCIVGAGGVEKIELELQLTAEKAMFAKSVAVRSL-V	309
✓HEC00426.1	231	AFYAPATAAISMAESYLKDKRLLPCAVELNGEYGVNGIYVGVVPIIGAGGVEKIVEISLNDDEKAGFDHSAVAVQGL-I	309
✓WP_121938586.1	231	AFYAPAAIAIQMAESYLKDKRLLPCAAYLDGAYGQSDLVYGVPTIIGAGGIEKIVEIKLNKEEQAMFDKSVDAVKGL-V	309
✓NCU46848.1	230	AYYAPASSAIEMAEAYLKDKKILPCAVYLDGEYGVDDL VYGVVPIIGAKGVEKIEIKFNPEEKEMFLKSVDSVKKL-T	308
✓MBI1328659.1	231	AFYAPATSAIQMAESYLKDKRVLPCAAYLDGAYGKIDLVGLPAVIGEKIERIVLELLETFEDERAQLAKSAGAVKGL-I	309
✓RCL75573.1	231	AYYAPASSAIQMAESYLKDKRLLPCASVFNQYVNLNGIYVGVVPIIGSQGIEKIVEISLSKEEQEMF5KSVDSVKKL-I	309
✓WP_099340841.1	230	AYYAPASSAIEMAEAYLKDKKILPCAVYLDGEYGVDDL VYGVVPIIGAKGVEKIEIKFNPEEKEMFLKSVDSVKKL-T	308
✓WP_056229719.1	231	AFYAPATSAIEMAESYLKDKKRVLPAAYLDGQYGVKGTVYGVVPIIGAGGAERIVEISLNSAEQKAFDKSVAVDGL-I	309
✓MBM5787331.1	230	AYYAPASSAIEMAEAYLKDKKILPCAVYLDGEYGVDDL VYGVVPIIGAKGVEKIEIKFNPEEKEMFLKSVDSVKKL-T	308
✓HIB19697.1	231	AFYAPASAAIEMAESYLKDKKRVLPCAAYLNGQYGVNGLVYGVVPIIGTKGVERIVEISLSKSENAQFQKSVASVRAS-V	309
✓WP_183417264.1	231	AFYAPASSAIEMAESYLKDKRVLPCAAYLDGQYGVDDL VYGVVPIIGEGGVERIVLELLETAEEQEMF5KSVTAVQGL-V	309
✓MQA65584.1	231	AFYAPASAAIQMAESYLKDKRVLPCAAYLDGAYGKGMFVGVVPIIGAKGVEKIEIPLTAAEKAEFDKSVGAVRGLS	310
✓PPR17482.1	231	AFYAPATAAISMAESYLKDKRVLPCAAYLNGQYGVNGLVYGVVPIIGAKGVERIVEIALNKSEKAFQKSVASVRGL-V	309
✓WP_108459774.1	231	AFYAPATSAIEMAESYLKDKKRVLPAAYLDGQYGVKGTVYGVVPIIGAGGAERIVEISLNSAEQKAFDKSVAVDGL-I	309
✓NBT38276.1	230	AYYAPASSAIEMAEAYLKDKKILPCAVYLDGEYGVDDL VYGVVPIIGAKGVEKIEIKFNPEEKEMFLKSVDSVKKL-T	308
✓WP_008943063.1	231	AFYAPASSAIQMAESYLKDKRVLPCAAYVKGAYGLDGLVYGVVPIIGAKGVERIVEIENLNADEKMF5KSVGAVKAL-V	309

<a href="#">RYE11063.1</a>	231	AFYAPATSAIEMAESYLKDKKRRLPVAAYLKGEYGVKTYVGVPAVIGAGGAERVVEISLNSAEQKAFKESVAAVGGL - I	309
<a href="#">MAL87662.1</a>	231	AFYAPAESAIAAMARSYLLDQKRVLPCAVWLSGEYGLSDLVYGVPPALIGANGVEKVEFSTNDDEKAMFKKSVESVQGL - I	309
<a href="#">MAP00672.1</a>	231	AYYAPASSAIQMAESYLKDKKRLLPCAFAFVEGKYNDLGLYVGVVWVIGGGQIERVIEISLSKEEQMEFNSVDSVKGL - I	309
<a href="#">PPR37875.1</a>	231	AFYAPASAAIEMAESYLKDKKRVLTCAAYLNGQYGVGRGLYVGVVWVIGIKGVERIVEISLSKSENAQFQKSVASVRAS - V	309
<a href="#">PPR36537.1</a>	231	AFYAPASAAIEMAESYLKDKKRVLTCAAYLNGQYGVGRGLYVGVVWVIGIKGVERIVEISLSKSENAQFQKSVASVRAS - V	309
<a href="#">WP_056254967.1</a>	231	AFYAPATSAIEMAESYLKDKKRVMPTAAAYLDGQYGVKTYVGVVWVIGAGGAEKVIEISLNSAEQKAFDQKSVGAVEGL - I	309
<a href="#">OUX44185.1</a>	231	AYYAPASSAIQMAESYLKDKKRLLPCASVFNQYVNGIYVGVVWVIGSQGIEKVEISLSKEEQMEFNSVDSVKGL - I	309
<a href="#">WP_200339844.1</a>	231	AFYAPASSAIQMAESYLKDKKRVLPTAAAYLTGQYGVDMYVGVVWVIGDQGIERIVELKFTHEQEMFNHVSVEVREL - V	309
<a href="#">XP_022589240.1</a>	231	AFYAPAAAGVLMAEAYLKDKKRVLPCAAYLTGQYGVSNLYVGVVWVIGGGVEKILEHLTSEERSMFEKSVESVREL - V	309
<a href="#">WP_166213281.1</a>	231	AFYAPAASAIQMAESYLKDKKRVLPCAAYLNGEYGVKDMYVGVPTVIGSKGVERIVEISLAGKDREAFDQKSVASVQGL - V	309
<a href="#">6VDH_A</a>	242	AYFAPAASAIAMAEAYLKDKKRVLPCSCYLEGQYGVKDLVYGVVWVIGNGVEKVEIELELTPEEKEMFDKSIIEVREL - V	320
<a href="#">TAH36160.1</a>	233	AFYAPAASAIEMAESYLKDKKRVLPCAAYLNGEYGVKDIYVGVVWVIGKGGVEKVEIEIQMNADEKSMFDKSVAAVQEL - V	311
<a href="#">WP_067555953.1</a>	231	AFYAPASSAIQMAESYLKDKKRVLPCAAYVKGAYLDGLYVGVVWVIGAKGVERIVEIELNADEKQMFNSVAVKAL - V	309
<a href="#">MBA2590478.1</a>	231	AYYAPATSAIQMAESYLKDKKRVLPCAVVNGAYGIKDLVGLVWVIGKEKVEKVVLELNADEKAGLDKSDAVRGL - I	309
<a href="#">MBO6506542.1</a>	231	AYYAPATSAIEMAESYLKDKRRLPCAFLSGEYGLNDMYVGVVWVIGANGVEKVEIEILIGEEKSGFEHSGAVKGL - M	309
<a href="#">PCI63361.1</a>	231	AFYAPATSAIEMAESYLKDKRRLPCAAYLNGEYGLNDMYVGVPTVIGAGGIEKVEIEILQGDEQTFDHSVDAVKGL - M	309
<a href="#">PPR79434.1</a>	231	AFYAPAASAIMVESYLYDKRRLPCAAYLNGEYVNVKGLYVGVVWVIGSKGVEKVEIEIKLNSDERSMFNKSVKAVKDL - V	309
<a href="#">WP_166300597.1</a>	231	AFYAPAASAIQMAESYLKDKKRVLPCAAYLNGEYGVKDMYVGVPTVIGSKGVERIVEIELTGKDREAFDQKSVAVQGL - V	309
<a href="#">MBI3675661.1</a>	231	AFYAPATSAIEMAESYLKDKKRVLPCACVYVNGPYGIKDLVYGVPAVIGKEKVERVEIELTAGEREAALNKSAAESVREL - I	309
<a href="#">MBT05681.1</a>	231	AFYAPATAAIEMAEAYIKDKRVLPCAFLNGQYGVKGIYVGVVWVIGSRGVERVEIELSRTEMSQFQKSVVAVKNL - V	309
<a href="#">MBK8174980.1</a>	231	AFYAPATSAVAMAEFLKDKKRRLPCAAYWCDGYPYQNGLYVGVPTIIGAGGIEKVEIEILNAEEKAMLDHNSINSVKTL - V	309
<a href="#">WP_029081325.1</a>	231	AFYAPAASAIQMAESYLKDKKRVLPCAAYLNGEYGVKDMYVGVPTVIGSKGVERIVEIELLAGKDREAFDQKSVASVQGL - V	309
<a href="#">WP_027287413.1</a>	231	AFYAPASSAIQMAESYLKDKKRVLPTAAAYLTGQYGVNDMYVGVVWVIGDKGIERIVELKFTDHEQEMFNHVSVEVREL - V	309
<a href="#">MBN9587800.1</a>	231	AYYAPATSAIEMAESYLKDKRVLPCAVHVNGPYGIKDLVGLVWVIGKEKVERVEIELNADEKQMFHDSVSAVKAL - V	309
<a href="#">MBC7134210.1</a>	231	AFYAPASSAIQMADSYLKDKKRVLPCAAYVKGAYGLDGLYVGVVWVIGAKGVERIVEIELNADEKQMFHDSVSAVKAL - V	309
<a href="#">WP_086463724.1</a>	231	AFYAPASSAIQMADSYLKDKKRVLPCAAYVKGAYGLDGLYVGVVWVIGAKGVERIVEIELNADEKQMFHDSVSAVKAL - V	309
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<a href="#">6R8G_A</a>	306	QKAFDL--IKAaL[7]	324
<a href="#">XP_966170.1</a>	306	QKAFDL--IK----	313
<a href="#">XP_012761998.1</a>	306	QKAFDL--IK----	313
<a href="#">CAC9696262.1</a>	306	QKAFDL--IK----	313
<a href="#">ETW50453.1</a>	302	QKAFDL--IK----	309
<a href="#">SOV74725.1</a>	306	QKAFNL--IK----	313
<a href="#">SOV21691.1</a>	306	QKAFDL--IN----	313
<a href="#">XP_018642816.1</a>	306	QKAFDL--IN----	313
<a href="#">XP_028537330.1</a>	306	EKAFDL--IK----	313
<a href="#">XP_028533952.1</a>	306	QKAFDM--IK----	313
<a href="#">XP_019915696.1</a>	306	QKAFAL--IN----	313
<a href="#">SBT38197.1</a>	306	QKAFNQ--IV----	313
<a href="#">SBS85361.1</a>	306	QKAFNQ--IV----	313
<a href="#">XP_012335265.1</a>	306	QKAFAL--IN----	313
<a href="#">XP_028544431.1</a>	306	QKAFAM--IN----	313
<a href="#">XP_008814730.1</a>	306	QKAFAL--IN----	313
<a href="#">XP_001616198.1</a>	306	QKAFAL--IN----	313
<a href="#">KMZ79541.1</a>	306	QKAFAL--IN----	313
<a href="#">XP_028526585.1</a>	306	HKAFNM--IN----	313
<a href="#">XP_002261491.1</a>	306	QKAFAL--IN----	313
<a href="#">XP_004223317.1</a>	306	QKAFAL--IN----	313
<a href="#">CAD2095064.1</a>	306	KKALDA--VN----	313
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<a href="#">KOB87837.1</a>	222	QKAFDL--IK----	229
<a href="#">SBT79735.1</a>	306	KKAFDI--IN----	313
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✓WP_193334840.1	310	EACKKI-APKL--A	320
✓WP_112321891.1	310	DACKGI-DDSL--S	320
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✓MBI1328659.1	310	DACKGL-EPKL--A	320
✓RCL75573.1	310	EACIKI-DPSL--G[2]	322
✓WP_099340841.1	309	QDLFKL-DPEVakI[7]	328
✓WP_056229719.1	310	EACKKI-APKL--A	320
✓MBM5787331.1	309	QDLFKL-DPEVakI[7]	328
✓HIB19697.1	310	AAVKKT-RKNQtnK[1]	323
✓WP_183417264.1	310	EACKKL---GFkgG[1]	321
✓MQA65584.1	311	ELAKLL-AKGKrkG[2]	325
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✓WP_108459774.1	310	EACKKI-APKL--A	320
✓NBT38276.1	309	QDLFKL-DPEVakI[7]	328
✓WP_008943063.1	310	EVVKNM-DASA--G	320
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✓WP_056254967.1	310	EACKKI-APKL--A	320
✓OUX44185.1	310	EACIKI-DPSL--G[2]	322
✓WP_200339844.1	310	DACKKL---GAl--	318
✓XP_022589240.1	310	EALPKN-----[2]	317
✓WP_166213281.1	310	DACKKI-APDLlgK	322
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✓WP_067555953.1	310	EIVKNM-DATA--G	320
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