NameNote:N	M. haemocanis str. Illinois unique CDSs	Role category (TIGR microbial role categories)		Biological Process Terms <sup>a</sup>	Cellular Component Terms <sup>a</sup>	Internal Helix <sup>b</sup>	Non-Cytoplasmic (signal peptide) <sup>b</sup>	Subcellular Localization <sup>b</sup>	GenBank Access Number
	Paralogous family 9	hypothetical protein		ion/chloride transport (41%)	membrane (42%)	1	no	cytoplasmic membrane	AEW45130.1
proteom         control         <	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,					1			AEW45133.1
بهديالعنهالحكةالح		hypothetical protein	transferase (33%)	transport (30%)	cytoplasm (53%)	1	no	cytoplasmic membrane	AEW45134.1
ParterProduct of the start of		hypothetical protein	nucleotide/ATP binding (39%)	metabolic process (32%)	cytoplasm (37%)	1	no	unknown	AEW45136.1
ParterProduct of the start of		hypothetical protein	catalytic activity (51%)	GTP metabolic process (32%	) cytoplasm (67%)	1	no	unknown	AFW45155.1
partial protection of the section of the sectin of the section of the section of the section of the se				carbohydrate metabolic					
protects of out of the second of t		hypothetical protein	ATP binding (39%)	process (37%)		1	no	unknown	AEW45158.1
hybrid biol         (DR)		hypothetical protein	electron carrier activity	,		1	no	cytoplasmic membrane	AEW45237.1
n performant of the performant		hypothetical protein	(38%)/oxidoreductase activity (38%0		membrane (46%)	1	no	unknown	AEW45238.1
Normal sector         Normal	4 in				cytoplasm (20%)/extracellular	0			
Image and the second of the second	lot in paralogous families	nypothetical protein	protein binding (46%)/ two-	two-component signal transduction system (46%)/ regulation of transcription, DNA-dependent (46%)/	(19%)	U	no	cytoplasmic membrane	AEW45062.1
Instructure		hypothetical protein			membrane (53%)	0	no	unknown	AEW45474.1
Instruction         Number (N)         No         Negation (N)         Negation (N) <td></td> <td>hypothetical protein</td> <td></td> <td></td> <td>chromosome (100%)</td> <td>2</td> <td>no</td> <td>cytoplasmic membrane</td> <td>AEW45815.1</td>		hypothetical protein			chromosome (100%)	2	no	cytoplasmic membrane	AEW45815.1
Non-the product of product				ATP biosynthetic process					
Normal sector         Normal		nypotnetical protein	ATP binding (37%)		membrane (70%)	1	no	cytoplasmic membrane	AEW45816.1
Number of problem (problem (problem (problem))         Number of problem (problem)         Number of problem (probl		hypothetical protein	hydrolase (71%)		membrane (71%)	1	no	unknown	AEW45817.1
Nombia			oxidoreductase						
Name         NA*         NA*         NA*         O        O        O         O									AEW45917.1
Nome         NA*         NA*         NA*         O         NO         No <th< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></th<>									
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Second (SM)         Sold isocone (CM)         Sold isocone (CM) <th< td=""><td>esent in other bacteria</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></th<>	esent in other bacteria								
congent         conduct         templane         membrane (00%)         (0%)	emofelis str. Ohio2)	phosphotransferase system	ribosome (100%)	translation (100%)	ribosome (100%)	0	no	unknown	AEW45065.1
Bis Start         Results         Results (R05)         Results (R05) <thresults (r05)<="" th="">         Results (R05)</thresults>			sugar:hydrogen symporter activity (100%)	transport (100%)	membrane (100%)	7	no	cytoplasmic membrane	AEW45748.
Maxmander SL. Observerser         Discretation (Title)         Disc						0			AE10/45025
unique COS         microlar los écosonarias         Molecular Function nor intering (MA)         Molecular function de los formalitadas participadas         Solucitad Processo Function         Calibration Constraints         Intering (MA)         Municipadas         Number           ratiogues family 8         Psycholicial processo         Psycholicial processolicial processo         Psycholicial processo	M haamafalia atr Ohia?		Tibosoffie (100%)	translation (100%)	hbosome (100%)	0		cytopiastriic	
seigenze family 8 hypothesized protein binding (65%) 4 h1***********************************				Biological Process Terms <sup>a</sup>	Cellular Component Terms <sup>a</sup>	Internal Helix <sup>b</sup>		Subcellular Localization <sup>b</sup>	
Nybridies profes	ralogous family 8	hypothetical protein		DNA integration (80%)	N.I.*	1	no	unknown	AEG72490.1
hypothetical probein         message (1%)         signal translation (3%)         signal translation (3%) <td></td> <td>hypothetical protein</td> <td>hydrolase (20%)</td> <td>lipid metabolism (20%)</td> <td>membrane (42%)</td> <td>1</td> <td>no</td> <td>cytoplasmic</td> <td></td>		hypothetical protein	hydrolase (20%)	lipid metabolism (20%)	membrane (42%)	1	no	cytoplasmic	
Nypotesia probe         Nameson (19%)         Nameso		hypothetical protein		signal transduction (54%)	membrane (56%)	1	no	unknown	AEG72503 1
Non-the call proteined         nucleic acd biologi (19%)         biological process (13%)         numbrane (40%)         1         no         optoplasmic         AEG72361           Nypoblecial protein         Nx4         mapper (19%)         shifts processing (19%) </td <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>									
<ul> <li>medica cad binding (28%)</li> <li>mRNA processing (29%)</li> <li>mRNA processing (29%)</li> <li>mRNA processing (29%)</li> <li>mrRNA processing (</li></ul>			nucleic acid binding (19%)	biological process (13%)	membrane (40%)	1		cytoplasmic	AEG72504.1
Nycofielical protein         Nycofieli		hypothetical protein		transport (91%)	chromosome (91%)	1	no	cytoplasmic	AEG73619.1
Inyochelical protein         hene binding (28)         transport (28)         membrane (24)         1         no         unknown         AEG7359.1           raidgoas family 11         hypothelical protein         hypothelical protein         hypothelical protein         hypothelical protein         hypothelical protein         hypothelical protein         heat shock protein hypothelical		hypothetical protein	hydrolase (39%)	mRNA processing (39%)	chromosome (72%)	1	no	unknown	AEG73558.1
rategous family 11 hypothetical protein in binding (35%) in a diametein (25%) in membrane (2%) in membrane (		hypothetical protein	heme binding (28%)	transport (28%)	membrane (24%)	1	no	unknown	AEG73559.1
hypothetical protein         hypotheti	aralogous family 11	hypothetical protein	ion binding (36%)	cell adhesion (23%)	membrane (27%)	1	no	unknown	AEG72489.1
hypothetical protein         (49%)         membrane (45%)         membrane (45%)         1         yes         unknown         REC748b.1           hypothetical protein         ohannel activity (5%)         transport (45%)         optoplasmi (35%)         1         yes         unknown         REG7260.1           nalogous family 12         hypothetical protein         protein binding (25%)         protein binding (25%)         optoplasmi (25%)         1         yes         unknown         REG72638.1           hypothetical protein         nucleotole/ATP binding (45%)         transport (25%)         optoplasmi (25%)         1         yes         extracellular         REG7363.1           hypothetical protein         nucleotole/ATP binding (45%)         transport (25%)         (27%)         (25%)         (27%) <t< td=""><td></td><td>hypothetical protein</td><td>hydrolase (41%)</td><td></td><td>chromosome (52%)</td><td>1</td><td>no</td><td>unknown</td><td>AEG72502.1</td></t<>		hypothetical protein	hydrolase (41%)		chromosome (52%)	1	no	unknown	AEG72502.1
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catalytic activity (28%) ATP       viral reproduction (69%)       N.A.*       2       no       cytoplasmic membrane       AEG73767.1         hypothetical protein       translation release factor       translational termination       membrane (42%)       1       yes       unknown       AEG73767.1         hypothetical protein       activity (24%)       (24%)       membrane (42%)       1       yes       unknown       AEG72694.1         hypothetical protein       (56%) receptor activity (59%) signal transduction (60%)       membrane (90%)       2       no       cytoplasmic membrane       AEG72554.1         (19%) receptor activity (59%) signal transduction (60%)       membrane (90%)       2       no       cytoplasmic membrane       AEG72554.1         (19%) receptor activity (59%) signal transduction (60%)       metalloen activity (59%) signal transduction (60%)       membrane (90%)       2       no       cytoplasmic membrane       AEG72554.1         (19%) receptor activity (59%) signal transduction (60%)       metalloen (34%)       metalloen activity       membrane (34%)       0       no       unknown       AEG73596.1         hypothetical protein       (34%)       metal lon binding (28%)       transport (18%)       membrane (50%)       2       no       cytoplasmic membrane       AEG72323.1         hypothetical protein		hypothetical protein	nucleotide binding (43%)			0	no	cytoplasmic	AEG73312.1
translation release factor       translational termination         hypothetical protein       activity (24%)       (24%)       membrane (42%)       1       yes       unknown       AEG72694.1         signal transducer activity       signal transducer activity       membrane (42%)       2       no       cytoplasmic membrane       AEG72694.1         hypothetical protein       (59%) receptor activity (59%) signal transduction (60%)       membrane (90%)       2       no       cytoplasmic membrane       AEG72554.1         hypothetical protein       (34%) metal ion binding       proteolysis (34%)/       pathogenesis (17%)       extracellular region (34%)       0       no       unknown       AEG73596.1         hypothetical protein       (34%)       metal ion binding (28%)       transport (18%)       membrane (50%)       2       no       cytoplasmic membrane       AEG725923.1         metal ion binding (24%)       transport (18%)       membrane (50%)       2       no       cytoplasmic membrane       AEG72523.1			catalytic activity (28%)/ ATP						
signal transducer activity hypothetical protein (59%) receptor activity (59%) signal transduction (60%) membrane (90%) 2 no cytoplasmic membrane AEG72554.1 metalloendopeptidase activity (34%) metal ion binding proteolysis (34%) hypothetical protein (34%) metal ion binding (28%) transport (18%) membrane (50%) 2 no cytoplasmic membrane AEG73596.1 metal ion binding (28%) transport (18%) membrane (50%) 2 no cytoplasmic membrane AEG72923.1 metal ion binding (34%) (24%) (24%) (24%) (24%) membrane (50%) 2 no cytoplasmic membrane AEG72923.1			translation release factor	translational termination		2			
hypothetical protein         (5%)/ receptor activity (5%) signal transduction (60%)         membrane (90%)         2         no         cytoplasmic membrane         AEG72554.1           metalioendopeptidase activity (34%) metal ion binding hypothetical protein         proteolysis (34%)         atracellular region (34%)         0         no         unknown         AEG73596.1           hypothetical protein         (34%)         pathogenesis (17%)         extracellular region (34%)         0         no         unknown         AEG73596.1           hypothetical protein         metal ion binding (28%)         transport (18%)         membrane (50%)         2         no         cytoplasmic membrane         AEG72523.1           metal ion binding (43%)/ DNA         metal ion binding (43%)/ DNA         transport (18%)         membrane (50%)         2         no         cytoplasmic membrane         AEG72523.1		nypothetical protein		(24%)	membrane (42%)	1	yes	unknown	AEG72694.1
(34%)/ metal ion binding     proteolysis (34%)/       hypothetical protein     (34%)       hypothetical protein     (34%)       hypothetical protein     (34%)       hypothetical protein     (34%)       metal ion binding (28%)     transport (18%)       metal ion binding (43%)/ DNA     membrane (50%)		hypothetical protein	(59%)/ receptor activity (59%)	signal transduction (60%)	membrane (90%)	2	no	cytoplasmic membrane	AEG72554.1
hypothetical protein metal ion binding (28%) transport (18%) membrane (50%) 2 no cytoplasmic membrane AEG72923.1 metal ion binding (43%)/ DNA									
metal ion binding (43%)/ DNA			(34%)/ metal ion binding						
			(34%)/ metal ion binding (34%)	pathogenesis (17%)					AEG73596.1
			(34%)/ metal ion binding (34%) metal ion binding (28%)	pathogenesis (17%)					

	hypothetical protein	DNA binding (27%)	transcription (27%)	membrane (51%)	0	no	unknown	AEG73391.1
	hypothetical protein	structural molecule activity (60%)	transport (17%)/ cell adhesion (15%)	cytoplasm (63%)/ cytoskeleton (63%)	1	no	cytoplasmic membrane	AEG72824.1
	hypothetical protein	nucleotide (49%)/ATP binding (31%)	translation (17%)	cytoplasm (36%)	1	no	cytoplasmic	AEG73591.1
	hypothetical protein	protein binding (36%)/ receptor activity (42%)	cell adhesion (31%)	membrane (50%)	1	no	cytoplasmic	AEG73116.1
	hypothetical protein	metallopeptidase activity (20%)	proteolysis (20%)	membrane (54%)	1	no	cytoplasmic	AEG73115.1
	hypothetical protein	protein binding (32%)	phosphate transport (19%)/ cell adhesion (19%)	cytoplasm (35%)	1	no	cytoplasmic	AEG73114.1
	hypothetical protein	RNA binding (99%)	evasion by virus of host immune response (99%)	cytoplasm (99%)/ chromosome (99%)	3	no	cytoplasmic membrane	AEG73017.1
	hypothetical protein	catalytic activity (56%)/ transferase (44%)	metabolic process (48%)	membrane (100%)	3	no	cytoplasmic membrane	AEG72385.1
	hypothetical protein	transaminase/isomerase (100%)	porphyrin byosynthetic process (100%)	cytoplasm (100%)	0	no	cytoplasmic	AEG72616.1
		nucleotide binding (34%)/ translation initiation factor	translational initiation (32%)/					
	hypothetical protein	activity (32%)	pathogenesis (20%)	membrane (42%)	1	no	unknown	AEG73324.1
CDSs with predicted function	hypothetical protein	N.A.*	N.A.*	N.A.*	2	no	cytoplasmic membrane	AEG73429.1
(present in several bacteria species, but absent in <i>M.</i> haemocanis str. illinois)	type II site-specific deoxyribonuclease	Type II site-specific deoxyribonuclease activity (83%)	DNA restriction-modification system (83%)	membrane (11%)	0	no	cytoplasmic	AEG73510.1
	Cytosine-specific methyltransferase	DNA (cytosine-5-)- methyltransferase activity (99%)	DNA methylation (99%)/ DNA restriction-modification system (99%)	chromosome (7%)	0	no	unknown	AEG73555.1
	C-5 cytosine-specific DNA methylase	DNA (cytosine-5-)- methyltransferase activity (100%)	DNA methylation (100%)/ DNA restriction-modification system (100%)	chromosome (9%)	0	no	cytoplasmic	AEG73509.1

<sup>a</sup> ESG software (sequence similarity-based function prediction) [36].

<sup>b</sup> prediction using PSORTb version 3 software [31].

\* N.A.: no function assigned by ESG software.