

Mass Spectrometry Unit

Assay Report: UniMS 95/19



Sponsor Identification:

M. Madalena Alves - BRIDGE - Universidade do Minho

Sample Identification:

Sample - Amostra 1, Amostra 2, Amostra 3, Amostra 4, Amostra 5, Amostra 6

Sample Type - Protein

Sample reception date - 22/05/2019

Assay:

Peptide mapping by nanoLC-MS using Sciex TripleTOF 6600 mass spectrometer.

Database search:

Generated mass spectra were processed using Protein Pilot Software v. 5.0 (Sciex) for protein identification. The search was performed against the UniProt (reviewed and unreviewed) protein sequences for *Methanobacterium formicicum*. Peptide identification was considered with >95% confidence.

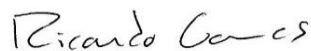
Assay Result:

Protein identification lists are displayed in *Amostra 1* to *Amostra 6* sections.
The total ion current chromatogram is displayed in *TIC* section.

Approval:



Bruno M. Alexandre, PhD
(MS specialist)



Ricardo Gomes, PhD
(MS specialist)

Oeiras, 25th June 2019

UniMS Results General Info



Proteins detected table

N	Protein rank
Unused	Unused ProtScore
Total	Total ProtScore
% Cov (95)	Percentage of aminoacids in a protein sequence identified with 95% confidence
Accession #	Protein unique ID in the database searched
Name	Protein name
Species	Sample species (if applicable)
Peptides(95%)	Number of distinct peptides identified with at least 95% confidence

ID statistics table

Unused (Conf) Cutoff	Threshold for unused protein score and corresponding identification confidence
Proteins Detected	Number of proteins groups identified for each cut off specifications
Proteins Before Grouping	Total number of proteins identified with a TotalScore above the Unused threshold specifications
Distinct Peptides	Number of unique peptides identified for each cut off specifications
Spectra Identified	Number of spectra with associated peptide identifications for each cut off specifications
% Total Spectra	Percentage of spectra with associated peptide identifications for each cut off specifications

The *Proteins detected table* shown includes all proteins identified. For identifications with a specific confidence level please refer to the following instructions:

Unused (Conf) Cutoff	
>2.0 (99)	For 99% identification confidence use proteins with Unused ProtScore >2
>1.3 (95)	For 95% identification confidence use proteins with Unused ProtScore >1.3
>0.47 (66)	For 66% identification confidence use proteins with Unused ProtScore >0.47

We recommend a data analysis using a confidence level of at least 95%, therefore we only report proteins that meet this threshold.

About the Total ProtScore and the Unused ProtScore

For each detected protein, the Pro Group Algorithm calculates the Total ProtScore and the Unused ProtScore.

The Total ProtScore measures all the peptide evidence for a protein and is analogous to protein scores reported by other protein identification software.

The Unused ProtScore measures all the peptide evidence for a protein that is not better explained by a higher ranked protein. It is the true indicator of protein confidence.

Amostra 1

1) Z:\Projects\UniMS2019_95 MALves\Data\CS1_9uL.wiff

Sample Type: Identification
Cys. Alkylation: Iodoacetamide
Digestion: Trypsin
Instrument: TripleTOF 6600
Special Factors: Gel-based ID
Species:
ID Focus: Biological modifications
 Amino acid substitutions
Database: 20190624_uniprot_methanobacterium+formicicum_6903entries.fasta
Search Effort: Thorough
FDR Analysis: Yes
User Modified Parameter Files: Yes



Proteins detected table

N	Unused	Total	% Cov (95	Accession #	Name	Species	Peptides(95%)
1	73.06	73.06	77.7	tr A0A090IAH6 A0A090IAH6_METFO	Thermosome subunit OS=Methanobacterium formicicum C METFO		291
2	72.01	72.21	51.1	tr A0A090I8L6 A0A090I8L6_METFO	Replication factor-A domain-containing protein OS=Methan METFO		45
3	61.86	61.86	40.6	tr A0A090I2R3 A0A090I2R3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO		53
4	56.4	56.4	59.1	tr A0A090I2M3 A0A090I2M3_METFO	V-type ATP synthase alpha chain OS=Methanobacterium f METFO		71
5	54.66	54.66	74.7	tr A0A090I2T3 A0A090I2T3_METFO	Methyl-coenzyme M reductase subunit beta OS=Methanob METFO		516
6	54	54.09	50.2	tr A0A090I3A9 A0A090I3A9_METFO	Chaperone protein DnaK OS=Methanobacterium formicicu METFO		55
7	50.93	50.93	97.5	tr A0A090I573 A0A090I573_METFO	5,10-methylenetetrahydromethanopterin reductase OS=Me METFO		259
8	46.92	48.78	71.3	tr A0A090I7W3 A0A090I7W3_METFO	Methyl-coenzyme M reductase subunit beta OS=Methanob METFO		194
9	46.11	46.2	65	tr A0A090I2R9 A0A090I2R9_METFO	F420-non-reducing hydrogenase subunit A OS=Methanob METFO		55
10	44.34	44.34	51.1	tr A0A090I2G6 A0A090I2G6_METFO	Methyl-coenzyme M reductase subunit alpha OS=Methano METFO		80
11	43.24	43.29	39.5	tr A0A090I7T4 A0A090I7T4_METFO	Phosphoenolpyruvate synthase OS=Methanobacterium for METFO		35
12	39.06	39.06	12.3	tr A0A090I3J2 A0A090I3J2_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO		31
13	39	39.01	33.4	tr A0A090I3T1 A0A090I3T1_METFO	Elongation factor 2 OS=Methanobacterium formicicum OX- METFO		28
14	38.34	40.04	58.7	tr A0A090I4W3 A0A090I4W3_METFO	F420-non-reducing hydrogenase vhc subunit A OS=Metha METFO		42

Amostra 1

15	36.42	36.42	50.3	tr A0A090I9A6 A0A090I9A6_METFO	Hydroxylamine reductase OS=Methanobacterium formicicu METFO	42
16	36.13	36.14	54.4	tr A0A0S4FR78 A0A0S4FR78_METFO	V-type ATP synthase beta chain OS=Methanobacterium fo METFO	80
17	35.67	35.77	43.3	tr A0A089ZDH4 A0A089ZDH4_METFO	Elongation factor 1-alpha OS=Methanobacterium formicicu METFO	39
18	34.7	34.74	35.7	tr A0A090I3G7 A0A090I3G7_METFO	CoB--CoM heterodisulfide reductase subunit A HdrA2 OS= METFO	41
19	33.89	33.93	49.3	tr A0A090I8W8 A0A090I8W8_METFO	Bifunctional enzyme Fae/Hps OS=Methanobacterium formi METFO	48
20	32.19	32.19	44.9	tr A0A090I7U6 A0A090I7U6_METFO	GDP-mannose 4,6-dehydratase OS=Methanobacterium fo METFO	26
21	30.19	43.66	61.5	tr A0A090IA40 A0A090IA40_METFO	Thermosome subunit OS=Methanobacterium formicicum C METFO	113
22	30.09	30.1	68.8	tr A0A090I4G9 A0A090I4G9_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO	189
23	29.91	30.04	62.8	tr A0A090I5H3 A0A090I5H3_METFO	Methenyltetrahydromethanopterin cyclohydrolase OS=Met METFO	33
24	29.91	29.95	42	tr A0A090JVC3 A0A090JVC3_METFO	Methyl-coenzyme M reductase subunit alpha OS=Methano METFO	47
25	28.63	28.98	34.2	tr A0A090I2L6 A0A090I2L6_METFO	D-3-phosphoglycerate dehydrogenase OS=Methanobacter METFO	19
26	28.48	28.49	47.1	tr A0A090I6W9 A0A090I6W9_METFO	Cell shape determining protein MreB/Mrl OS=Methanobact METFO	36
27	27.75	27.83	47.6	tr A0A090JTE7 A0A090JTE7_METFO	30S ribosomal protein S3 OS=Methanobacterium formicicu METFO	19
28	26.58	26.63	63.9	tr A0A090I1H9 A0A090I1H9_METFO	30S ribosomal protein S4e OS=Methanobacterium formicic METFO	27
29	26	26	67	tr A0A090I8V8 A0A090I8V8_METFO	F420-dependent methylenetetrahydromethanopterin dehyd METFO	49
30	25.53	25.58	39.5	tr A0A089ZIP7 A0A089ZIP7_METFO	DNA primase DnaG OS=Methanobacterium formicicum O METFO	21
31	24.49	24.49	54.1	tr A0A090I5T3 A0A090I5T3_METFO	Methyl-coenzyme M reductase subunit gamma OS=Methar METFO	21
32	23.71	23.71	35.3	tr A0A090I281 A0A090I281_METFO	Pyruvate synthase subunit PorA OS=Methanobacterium fo METFO	20
33	23.35	23.36	55.6	tr A0A090I842 A0A090I842_METFO	CBS domain-containing membrane protein OS=Methanoba METFO	28
34	23.21	23.25	37.7	tr A0A090I2P0 A0A090I2P0_METFO	CBS domain-containing protein OS=Methanobacterium fo METFO	15
35	23.11	23.14	34.3	tr A0A090I7L2 A0A090I7L2_METFO	Acetyl-CoA decarbonylase/synthase complex subunit gamr METFO	15
36	23	23.06	62.5	tr A0A090I5H7 A0A090I5H7_METFO	Tetrahydromethanopterin S-methyltransferase subunit H O METFO	40
37	22.49	22.62	41.1	tr A0A090JUK8 A0A090JUK8_METFO	V-type proton ATPase subunit E OS=Methanobacterium fo METFO	16
38	22.32	22.4	41.7	tr A0A089ZBS9 A0A089ZBS9_METFO	Acetyl-CoA acetyltransferase OS=Methanobacterium formi METFO	34
39	22.27	22.38	42.2	tr A0A089ZVL0 A0A089ZVL0_METFO	Cell division protein FtsZ OS=Methanobacterium formicicu METFO	15
40	22.16	22.21	38.5	tr A0A090I210 A0A090I210_METFO	Putative aminotransferase MJ0959 OS=Methanobacterium METFO	23
41	21.87	21.95	20.4	tr A0A089ZHH5 A0A089ZHH5_METFO	Phosphoserine phosphatase SerB OS=Methanobacterium METFO	12
42	21.74	21.78	60.4	tr A0A089ZEV2 A0A089ZEV2_METFO	CBS domain-containing protein OS=Methanobacterium fo METFO	29
43	21.36	21.44	30.7	tr A0A090I2C6 A0A090I2C6_METFO	Methyl-coenzyme M reductase component A2 AtwA1 OS= METFO	13
44	21.2	21.24	62.4	tr A0A090I2W9 A0A090I2W9_METFO	Proteasome subunit beta OS=Methanobacterium formicicu METFO	29
45	20.03	20.05	35.4	tr A0A089ZUL5 A0A089ZUL5_METFO	Tryptophan synthase beta chain OS=Methanobacterium fo METFO	12
46	20	20	53.8	tr A0A090IB20 A0A090IB20_METFO	Proteasome subunit alpha OS=Methanobacterium formicic METFO	27
47	19.91	20.12	27.1	tr A0A089ZGQ5 A0A089ZGQ5_METFO	Peptidase U62 family OS=Methanobacterium formicicum C METFO	13

Amostra 1

48	19.77	19.77	49.4	tr A0A090I5U4 A0A090I5U4_METFO	SPFH domain/Band 7 family protein OS=Methanobacterium METFO	17
49	19.72	19.72	50.3	tr A0A090I613 A0A090I613_METFO	Coenzyme F420 hydrogenase subunit beta OS=Methanobacterium METFO	33
50	19.69	20.48	33.1	tr A0A090I4G3 A0A090I4G3_METFO	LL-diaminopimelate aminotransferase OS=Methanobacterium METFO	14
51	19.65	19.8	33.9	tr A0A090I4Q7 A0A090I4Q7_METFO	Aspartate--tRNA(Asp/Asn) ligase OS=Methanobacterium formicicun METFO	12
52	19.2	19.29	36.1	tr A0A090JWH2 A0A090JWH2_METFO	Phosphoglucosamine mutase GlmM2 OS=Methanobacterium formicicun METFO	14
53	19.19	19.33	36.6	tr A0A089ZUT3 A0A089ZUT3_METFO	50S ribosomal protein L3 OS=Methanobacterium formicicun METFO	17
54	19.09	19.17	46.4	tr A0A090I5W3 A0A090I5W3_METFO	30S ribosomal protein S3Ae OS=Methanobacterium formicicun METFO	17
55	18.97	19.08	42.7	tr A0A090I1P7 A0A090I1P7_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	11
56	18.93	18.96	56.5	tr A0A090JTE0 A0A090JTE0_METFO	50S ribosomal protein L6 OS=Methanobacterium formicicun METFO	18
57	18.31	18.54	51	tr A0A089ZAX5 A0A089ZAX5_METFO	30S ribosomal protein S2 OS=Methanobacterium formicicun METFO	12
58	18.18	18.24	21.8	tr A0A090I2I6 A0A090I2I6_METFO	Archaeal glutamate synthase [NADPH] OS=Methanobacterium formicicun METFO	12
59	17.66	17.68	54.5	tr A0A090I2I9 A0A090I2I9_METFO	Translation initiation factor 6 OS=Methanobacterium formicicun METFO	19
60	17.55	17.56	50	tr A0A090I9S3 A0A090I9S3_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	24
61	17.46	17.53	23	tr A0A089ZAI4 A0A089ZAI4_METFO	Formylmethanofuran dehydrogenase subunit A FwdA OS=Methanobacterium formicicun METFO	12
62	17.37	17.41	18.9	tr A0A090I3H2 A0A090I3H2_METFO	Phosphoribosylformylglycinamide synthase subunit PurL OS=Methanobacterium formicicun METFO	10
63	17.25	17.34	37.5	tr A0A090I9D3 A0A090I9D3_METFO	Succinate--CoA ligase [ADP-forming] subunit beta OS=Methanobacterium formicicun METFO	11
64	17.18	18.51	38.8	tr A0A090I305 A0A090I305_METFO	Coenzyme F420 hydrogenase alpha subunit FrhA OS=Methanobacterium formicicun METFO	25
65	16.84	16.9	37.3	tr A0A089ZG02 A0A089ZG02_METFO	DNA repair and recombination protein RadA OS=Methanobacterium formicicun METFO	13
66	16.81	16.91	48.7	tr A0A089Z979 A0A089Z979_METFO	Site-determining protein OS=Methanobacterium formicicun METFO	23
67	16.2	16.25	25.3	tr A0A090I3J1 A0A090I3J1_METFO	Formate dehydrogenase beta subunit FdhB OS=Methanobacterium formicicun METFO	8
68	16.18	16.27	48.7	tr A0A090I0N7 A0A090I0N7_METFO	PyrE-like protein OS=Methanobacterium formicicun METFO	9
69	16.05	16.11	25.9	tr A0A090I6I2 A0A090I6I2_METFO	Adenylosuccinate synthetase OS=Methanobacterium formicicun METFO	9
70	15.91	15.94	39.4	tr A0A090I6Q2 A0A090I6Q2_METFO	Formylmethanofuran dehydrogenase subunit C FwdC OS=Methanobacterium formicicun METFO	15
71	15.52	15.58	27.8	tr A0A090I3H9 A0A090I3H9_METFO	5-formaminoimidazole-4-carboxamide-1-(beta)-D-ribofuran METFO	9
72	15.16	15.18	30.7	tr A0A089ZI64 A0A089ZI64_METFO	ATP phosphoribosyltransferase OS=Methanobacterium formicicun METFO	8
73	15.09	15.11	25.7	tr A0A090JXJ6 A0A090JXJ6_METFO	3-dehydroquinate synthase OS=Methanobacterium formicicun METFO	12
74	14.9	14.97	26.4	tr A0A090I8M3 A0A090I8M3_METFO	S-adenosylmethionine synthase OS=Methanobacterium formicicun METFO	9
75	14.9	14.91	44.7	tr A0A089ZGF9 A0A089ZGF9_METFO	30S ribosomal protein S5 OS=Methanobacterium formicicun METFO	16
76	14.88	14.9	30.3	tr A0A090JVV9 A0A090JVV9_METFO	Aspartate carbamoyltransferase OS=Methanobacterium formicicun METFO	9
77	14.86	14.9	61.7	tr A0A089ZUS9 A0A089ZUS9_METFO	50S ribosomal protein L18 OS=Methanobacterium formicicun METFO	8
78	14.82	14.89	26.5	tr A0A090I5S8 A0A090I5S8_METFO	Argininosuccinate synthase OS=Methanobacterium formicicun METFO	8
79	14.78	14.85	10.3	tr A0A090I151 A0A090I151_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	11
80	14.64	14.8	30.7	tr A0A090I781 A0A090I781_METFO	Fructose-1,6-bisphosphate aldolase/phosphatase OS=Methanobacterium formicicun METFO	8

Amostra 1

81	14.56	14.65	37.2	tr A0A090I1I9 A0A090I1I9_METFO	CoB-CoM heterodisulfide reductase iron-sulfur subunit C O METFO	14
82	14.51	14.54	68.7	tr A0A089ZCU1 A0A089ZCU1_METFO	Transcription elongation factor Spt5 OS=Methanobacterium METFO	9
83	14.45	14.47	30.2	tr A0A090I345 A0A090I345_METFO	3-isopropylmalate dehydrogenase OS=Methanobacterium METFO	11
84	14.25	14.32	57.8	tr A0A090I579 A0A090I579_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	12
85	14.19	14.3	23.8	tr A0A090I3S6 A0A090I3S6_METFO	DNA-directed RNA polymerase subunit A' OS=Methanobacterium METFO	16
86	14.13	14.18	68	tr A0A090I170 A0A090I170_METFO	TATA-box-binding protein OS=Methanobacterium formicicum METFO	17
87	14.13	14.14	33.7	tr A0A090I192 A0A090I192_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	9
88	14.04	14.04	47	tr A0A089ZGG4 A0A089ZGG4_METFO	50S ribosomal protein L14 OS=Methanobacterium formicicum METFO	11
89	14	14	28	tr A0A090I2K4 A0A090I2K4_METFO	Putative ATP-binding protein MJ0685 OS=Methanobacterium METFO	7
90	14	14	41.2	tr A0A090JW64 A0A090JW64_METFO	LemA family protein OS=Methanobacterium formicicum OX= METFO	10
91	14	14	26.3	tr A0A090I471 A0A090I471_METFO	GDP-mannose 4,6-dehydratase OS=Methanobacterium formicicum METFO	10
92	13.83	14.01	23.6	tr A0A090JXT2 A0A090JXT2_METFO	O-acetylhomoserine (Thiol)-lyase OS=Methanobacterium formicicum METFO	8
93	13.53	13.8	21.7	tr A0A089ZCR8 A0A089ZCR8_METFO	Proteasome-activating nucleotidase OS=Methanobacterium METFO	11
94	13.52	13.79	29.6	tr A0A090I514 A0A090I514_METFO	UPF0219 protein DSM1535_2142 OS=Methanobacterium formicicum METFO	40
95	13.51	13.62	45.2	tr A0A090I7T8 A0A090I7T8_METFO	Peptidyl-prolyl cis-trans isomerase OS=Methanobacterium formicicum METFO	19
96	13.2	13.37	28.3	tr A0A090JV64 A0A090JV64_METFO	CBS domain-containing membrane protein OS=Methanobacterium formicicum METFO	12
97	13.16	13.4	25.6	tr A0A090JTX8 A0A090JTX8_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	7
98	13.12	13.22	22.4	tr A0A089ZGM2 A0A089ZGM2_METFO	CoB--CoM heterodisulfide reductase subunit B HdrB1 OS= METFO	12
99	13.1	13.16	54	tr A0A090I4T3 A0A090I4T3_METFO	Orotate phosphoribosyltransferase OS=Methanobacterium METFO	8
100	13.08	13.21	26.6	tr A0A090I433 A0A090I433_METFO	GMP synthase [glutamine-hydrolyzing] subunit B OS=Methanobacterium METFO	7
101	13.03	13.08	18.2	tr A0A090I3Y0 A0A090I3Y0_METFO	Phenylalanine--tRNA ligase beta subunit OS=Methanobacterium METFO	8
102	13.02	20.75	22.6	tr A0A0S4FLI0 A0A0S4FLI0_METFO	Putative ABC transporter ATP-binding protein MJ1242 OS= METFO	12
103	13.01	13.07	20.5	tr A0A090I3U3 A0A090I3U3_METFO	Peptidase U62 modulator of DNA gyrase OS=Methanobacterium METFO	7
104	12.94	13.05	18.7	tr A0A090JY31 A0A090JY31_METFO	Aspartokinase OS=Methanobacterium formicicum OX=216 METFO	7
105	12.9	13.02	35	tr A0A0S4FRT9 A0A0S4FRT9_METFO	Formylmethanofuran--tetrahydromethanopterin formyltransferase METFO	14
106	12.69	12.79	13.9	tr A0A089ZHM6 A0A089ZHM6_METFO	Methyl-coenzyme M reductase component A2 AtwA2 OS=Methanobacterium METFO	6
107	12.68	12.74	20.2	tr A0A090JTT4 A0A090JTT4_METFO	Methanogenesis marker protein 15 OS=Methanobacterium METFO	6
108	12.59	12.65	17.4	tr A0A090I796 A0A090I796_METFO	Pyridoxal 5'-phosphate synthase subunit PdxS OS=Methanobacterium METFO	8
109	12.58	12.66	25.7	tr A0A090I166 A0A090I166_METFO	Enolase OS=Methanobacterium formicicum OX=2162 GN= METFO	8
110	12.39	12.47	18.7	tr A0A090JUQ9 A0A090JUQ9_METFO	Putative nickel insertion protein OS=Methanobacterium formicicum METFO	6
111	12.29	12.42	21.2	tr A0A090IAD3 A0A090IAD3_METFO	Homoserine dehydrogenase OS=Methanobacterium formicicum METFO	6
112	12.15	12.23	23.4	tr A0A090I0T1 A0A090I0T1_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	11
113	12.02	12.14	21.9	tr A0A089ZAG5 A0A089ZAG5_METFO	Transcriptional regulator with CBS domains OS=Methanobacterium METFO	8

Amostra 1

114	12	12	39.9	tr A0A090I180 A0A090I180_METFO	50S ribosomal protein L5 OS=Methanobacterium formicicu METFO	12
115	11.92	12.06	30.7	tr A0A089ZJ55 A0A089ZJ55_METFO	DNA polymerase sliding clamp OS=Methanobacterium forr METFO	8
116	11.89	11.98	36.1	tr A0A089ZCQ3 A0A089ZCQ3_METFO	Putative rubrerythrin OS=Methanobacterium formicicum O) METFO	9
117	11.78	11.84	24.1	tr A0A090I246 A0A090I246_METFO	3-hydroxy-3-methylglutaryl coenzyme A reductase OS=Met METFO	6
118	11.77	11.82	31.3	tr A0A089ZH50 A0A089ZH50_METFO	Phosphate ABC transporter phosphate-binding protein Pst METFO	7
119	11.57	11.65	31.6	tr A0A089ZER7 A0A089ZER7_METFO	Exosome complex component Rrp4 OS=Methanobacteriun METFO	10
120	11.43	11.5	14.4	tr A0A090I599 A0A090I599_METFO	Acetyl-CoA decarbonylase/synthase complex subunit beta METFO	7
121	11.41	11.44	29.3	tr A0A090I2T7 A0A090I2T7_METFO	Methyl-coenzyme M reductase subunit gamma OS=Methar METFO	7
122	11.36	11.49	43.9	tr A0A090I424 A0A090I424_METFO	Translation initiation factor 5A OS=Methanobacterium form METFO	12
123	11.27	11.35	30.7	tr A0A090I4Y4 A0A090I4Y4_METFO	Circadian clock protein KaiC OS=Methanobacterium formic METFO	9
124	11.24	11.31	21.2	tr A0A089ZVL1 A0A089ZVL1_METFO	50S ribosomal protein L10 OS=Methanobacterium formicic METFO	6
125	11.23	11.31	18.8	tr A0A090I428 A0A090I428_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	8
126	11.23	11.27	22.1	tr A0A090JW72 A0A090JW72_METFO	Arsenite-activated ATPase ArsA OS=Methanobacterium fo METFO	10
127	11.16	11.2	44.6	tr A0A090JWN0 A0A090JWN0_METFO	Putative secreted protein OS=Methanobacterium formicicu METFO	26
128	10.96	11.07	28.5	tr A0A090I6I6 A0A090I6I6_METFO	Isopentenyl-diphosphate delta-isomerase OS=Methanobac METFO	6
129	10.75	11.06	32.2	tr A0A090I3I7 A0A090I3I7_METFO	Putative sugar kinase MTH_1544 OS=Methanobacterium f METFO	6
130	10.71	10.82	29	tr A0A089ZGG9 A0A089ZGG9_METFO	50S ribosomal protein L4 OS=Methanobacterium formicicu METFO	9
131	10.63	10.77	17.9	tr A0A090I2F4 A0A090I2F4_METFO	Polyferredoxin protein MvhB OS=Methanobacterium formic METFO	10
132	10.57	10.61	31.8	tr A0A090I2G3 A0A090I2G3_METFO	Tetrahydromethanopterin S-methyltransferase subunit A O METFO	23
133	10.56	10.6	17	tr A0A0S4FMQ4 A0A0S4FMQ4_METFO	Putative hydrogenase expression/formation protein MJ067 METFO	6
134	10.39	10.42	16.8	tr A0A090I518 A0A090I518_METFO	Digeranylgeranyllycerophospholipid reductase OS=Metha METFO	6
135	10.36	10.44	30.2	tr A0A090I8S8 A0A090I8S8_METFO	ABC transporter ATP-binding protein OS=Methanobacteriu METFO	6
136	10.25	10.63	9.3	tr A0A089ZCL2 A0A089ZCL2_METFO	Lon protease OS=Methanobacterium formicicum OX=2162 METFO	7
137	10.21	10.33	20.5	tr A0A089ZG23 A0A089ZG23_METFO	Formylmethanofuran dehydrogenase subunit F FwdF1 OS METFO	5
138	10.19	10.21	19.2	tr A0A090I7B6 A0A090I7B6_METFO	Inosine-5'-monophosphate dehydrogenase OS=Methanob METFO	8
139	10.13	10.31	21.5	tr A0A090I672 A0A090I672_METFO	dTDP-glucose 4,6-dehydratase OS=Methanobacterium for METFO	6
140	10.1	10.28	30.6	tr A0A090I552 A0A090I552_METFO	Exosome complex component Rrp42 OS=Methanobacteriu METFO	11
141	10.02	10.03	19.9	tr A0A090I4Y0 A0A090I4Y0_METFO	Threonine synthase OS=Methanobacterium formicicum OX METFO	5
142	10	10	36.3	tr A0A090I5G8 A0A090I5G8_METFO	F420-non-reducing hydrogenase subunit G OS=Methanob METFO	15
143	10	10	16.1	tr A0A090I496 A0A090I496_METFO	N-acetyl-gamma-glutamyl-phosphate reductase OS=Metha METFO	5
144	10	10	46.1	tr K2QDP1 K2QDP1_METFP	30S ribosomal protein S10 OS=Methanobacterium formicic METFP	5
145	9.98	10.82	25.9	tr A0A090I7S6 A0A090I7S6_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	11
146	9.92	10.15	36.8	tr A0A090I729 A0A090I729_METFO	TrkA domain-containing protein OS=Methanobacterium for METFO	6

Amostra 1

147	9.91	10.02	23.6 tr A0A089ZDP0 A0A089ZDP0_METFO	Thiamine thiazole synthase OS=Methanobacterium formicicum METFO	5
148	9.84	10.03	37 tr A0A089ZGF5 A0A089ZGF5_METFO	CBS domain-containing protein OS=Methanobacterium formicicum METFO	6
149	9.82	9.9	29 tr A0A090I622 A0A090I622_METFO	Translation initiation factor 2 subunit alpha OS=Methanobacterium formicicum METFO	8
150	9.64	9.75	17.5 tr A0A089ZV33 A0A089ZV33_METFO	FeS assembly protein SufBD OS=Methanobacterium formicicum METFO	7
151	9.6	9.77	22 tr A0A090I7U4 A0A090I7U4_METFO	ABC transporter OS=Methanobacterium formicicum OX=21 METFO	6
152	9.34	9.49	15 tr A0A0S4FN62 A0A0S4FN62_METFO	UDP-N-acetylglucosamine 2-epimerase OS=Methanobacterium formicicum METFO	5
153	9.3	11.5	10.5 tr A0A089ZDA2 A0A089ZDA2_METFO	Cell division control protein Cdc48 OS=Methanobacterium formicicum METFO	8
154	9.28	9.45	16.1 tr A0A090I938 A0A090I938_METFO	Phosphomethylpyrimidine synthase OS=Methanobacterium formicicum METFO	8
155	9.18	9.41	27.1 tr A0A090I560 A0A090I560_METFO	Putative hydrogenase nickel incorporation protein HypB OS=Methanobacterium formicicum METFO	5
156	9.15	9.33	38.6 tr A0A090I340 A0A090I340_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	5
157	9.08	9.13	7.2 tr A0A090I8V0 A0A090I8V0_METFO	Threonine--tRNA ligase OS=Methanobacterium formicicum METFO	5
158	9.04	9.1	33 tr A0A090JWL2 A0A090JWL2_METFO	IMP cyclohydrolase OS=Methanobacterium formicicum OX METFO	10
159	9.02	9.13	30.1 tr A0A089ZAY7 A0A089ZAY7_METFO	30S ribosomal protein S4 OS=Methanobacterium formicicum METFO	7
160	9.01	9.17	37.1 tr A0A089Z8Q6 A0A089Z8Q6_METFO	30S ribosomal protein S11 OS=Methanobacterium formicicum METFO	14
161	8.89	9.04	27.1 tr A0A090I958 A0A090I958_METFO	Extracellular solute-binding protein OS=Methanobacterium formicicum METFO	13
162	8.85	8.93	23.3 tr A0A090I3Q7 A0A090I3Q7_METFO	Nucleotidyl transferase OS=Methanobacterium formicicum METFO	10
163	8.65	8.92	11.6 tr A0A090I0Z8 A0A090I0Z8_METFO	Type 2 DNA topoisomerase 6 subunit B OS=Methanobacterium formicicum METFO	5
164	8.64	8.68	32.1 tr A0A089ZF65 A0A089ZF65_METFO	PRC-barrel domain-containing protein OS=Methanobacterium formicicum METFO	8
165	8.62	8.77	34.9 tr A0A090JVL3 A0A090JVL3_METFO	Coenzyme F420 hydrogenase gamma subunit FrhG OS=Methanobacterium formicicum METFO	8
166	8.54	9	9.5 tr A0A090I904 A0A090I904_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	5
167	8.53	8.58	12.5 tr A0A089ZGS2 A0A089ZGS2_METFO	Replication factor C small subunit OS=Methanobacterium formicicum METFO	4
168	8.44	8.55	61.9 tr A0A089ZBS5 A0A089ZBS5_METFO	30S ribosomal protein S6e OS=Methanobacterium formicicum METFO	6
169	8.36	8.56	15.6 tr A0A090IB58 A0A090IB58_METFO	Carbamoyl-phosphate synthase small chain OS=Methanobacterium formicicum METFO	5
170	8.16	8.31	19.2 tr A0A090I2K0 A0A090I2K0_METFO	Phosphoribosylformylglycinamide cyclo-ligase OS=Methanobacterium formicicum METFO	5
171	8.14	8.23	26.6 tr A0A090JSP3 A0A090JSP3_METFO	Uridylate kinase OS=Methanobacterium formicicum OX=21 METFO	10
172	8.11	8.2	28 tr A0A089ZC51 A0A089ZC51_METFO	Extracellular phosphate-binding protein OS=Methanobacterium formicicum METFO	5
173	8.09	8.11	40.6 tr A0A090JTC3 A0A090JTC3_METFO	30S ribosomal protein S9 OS=Methanobacterium formicicum METFO	7
174	8.08	8.27	12.5 tr A0A089ZGW2 A0A089ZGW2_METFO	Translation initiation factor 2 subunit gamma OS=Methanobacterium formicicum METFO	5
175	8.07	8.35	15.7 tr A0A090I3I6 A0A090I3I6_METFO	Putative lipoprotein MJ0085 OS=Methanobacterium formicicum METFO	5
176	8.07	8.08	15.9 tr A0A090I731 A0A090I731_METFO	Glucose-1-phosphate thymidyltransferase OS=Methanobacterium formicicum METFO	4
177	8.03	8.03	37.1 tr A0A089ZGF2 A0A089ZGF2_METFO	50S ribosomal protein L13 OS=Methanobacterium formicicum METFO	12
178	8.02	8.02	44.1 tr A0A089ZGZ1 A0A089ZGZ1_METFO	30S ribosomal protein S8e OS=Methanobacterium formicicum METFO	7
179	8.02	8.02	12.7 tr A0A090JTB4 A0A090JTB4_METFO	Ribonuclease J OS=Methanobacterium formicicum OX=21 METFO	6

Amostra 1

180	8	8.04	18.2	tr A0A089ZA17 A0A089ZA17_METFO	Peptidase U32 family OS=Methanobacterium formicicum C METFO	4
181	7.91	8.05	24.7	tr A0A090I443 A0A090I443_METFO	Superoxide dismutase OS=Methanobacterium formicicum C METFO	5
182	7.87	8.09	19	tr A0A090JYU9 A0A090JYU9_METFO	Phosphosulfolactate synthase OS=Methanobacterium formicicum C METFO	5
183	7.86	7.93	11.1	tr A0A090I6T0 A0A090I6T0_METFO	Glutamine synthetase OS=Methanobacterium formicicum C METFO	4
184	7.86	7.93	36.4	tr A0A089ZHN5 A0A089ZHN5_METFO	Probable transcription termination protein NusA OS=Methanobacterium formicicum C METFO	4
185	7.83	7.98	22.2	tr A0A089ZEW4 A0A089ZEW4_METFO	50S ribosomal protein L11 OS=Methanobacterium formicicum C METFO	5
186	7.68	7.77	50	tr K2QX04 K2QX04_METFP	Deoxyribonuclease/rho motif-related TRAM OS=Methanobacterium formicicum C METFP	4
187	7.66	7.91	12	tr A0A090JW43 A0A090JW43_METFO	Glutamyl-tRNA(Gln) amidotransferase subunit A OS=Methanobacterium formicicum C METFO	4
188	7.63	7.75	52.3	tr A0A090I6K9 A0A090I6K9_METFO	30S ribosomal protein S17 OS=Methanobacterium formicicum C METFO	7
189	7.61	7.85	34.7	tr A0A089ZV28 A0A089ZV28_METFO	Heat shock protein Hsp20 OS=Methanobacterium formicicum C METFO	8
190	7.57	7.64	20.6	tr A0A090I6D3 A0A090I6D3_METFO	Ornithine carbamoyltransferase OS=Methanobacterium formicicum C METFO	4
191	7.55	7.64	9.6	tr A0A0S4FQD8 A0A0S4FQD8_METFO	Putative ABC transporter ATP-binding protein MJ0719 OS=Methanobacterium formicicum C METFO	5
192	7.52	7.59	27.6	tr A0A090JUF5 A0A090JUF5_METFO	Pyruvate synthase subunit PorC OS=Methanobacterium formicicum C METFO	4
193	7.49	7.68	16.2	tr A0A090JYL6 A0A090JYL6_METFO	Peptidase C60 sortase A and B OS=Methanobacterium formicicum C METFO	5
194	7.25	7.36	34.8	tr A0A089ZCA7 A0A089ZCA7_METFO	Thioesterase OS=Methanobacterium formicicum C OX=2162 METFO	6
195	7.22	7.29	15.3	tr A0A090I3J9 A0A090I3J9_METFO	Tungsten-containing formylmethanofuran dehydrogenase 2 METFO	4
196	7.21	7.29	17.6	tr A0A090I5G4 A0A090I5G4_METFO	Exosome complex component Rrp41 OS=Methanobacterium formicicum C METFO	4
197	7.17	7.48	29.5	tr A0A090JV59 A0A090JV59_METFO	Transcription elongation factor NusA-like protein OS=Methanobacterium formicicum C METFO	4
198	7.17	7.26	23.2	tr A0A090JX40 A0A090JX40_METFO	(5-formylfuran-3-yl)methyl phosphate synthase OS=Methanobacterium formicicum C METFO	8
199	7.17	7.23	13.9	tr A0A090I391 A0A090I391_METFO	Daunorubicin resistance ABC transporter ATPase subunit C METFO	5
200	7.12	7.18	35.9	tr A0A089ZG55 A0A089ZG55_METFO	Uncharacterized protein OS=Methanobacterium formicicum C METFO	8
201	7.02	9.41	22.9	tr A0A090JXN7 A0A090JXN7_METFO	Uncharacterized protein OS=Methanobacterium formicicum C METFO	17
202	6.99	7.17	12.8	tr A0A090I8R6 A0A090I8R6_METFO	Acetylornithine aminotransferase OS=Methanobacterium formicicum C METFO	4
203	6.94	7.44	19.2	tr K2QY77 K2QY77_METFP	Transcription initiation factor IIB OS=Methanobacterium formicicum C METFP	5
204	6.91	7	7.2	tr A0A090JWG4 A0A090JWG4_METFO	DNA ligase OS=Methanobacterium formicicum C OX=2162 C METFO	4
205	6.89	7.02	32.5	tr A0A090JU72 A0A090JU72_METFO	Putative secreted protein OS=Methanobacterium formicicum C METFO	4
206	6.86	6.98	31.9	tr A0A089ZEU2 A0A089ZEU2_METFO	Uncharacterized protein OS=Methanobacterium formicicum C METFO	4
207	6.79	7.39	21.3	tr A0A089Z8F8 A0A089Z8F8_METFO	CBS domain-containing protein OS=Methanobacterium formicicum C METFO	5
208	6.79	6.95	16.8	tr A0A090IAU5 A0A090IAU5_METFO	Choloylglycine hydrolase OS=Methanobacterium formicicum C METFO	4
209	6.77	6.99	17.7	tr A0A090I521 A0A090I521_METFO	4-hydroxy-tetrahydrodipicolinate reductase OS=Methanobacterium formicicum C METFO	6
210	6.76	6.92	24.4	tr A0A090I494 A0A090I494_METFO	Short-chain dehydrogenase family protein OS=Methanobacterium formicicum C METFO	5
211	6.74	7.59	9.8	tr A0A090I3V1 A0A090I3V1_METFO	Formate dehydrogenase alpha subunit FdhA OS=Methanobacterium formicicum C METFO	7
212	6.73	6.93	12.9	tr A0A0S4FSL7 A0A0S4FSL7_METFO	Diaminopimelate decarboxylase OS=Methanobacterium formicicum C METFO	4

Amostra 1

213	6.72	7.03	15.7 tr A0A090I3S2 A0A090I3S2_METFO	Phosphoglycerate kinase OS=Methanobacterium formicicu METFO	4
214	6.71	7.21	10.9 tr A0A090I8R0 A0A090I8R0_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	4
215	6.6	6.74	14.4 tr A0A090I3P4 A0A090I3P4_METFO	Alanine dehydrogenase OS=Methanobacterium formicicun METFO	5
216	6.56	6.75	8.6 tr A0A090I2M9 A0A090I2M9_METFO	Catalase-peroxidase OS=Methanobacterium formicicum O METFO	5
217	6.51	8.01	9.3 tr A0A090I333 A0A090I333_METFO	Signal recognition particle 54 kDa protein OS=Methanobac METFO	4
218	6.48	6.74	8.9 tr A0A090JW16 A0A090JW16_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	7
219	6.46	6.5	13.8 tr A0A0S4FNG0 A0A0S4FNG0_METFO	Formylmethanofuran-tetrahydromethanopterin formyltransf METFO	3
220	6.4	6.55	14.2 tr A0A090I135 A0A090I135_METFO	UTP--glucose-1-phosphate uridylyltransferase OS=Methan METFO	4
221	6.39	6.44	18.2 tr A0A090JUT3 A0A090JUT3_METFO	F420-non-reducing hydrogenase iron-sulfur subunit D OS= METFO	6
222	6.34	6.64	29.3 tr A0A089ZH87 A0A089ZH87_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	6
223	6.33	6.64	14.1 tr A0A089ZBE1 A0A089ZBE1_METFO	UPF0288 protein BRM9_0509 OS=Methanobacterium form METFO	5
224	6.32	6.43	5.6 tr A0A089Z9Y9 A0A089Z9Y9_METFO	Type II secretion system protein E GspE OS=Methanobacti METFO	3
225	6.14	6.27	30.3 tr A0A090I7B8 A0A090I7B8_METFO	30S ribosomal protein S19e OS=Methanobacterium formici METFO	3
226	6.09	6.1	27.4 tr A0A089ZA11 A0A089ZA11_METFO	UPF0145 protein BRM9_0823 OS=Methanobacterium form METFO	5
227	6.07	6.3	15 tr A0A090JUJ4 A0A090JUJ4_METFO	Probable L-aspartate dehydrogenase OS=Methanobacteriu METFO	4
228	6.04	6.05	18 tr A0A090I4F5 A0A090I4F5_METFO	Putative cobalt-precorrin-4 C(11)-methyltransferase OS=M METFO	4
229	6.03	6.03	23.1 tr A0A090I8J3 A0A090I8J3_METFO	Cobalt-precorrin-8X methylmutase OS=Methanobacterium METFO	3
230	6.02	6.02	9.8 tr A0A090JSU7 A0A090JSU7_METFO	Glyceraldehyde-3-phosphate dehydrogenase OS=Methanc METFO	3
231	6.02	6.02	9.8 tr A0A090I9D6 A0A090I9D6_METFO	Triosephosphate isomerase OS=Methanobacterium formic METFO	3
232	6.01	6.01	24.4 tr A0A089ZFP6 A0A089ZFP6_METFO	Peptidase S26B, signal peptidase OS=Methanobacterium f METFO	5
233	6	6	9.4 tr A0A090I657 A0A090I657_METFO	3-isopropylmalate dehydratase large subunit OS=Methanol METFO	4
234	5.97	6.13	20.8 tr A0A090I912 A0A090I912_METFO	NH(3)-dependent NAD(+) synthetase OS=Methanobacteriu METFO	4
235	5.97	6.01	10 tr A0A0S4FM80 A0A0S4FM80_METFO	2,3-bisphosphoglycerate-independent phosphoglycerate m METFO	3
236	5.94	6.06	34.5 tr A0A090JWM7 A0A090JWM7_METFO	2-oxoglutarate synthase subunit KorC OS=Methanobacteriu METFO	4
237	5.92	6.02	53.5 tr A0A089ZB18 A0A089ZB18_METFO	50S ribosomal protein L23 OS=Methanobacterium formicic METFO	6
238	5.91	6.01	11.1 tr A0A089ZE87 A0A089ZE87_METFO	ABC transporter ATP-binding protein OS=Methanobacteriu METFO	3
239	5.9	5.97	42.9 tr A0A090JUU7 A0A090JUU7_METFO	Tetrahydromethanopterin S-methyltransferase subunit G O METFO	11
240	5.88	5.98	23.5 tr A0A090I9E4 A0A090I9E4_METFO	30S ribosomal protein S7 OS=Methanobacterium formicicu METFO	3
241	5.87	6.04	17.7 tr A0A090I7Q9 A0A090I7Q9_METFO	2-amino-3,7-dideoxy-D-threo-hept-6-ulosonate synthase O METFO	3
242	5.84	6.03	11.8 tr A0A090I409 A0A090I409_METFO	Glutamyl-tRNA(Gln) amidotransferase subunit D OS=Meth METFO	4
243	5.68	5.74	38.8 tr A0A090I442 A0A090I442_METFO	50S ribosomal protein L30e OS=Methanobacterium formici METFO	4
244	5.62	6	9.8 tr A0A090I6C9 A0A090I6C9_METFO	Ketol-acid reductoisomerase (NADP(+)) OS=Methanobact METFO	4
245	5.58	5.7	6.6 tr A0A089ZGX6 A0A089ZGX6_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	4

Amostra 1

246	5.54	5.63	7.6 tr A0A090I4R4 A0A090I4R4_METFO	Type A flavoprotein FprA OS=Methanobacterium formicicum METFO	3
247	5.52	5.92	7.2 tr A0A090I9E0 A0A090I9E0_METFO	DNA-directed RNA polymerase subunit OS=Methanobacte METFO	5
248	5.51	5.59	11.3 tr A0A090I6J2 A0A090I6J2_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
249	5.47	5.73	14 tr A0A090I455 A0A090I455_METFO	Type 2 DNA topoisomerase 6 subunit A OS=Methanobacte METFO	4
250	5.47	5.56	14.2 tr A0A090I5U3 A0A090I5U3_METFO	Geranylgeranyl glyceryl phosphate synthase OS=Methanob METFO	3
251	5.45	5.79	12 tr A0A0S4FRZ5 A0A0S4FRZ5_METFO	Digeranylgeranyl glycerophospholipid reductase OS=Metha METFO	4
252	5.44	5.53	23.5 tr A0A090I9B3 A0A090I9B3_METFO	GTP cyclohydrolase III OS=Methanobacterium formicicum METFO	5
253	5.4	5.5	15.9 tr A0A090I4X8 A0A090I4X8_METFO	F420-dependent NADP reductase OS=Methanobacterium METFO	3
254	5.36	5.56	13.2 tr A0A090JXZ1 A0A090JXZ1_METFO	Delta-aminolevulinic acid dehydratase OS=Methanobacteri METFO	3
255	5.32	5.59	16.3 tr A0A090I7K3 A0A090I7K3_METFO	Phosphate import ATP-binding protein PstB OS=Methanob METFO	4
256	5.32	5.48	19.1 tr A0A090JU33 A0A090JU33_METFO	DNA-directed RNA polymerase OS=Methanobacterium for METFO	4
257	5.31	5.4	13.9 tr A0A090I1J8 A0A090I1J8_METFO	Putative methylthioribose-1-phosphate isomerase OS=Metl METFO	4
258	5.3	5.39	18.1 tr A0A090JU20 A0A090JU20_METFO	3-hexulose-6-phosphate isomerase HxIB2 OS=Methanoba METFO	3
259	5.28	5.7	21.2 tr A0A090I465 A0A090I465_METFO	Spore coat polysaccharide biosynthesis protein SpsK OS=I METFO	4
260	5.18	5.35	9.9 tr A0A0S4FLD6 A0A0S4FLD6_METFO	ABC transporter substrate-binding protein OS=Methanobac METFO	4
261	5.17	5.25	25.4 tr A0A090I174 A0A090I174_METFO	Adenylate kinase OS=Methanobacterium formicicum OX=2 METFO	3
262	5.14	5.22	22.2 tr A0A090JX27 A0A090JX27_METFO	Amino acid-binding ACT domain-containing protein OS=Me METFO	4
263	5.12	5.21	27.8 tr K2REW5 K2REW5_METFP	30S ribosomal protein S15 OS=Methanobacterium formicic METFP	4
264	5.09	5.32	19.3 tr A0A090I950 A0A090I950_METFO	Formylmethanofuran dehydrogenase subunit D FwdD OS= METFO	3
265	5.09	5.29	7.8 tr A0A090IB52 A0A090IB52_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
266	5.05	5.14	14.7 tr K2QDZ9 K2QDZ9_METFP	RNA-processing protein OS=Methanobacterium formicicum METFP	4
267	5.04	5.13	10.7 tr A0A0S4FSN1 A0A0S4FSN1_METFO	Proline--tRNA ligase OS=Methanobacterium formicicum O METFO	3
268	5.02	5.29	16.4 tr A0A090I4T1 A0A090I4T1_METFO	Aspartate-semialdehyde dehydrogenase OS=Methanobact METFO	4
269	5.02	5.11	12.5 tr A0A090I8Z8 A0A090I8Z8_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	4
270	4.98	5.12	7.9 tr A0A090JVX7 A0A090JVX7_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
271	4.95	5.09	13.2 tr A0A090IA04 A0A090IA04_METFO	5-amino-6-(D-ribitylamino)uracil--L-tyrosine 4-hydroxyphen METFO	3
272	4.92	5.19	19.8 tr A0A090I582 A0A090I582_METFO	50S ribosomal protein L1 OS=Methanobacterium formicicu METFO	8
273	4.91	5.15	12.5 tr A0A090I4P4 A0A090I4P4_METFO	Endonuclease NucS OS=Methanobacterium formicicum O METFO	3
274	4.9	4.98	10.1 tr A0A089ZFA3 A0A089ZFA3_METFO	Acetyl-CoA decarbonylase/synthase complex subunit delta METFO	4
275	4.88	5	26.7 tr A0A090I4J8 A0A090I4J8_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
276	4.87	4.96	11.1 tr A0A0S4FN18 A0A0S4FN18_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
277	4.85	4.94	23 tr A0A090I308 A0A090I308_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
278	4.83	5.07	8.9 tr A0A090I100 A0A090I100_METFO	S-inosyl-L-homocysteine hydrolase OS=Methanobacterium METFO	5

Amostra 1

279	4.79	4.99	9.8 tr A0A090I6B5 A0A090I6B5_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
280	4.77	4.91	10.6 tr A0A090I4G1 A0A090I4G1_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
281	4.77	4.87	29.5 tr A0A090JVY8 A0A090JVY8_METFO	Putative acetolactate synthase small subunit OS=Methanobacterium formicicum METFO	6
282	4.69	4.9	12.1 tr A0A090I866 A0A090I866_METFO	4-hydroxy-tetrahydrodipicolinate synthase OS=Methanobacterium formicicum METFO	3
283	4.68	4.76	10.5 tr A0A090I2X2 A0A090I2X2_METFO	L-sulfolactate dehydrogenase OS=Methanobacterium formicicum METFO	3
284	4.66	4.74	15.8 tr A0A090I1G0 A0A090I1G0_METFO	DNA-directed RNA polymerase subunit D OS=Methanobacterium formicicum METFO	3
285	4.6	4.86	20.7 tr A0A090I653 A0A090I653_METFO	Methanogenesis marker protein 11 OS=Methanobacterium formicicum METFO	7
286	4.46	4.8	7.2 tr A0A089ZUP9 A0A089ZUP9_METFO	Energy-converting hydrogenase B subunit N EhbN OS=Methanobacterium formicicum METFO	3
287	4.44	4.49	20.5 tr A0A089ZGC1 A0A089ZGC1_METFO	Pyridoxamine 5'-phosphate oxidase family protein OS=Methanobacterium formicicum METFO	4
288	4.39	4.44	6.3 tr A0A090JU38 A0A090JU38_METFO	Argininosuccinate lyase OS=Methanobacterium formicicum METFO	3
289	4.34	4.4	5.5 tr K2QYE4 K2QYE4_METFP	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit METFP	2
290	4.3	4.34	28.3 tr A0A090I4H6 A0A090I4H6_METFO	50S ribosomal protein L15 OS=Methanobacterium formicicum METFO	3
291	4.29	4.49	22.2 tr A0A090I618 A0A090I618_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	4
292	4.27	4.46	6.2 tr A0A090I298 A0A090I298_METFO	Archaeal glutamate synthase [NADPH] OS=Methanobacterium formicicum METFO	3
293	4.26	4.44	7.4 tr A0A090I583 A0A090I583_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
294	4.23	4.41	4.6 tr A0A090I3L1 A0A090I3L1_METFO	Acetyl-CoA synthetase AcsA1 OS=Methanobacterium formicicum METFO	3
295	4.12	4.29	21 tr A0A090IA48 A0A090IA48_METFO	Nitrite reductase (NAD(P)H) OS=Methanobacterium formicicum METFO	4
296	4.1	4.11	20.4 tr A0A089ZDW1 A0A089ZDW1_METFO	Methyl-coenzyme M reductase II D subunit MtrD OS=Methanobacterium formicicum METFO	2
297	4.09	4.11	10.6 tr A0A089ZV26 A0A089ZV26_METFO	Inositol-3-phosphate synthase OS=Methanobacterium formicicum METFO	3
298	4.09	4.1	16.6 tr A0A090JSW7 A0A090JSW7_METFO	CBS domain-containing membrane protein OS=Methanobacterium formicicum METFO	2
299	4.08	4.1	22 tr A0A089ZVR0 A0A089ZVR0_METFO	30S ribosomal protein S12 OS=Methanobacterium formicicum METFO	6
300	4.06	4.08	7.8 tr A0A0S4FLK3 A0A0S4FLK3_METFO	Coenzyme F420:L-glutamate ligase OS=Methanobacterium formicicum METFO	2
301	4.05	4.06	5.7 tr A0A089ZH78 A0A089ZH78_METFO	V-type ATP synthase subunit C OS=Methanobacterium formicicum METFO	2
302	4.04	4.3	8.1 tr A0A089ZI25 A0A089ZI25_METFO	Serine hydroxymethyltransferase OS=Methanobacterium formicicum METFO	3
303	4.04	4.04	6.1 tr A0A090I3N5 A0A090I3N5_METFO	2-isopropylmalate synthase LeuA OS=Methanobacterium formicicum METFO	2
304	4.03	8.29	12.1 tr A0A090IAQ7 A0A090IAQ7_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	9
305	4.03	4.04	7.3 tr A0A090I3M2 A0A090I3M2_METFO	Cell division ATPase MinD1 OS=Methanobacterium formicicum METFO	2
306	4.02	4.02	12.5 tr A0A090I810 A0A090I810_METFO	Dihydroorotate dehydrogenase OS=Methanobacterium formicicum METFO	2
307	4.02	4.02	18.6 tr A0A089ZA06 A0A089ZA06_METFO	PRC-barrel domain-containing protein OS=Methanobacterium formicicum METFO	2
308	4.01	4.03	13.1 tr A0A0S4FSE6 A0A0S4FSE6_METFO	Putative ABC transporter ATP-binding protein MJ0089 OS=Methanobacterium formicicum METFO	2
309	4.01	4.01	13.8 tr A0A090I640 A0A090I640_METFO	Exosome complex component Csl4 OS=Methanobacterium formicicum METFO	2
310	4.01	4.01	22.6 tr A0A089ZVK3 A0A089ZVK3_METFO	CBS domain-containing protein OS=Methanobacterium formicicum METFO	2
311	4	4	10.9 tr K2RAP2 K2RAP2_METFP	Tetrahydromethanopterin S-methyltransferase subunit E OS=Methanobacterium formicicum METFO	3

Amostra 1

312	4	4	14 tr A0A090I7B5 A0A090I7B5_METFO	Flavin prenyltransferase UbiX OS=Methanobacterium form METFO	2
313	4	4	7 tr A0A090JWU9 A0A090JWU9_METFO	Protein-export membrane protein SecD OS=Methanobacte METFO	2
314	4	4	11.7 tr A0A090I368 A0A090I368_METFO	Formylmethanofuran dehydrogenase subunit E OS=Metha METFO	2
315	4	4	13.3 tr A0A089ZDH3 A0A089ZDH3_METFO	Putative membrane protein OS=Methanobacterium formici METFO	2
316	4	4	18 tr A0A090JY14 A0A090JY14_METFO	Phenylacetic acid degradation-like protein OS=Methanoba METFO	2
317	4	4	8.6 tr A0A090I231 A0A090I231_METFO	Methyl viologen-reducing hydrogenase gamma subunit MvI METFO	2
318	4	4	16 tr A0A089ZVX2 A0A089ZVX2_METFO	Putative membrane protein OS=Methanobacterium formici METFO	3
319	3.89	4.01	35.6 tr A0A089ZGN8 A0A089ZGN8_METFO	PRC-barrel domain-containing protein OS=Methanobacteri METFO	3
320	3.85	4.03	6.7 tr A0A090JV74 A0A090JV74_METFO	Homoserine dehydrogenase OS=Methanobacterium formic METFO	4
321	3.83	3.95	12.1 tr A0A0S4FPI8 A0A0S4FPI8_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO	2
322	3.82	4.05	11.6 tr A0A090I7Z4 A0A090I7Z4_METFO	O-acetylserine sulfhydrylase OS=Methanobacterium formic METFO	3
323	3.82	3.91	14.8 tr A0A090I8C8 A0A090I8C8_METFO	Flavodoxin/nitric oxide synthase OS=Methanobacterium fo METFO	2
324	3.8	3.92	6.6 tr A0A090I524 A0A090I524_METFO	tRNA-splicing ligase RtcB OS=Methanobacterium formicic METFO	2
325	3.78	4.1	20.3 tr A0A090I8S1 A0A090I8S1_METFO	Universal stress protein UspA5 OS=Methanobacterium forr METFO	4
326	3.77	3.85	8.4 tr K2R511 K2R511_METFP	TOPRIM domain-containing protein OS=Methanobacteriurr METFP	2
327	3.75	3.94	8 tr A0A089ZHE0 A0A089ZHE0_METFO	Molybdenum cofactor synthesis domain-containing protein METFO	3
328	3.7	3.86	9.1 tr K2R423 K2R423_METFP	50S ribosomal protein L2 OS=Methanobacterium formicicu METFP	2
329	3.66	4.11	7.3 tr A0A090JW77 A0A090JW77_METFO	ATP phosphoribosyltransferase OS=Methanobacterium for METFO	2
330	3.66	3.77	12.2 tr A0A090JTT8 A0A090JTT8_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO	2
331	3.64	3.72	7.5 tr A0A089ZG19 A0A089ZG19_METFO	Formate/nitrite transporter FdhC OS=Methanobacterium fo METFO	2
332	3.61	3.8	21.9 tr A0A090I7Y5 A0A090I7Y5_METFO	AsnC family transcriptional regulator OS=Methanobacteriur METFO	3
333	3.59	4.06	25.3 tr A0A090JTX4 A0A090JTX4_METFO	dCTP deaminase, dUMP-forming OS=Methanobacterium f METFO	5
334	3.59	3.68	4.8 tr A0A0S4FS90 A0A0S4FS90_METFO	Putative secreted protein OS=Methanobacterium formicicu METFO	2
335	3.57	3.68	8.2 tr A0A090I4Z6 A0A090I4Z6_METFO	Aminotransferase OS=Methanobacterium formicicum OX=: METFO	3
336	3.55	3.85	18.1 tr A0A090I5C9 A0A090I5C9_METFO	Phosphoribosylformylglycinamide synthase subunit PurQ METFO	3
337	3.54	3.73	13.3 tr A0A090I4H9 A0A090I4H9_METFO	UDP-glucose 4-epimerase OS=Methanobacterium formicic METFO	3
338	3.51	3.86	12.8 tr A0A090I3D2 A0A090I3D2_METFO	PQQ repeat-containing cell surface protein OS=Methanoba METFO	3
339	3.51	3.63	7.6 tr A0A090I6D0 A0A090I6D0_METFO	Tryptophan synthase beta chain OS=Methanobacterium fo METFO	3
340	3.5	4.04	6.4 tr A0A089ZBN0 A0A089ZBN0_METFO	PIN domain-containing protein OS=Methanobacterium forr METFO	4
341	3.5	3.59	8.5 tr A0A090I420 A0A090I420_METFO	Probable porphobilinogen deaminase OS=Methanobacteriu METFO	2
342	3.47	3.8	11.7 tr A0A090IAE6 A0A090IAE6_METFO	Putative aminopeptidase MJ0555 OS=Methanobacterium f METFO	3
343	3.47	3.69	7.4 tr A0A0S4FQI5 A0A0S4FQI5_METFO	Cell division cycle protein 48 homolog MJ1156 OS=Methan METFO	4
344	3.44	3.61	14.5 tr A0A089ZA94 A0A089ZA94_METFO	CobQ/CobB/MinD/ParA nucleotide binding domain-containi METFO	3

Amostra 1

345	3.42	3.58	8.9 tr A0A0S4FPY7 A0A0S4FPY7_METFO	Aminotransferase OS=Methanobacterium formicicum OX=:METFO	3
346	3.39	3.78	17.9 tr A0A090I1Q2 A0A090I1Q2_METFO	Nicotinate-nucleotide pyrophosphorylase [carboxylating] OX=:METFO	7
347	3.36	3.46	15.9 tr A0A089Z7Q8 A0A089Z7Q8_METFO	TetR family transcriptional regulator OS=Methanobacterium formicicum METFO	2
348	3.35	3.44	19 tr A0A090I1Y5 A0A090I1Y5_METFO	Molybdenum cofactor synthesis domain-containing protein METFO	3
349	3.31	3.46	11.2 tr A0A090I431 A0A090I431_METFO	2-oxoglutarate synthase subunit KorA OS=Methanobacterium formicicum METFO	3
350	3.27	3.43	8.8 tr A0A090I8F3 A0A090I8F3_METFO	Methionine aminopeptidase OS=Methanobacterium formicicum METFO	2
351	3.26	3.72	6 tr A0A090JTZ4 A0A090JTZ4_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
352	3.25	5.46	16.9 tr A0A0S4FPN3 A0A0S4FPN3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	4
353	3.25	3.41	10.6 tr A0A090JWV3 A0A090JWV3_METFO	Acetylglutamate kinase OS=Methanobacterium formicicum METFO	3
354	3.23	3.54	10.6 tr A0A090I4C0 A0A090I4C0_METFO	Indole-3-glycerol phosphate synthase OS=Methanobacterium formicicum METFO	2
355	3.12	3.31	4.9 tr A0A089ZVM8 A0A089ZVM8_METFO	Peptide chain release factor subunit 1 OS=Methanobacterium formicicum METFO	2
356	3.08	3.35	10 tr A0A090I4G2 A0A090I4G2_METFO	Bifunctional short chain isoprenyl diphosphate synthase Lds OS=METHANOBACTERIUM FORMICICUM METFO	3
357	3.07	3.28	24.5 tr A0A090I8N6 A0A090I8N6_METFO	Carboxymuconolactone decarboxylase family protein OS=METHANOBACTERIUM FORMICICUM METFO	2
358	3.02	3.16	15.6 tr A0A089ZVK5 A0A089ZVK5_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
359	3.01	3.11	20.7 tr A0A090I168 A0A090I168_METFO	50S ribosomal protein L18e OS=Methanobacterium formicicum METFO	2
360	2.99	3.09	11.4 tr A0A0S4FN48 A0A0S4FN48_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
361	2.94	3.15	5.1 tr A0A090I5E9 A0A090I5E9_METFO	Pyruvate carboxylase subunit B OS=Methanobacterium formicicum METFO	3
362	2.92	3.01	8.8 tr A0A090I3Z3 A0A090I3Z3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
363	2.87	3.07	8.5 tr A0A089ZH11 A0A089ZH11_METFO	Thiamine thiazole synthase OS=Methanobacterium formicicum METFO	2
364	2.86	3.18	8.7 tr A0A090I4Y9 A0A090I4Y9_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
365	2.85	2.98	10.8 tr A0A090I2L4 A0A090I2L4_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	4
366	2.83	3.14	19.3 tr A0A089ZGF4 A0A089ZGF4_METFO	30S ribosomal protein S13 OS=Methanobacterium formicicum METFO	3
367	2.79	2.95	31.8 tr K2R0W5 K2R0W5_METFP	30S ribosomal protein S17e OS=Methanobacterium formicicum METFP	2
368	2.73	2.88	4 tr A0A090JTF6 A0A090JTF6_METFO	Biotin-(Acetyl-CoA carboxylase) ligase OS=Methanobacterium formicicum METFO	1
369	2.71	2.8	1.8 tr A0A0S4FL46 A0A0S4FL46_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
370	2.69	9.61	15.4 tr A0A090IAA4 A0A090IAA4_METFO	Pyridoxal 5'-phosphate synthase subunit PdxS OS=Methanobacterium formicicum METFO	6
371	2.67	2.77	3.4 tr K2QDN1 K2QDN1_METFP	DNA-directed RNA polymerase subunit B OS=Methanobacterium formicicum METFP	2
372	2.62	2.68	49.1 tr A0A090I260 A0A090I260_METFO	50S ribosomal protein L24e OS=Methanobacterium formicicum METFO	2
373	2.6	2.66	8.3 tr A0A089ZAI2 A0A089ZAI2_METFO	Molybdate transport system regulatory protein ModE OS=METHANOBACTERIUM FORMICICUM METFO	2
374	2.55	2.61	7.1 tr A0A090I503 A0A090I503_METFO	Malate dehydrogenase OS=Methanobacterium formicicum METFO	2
375	2.54	2.75	5.2 tr A0A090JXY4 A0A090JXY4_METFO	Chorismate synthase OS=Methanobacterium formicicum METFO	2
376	2.54	2.61	4.1 tr A0A090I2H7 A0A090I2H7_METFO	Glutamate decarboxylase OS=Methanobacterium formicicum METFO	2
377	2.52	2.58	17.2 tr A0A0S4FLM0 A0A0S4FLM0_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	4

Amostra 1

378	2.51	2.8	20.7	tr A0A0S4FPE1 A0A0S4FPE1_METFO	Probable cobalt-precorrin-6B C(15)-methyltransferase (dec METFO	3
379	2.47	2.53	8	tr A0A090I2J1 A0A090I2J1_METFO	Pyruvate ferredoxin oxidoreductase beta subunit PorB OS= METFO	2
380	2.44	2.49	5.5	tr K2QEI4 K2QEI4_METFP	Arginine biosynthesis bifunctional protein ArgJ OS=Methan METFP	2
381	2.42	3.02	12	tr A0A090I609 A0A090I609_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	2
382	2.4	2.59	6	tr A0A090I4Q8 A0A090I4Q8_METFO	Phenylalanine--tRNA ligase alpha subunit OS=Methanobac METFO	2
383	2.38	2.43	9.2	tr A0A090I5P8 A0A090I5P8_METFO	Coenzyme A biosynthesis bifunctional protein CoaBC OS= METFO	3
384	2.35	2.5	24.3	tr A0A090I489 A0A090I489_METFO	GTP-binding protein Rab-like protein OS=Methanobacteriu METFO	3
385	2.33	2.37	4.3	tr A0A090I5J7 A0A090I5J7_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	2
386	2.3	2.34	3.2	tr K2QC11 K2QC11_METFP	Shikimate dehydrogenase (NADP(+)) OS=Methanobacteriu METFP	1
387	2.23	2.37	8.6	tr A0A090I525 A0A090I525_METFO	Shikimate kinase OS=Methanobacterium formicicum OX=2 METFO	2
388	2.23	2.26	7.7	tr A0A0S4FPT9 A0A0S4FPT9_METFO	dTDP-glucose 4,6-dehydratase-like protein OS=Methanobac METFO	2
389	2.21	2.24	5.6	tr A0A090I8P6 A0A090I8P6_METFO	Ribose-phosphate pyrophosphokinase OS=Methanobacter METFO	1
390	2.2	2.23	6	tr A0A090JTD5 A0A090JTD5_METFO	50S ribosomal protein L30 OS=Methanobacterium formicic METFO	1
391	2.18	2.21	2.1	tr A0A090I4P0 A0A090I4P0_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
392	2.16	2.17	3.1	tr A0A090I6X8 A0A090I6X8_METFO	2-oxoglutarate ferredoxin oxidoreductase subunit beta KorE METFO	1
393	2.15	2.27	5.7	tr A0A090I574 A0A090I574_METFO	Glutamine-fructose-6-phosphate transaminase OS=Methar METFO	2
394	2.14	2.16	7.1	tr A0A089ZBJ3 A0A089ZBJ3_METFO	ZPR1 zinc-finger domain-containing protein OS=Methanob METFO	1
395	2.13	2.15	8.7	tr A0A090I806 A0A090I806_METFO	Putative pantothenate synthetase OS=Methanobacterium f METFO	1
396	2.13	2.14	1.8	tr A0A090I8E3 A0A090I8E3_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
397	2.12	2.14	2.3	tr A0A090I5F2 A0A090I5F2_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
398	2.12	2.13	7.9	tr A0A089ZEK2 A0A089ZEK2_METFO	MarR family transcriptional regulator OS=Methanobacteriur METFO	1
399	2.09	2.1	2.7	tr A0A090I360 A0A090I360_METFO	F420H2 oxidase FprA OS=Methanobacterium formicicum (METFO	1
400	2.08	5.68	48.7	tr A0A090IAT6 A0A090IAT6_METFO	TRAM domain-containing protein OS=Methanobacterium fc METFO	3
401	2.08	2.09	9.8	tr A0A089Z9L4 A0A089Z9L4_METFO	Nitrogen regulatory protein P-II GlnK1 OS=Methanobacteriu METFO	1
402	2.07	2.08	3.6	tr A0A090I7X7 A0A090I7X7_METFO	Glutamine-scyllo-inositol transaminase OS=Methanobacter METFO	1
403	2.06	2.07	17.7	tr A0A090I3M8 A0A090I3M8_METFO	Imidazoleglycerol-phosphate dehydratase OS=Methanobac METFO	2
404	2.04	2.08	12.6	tr A0A089Z8B7 A0A089Z8B7_METFO	Energy-converting hydrogenase B subunit A EhbA OS=Mei METFO	1
405	2.04	2.06	1.5	tr A0A089ZUK9 A0A089ZUK9_METFO	Dihydroxy-acid dehydratase OS=Methanobacterium formici METFO	1
406	2.03	2.04	4.7	tr A0A089ZI49 A0A089ZI49_METFO	Sensory transduction histidine kinase OS=Methanobacteriu METFO	1
407	2.03	2.04	4.7	tr A0A090I4E1 A0A090I4E1_METFO	Histidinol dehydrogenase OS=Methanobacterium formicicu METFO	1
408	2.03	2.03	2.8	tr A0A0S4FLU0 A0A0S4FLU0_METFO	Dihydrolipoyl dehydrogenase OS=Methanobacterium formi METFO	1
409	2.03	2.03	27.5	tr K2RD75 K2RD75_METFP	Putative snRNP Sm-like protein OS=Methanobacterium for METFP	2
410	2.02	2.03	1.3	tr K2RPE1 K2RPE1_METFP	DNA-binding protein MutS2 OS=Methanobacterium formici METFP	1

Amostra 1

411	2.02	2.03	8.6 tr K2R5U5 K2R5U5_METFP	Uncharacterized protein OS=Methanobacterium formicicum METFP	1
412	2.02	2.03	3.9 tr A0A089Z928 A0A089Z928_METFO	Nitrogenase cofactor biosynthesis protein NifB OS=Methanobacterium formicicum METFO	1
413	2.02	2.02	2.8 tr A0A090JX53 A0A090JX53_METFO	Cell wall biosynthesis protein Mur ligase family OS=Methanobacterium formicicum METFO	2
414	2.02	2.02	5 tr A0A089ZGR4 A0A089ZGR4_METFO	Deoxyhypusine synthase Dys OS=Methanobacterium formicicum METFO	1
415	2.01	3.17	3 tr K2RQD8 K2RQD8_METFP	Acetate/CoA ligase OS=Methanobacterium formicicum (str. formicicum) METFP	2
416	2.01	2.02	5.8 tr A0A090JWI9 A0A090JWI9_METFO	Thioredoxin reductase OS=Methanobacterium formicicum METFO	1
417	2.01	2.02	1.8 tr A0A090I8U6 A0A090I8U6_METFO	Arginine--tRNA ligase OS=Methanobacterium formicicum METFO	1
418	2.01	2.01	6 tr K2R0A8 K2R0A8_METFP	Uncharacterized protein OS=Methanobacterium formicicum METFP	1
419	2.01	2.01	4.2 tr A0A090I3L5 A0A090I3L5_METFO	UPF0285 protein DSM1535_1340 OS=Methanobacterium formicicum METFO	1
420	2.01	2.01	7.8 tr A0A089ZC90 A0A089ZC90_METFO	V-type ATP synthase subunit D OS=Methanobacterium formicicum METFO	1
421	2.01	2.01	2.5 tr K2QE06 K2QE06_METFP	Uncharacterized protein OS=Methanobacterium formicicum METFP	1
422	2.01	2.01	4.5 tr A0A090JUW9 A0A090JUW9_METFO	2-phosphosulfolactate phosphatase OS=Methanobacterium formicicum METFO	1
423	2.01	2.01	3.8 tr A0A090I4E0 A0A090I4E0_METFO	Pleiotropic regulatory protein OS=Methanobacterium formicicum METFO	1
424	2	3.89	11.1 tr A0A090I9F1 A0A090I9F1_METFO	Tetrahydromethanopterin S-methyltransferase subunit A OS=Methanobacterium formicicum METFO	2
425	2	3.84	38.4 tr K2R0A1 K2R0A1_METFP	50S ribosomal protein L23 OS=Methanobacterium formicicum METFP	4
426	2	2.08	0.8 tr A0A089ZGE0 A0A089ZGE0_METFO	Adhesin-like protein with PMBR domains OS=Methanobacterium formicicum METFO	2
427	2	2.07	8.2 tr A0A090I5Z1 A0A090I5Z1_METFO	Isochorismatase family protein OS=Methanobacterium formicicum METFO	1
428	2	2.03	3 tr A0A090JU62 A0A090JU62_METFO	Glutamine amidotransferase OS=Methanobacterium formicicum METFO	1
429	2	2.01	1.6 tr K2RQB5 K2RQB5_METFP	Methionine--tRNA ligase OS=Methanobacterium formicicum METFP	1
430	2	2.01	10.6 tr K2RB04 K2RB04_METFP	Phosphoribosyl-AMP cyclohydrolase OS=Methanobacterium formicicum METFP	1
431	2	2.01	9.3 tr K2QYV5 K2QYV5_METFP	Nucleoside diphosphate kinase OS=Methanobacterium formicicum METFP	1
432	2	2	6 tr A0A090I2K2 A0A090I2K2_METFO	PBS lyase HEAT domain-containing protein OS=Methanobacterium formicicum METFO	2
433	2	2	6.3 tr A0A089ZCI8 A0A089ZCI8_METFO	Methanogenesis marker protein 7 OS=Methanobacterium formicicum METFO	1
434	2	2	2.9 tr K2RVK9 K2RVK9_METFP	Uncharacterized protein OS=Methanobacterium formicicum METFP	1
435	2	2	10.4 tr K2R8M5 K2R8M5_METFP	Roadblock/LC7 family protein OS=Methanobacterium formicicum METFP	3
436	2	2	5.7 tr K2R1L9 K2R1L9_METFP	Aspartate carbamoyltransferase regulatory chain OS=Methanobacterium formicicum METFP	1
437	2	2	8 tr A0A0S4FP85 A0A0S4FP85_METFO	Putative secreted protein OS=Methanobacterium formicicum METFO	1
438	2	2	2.5 tr A0A0S4FNE3 A0A0S4FNE3_METFO	Triphosphoribosyl-dephospho-CoA protein OS=Methanobacterium formicicum METFO	1
439	2	2	5.5 tr A0A090JX71 A0A090JX71_METFO	CRISPR locus-related DNA-binding protein OS=Methanobacterium formicicum METFO	1
440	2	2	9 tr A0A090I6A2 A0A090I6A2_METFO	Cyclophilin type peptidyl-prolyl cis-trans isomerase OS=Methanobacterium formicicum METFO	1
441	2	2	10.6 tr A0A090I4F8 A0A090I4F8_METFO	Iron-sulfur flavoprotein MJ1083 OS=Methanobacterium formicicum METFO	1
442	2	2	2.6 tr A0A089ZVW0 A0A089ZVW0_METFO	NADH oxidase Nox OS=Methanobacterium formicicum OX METFO	2
443	2	2	4.1 tr A0A089ZV44 A0A089ZV44_METFO	GTP cyclohydrolase MptA OS=Methanobacterium formicicum METFO	1

Amostra 1

444	2	2	8.7 tr A0A089ZHA1 A0A089ZHA1_METFO	Ferripyochelin binding protein OS=Methanobacterium form METFO	1
445	2	2	3 tr A0A089ZGK4 A0A089ZGK4_METFO	Polysaccharide biosynthesis protein OS=Methanobacterium METFO	1
446	2	2	20.7 tr K2REJ5 K2REJ5_METFP	30S ribosomal protein S27e OS=Methanobacterium formicic METFP	1
447	2	2	13.4 tr K2RBN6 K2RBN6_METFP	Archaeoflavoprotein AfpA OS=Methanobacterium formicic METFP	1
448	2	2	11.9 tr K2R290 K2R290_METFP	Amino acid-binding ACT domain-containing protein OS=Methanobacterium METFP	1
449	2	2	8.2 tr K2QD32 K2QD32_METFP	DNA-directed RNA polymerase subunit K OS=Methanobacterium METFP	1
450	2	2	4.3 tr A0A0S4FNA9 A0A0S4FNA9_METFO	Deoxyribose-phosphate aldolase OS=Methanobacterium formicic METFO	1
451	2	2	3.3 tr A0A090JUV1 A0A090JUV1_METFO	Tetrahydromethanopterin S-methyltransferase subunit D OS=Methanobacterium METFO	1
452	2	2	4.4 tr A0A090JUP7 A0A090JUP7_METFO	Phosphonate-transporting ATPase OS=Methanobacterium METFO	1
453	2	2	5.9 tr A0A090JTA3 A0A090JTA3_METFO	Putative membrane protein OS=Methanobacterium formicic METFO	1
454	2	2	8.2 tr A0A090I9J6 A0A090I9J6_METFO	Protein-export membrane protein SecF OS=Methanobacterium METFO	1
455	2	2	1.5 tr A0A090I8L0 A0A090I8L0_METFO	Ferrous iron transport protein B, FeoB OS=Methanobacterium METFO	1
456	2	2	4.9 tr A0A090I626 A0A090I626_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
457	2	2	5.6 tr A0A090I5I0 A0A090I5I0_METFO	Tetrahydromethanopterin S-methyltransferase subunit C OS=Methanobacterium METFO	2
458	2	2	4.8 tr A0A090I4Y2 A0A090I4Y2_METFO	Putative membrane protein OS=Methanobacterium formicic METFO	1
459	2	2	3 tr A0A090I4S4 A0A090I4S4_METFO	Family 2 glycosyl transferase OS=Methanobacterium formicic METFO	1
460	2	2	4.3 tr A0A090I4Q2 A0A090I4Q2_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
461	2	2	11.8 tr A0A089ZUR3 A0A089ZUR3_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	2
462	2	2	8.8 tr A0A089ZJ52 A0A089ZJ52_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	2
463	2	2	6.7 tr A0A089ZGY8 A0A089ZGY8_METFO	Putative membrane protein OS=Methanobacterium formicic METFO	1
464	2	2	15.7 tr A0A089ZDV5 A0A089ZDV5_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
465	1.96	2	13 tr K2R1S1 K2R1S1_METFP	50S ribosomal protein L12 OS=Methanobacterium formicic METFP	1
466	1.93	2.01	7 tr A0A090I5Q4 A0A090I5Q4_METFO	CBS domain-containing protein OS=Methanobacterium formicic METFO	1
467	1.92	2	2.6 tr K2RR54 K2RR54_METFP	Glucosamine-1-phosphate N-acetyltransferase OS=Methanobacterium METFP	1
468	1.92	2	19.1 tr K2QD78 K2QD78_METFP	Uncharacterized protein OS=Methanobacterium formicicun METFP	1
469	1.91	2.03	4 tr A0A090I3L4 A0A090I3L4_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
470	1.89	2	5.4 tr A0A089ZGT2 A0A089ZGT2_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
471	1.89	2	10.6 tr A0A090I4X2 A0A090I4X2_METFO	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylidene]thiazole METFO	1
472	1.85	1.96	7.9 tr A0A090I9P0 A0A090I9P0_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
473	1.84	1.94	3.4 tr A0A0S4FPT3 A0A0S4FPT3_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
474	1.8	1.89	7.1 tr K2RPH4 K2RPH4_METFP	Uncharacterized protein OS=Methanobacterium formicicun METFP	1
475	1.8	1.89	7.1 tr A0A090I8N7 A0A090I8N7_METFO	Precorrin-2 C20-methyltransferase OS=Methanobacterium METFO	1
476	1.78	1.87	1.6 tr A0A089ZAV8 A0A089ZAV8_METFO	RNA-metabolising metallo-beta-lactamase OS=Methanobacterium METFO	1

Amostra 1

477	1.74	1.85	2.2 tr K2RWA6 K2RWA6_METFP	Adenylosuccinate lyase OS=Methanobacterium formicicum METFP	1
478	1.7	1.89	12.6 tr A0A090I1S6 A0A090I1S6_METFO	Succinate--CoA ligase [ADP-forming] subunit alpha OS=Methanobacterium formicicum METFO	2
479	1.68	1.86	9.7 tr A0A090I0P3 A0A090I0P3_METFO	Inositol-1-monophosphatase OS=Methanobacterium formicicum METFO	2
480	1.68	1.8	4.5 tr A0A089ZHU8 A0A089ZHU8_METFO	Response regulator domain-containing protein OS=Methanobacterium formicicum METFO	1
481	1.66	1.87	10.3 tr A0A090I679 A0A090I679_METFO	UDP-glucose 4-epimerase OS=Methanobacterium formicicum METFO	2
482	1.65	1.82	25.3 tr K2RRN0 K2RRN0_METFP	Uncharacterized protein OS=Methanobacterium formicicum METFP	2
483	1.64	1.74	4 tr A0A0S4FM70 A0A0S4FM70_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
484	1.63	1.76	21.7 tr A0A089ZAK4 A0A089ZAK4_METFO	Molybdenum-pterin binding protein Mop1 OS=Methanobacterium formicicum METFO	1
485	1.62	1.72	2.2 tr A0A0S4FM93 A0A0S4FM93_METFO	Histidinol-phosphate aminotransferase OS=Methanobacterium formicicum METFO	1
486	1.61	1.73	4.1 tr A0A090I8S7 A0A090I8S7_METFO	tRNA (Adenine(57)-N(1)/adenine(58)-N(1))-methyltransferase OS=Methanobacterium formicicum METFO	1
487	1.58	1.76	6.7 tr A0A090I4P9 A0A090I4P9_METFO	Glucose-methanol-choline oxidoreductase OS=Methanobacterium formicicum METFO	2
488	1.57	1.68	5.2 tr A0A090I1M8 A0A090I1M8_METFO	UPF0173 metal-dependent hydrolase DSM1535_0376 OS=Methanobacterium formicicum METFO	1
489	1.54	1.73	13.7 tr A0A090I3X8 A0A090I3X8_METFO	Formylmethanofuran dehydrogenase, subunit E region OS=Methanobacterium formicicum METFO	2
490	1.53	1.62	2.5 tr A0A090I7C8 A0A090I7C8_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
491	1.5	1.67	6.2 tr A0A090JVY2 A0A090JVY2_METFO	Branched-chain-amino-acid aminotransferase OS=Methanobacterium formicicum METFO	2
492	1.49	1.61	4.3 tr A0A090I4Z8 A0A090I4Z8_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
493	1.49	1.6	5.3 tr A0A090I548 A0A090I548_METFO	Metallophosphoesterase OS=Methanobacterium formicicum METFO	1
494	1.48	1.68	16.4 tr K2RTG9 K2RTG9_METFP	Archaeoflavoprotein AfpA OS=Methanobacterium formicicum METFP	2
495	1.48	1.61	7.4 tr A0A090IB44 A0A090IB44_METFO	Universal stress protein UspA4 OS=Methanobacterium formicicum METFO	1
496	1.46	1.58	8.6 tr A0A090I0V7 A0A090I0V7_METFO	Nuclease domain-containing protein OS=Methanobacterium formicicum METFO	1
497	1.46	1.57	32.4 tr K2RQ61 K2RQ61_METFP	Transcription factor CBF/NF-Y/histone domain-containing protein OS=Methanobacterium formicicum METFP	3
498	1.45	1.62	2.4 tr A0A0S4FN19 A0A0S4FN19_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
499	1.41	1.6	12 tr A0A090I5D6 A0A090I5D6_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
500	1.41	1.52	4.1 tr A0A090JW59 A0A090JW59_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
501	1.4	1.59	13.7 tr A0A090JSW3 A0A090JSW3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
502	1.39	2	13 tr K2RAP6 K2RAP6_METFP	Tetrahydromethanopterin S-methyltransferase subunit F OS=Methanobacterium formicicum METFP	1
503	1.38	1.49	8.4 tr A0A090I852 A0A090I852_METFO	Cupin OS=Methanobacterium formicicum OX=2162 GN=B1 METFO	1
504	1.37	1.47	4 tr A0A090I4X0 A0A090I4X0_METFO	3-dehydroquinate dehydratase OS=Methanobacterium formicicum METFO	1
505	1.32	1.5	7.3 tr A0A090JWB1 A0A090JWB1_METFO	Sulfur carrier protein FdhD OS=Methanobacterium formicicum METFO	2
506	1.32	1.44	3.8 tr A0A089ZI47 A0A089ZI47_METFO	PAS/PAC sensor protein OS=Methanobacterium formicicum METFO	1

Amostra 1



ID statistics table

Unused (Conf) Cutoff	Proteins Detected	Proteins Before Grouping	Distinct Peptides	Spectra Identified	% Total Spectra
>2.0 (99)	423	881	7200	28812	18.4
>1.3 (95)	506	1109	7387	29197	18.6
>0.47 (66)	575	1275	7575	29531	18.8
Cutoff Applied: >0.05 (10%)	740	1640	7892	30014	19.1

Amostra 2

1) Z:\Projects\UniMS2019_95 MALves\Data\CS2_4uL.wiff

Sample Type: Identification
Cys. Alkylation: Iodoacetamide
Digestion: Trypsin
Instrument: TripleTOF 6600
Special Factors: Gel-based ID
Species:
ID Focus: Biological modifications
 Amino acid substitutions
Database: 20190624_uniprot_methanobacterium+formicicum_6903entries.fasta
Search Effort: Thorough
FDR Analysis: Yes
User Modified Parameter Files: Yes



Proteins detected table

N	Unused	Total	% Cov (95	Accession #	Name	Species	Peptides(95%)
1	92.83	92.83	85.8	tr A0A090I2T3 A0A090I2T3_METFO	Methyl-coenzyme M reductase subunit beta OS=Methanob METFO		751
2	81.67	81.67	61.3	tr A0A090I8L6 A0A090I8L6_METFO	Replication factor-A domain-containing protein OS=Methan METFO		73
3	74.31	74.37	77.8	tr A0A090IAH6 A0A090IAH6_METFO	Thermosome subunit OS=Methanobacterium formicicum C METFO		330
4	74.13	74.17	63.7	tr A0A090I2M3 A0A090I2M3_METFO	V-type ATP synthase alpha chain OS=Methanobacterium f METFO		109
5	70.88	70.88	96	tr A0A090I573 A0A090I573_METFO	5,10-methylenetetrahydromethanopterin reductase OS=Me METFO		358
6	63.97	63.97	57.2	tr A0A090I3T1 A0A090I3T1_METFO	Elongation factor 2 OS=Methanobacterium formicicum OX- METFO		57
7	63.28	63.29	53.1	tr A0A090I7T4 A0A090I7T4_METFO	Phosphoenolpyruvate synthase OS=Methanobacterium for METFO		69
8	62.46	62.5	57.5	tr A0A090I3A9 A0A090I3A9_METFO	Chaperone protein DnaK OS=Methanobacterium formicicu METFO		85
9	62.35	62.41	77.3	tr A0A090I2R9 A0A090I2R9_METFO	F420-non-reducing hydrogenase subunit A OS=Methanoba METFO		124
10	62	62.09	42.1	tr A0A090I2R3 A0A090I2R3_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO		64
11	59.54	59.54	84	tr A0A090I7W3 A0A090I7W3_METFO	Methyl-coenzyme M reductase subunit beta OS=Methanob METFO		224
12	53.49	53.49	52.7	tr A0A090I3G7 A0A090I3G7_METFO	CoB--CoM heterodisulfide reductase subunit A HdrA2 OS= METFO		82
13	53.42	53.44	16.4	tr A0A090I3J2 A0A090I3J2_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO		46
14	49.01	51.01	61.6	tr A0A090I4W3 A0A090I4W3_METFO	F420-non-reducing hydrogenase vhc subunit A OS=Metha METFO		63

Amostra 2

15	47.7	47.7	66.6	tr A0A090I9A6 A0A090I9A6_METFO	Hydroxylamine reductase OS=Methanobacterium formicicu METFO	78
16	47.16	47.23	59.1	tr A0A089ZDH4 A0A089ZDH4_METFO	Elongation factor 1-alpha OS=Methanobacterium formicicu METFO	122
17	46.66	46.74	58.9	tr A0A090I2G6 A0A090I2G6_METFO	Methyl-coenzyme M reductase subunit alpha OS=Methano METFO	167
18	42.23	42.23	68.2	tr A0A090JVC3 A0A090JVC3_METFO	Methyl-coenzyme M reductase subunit alpha OS=Methano METFO	190
19	40.04	40.04	57.7	tr A0A090I6W9 A0A090I6W9_METFO	Cell shape determining protein MreB/Mrl OS=Methanobact METFO	70
20	38.35	38.35	46.1	tr A0A090I8W8 A0A090I8W8_METFO	Bifunctional enzyme Fae/Hps OS=Methanobacterium formi METFO	58
21	38.33	38.34	56.1	tr A0A090I7U6 A0A090I7U6_METFO	GDP-mannose 4,6-dehydratase OS=Methanobacterium fo METFO	50
22	36.78	36.78	39.9	tr A0A089ZAI4 A0A089ZAI4_METFO	Formylmethanofuran dehydrogenase subunit A FwdA OS= METFO	43
23	36.52	36.53	34.9	tr A0A089ZDA2 A0A089ZDA2_METFO	Cell division control protein Cdc48 OS=Methanobacterium METFO	22
24	36.17	45.22	59.9	tr A0A090IA40 A0A090IA40_METFO	Thermosome subunit OS=Methanobacterium formicicum C METFO	140
25	34.99	35.01	51.7	tr A0A090JTE7 A0A090JTE7_METFO	30S ribosomal protein S3 OS=Methanobacterium formicicu METFO	44
26	34.56	34.56	58.8	tr A0A0S4FR78 A0A0S4FR78_METFO	V-type ATP synthase beta chain OS=Methanobacterium fo METFO	129
27	34.15	34.16	36.3	tr A0A090I2L6 A0A090I2L6_METFO	D-3-phosphoglycerate dehydrogenase OS=Methanobacter METFO	34
28	33.85	33.89	51.8	tr A0A089ZUT3 A0A089ZUT3_METFO	50S ribosomal protein L3 OS=Methanobacterium formicicu METFO	40
29	33.81	33.86	68.4	tr A0A090I5H3 A0A090I5H3_METFO	Methenyltetrahydromethanopterin cyclohydrolase OS=Met METFO	42
30	32.59	32.6	67.9	tr A0A090I4G9 A0A090I4G9_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO	212
31	32.07	32.07	69.7	tr A0A090I5H7 A0A090I5H7_METFO	Tetrahydromethanopterin S-methyltransferase subunit H O METFO	77
32	31.87	31.91	30.4	tr A0A090I0Y6 A0A090I0Y6_METFO	Phosphoserine phosphatase SerB OS=Methanobacterium METFO	22
33	30.59	30.59	58.5	tr A0A090JUK8 A0A090JUK8_METFO	V-type proton ATPase subunit E OS=Methanobacterium fo METFO	26
34	30.03	30.03	58.7	tr A0A090I6Q2 A0A090I6Q2_METFO	Formylmethanofuran dehydrogenase subunit C FwdC OS= METFO	37
35	29.84	29.84	39	tr A0A0S4FLI0 A0A0S4FLI0_METFO	Putative ABC transporter ATP-binding protein MJ1242 OS= METFO	22
36	29.64	29.65	75.3	tr A0A089ZAX5 A0A089ZAX5_METFO	30S ribosomal protein S2 OS=Methanobacterium formicicu METFO	32
37	29.21	29.23	42.6	tr A0A089ZIP7 A0A089ZIP7_METFO	DNA primase DnaG OS=Methanobacterium formicicum O METFO	22
38	28.73	28.76	68.5	tr A0A090I1H9 A0A090I1H9_METFO	30S ribosomal protein S4e OS=Methanobacterium formicic METFO	67
39	28.67	28.74	26.1	tr A0A090I2M9 A0A090I2M9_METFO	Catalase-peroxidase OS=Methanobacterium formicicum O METFO	19
40	28.61	28.65	45.1	tr A0A089ZGQ5 A0A089ZGQ5_METFO	Peptidase U62 family OS=Methanobacterium formicicum C METFO	18
41	28.05	28.08	74.3	tr A0A090I2W9 A0A090I2W9_METFO	Proteasome subunit beta OS=Methanobacterium formicicu METFO	65
42	27.48	27.49	64.6	tr A0A090I613 A0A090I613_METFO	Coenzyme F420 hydrogenase subunit beta OS=Methanob METFO	60
43	27.29	27.34	36.7	tr A0A090I4Q7 A0A090I4Q7_METFO	Aspartate--tRNA(Asp/Asn) ligase OS=Methanobacterium fc METFO	16
44	27.23	27.32	19.3	tr A0A090I151 A0A090I151_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO	18
45	27.18	27.27	61.7	tr A0A090I842 A0A090I842_METFO	CBS domain-containing membrane protein OS=Methanoba METFO	49
46	26.9	26.99	58.1	tr A0A089ZBS9 A0A089ZBS9_METFO	Acetyl-CoA acetyltransferase OS=Methanobacterium formi METFO	68
47	26.6	26.62	60.4	tr A0A089ZEV2 A0A089ZEV2_METFO	CBS domain-containing protein OS=Methanobacterium fo METFO	42

Amostra 2

48	26.57	26.6	44.8	tr A0A090I210 A0A090I210_METFO	Putative aminotransferase MJ0959 OS=Methanobacterium METFO	58
49	26.43	30.48	49.1	tr A0A090I305 A0A090I305_METFO	Coenzyme F420 hydrogenase alpha subunit FrhA OS=Met METFO	51
50	25.92	25.92	38	tr A0A090I2P0 A0A090I2P0_METFO	CBS domain-containing protein OS=Methanobacterium fori METFO	19
51	25.65	25.68	16.8	tr A0A090I9E0 A0A090I9E0_METFO	DNA-directed RNA polymerase subunit OS=Methanobacte METFO	14
52	25.46	25.52	65.3	tr A0A089ZG02 A0A089ZG02_METFO	DNA repair and recombination protein RadA OS=Methanok METFO	28
53	25.2	25.34	59.8	tr A0A090I5T3 A0A090I5T3_METFO	Methyl-coenzyme M reductase subunit gamma OS=Methar METFO	33
54	24.89	24.91	63.6	tr A0A090I7T8 A0A090I7T8_METFO	Peptidyl-prolyl cis-trans isomerase OS=Methanobacterium METFO	25
55	24.84	24.88	27.5	tr A0A090I904 A0A090I904_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	19
56	24.8	24.84	67.4	tr A0A090I8V8 A0A090I8V8_METFO	F420-dependent methylenetetrahydromethanopterin dehyd METFO	45
57	24.71	24.78	49.2	tr A0A090I281 A0A090I281_METFO	Pyruvate synthase subunit PorA OS=Methanobacterium fo METFO	48
58	24.65	24.71	47.6	tr A0A089ZVL0 A0A089ZVL0_METFO	Cell division protein FtsZ OS=Methanobacterium formicicun METFO	21
59	24.2	24.23	48.5	tr A0A090I6I2 A0A090I6I2_METFO	Adenylosuccinate synthetase OS=Methanobacterium formi METFO	27
60	24.15	26.35	32.2	tr A0A089ZCR8 A0A089ZCR8_METFO	Proteasome-activating nucleotidase OS=Methanobacteriun METFO	19
61	24.13	24.21	20.6	tr A0A090I5F3 A0A090I5F3_METFO	Putative secreted protein OS=Methanobacterium formicicu METFO	17
62	24.02	24.12	42.7	tr A0A090I3C5 A0A090I3C5_METFO	Tryptophan synthase beta chain OS=Methanobacterium fo METFO	31
63	23.86	23.86	33.1	tr A0A090I3H9 A0A090I3H9_METFO	5-formaminoimidazole-4-carboxamide-1-(beta)-D-ribofuran METFO	20
64	23.75	23.87	34.1	tr A0A090I7L2 A0A090I7L2_METFO	Acetyl-CoA decarbonylase/synthase complex subunit gamr METFO	19
65	23.7	23.74	51.5	tr A0A090I246 A0A090I246_METFO	3-hydroxy-3-methylglutaryl coenzyme A reductase OS=Met METFO	18
66	23.6	23.76	23.7	tr A0A090I3V1 A0A090I3V1_METFO	Formate dehydrogenase alpha subunit FdhA OS=Methano METFO	19
67	23.33	23.38	47.8	tr A0A090I1P7 A0A090I1P7_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	17
68	22.96	22.99	40.1	tr A0A090JXJ6 A0A090JXJ6_METFO	3-dehydroquinate synthase OS=Methanobacterium formici METFO	20
69	22.9	23.01	29.9	tr A0A090I0Z8 A0A090I0Z8_METFO	Type 2 DNA topoisomerase 6 subunit B OS=Methanobacte METFO	14
70	22.83	22.87	45.7	tr A0A090I3Q7 A0A090I3Q7_METFO	Nucleotidyl transferase OS=Methanobacterium formicicum METFO	19
71	22.61	22.7	39.2	tr A0A090I781 A0A090I781_METFO	Fructose-1,6-bisphosphate aldolase/phosphatase OS=Metl METFO	17
72	22.3	22.32	55.1	tr A0A090I5W3 A0A090I5W3_METFO	30S ribosomal protein S3Ae OS=Methanobacterium formic METFO	34
73	22.22	22.27	39.7	tr A0A090I8M3 A0A090I8M3_METFO	S-adenosylmethionine synthase OS=Methanobacterium fo METFO	16
74	22.07	22.12	57.6	tr A0A090I1I9 A0A090I1I9_METFO	CoB-CoM heterodisulfide reductase iron-sulfur subunit C O METFO	36
75	22.05	22.05	50.2	tr A0A090I5U4 A0A090I5U4_METFO	SPFH domain/Band 7 family protein OS=Methanobacteriun METFO	28
76	21.47	21.52	18.4	tr A0A090I3L1 A0A090I3L1_METFO	Acetyl-CoA synthetase AcsA1 OS=Methanobacterium form METFO	11
77	21.26	21.3	56.3	tr A0A090JV64 A0A090JV64_METFO	CBS domain-containing membrane protein OS=Methanoba METFO	15
78	21.07	21.11	43.1	tr A0A090JXT2 A0A090JXT2_METFO	O-acetylhomoserine (Thiol)-lyase OS=Methanobacterium f METFO	15
79	20.88	20.94	47.6	tr A0A090I6C9 A0A090I6C9_METFO	Ketol-acid reductoisomerase (NADP(+)) OS=Methanobacte METFO	22
80	20.85	20.87	56.5	tr A0A090JTE0 A0A090JTE0_METFO	50S ribosomal protein L6 OS=Methanobacterium formicicu METFO	31

Amostra 2

81	20.63	20.64	59.8 tr A0A090IB20 A0A090IB20_METFO	Proteasome subunit alpha OS=Methanobacterium formicic METFO	35
82	20.62	20.64	35.8 tr A0A090I428 A0A090I428_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	27
83	20.57	20.66	26 tr A0A089ZHM6 A0A089ZHM6_METFO	Methyl-coenzyme M reductase component A2 AtwA2 OS=M METFO	11
84	20.54	20.6	20.9 tr A0A090I3H2 A0A090I3H2_METFO	Phosphoribosylformylglycinamide synthase subunit PurL METFO	12
85	20.43	20.49	35 tr A0A090I4G3 A0A090I4G3_METFO	LL-diaminopimelate aminotransferase OS=Methanobacteri METFO	12
86	20.08	20.16	43.5 tr A0A090I9D3 A0A090I9D3_METFO	Succinate--CoA ligase [ADP-forming] subunit beta OS=MelADP-formin	13
87	20.08	20.1	47 tr A0A089ZGG9 A0A089ZGG9_METFO	50S ribosomal protein L4 OS=Methanobacterium formicicu METFO	15
88	20.06	28.85	42.1 tr A0A090I2C6 A0A090I2C6_METFO	Methyl-coenzyme M reductase component A2 AtwA1 OS=M METFO	18
89	20.05	20.05	35.5 tr A0A090I796 A0A090I796_METFO	Pyridoxal 5'-phosphate synthase subunit PdxS OS=Methan METFO	11
90	20.02	21.94	61 tr A0A089ZD82 A0A089ZD82_METFO	Peptidoglycan binding domain-containing protein OS=Meth METFO	32
91	19.99	20.12	35.2 tr A0A090JVV9 A0A090JVV9_METFO	Aspartate carbamoyltransferase OS=Methanobacterium foi METFO	13
92	19.95	19.99	50.9 tr A0A090I192 A0A090I192_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	14
93	19.77	19.89	25.3 tr A0A0S4FN19 A0A0S4FN19_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	11
94	19.66	19.7	48.7 tr A0A089Z979 A0A089Z979_METFO	Site-determining protein OS=Methanobacterium formicicun METFO	26
95	19.61	19.72	30.8 tr A0A090JTT4 A0A090JTT4_METFO	Methanogenesis marker protein 15 OS=Methanobacterium METFO	11
96	19.59	19.62	45.4 tr A0A090I424 A0A090I424_METFO	Translation initiation factor 5A OS=Methanobacterium form METFO	36
97	19.46	19.58	30.2 tr A0A090I4J0 A0A090I4J0_METFO	Pyruvate carboxylase subunit A OS=Methanobacterium for METFO	10
98	19.27	19.36	40.6 tr A0A089ZVL1 A0A089ZVL1_METFO	50S ribosomal protein L10 OS=Methanobacterium formicic METFO	16
99	19.27	19.31	31.2 tr A0A090JTB4 A0A090JTB4_METFO	Ribonuclease J OS=Methanobacterium formicicum OX=21 METFO	10
100	19.06	19.1	27.4 tr A0A090JW72 A0A090JW72_METFO	Arsenite-activated ATPase ArsA OS=Methanobacterium fo METFO	22
101	18.97	19.12	33.3 tr A0A089ZBE1 A0A089ZBE1_METFO	UPF0288 protein BRM9_0509 OS=Methanobacterium forr METFO	11
102	18.92	19.01	36.7 tr A0A090JTX8 A0A090JTX8_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	19
103	18.9	18.97	50.6 tr A0A090I0T1 A0A090I0T1_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	22
104	18.87	18.97	42.2 tr A0A089ZJ55 A0A089ZJ55_METFO	DNA polymerase sliding clamp OS=Methanobacterium forr METFO	17
105	18.71	18.85	13.3 tr A0A090I571 A0A090I571_METFO	Carbamoyl-phosphate synthase large chain OS=Methanob METFO	11
106	18.69	18.81	66.4 tr A0A089ZER7 A0A089ZER7_METFO	Exosome complex component Rrp4 OS=Methanobacteriun METFO	28
107	18.63	18.73	27.3 tr A0A090I5E9 A0A090I5E9_METFO	Pyruvate carboxylase subunit B OS=Methanobacterium for METFO	12
108	18.4	18.47	28.8 tr A0A090JUQ9 A0A090JUQ9_METFO	Putative nickel insertion protein OS=Methanobacterium for METFO	12
109	18.39	18.5	27.4 tr A0A090I7B6 A0A090I7B6_METFO	Inosine-5'-monophosphate dehydrogenase OS=Methanob METFO	21
110	18.38	18.44	38.5 tr A0A090I4Y4 A0A090I4Y4_METFO	Circadian clock protein KaiC OS=Methanobacterium formic METFO	16
111	18.23	18.43	20.3 tr A0A089ZBN0 A0A089ZBN0_METFO	PIN domain-containing protein OS=Methanobacterium forr METFO	11
112	18.13	18.13	48.7 tr A0A090I0N7 A0A090I0N7_METFO	PyrE-like protein OS=Methanobacterium formicicum OX=2 METFO	15
113	18.09	18.18	44.7 tr A0A089Z8Q6 A0A089Z8Q6_METFO	30S ribosomal protein S11 OS=Methanobacterium formicic METFO	37

Amostra 2

114	18.01	18.01	34.1	tr A0A090I672 A0A090I672_METFO	dTDP-glucose 4,6-dehydratase OS=Methanobacterium formicicum METFO	11
115	18	18	38.4	tr A0A090I345 A0A090I345_METFO	3-isopropylmalate dehydrogenase OS=Methanobacterium formicicum METFO	20
116	18	18	68.7	tr A0A089ZCU1 A0A089ZCU1_METFO	Transcription elongation factor Spt5 OS=Methanobacterium formicicum METFO	16
117	18	18	35.7	tr A0A090I3I6 A0A090I3I6_METFO	Putative lipoprotein MJ0085 OS=Methanobacterium formicicum METFO	14
118	17.96	18	53.1	tr A0A090I7B8 A0A090I7B8_METFO	30S ribosomal protein S19e OS=Methanobacterium formicicum METFO	16
119	17.88	18	20.9	tr A0A089Z9Y9 A0A089Z9Y9_METFO	Type II secretion system protein E GspE OS=Methanobacterium formicicum METFO	13
120	17.85	17.89	59.1	tr A0A089ZGG4 A0A089ZGG4_METFO	50S ribosomal protein L14 OS=Methanobacterium formicicum METFO	18
121	17.77	17.86	20.5	tr A0A090I3Y0 A0A090I3Y0_METFO	Phenylalanine--tRNA ligase beta subunit OS=Methanobacterium formicicum METFO	13
122	17.76	17.82	24.2	tr A0A090JW43 A0A090JW43_METFO	Glutamyl-tRNA(Gln) amidotransferase subunit A OS=Methanobacterium formicicum METFO	12
123	17.73	17.84	19.4	tr A0A090I2I6 A0A090I2I6_METFO	Archaeal glutamate synthase [NADPH] OS=Methanobacterium formicicum METFO	11
124	17.72	18.02	16.9	tr A0A089ZUX5 A0A089ZUX5_METFO	ATPase RIL OS=Methanobacterium formicicum OX=2162 METFO	9
125	17.68	17.78	69.4	tr A0A089ZUS9 A0A089ZUS9_METFO	50S ribosomal protein L18 OS=Methanobacterium formicicum METFO	30
126	17.62	17.7	41.9	tr A0A090I958 A0A090I958_METFO	Extracellular solute-binding protein OS=Methanobacterium formicicum METFO	32
127	17.52	17.67	27	tr A0A090I5S8 A0A090I5S8_METFO	Argininosuccinate synthase OS=Methanobacterium formicicum METFO	13
128	17.45	17.66	41.6	tr A0A090I5I4 A0A090I5I4_METFO	UPF0219 protein DSM1535_2142 OS=Methanobacterium formicicum METFO	28
129	17.31	17.64	20.3	tr A0A090I8V0 A0A090I8V0_METFO	Threonine--tRNA ligase OS=Methanobacterium formicicum METFO	12
130	17.28	17.38	32	tr A0A090I3S2 A0A090I3S2_METFO	Phosphoglycerate kinase OS=Methanobacterium formicicum METFO	9
131	17.22	17.36	25.3	tr A0A090I3J1 A0A090I3J1_METFO	Formate dehydrogenase beta subunit FdhB OS=Methanobacterium formicicum METFO	9
132	16.89	17.26	37.1	tr A0A090I3S6 A0A090I3S6_METFO	DNA-directed RNA polymerase subunit A' OS=Methanobacterium formicicum METFO	28
133	16.73	16.83	75.5	tr A0A090JWL2 A0A090JWL2_METFO	IMP cyclohydrolase OS=Methanobacterium formicicum OX METFO	22
134	16.7	16.75	42.1	tr A0A0S4FRT9 A0A0S4FRT9_METFO	Formylmethanofuran--tetrahydromethanopterin formyltransferase METFO	27
135	16.49	16.59	35	tr A0A089ZI64 A0A089ZI64_METFO	ATP phosphoribosyltransferase OS=Methanobacterium formicicum METFO	11
136	16.42	16.45	35.5	tr A0A090I622 A0A090I622_METFO	Translation initiation factor 2 subunit alpha OS=Methanobacterium formicicum METFO	20
137	16.4	16.42	32.1	tr A0A090I8R6 A0A090I8R6_METFO	Acetylornithine aminotransferase OS=Methanobacterium formicicum METFO	10
138	16.18	16.19	59.4	tr A0A090I2G3 A0A090I2G3_METFO	Tetrahydromethanopterin S-methyltransferase subunit A OS=Methanobacterium formicicum METFO	82
139	16.1	16.1	29.9	tr A0A090I8Z8 A0A090I8Z8_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	8
140	16.04	16.04	31.9	tr A0A090I653 A0A090I653_METFO	Methanogenesis marker protein 11 OS=Methanobacterium formicicum METFO	15
141	16.04	16.04	45.1	tr A0A089ZGF9 A0A089ZGF9_METFO	30S ribosomal protein S5 OS=Methanobacterium formicicum METFO	18
142	16	16	67.4	tr A0A090I170 A0A090I170_METFO	TATA-box-binding protein OS=Methanobacterium formicicum METFO	27
143	16	16	34.7	tr A0A090JUJ4 A0A090JUJ4_METFO	Probable L-aspartate dehydrogenase OS=Methanobacterium formicicum METFO	8
144	15.75	15.82	61.6	tr A0A090I2I9 A0A090I2I9_METFO	Translation initiation factor 6 OS=Methanobacterium formicicum METFO	27
145	15.75	15.77	44	tr A0A090I560 A0A090I560_METFO	Putative hydrogenase nickel incorporation protein HypB OS=Methanobacterium formicicum METFO	9
146	15.74	15.79	22.7	tr A0A090JY31 A0A090JY31_METFO	Aspartokinase OS=Methanobacterium formicicum OX=216 METFO	8

Amostra 2

147	15.69	15.82	33.6	tr A0A090I6V8 A0A090I6V8_METFO	CoB-CoM heterodisulfide reductase subunit B OS=Methanobacterium formicicum METFO	16
148	15.57	15.64	43.3	tr A0A090I518 A0A090I518_METFO	Digeranylglycerophospholipid reductase OS=Methanobacterium formicicum METFO	13
149	15.51	15.62	23.8	tr A0A090JWH2 A0A090JWH2_METFO	Phosphoglucosamine mutase GlmM2 OS=Methanobacterium formicicum METFO	12
150	15.3	15.47	16.3	tr A0A0S4FQI5 A0A0S4FQI5_METFO	Cell division cycle protein 48 homolog MJ1156 OS=Methanobacterium formicicum METFO	10
151	15.29	15.39	34.5	tr A0A090I7Z4 A0A090I7Z4_METFO	O-acetylserine sulfhydrylase OS=Methanobacterium formicicum METFO	9
152	15.24	15.45	38.2	tr A0A090I166 A0A090I166_METFO	Enolase OS=Methanobacterium formicicum OX=2162 GN= METFO	13
153	15.15	15.29	20.2	tr A0A090I4Q8 A0A090I4Q8_METFO	Phenylalanine--tRNA ligase alpha subunit OS=Methanobacterium formicicum METFO	11
154	15.13	16.23	27.8	tr A0A090I7S6 A0A090I7S6_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	13
155	15.04	15.18	27.1	tr A0A090IAD3 A0A090IAD3_METFO	Homoserine dehydrogenase OS=Methanobacterium formicicum METFO	10
156	15.03	15.08	43.5	tr A0A089ZAY7 A0A089ZAY7_METFO	30S ribosomal protein S4 OS=Methanobacterium formicicum METFO	14
157	14.96	15.01	41.7	tr A0A090I740 A0A090I740_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	10
158	14.77	14.93	19.6	tr A0A090JYJ5 A0A090JYJ5_METFO	Glutamine--fructose-6-phosphate aminotransferase [isozyme 1] OS=Methanobacterium formicicum METFO	8
159	14.77	14.91	28.3	tr K2QY77 K2QY77_METFP	Transcription initiation factor IIB OS=Methanobacterium formicicum METFP	9
160	14.71	14.82	38.6	tr A0A090I433 A0A090I433_METFO	GMP synthase [glutamine-hydrolyzing] subunit B OS=Methanobacterium formicicum METFO	11
161	14.57	14.79	30.2	tr A0A090I3J9 A0A090I3J9_METFO	Tungsten-containing formylmethanofuran dehydrogenase 2 OS=Methanobacterium formicicum METFO	26
162	14.44	14.47	19.9	tr A0A090JVX7 A0A090JVX7_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	7
163	14.41	14.5	21	tr A0A090I3U3 A0A090I3U3_METFO	Peptidase U62 modulator of DNA gyrase OS=Methanobacterium formicicum METFO	9
164	14.39	14.46	37	tr A0A090I7Q9 A0A090I7Q9_METFO	2-amino-3,7-dideoxy-D-threo-hept-6-ulosonate synthase O METFO	14
165	14.32	14.75	21.6	tr A0A089ZGW2 A0A089ZGW2_METFO	Translation initiation factor 2 subunit gamma OS=Methanobacterium formicicum METFO	9
166	14.19	14.23	59.9	tr A0A090I340 A0A090I340_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	13
167	14.17	14.25	41.2	tr A0A090I9E4 A0A090I9E4_METFO	30S ribosomal protein S7 OS=Methanobacterium formicicum METFO	17
168	14.11	14.12	61.5	tr A0A090JUT3 A0A090JUT3_METFO	F420-non-reducing hydrogenase iron-sulfur subunit D OS= METFO	14
169	14	14	42.7	tr A0A090I5G8 A0A090I5G8_METFO	F420-non-reducing hydrogenase subunit G OS=Methanobacterium formicicum METFO	22
170	14	14	41.2	tr A0A090JW64 A0A090JW64_METFO	LemA family protein OS=Methanobacterium formicicum OX= METFO	18
171	14	14	26.3	tr A0A090I471 A0A090I471_METFO	GDP-mannose 4,6-dehydratase OS=Methanobacterium formicicum METFO	10
172	13.92	13.96	52	tr A0A090JTD5 A0A090JTD5_METFO	50S ribosomal protein L30 OS=Methanobacterium formicicum METFO	21
173	13.77	13.83	18.8	tr A0A090I8U4 A0A090I8U4_METFO	Acetolactate synthase OS=Methanobacterium formicicum (METFO	7
174	13.66	13.88	29.9	tr A0A089ZGS2 A0A089ZGS2_METFO	Replication factor C small subunit OS=Methanobacterium formicicum METFO	10
175	13.63	13.76	36.4	tr A0A089ZAG5 A0A089ZAG5_METFO	Transcriptional regulator with CBS domains OS=Methanobacterium formicicum METFO	12
176	13.55	13.59	26.1	tr A0A090I7U4 A0A090I7U4_METFO	ABC transporter OS=Methanobacterium formicicum OX=21 METFO	9
177	13.49	13.53	57.8	tr A0A090I579 A0A090I579_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	13
178	13.42	13.47	42.8	tr A0A090JY8 A0A090JY8_METFO	Putative acetolactate synthase small subunit OS=Methanobacterium formicicum METFO	11
179	13.39	13.44	41.6	tr A0A090IA48 A0A090IA48_METFO	Nitrite reductase (NAD(P)H) OS=Methanobacterium formicicum METFO	7

Amostra 2

180	13.29	13.41	35.4	tr A0A090I582 A0A090I582_METFO	50S ribosomal protein L1 OS=Methanobacterium formicicu METFO	11
181	13.23	13.28	54	tr A0A090I4T3 A0A090I4T3_METFO	Orotate phosphoribosyltransferase OS=Methanobacterium METFO	11
182	13.22	13.28	21.3	tr A0A090I383 A0A090I383_METFO	Diaminopimelate decarboxylase OS=Methanobacterium fo METFO	11
183	13.16	13.3	31.7	tr A0A090IB58 A0A090IB58_METFO	Carbamoyl-phosphate synthase small chain OS=Methanob METFO	15
184	13.15	13.29	32.2	tr A0A090I4Y0 A0A090I4Y0_METFO	Threonine synthase OS=Methanobacterium formicicum OX METFO	11
185	13.04	13.09	21.5	tr A0A090I409 A0A090I409_METFO	Glutamyl-tRNA(Gln) amidotransferase subunit D OS=Meth METFO	8
186	12.88	12.99	21.7	tr A0A090I455 A0A090I455_METFO	Type 2 DNA topoisomerase 6 subunit A OS=Methanobacte METFO	7
187	12.87	12.92	51.2	tr A0A089ZF65 A0A089ZF65_METFO	PRC-barrel domain-containing protein OS=Methanobacteri METFO	11
188	12.78	12.85	33.6	tr A0A090I6D3 A0A090I6D3_METFO	Ornithine carbamoyltransferase OS=Methanobacterium for METFO	7
189	12.69	12.72	29.5	tr A0A090I494 A0A090I494_METFO	Short-chain dehydrogenase family protein OS=Methanobac METFO	12
190	12.66	12.95	27.4	tr A0A090I4Y9 A0A090I4Y9_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO	8
191	12.61	12.71	11	tr A0A090JW16 A0A090JW16_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO	12
192	12.51	12.54	62.6	tr A0A090I6K9 A0A090I6K9_METFO	30S ribosomal protein S17 OS=Methanobacterium formicic METFO	15
193	12.42	12.5	31.3	tr A0A090JUG7 A0A090JUG7_METFO	Phosphate binding protein OS=Methanobacterium formicic METFO	8
194	12.35	12.48	42.2	tr A0A089ZGF5 A0A089ZGF5_METFO	CBS domain-containing protein OS=Methanobacterium for METFO	10
195	12.29	12.45	27.8	tr A0A090I135 A0A090I135_METFO	UTP--glucose-1-phosphate uridylyltransferase OS=Methan METFO	7
196	12.19	12.21	36.1	tr A0A089ZCQ3 A0A089ZCQ3_METFO	Putative rubrerythrin OS=Methanobacterium formicicum O METFO	8
197	12.06	12.06	39.9	tr A0A090I180 A0A090I180_METFO	50S ribosomal protein L5 OS=Methanobacterium formicicu METFO	21
198	12.04	12.16	34.2	tr A0A090I3I7 A0A090I3I7_METFO	Putative sugar kinase MTH_1544 OS=Methanobacterium f METFO	7
199	12.01	12.01	62.8	tr A0A089ZB18 A0A089ZB18_METFO	50S ribosomal protein L23 OS=Methanobacterium formicic METFO	19
200	12	14	38.9	tr A0A089ZVR2 A0A089ZVR2_METFO	Peptidoglycan binding domain-containing protein OS=Meth METFO	35
201	12	12	47.1	tr K2QDP1 K2QDP1_METFP	30S ribosomal protein S10 OS=Methanobacterium formicic METFP	9
202	11.83	11.89	37.3	tr A0A090I552 A0A090I552_METFO	Exosome complex component Rrp42 OS=Methanobacteriu METFO	14
203	11.71	11.86	27.4	tr A0A090I6I6 A0A090I6I6_METFO	Isopentenyl-diphosphate delta-isomerase OS=Methanobac METFO	6
204	11.68	11.72	27.7	tr A0A090I1X5 A0A090I1X5_METFO	3-isopropylmalate dehydrogenase OS=Methanobacterium METFO	6
205	11.66	11.7	36.9	tr A0A090I7Y5 A0A090I7Y5_METFO	AsnC family transcriptional regulator OS=Methanobacteriur METFO	8
206	11.62	11.67	18.6	tr A0A090I6T0 A0A090I6T0_METFO	Glutamine synthetase OS=Methanobacterium formicicum C METFO	8
207	11.57	11.62	19.8	tr A0A0S4FMQ4 A0A0S4FMQ4_METFO	Putative hydrogenase expression/formation protein MJ067 METFO	7
208	11.51	11.67	42.2	tr A0A089ZH87 A0A089ZH87_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO	10
209	11.5	11.64	10.5	tr A0A090I8M1 A0A090I8M1_METFO	Lon protease OS=Methanobacterium formicicum OX=2162 METFO	6
210	11.43	11.53	28.8	tr A0A090I2K4 A0A090I2K4_METFO	Putative ATP-binding protein MJ0685 OS=Methanobacteri METFO	8
211	11.42	11.51	32.1	tr A0A090I0T5 A0A090I0T5_METFO	Toprim domain-containing protein OS=Methanobacterium f METFO	10
212	11.41	11.51	14.9	tr A0A090I8R0 A0A090I8R0_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO	6

Amostra 2

213	11.4	11.46	21.2	tr A0A090JX22 A0A090JX22_METFO	Proline--tRNA ligase OS=Methanobacterium formicicum O METFO	11
214	11.38	11.45	62.2	tr A0A090JYF1 A0A090JYF1_METFO	TRAM domain-containing protein OS=Methanobacterium formicicum METFO	14
215	11.26	11.5	24.7	tr A0A090I314 A0A090I314_METFO	CBS domain-containing protein OS=Methanobacterium formicicum METFO	6
216	11.19	11.28	17.7	tr A0A0S4FN62 A0A0S4FN62_METFO	UDP-N-acetylglucosamine 2-epimerase OS=Methanobacterium formicicum METFO	7
217	11.14	11.19	28.7	tr A0A090JW77 A0A090JW77_METFO	ATP phosphoribosyltransferase OS=Methanobacterium formicicum METFO	7
218	11.09	11.2	47.1	tr A0A089ZGF2 A0A089ZGF2_METFO	50S ribosomal protein L13 OS=Methanobacterium formicicum METFO	24
219	11	11.05	34.6	tr A0A089ZE87 A0A089ZE87_METFO	ABC transporter ATP-binding protein OS=Methanobacterium formicicum METFO	11
220	10.99	11.07	37.3	tr A0A090I729 A0A090I729_METFO	TrkA domain-containing protein OS=Methanobacterium formicicum METFO	8
221	10.98	11.26	12.4	tr A0A090I583 A0A090I583_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	5
222	10.91	11.06	41.3	tr A0A090I1Y5 A0A090I1Y5_METFO	Molybdenum cofactor synthesis domain-containing protein METFO	8
223	10.87	11.05	29.2	tr A0A090JTX4 A0A090JTX4_METFO	dCTP deaminase, dUMP-forming OS=Methanobacterium formicicum METFO	6
224	10.81	10.86	51.1	tr A0A090JTC3 A0A090JTC3_METFO	30S ribosomal protein S9 OS=Methanobacterium formicicum METFO	12
225	10.78	10.89	33.2	tr A0A090JSP3 A0A090JSP3_METFO	Uridylate kinase OS=Methanobacterium formicicum OX=21 METFO	13
226	10.78	10.84	22.7	tr A0A090I3A4 A0A090I3A4_METFO	Phosphoribosylamine--glycine ligase OS=Methanobacterium formicicum METFO	6
227	10.7	10.78	20.2	tr A0A090I5P8 A0A090I5P8_METFO	Coenzyme A biosynthesis bifunctional protein CoaBC OS=Methanobacterium formicicum METFO	6
228	10.6	10.76	20.7	tr A0A089ZV33 A0A089ZV33_METFO	FeS assembly protein SufBD OS=Methanobacterium formicicum METFO	9
229	10.51	10.55	14.7	tr A0A090I4R4 A0A090I4R4_METFO	Type A flavoprotein FprA OS=Methanobacterium formicicum METFO	6
230	10.46	10.5	22.9	tr A0A090I1Q2 A0A090I1Q2_METFO	Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Methanobacterium formicicum METFO	8
231	10.35	10.39	19	tr A0A090JYU9 A0A090JYU9_METFO	Phosphosulfolactate synthase OS=Methanobacterium formicicum METFO	7
232	10.26	10.28	19.7	tr A0A090I360 A0A090I360_METFO	F420H2 oxidase FprA OS=Methanobacterium formicicum METFO	6
233	10.18	10.35	16.8	tr A0A090I6D0 A0A090I6D0_METFO	Tryptophan synthase beta chain OS=Methanobacterium formicicum METFO	6
234	10.11	10.13	13.7	tr A0A090I100 A0A090I100_METFO	S-inosyl-L-homocysteine hydrolase OS=Methanobacterium formicicum METFO	7
235	10.11	10.12	61.9	tr A0A089ZBS5 A0A089ZBS5_METFO	30S ribosomal protein S6e OS=Methanobacterium formicicum METFO	13
236	10.09	10.36	23.2	tr A0A090I4K5 A0A090I4K5_METFO	Glutamate dehydrogenase OS=Methanobacterium formicicum METFO	7
237	10.08	10.97	22.9	tr A0A090I3P4 A0A090I3P4_METFO	Alanine dehydrogenase OS=Methanobacterium formicicum METFO	8
238	10.07	10.08	33.7	tr A0A090I8S8 A0A090I8S8_METFO	ABC transporter ATP-binding protein OS=Methanobacterium formicicum METFO	11
239	10.04	10.04	12	tr A0A090I599 A0A090I599_METFO	Acetyl-CoA decarbonylase/synthase complex subunit beta METFO	8
240	10.01	10.01	47.2	tr A0A089ZGZ1 A0A089ZGZ1_METFO	30S ribosomal protein S8e OS=Methanobacterium formicicum METFO	14
241	10	10	21.2	tr A0A090I5G4 A0A090I5G4_METFO	Exosome complex component Rrp41 OS=Methanobacterium formicicum METFO	8
242	10	10	48.9	tr A0A089ZCA7 A0A089ZCA7_METFO	Thioesterase OS=Methanobacterium formicicum OX=2162 METFO	9
243	10	10	38	tr A0A090JX40 A0A090JX40_METFO	(5-formylfuran-3-yl)methyl phosphate synthase OS=Methanobacterium formicicum METFO	10
244	10	10	21.2	tr A0A090I657 A0A090I657_METFO	3-isopropylmalate dehydratase large subunit OS=Methanobacterium formicicum METFO	8
245	9.94	10.13	23.2	tr A0A090I536 A0A090I536_METFO	Signal recognition particle receptor FtsY OS=Methanobacterium formicicum METFO	6

Amostra 2

246	9.83	9.89	12.6	tr A0A090I298 A0A090I298_METFO	Archaeal glutamate synthase [NADPH] OS=Methanobacteri NADPH	5
247	9.82	9.89	34.7	tr A0A089ZV28 A0A089ZV28_METFO	Heat shock protein Hsp20 OS=Methanobacterium formicic METFO	8
248	9.82	9.89	35.5	tr A0A090JV59 A0A090JV59_METFO	Transcription elongation factor NusA-like protein OS=Meth METFO	5
249	9.8	9.92	24.8	tr A0A0S4FLD6 A0A0S4FLD6_METFO	ABC transporter substrate-binding protein OS=Methanobac METFO	9
250	9.77	9.94	10.9	tr A0A089ZUP9 A0A089ZUP9_METFO	Energy-converting hydrogenase B subunit N EhbN OS=Me METFO	4
251	9.65	9.73	14.9	tr A0A089ZI25 A0A089ZI25_METFO	Serine hydroxymethyltransferase OS=Methanobacterium fc METFO	5
252	9.64	9.83	20.3	tr A0A090I3L6 A0A090I3L6_METFO	Type 11 methyltransferase OS=Methanobacterium formicic METFO	6
253	9.63	9.78	28.5	tr A0A090I2T7 A0A090I2T7_METFO	Methyl-coenzyme M reductase subunit gamma OS=Methar METFO	9
254	9.62	9.82	19.2	tr A0A0S4FPY7 A0A0S4FPY7_METFO	Aminotransferase OS=Methanobacterium formicicum OX= METFO	6
255	9.59	9.68	9.1	tr A0A089ZAV8 A0A089ZAV8_METFO	RNA-metabolising metallo-beta-lactamase OS=Methanoba METFO	5
256	9.59	9.66	16.1	tr A0A090I496 A0A090I496_METFO	N-acetyl-gamma-glutamyl-phosphate reductase OS=Metha METFO	5
257	9.55	9.82	26.9	tr A0A090I7X7 A0A090I7X7_METFO	Glutamine-scylo-inositol transaminase OS=Methanobacter METFO	6
258	9.55	9.63	24.9	tr A0A089ZGX6 A0A089ZGX6_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	14
259	9.55	9.62	27.3	tr A0A090JVL3 A0A090JVL3_METFO	Coenzyme F420 hydrogenase gamma subunit FrhG OS=M METFO	7
260	9.46	9.61	14.7	tr A0A090JWA7 A0A090JWA7_METFO	Lysine--tRNA ligase OS=Methanobacterium formicicum O METFO	6
261	9.42	9.62	16.5	tr A0A090I116 A0A090I116_METFO	Amidophosphoribosyltransferase OS=Methanobacterium fc METFO	6
262	9.36	9.42	23.4	tr A0A0S4FLK3 A0A0S4FLK3_METFO	Coenzyme F420:L-glutamate ligase OS=Methanobacteriun METFO	6
263	9.31	9.36	40.9	tr A0A090I3Y5 A0A090I3Y5_METFO	Flavodoxin OS=Methanobacterium formicicum OX=2162 G METFO	6
264	9.21	9.63	21	tr A0A089ZGH1 A0A089ZGH1_METFO	Bifunctional biotin operon repressor/biotin-acetyl-CoA-carb METFO	6
265	9.18	14.47	15.1	tr A0A090IAQ7 A0A090IAQ7_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	12
266	9.15	9.25	20.9	tr A0A090I2K0 A0A090I2K0_METFO	Phosphoribosylformylglycinamide cyclo-ligase OS=Metha METFO	5
267	9.11	9.21	29.4	tr A0A090I912 A0A090I912_METFO	NH(3)-dependent NAD(+) synthetase OS=Methanobacteri METFO	6
268	9.05	11.28	27.5	tr A0A090I938 A0A090I938_METFO	Phosphomethylpyrimidine synthase OS=Methanobacteriun METFO	21
269	9.04	9.36	12.3	tr A0A090JWN5 A0A090JWN5_METFO	DNA-directed RNA polymerase subunit beta OS=Methanok METFO	8
270	9.04	9.13	13	tr A0A090JWG4 A0A090JWG4_METFO	DNA ligase OS=Methanobacterium formicicum OX=2162 C METFO	5
271	8.9	8.97	19.1	tr A0A090I0K3 A0A090I0K3_METFO	Histidinol-phosphate aminotransferase OS=Methanobacter METFO	5
272	8.88	8.94	15.4	tr A0A090IB52 A0A090IB52_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	5
273	8.87	9.01	30.4	tr A0A089Z928 A0A089Z928_METFO	Nitrogenase cofactor biosynthesis protein NifB OS=Methan METFO	10
274	8.87	8.95	35.4	tr A0A090I8J3 A0A090I8J3_METFO	Cobalt-precorrin-8X methylmutase OS=Methanobacterium METFO	6
275	8.82	8.89	23	tr A0A090I4H9 A0A090I4H9_METFO	UDP-glucose 4-epimerase OS=Methanobacterium formicic METFO	5
276	8.79	8.89	19.2	tr A0A089ZA17 A0A089ZA17_METFO	Peptidase U32 family OS=Methanobacterium formicicum C METFO	6
277	8.73	8.91	24.4	tr A0A090JVT4 A0A090JVT4_METFO	Putative ABC transporter ATP-binding protein MJ0089 OS= METFO	7
278	8.68	8.73	18.3	tr A0A090I574 A0A090I574_METFO	Glutamine-fructose-6-phosphate transaminase OS=Methar METFO	7

Amostra 2

279	8.63	8.86	15.2	tr A0A090I5M1 A0A090I5M1_METFO	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit METFO	5
280	8.59	8.64	23.1	tr A0A089ZC51 A0A089ZC51_METFO	Extracellular phosphate-binding protein OS=Methanobacte METFO	6
281	8.55	8.59	55.9	tr A0A090I6A2 A0A090I6A2_METFO	Cyclophilin type peptidyl-prolyl cis-trans isomerase OS=Me METFO	6
282	8.49	8.62	23.6	tr A0A090I6J2 A0A090I6J2_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	7
283	8.4	8.44	16.5	tr A0A090I2F4 A0A090I2F4_METFO	Polyferredoxin protein MvhB OS=Methanobacterium formic METFO	5
284	8.36	13.95	19.4	tr A0A090JXN7 A0A090JXN7_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	17
285	8.28	8.48	18.4	tr A0A090I6B5 A0A090I6B5_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	7
286	8.22	8.29	46.2	tr A0A089ZHN5 A0A089ZHN5_METFO	Probable transcription termination protein NusA OS=Metha METFO	6
287	8.16	8.26	27	tr A0A090I640 A0A090I640_METFO	Exosome complex component Csl4 OS=Methanobacterium METFO	4
288	8.11	8.12	28.3	tr A0A090I4X8 A0A090I4X8_METFO	F420-dependent NADP reductase OS=Methanobacterium METFO	9
289	8.09	8.17	28.4	tr A0A089ZEW4 A0A089ZEW4_METFO	50S ribosomal protein L11 OS=Methanobacterium formicic METFO	6
290	8.06	8.22	21.2	tr A0A090I465 A0A090I465_METFO	Spore coat polysaccharide biosynthesis protein SpsK OS=I METFO	7
291	8.05	8.05	20.9	tr A0A090I9D6 A0A090I9D6_METFO	Triosephosphate isomerase OS=Methanobacterium formic METFO	6
292	8.04	8.12	27.3	tr A0A090I950 A0A090I950_METFO	Formylmethanofuran dehydrogenase subunit D FwdD OS= METFO	4
293	8.02	8.02	22.4	tr A0A090I1I6 A0A090I1I6_METFO	50S ribosomal protein L2 OS=Methanobacterium formicicu METFO	5
294	8.01	8.02	16.8	tr A0A090IAU5 A0A090IAU5_METFO	Choloylglycine hydrolase OS=Methanobacterium formicicu METFO	4
295	8	8	44.7	tr A0A089ZVR0 A0A089ZVR0_METFO	30S ribosomal protein S12 OS=Methanobacterium formicic METFO	12
296	8	8	18	tr A0A090I4P4 A0A090I4P4_METFO	Endonuclease NucS OS=Methanobacterium formicicum O METFO	5
297	8	8	22.3	tr A0A090I2J1 A0A090I2J1_METFO	Pyruvate ferredoxin oxidoreductase beta subunit PorB OS= METFO	5
298	8	8	17.9	tr A0A090I4G2 A0A090I4G2_METFO	Bifunctional short chain isoprenyl diphosphate synthase Ids METFO	4
299	8	8	33.8	tr A0A089ZFP6 A0A089ZFP6_METFO	Peptidase S26B, signal peptidase OS=Methanobacterium f METFO	7
300	8	8	47.8	tr A0A089ZA11 A0A089ZA11_METFO	UPF0145 protein BRM9_0823 OS=Methanobacterium form METFO	11
301	8	8	17.8	tr A0A090IA04 A0A090IA04_METFO	5-amino-6-(D-ribitylamino)uracil--L-tyrosine 4-hydroxyphen METFO	5
302	7.92	8	38.5	tr A0A090I2G1 A0A090I2G1_METFO	Universal stress protein MTBMA_c15380 OS=Methanobac METFO	4
303	7.89	9.47	13.1	tr A0A090I3X2 A0A090I3X2_METFO	Probable phosphoglucosamine mutase OS=Methanobacte METFO	6
304	7.87	8.08	16.7	tr A0A090I503 A0A090I503_METFO	Malate dehydrogenase OS=Methanobacterium formicicum METFO	4
305	7.87	7.94	12.2	tr A0A090I524 A0A090I524_METFO	tRNA-splicing ligase RtcB OS=Methanobacterium formicicu METFO	5
306	7.84	8.08	34	tr A0A090JU33 A0A090JU33_METFO	DNA-directed RNA polymerase OS=Methanobacterium form METFO	8
307	7.82	7.94	25.7	tr A0A090IA01 A0A090IA01_METFO	Beta-lactamase domain protein OS=Methanobacterium form METFO	4
308	7.78	7.87	17.6	tr A0A090I2L0 A0A090I2L0_METFO	CBS domain-containing protein OS=Methanobacterium form METFO	5
309	7.71	7.97	22.1	tr A0A0S4FRZ5 A0A0S4FRZ5_METFO	Digeranylglycerolphospholipid reductase OS=Metha METFO	6
310	7.7	7.77	10.4	tr A0A0S4FM80 A0A0S4FM80_METFO	2,3-bisphosphoglycerate-independent phosphoglycerate m METFO	4
311	7.69	7.98	20	tr A0A089ZDP0 A0A089ZDP0_METFO	Thiamine thiazole synthase OS=Methanobacterium formici METFO	7

Amostra 2

312	7.64	7.7	14.9	tr A0A090I431 A0A090I431_METFO	2-oxoglutarate synthase subunit KorA OS=Methanobacteriu METFO	7
313	7.62	7.82	6.6	tr A0A090I5I4 A0A090I5I4_METFO	ATP-dependent protease S16 family OS=Methanobacteriu METFO	4
314	7.62	7.75	42.4	tr A0A090JWM7 A0A090JWM7_METFO	2-oxoglutarate synthase subunit KorC OS=Methanobacteriu METFO	6
315	7.62	7.7	19.2	tr A0A090I3L5 A0A090I3L5_METFO	UPF0285 protein DSM1535_1340 OS=Methanobacterium i METFO	4
316	7.57	7.71	12	tr A0A089ZH78 A0A089ZH78_METFO	V-type ATP synthase subunit C OS=Methanobacterium fori METFO	6
317	7.55	7.64	14.6	tr A0A089ZHE0 A0A089ZHE0_METFO	Molybdenum cofactor synthesis domain-containing protein METFO	6
318	7.53	7.67	31.9	tr A0A089ZEU2 A0A089ZEU2_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO	5
319	7.49	7.72	9.2	tr A0A090I4F2 A0A090I4F2_METFO	Methionine--tRNA ligase OS=Methanobacterium formicicu METFO	5
320	7.49	7.61	37.5	tr A0A090I2E9 A0A090I2E9_METFO	50S ribosomal protein L10e OS=Methanobacterium formici METFO	5
321	7.41	7.68	24.7	tr A0A090I443 A0A090I443_METFO	Superoxide dismutase OS=Methanobacterium formicicum i METFO	6
322	7.39	7.53	29.3	tr A0A090I420 A0A090I420_METFO	Probable porphobilinogen deaminase OS=Methanobacteriu METFO	6
323	7.29	7.37	23.2	tr A0A090JW24 A0A090JW24_METFO	PHP domain-containing protein OS=Methanobacterium fori METFO	4
324	7.24	7.32	30.3	tr A0A090I8C8 A0A090I8C8_METFO	Flavodoxin/nitric oxide synthase OS=Methanobacterium fori METFO	4
325	7.2	7.29	16.4	tr A0A0S4FLL3 A0A0S4FLL3_METFO	Exodeoxyribonuclease III OS=Methanobacterium formicicu METFO	4
326	7.19	7.42	39.6	tr A0A090I0S1 A0A090I0S1_METFO	KH domain-containing protein OS=Methanobacterium form METFO	6
327	7.11	7.33	32.1	tr A0A090I3K4 A0A090I3K4_METFO	Diaminopimelate epimerase OS=Methanobacterium formic METFO	11
328	7.08	7.19	32.4	tr A0A090I521 A0A090I521_METFO	4-hydroxy-tetrahydrodipicolinate reductase OS=Methanoba METFO	11
329	7.07	7.16	10.6	tr A0A090I9P2 A0A090I9P2_METFO	Phenylacetate-coenzyme A ligase OS=Methanobacterium i METFO	5
330	7.04	7.11	27.3	tr A0A089ZGF4 A0A089ZGF4_METFO	30S ribosomal protein S13 OS=Methanobacterium formicic METFO	5
331	7.01	7.29	15.1	tr A0A090I8Q5 A0A090I8Q5_METFO	Probable cobyric acid synthase OS=Methanobacterium fori METFO	6
332	7.01	7.28	23.1	tr A0A090I731 A0A090I731_METFO	Glucose-1-phosphate thymidyltransferase OS=Methanob. METFO	5
333	7.01	7.15	21	tr A0A090I5E6 A0A090I5E6_METFO	Inositol-3-phosphate synthase OS=Methanobacterium forr METFO	7
334	6.92	7.21	24.3	tr A0A090I7K3 A0A090I7K3_METFO	Phosphate import ATP-binding protein PstB OS=Methanob METFO	7
335	6.91	7.25	16.2	tr A0A090JYL6 A0A090JYL6_METFO	Peptidase C60 sortase A and B OS=Methanobacterium for METFO	6
336	6.82	6.95	31.6	tr A0A090I489 A0A090I489_METFO	GTP-binding protein Rab-like protein OS=Methanobacteriu METFO	4
337	6.77	6.99	8.9	tr A0A090I3L9 A0A090I3L9_METFO	Dihydroxy-acid dehydratase OS=Methanobacterium formici METFO	4
338	6.77	6.92	29.9	tr A0A090I2W0 A0A090I2W0_METFO	Glutamate synthase beta subunit GltB2 OS=Methanobacte METFO	4
339	6.75	6.83	16.4	tr A0A090JXR2 A0A090JXR2_METFO	Formylmethanofuran-tetrahydromethanopterin formyltransf METFO	5
340	6.7	6.8	23.7	tr A0A090I5D2 A0A090I5D2_METFO	MarR family transcriptional regulator OS=Methanobacteriu METFO	5
341	6.6	6.76	26.4	tr A0A090I684 A0A090I684_METFO	Formylmethanofuran dehydrogenase subunit E OS=Metha METFO	4
342	6.5	6.83	15.5	tr A0A090I0L2 A0A090I0L2_METFO	Dimethylmenaquinone methyltransferase OS=Methanobac METFO	3
343	6.45	6.55	30.5	tr A0A090I5U3 A0A090I5U3_METFO	Geranylgeranylglyceryl phosphate synthase OS=Methanob METFO	5
344	6.43	6.6	41.4	tr A0A089ZDW1 A0A089ZDW1_METFO	Methyl-coenzyme M reductase II D subunit MrtD OS=Meth METFO	6

Amostra 2

345	6.33	6.35	11.5	tr A0A090I391 A0A090I391_METFO	Daunorubicin resistance ABC transporter ATPase subunit (METFO	5
346	6.32	6.35	14.2	tr A0A090I3L4 A0A090I3L4_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
347	6.29	6.43	12.7	tr A0A090JXY4 A0A090JXY4_METFO	Chorismate synthase OS=Methanobacterium formicicum CMETFO	4
348	6.28	10.04	58.1	tr A0A090IAT6 A0A090IAT6_METFO	TRAM domain-containing protein OS=Methanobacterium fo METFO	6
349	6.21	6.25	11.1	tr A0A090I3M2 A0A090I3M2_METFO	Cell division ATPase MinD1 OS=Methanobacterium formici METFO	3
350	6.21	6.23	37.4	tr K2RRN0 K2RRN0_METFP	Uncharacterized protein OS=Methanobacterium formicicum METFP	5
351	6.19	6.22	8.9	tr A0A090JXZ1 A0A090JXZ1_METFO	Delta-aminolevulinic acid dehydratase OS=Methanobacteri METFO	3
352	6.16	6.35	27.1	tr K2REW5 K2REW5_METFP	30S ribosomal protein S15 OS=Methanobacterium formicic METFP	4
353	6.15	6.17	12.3	tr A0A090JYQ2 A0A090JYQ2_METFO	Vitamin-B12 independent methionine synthase OS=Methar METFO	3
354	6.11	6.2	20	tr A0A090I525 A0A090I525_METFO	Shikimate kinase OS=Methanobacterium formicicum OX=2 METFO	4
355	6.08	6.09	27.6	tr A0A090JUF5 A0A090JUF5_METFO	Pyruvate synthase subunit PorC OS=Methanobacterium fo METFO	7
356	6.05	6.05	23.5	tr A0A090I9B3 A0A090I9B3_METFO	GTP cyclohydrolase III OS=Methanobacterium formicicum METFO	6
357	6.02	6.03	28	tr A0A090I528 A0A090I528_METFO	Probable cyclic pyranopterin monophosphate synthase OS METFO	3
358	6.02	6.02	11.7	tr A0A090IAE6 A0A090IAE6_METFO	Putative aminopeptidase MJ0555 OS=Methanobacterium f METFO	4
359	6.02	6.02	37.7	tr A0A090I8N6 A0A090I8N6_METFO	Carboxymuconolactone decarboxylase family protein OS=M METFO	3
360	6.02	6.02	14.2	tr A0A090I3N1 A0A090I3N1_METFO	Ketoisovalerate oxidoreductase subunit VorB OS=Methano METFO	3
361	6.02	6.02	23.7	tr A0A090I3I4 A0A090I3I4_METFO	Putative secreted protein OS=Methanobacterium formicicu METFO	3
362	6.02	6.02	18.1	tr A0A090JU20 A0A090JU20_METFO	3-hexulose-6-phosphate isomerase HxIB2 OS=Methanoba METFO	3
363	6.02	6.02	37.7	tr A0A089ZUT2 A0A089ZUT2_METFO	50S ribosomal protein L22 OS=Methanobacterium formicic METFO	19
364	6.01	6.12	25.6	tr A0A090JU72 A0A090JU72_METFO	Putative secreted protein OS=Methanobacterium formicicu METFO	3
365	6.01	6.03	9.2	tr A0A090I7C8 A0A090I7C8_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
366	6.01	6.01	23.1	tr A0A090I7B5 A0A090I7B5_METFO	Flavin prenyltransferase UbiX OS=Methanobacterium form METFO	3
367	6.01	6.01	12.6	tr A0A090I342 A0A090I342_METFO	N5-carboxyaminoimidazole ribonucleotide mutase OS=Met METFO	3
368	6.01	6.01	28	tr A0A089ZGC1 A0A089ZGC1_METFO	Pyridoxamine 5'-phosphate oxidase family protein OS=Met METFO	3
369	6.01	6.01	38.8	tr A0A090I442 A0A090I442_METFO	50S ribosomal protein L30e OS=Methanobacterium formici METFO	4
370	6	6.07	12	tr A0A090I4Z6 A0A090I4Z6_METFO	Aminotransferase OS=Methanobacterium formicicum OX=: METFO	5
371	6	6.01	23	tr A0A090JSW3 A0A090JSW3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	5
372	6	6	42.9	tr A0A090JUU7 A0A090JUU7_METFO	Tetrahydromethanopterin S-methyltransferase subunit G O METFO	9
373	6	6	12.7	tr A0A090JWU9 A0A090JWU9_METFO	Protein-export membrane protein SecD OS=Methanobacte METFO	4
374	6	6	22.7	tr A0A090JUH9 A0A090JUH9_METFO	Acetyl-CoA decarbonylase/synthase complex subunit epsik METFO	3
375	6	6	18.1	tr A0A090I5C9 A0A090I5C9_METFO	Phosphoribosylformylglycinamide synthase subunit PurQ METFO	3
376	6	6	12.6	tr A0A090I4Z8 A0A090I4Z8_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
377	6	6	7	tr A0A090I4A2 A0A090I4A2_METFO	Putative secreted protein OS=Methanobacterium formicicu METFO	4

Amostra 2

378	5.93	6.09	12.9	tr A0A090I4V7 A0A090I4V7_METFO	Cysteine desulfurase IscS OS=Methanobacterium formicicum METFO	3
379	5.9	6.22	22	tr A0A090I8N8 A0A090I8N8_METFO	Putative thymidylate synthase OS=Methanobacterium formicicum METFO	4
380	5.84	5.99	11.3	tr A0A090I2X2 A0A090I2X2_METFO	L-sulfolactate dehydrogenase OS=Methanobacterium formicicum METFO	3
381	5.84	5.98	18.3	tr A0A089ZI49 A0A089ZI49_METFO	Sensory transduction histidine kinase OS=Methanobacterium formicicum METFO	3
382	5.78	5.99	7.5	tr A0A089ZC05 A0A089ZC05_METFO	MCM family protein OS=Methanobacterium formicicum OX METFO	4
383	5.71	5.83	15.8	tr A0A090I549 A0A090I549_METFO	Beta-ribofuranosylaminobenzene 5'-phosphate synthase O METFO	3
384	5.69	5.95	11.2	tr A0A0S4FPT9 A0A0S4FPT9_METFO	dTDP-glucose 4,6-dehydratase-like protein OS=Methanobacterium formicicum METFO	5
385	5.66	5.81	8	tr A0A090I706 A0A090I706_METFO	Glycine-tRNA ligase OS=Methanobacterium formicicum OX METFO	3
386	5.62	5.75	10.3	tr A0A089ZI10 A0A089ZI10_METFO	Energy-converting hydrogenase A subunit O EhaO OS=Me METFO	3
387	5.58	5.78	30.4	tr A0A090I231 A0A090I231_METFO	Methyl viologen-reducing hydrogenase gamma subunit Mvi METFO	5
388	5.52	5.65	10.6	tr A0A090I4G1 A0A090I4G1_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	4
389	5.52	5.63	12.8	tr A0A090I1I5 A0A090I1I5_METFO	2-phosphoglycerate kinase OS=Methanobacterium formicicum METFO	3
390	5.52	5.6	16.7	tr A0A090I2Q1 A0A090I2Q1_METFO	7-cyano-7-deazaguanine synthase OS=Methanobacterium formicicum METFO	3
391	5.48	5.65	2.9	tr A0A090I3E3 A0A090I3E3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	4
392	5.31	5.56	9.1	tr A0A090JYM0 A0A090JYM0_METFO	Glutamine synthetase OS=Methanobacterium formicicum METFO	3
393	5.29	5.54	8.8	tr A0A090JY2 A0A090JY2_METFO	Branched-chain-amino-acid aminotransferase OS=Methanobacterium formicicum METFO	3
394	5.18	5.49	8.9	tr A0A090I4P0 A0A090I4P0_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	5
395	5.17	5.38	18.1	tr A0A090JWV3 A0A090JWV3_METFO	Acetylglutamate kinase OS=Methanobacterium formicicum METFO	5
396	5.15	5.24	15.1	tr A0A090JSU7 A0A090JSU7_METFO	Glyceraldehyde-3-phosphate dehydrogenase OS=Methanobacterium formicicum METFO	6
397	5.15	5.23	15.6	tr A0A090I171 A0A090I171_METFO	Probable tRNA pseudouridine synthase B OS=Methanobacterium formicicum METFO	3
398	5.13	5.21	23	tr A0A090I308 A0A090I308_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	4
399	5.09	5.19	6.7	tr A0A090I3Y4 A0A090I3Y4_METFO	Transcriptional repressor of nif and glnA operons NrpR OS=Methanobacterium formicicum METFO	3
400	5.05	5.29	32.4	tr A0A090I8S1 A0A090I8S1_METFO	Universal stress protein UspA5 OS=Methanobacterium formicicum METFO	5
401	5.03	5.13	21.2	tr A0A089ZVS2 A0A089ZVS2_METFO	Cupin OS=Methanobacterium formicicum OX=2162 GN=BI METFO	4
402	5.02	5.12	9	tr A0A090I1N1 A0A090I1N1_METFO	Coenzyme F390 synthetase FtsA2 OS=Methanobacterium formicicum METFO	4
403	5.01	5.11	16.4	tr A0A0S4FPQ0 A0A0S4FPQ0_METFO	Family 2 glycosyl transferase OS=Methanobacterium formicicum METFO	3
404	5.01	5.1	14.5	tr A0A090IA97 A0A090IA97_METFO	PfkB domain-containing protein OS=Methanobacterium formicicum METFO	4
405	5	5.08	23	tr A0A090I567 A0A090I567_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	4
406	4.99	5.33	6.6	tr A0A090JW98 A0A090JW98_METFO	Anaerobic ribonucleoside-triphosphate reductase OS=Methanobacterium formicicum METFO	4
407	4.93	5.21	9.1	tr A0A090JXV9 A0A090JXV9_METFO	CTP synthase OS=Methanobacterium formicicum OX=216 METFO	4
408	4.91	4.99	8.7	tr A0A090I8G0 A0A090I8G0_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
409	4.9	4.98	12.1	tr A0A090I866 A0A090I866_METFO	4-hydroxy-tetrahydrodipicolinate synthase OS=Methanobacterium formicicum METFO	3
410	4.89	5.16	17.4	tr A0A0S4FLH0 A0A0S4FLH0_METFO	UBA/THiF-type NAD/FAD binding protein OS=Methanobacterium formicicum METFO	5

Amostra 2

411	4.79	5.09	17.4 tr A0A090I679 A0A090I679_METFO	UDP-glucose 4-epimerase OS=Methanobacterium formicic METFO	4
412	4.79	5.04	35.9 tr A0A089ZG55 A0A089ZG55_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	7
413	4.78	4.88	7 tr A0A090I333 A0A090I333_METFO	Signal recognition particle 54 kDa protein OS=Methanobac METFO	3
414	4.76	4.85	9.7 tr A0A090JWI9 A0A090JWI9_METFO	Thioredoxin reductase OS=Methanobacterium formicicum METFO	3
415	4.74	4.91	6.9 tr A0A089ZG11 A0A089ZG11_METFO	ABC transporter permease protein OS=Methanobacterium METFO	3
416	4.74	4.85	6.7 tr A0A0S4FR34 A0A0S4FR34_METFO	Acetyl-CoA decarboxylase/synthase complex subunit alpha METFO	3
417	4.72	5.15	13.8 tr A0A090I4V1 A0A090I4V1_METFO	Probable tRNA sulfurtransferase OS=Methanobacterium fo METFO	4
418	4.68	4.85	24.5 tr A0A090JWL7 A0A090JWL7_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	4
419	4.67	4.86	9.7 tr A0A0S4FN23 A0A0S4FN23_METFO	UDP-N-acetyl-D-mannosamine dehydrogenase OS=Metha METFO	3
420	4.67	4.85	12.5 tr A0A089ZG23 A0A089ZG23_METFO	Formylmethanofuran dehydrogenase subunit F FwdF1 OS= METFO	3
421	4.61	4.65	17.4 tr A0A090JV79 A0A090JV79_METFO	Formamidopyrimidine-DNA glycosylase OS=Methanobacte METFO	3
422	4.58	4.62	13.9 tr A0A090I1J8 A0A090I1J8_METFO	Putative methylthioribose-1-phosphate isomerase OS=Metl METFO	3
423	4.57	4.96	8.5 tr K2QDN1 K2QDN1_METFP	DNA-directed RNA polymerase subunit B OS=Methanobac METFP	5
424	4.57	4.63	11.6 tr A0A090I3B2 A0A090I3B2_METFO	Cobyrinate a,c-diamide synthase OS=Methanobacterium fc METFO	4
425	4.48	4.52	5 tr A0A090I9W6 A0A090I9W6_METFO	Adenine specific DNA methylase Mod OS=Methanobacterii METFO	3
426	4.44	4.48	12.1 tr A0A090I4C0 A0A090I4C0_METFO	Indole-3-glycerol phosphate synthase OS=Methanobacterii METFO	3
427	4.41	4.45	28.3 tr A0A089ZJ62 A0A089ZJ62_METFO	Sirohydrochlorin cobaltochelataase OS=Methanobacterium l METFO	3
428	4.39	4.43	4.9 tr A0A090JTW9 A0A090JTW9_METFO	Indolepyruvate oxidoreductase subunit IorA OS=Methanob: METFO	2
429	4.39	4.42	5.3 tr A0A090I5D7 A0A090I5D7_METFO	Glutamate-1-semialdehyde 2,1-aminomutase OS=Methanc METFO	2
430	4.36	4.5	13.2 tr A0A090I8P6 A0A090I8P6_METFO	Ribose-phosphate pyrophosphokinase OS=Methanobacter METFO	3
431	4.3	4.37	8.6 tr A0A090I306 A0A090I306_METFO	Restriction endonuclease OS=Methanobacterium formicicu METFO	3
432	4.3	4.33	28.3 tr A0A090I4H6 A0A090I4H6_METFO	50S ribosomal protein L15 OS=Methanobacterium formicic METFO	5
433	4.29	4.32	30.2 tr A0A089ZA06 A0A089ZA06_METFO	PRC-barrel domain-containing protein OS=Methanobacteri METFO	4
434	4.28	4.31	14.2 tr A0A089ZG68 A0A089ZG68_METFO	Energy-converting hydrogenase B subunit M EhbM OS=Me METFO	2
435	4.28	4.31	42 tr A0A089ZAK4 A0A089ZAK4_METFO	Molybdenum-pterin binding protein Mop1 OS=Methanobac: METFO	2
436	4.27	4.3	7.2 tr A0A090I666 A0A090I666_METFO	Nitrogenase iron protein 2 OS=Methanobacterium formicici METFO	2
437	4.27	4.3	7.6 tr A0A090JT90 A0A090JT90_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	2
438	4.25	4.33	9.2 tr A0A089ZVK9 A0A089ZVK9_METFO	Fe-S cluster domain-containing protein OS=Methanobacter METFO	2
439	4.23	4.37	19.8 tr A0A089ZH11 A0A089ZH11_METFO	Thiamine thiazole synthase OS=Methanobacterium formici METFO	3
440	4.21	4.84	51.5 tr K2RQ61 K2RQ61_METFP	Transcription factor CBF/NF-Y/histone domain-containing p METFP	3
441	4.2	4.22	17.7 tr A0A090I3M8 A0A090I3M8_METFO	Imidazoleglycerol-phosphate dehydratase OS=Methanobac METFO	3
442	4.19	4.22	8.1 tr A0A090JXI6 A0A090JXI6_METFO	Cyclic 2,3-diphosphoglycerate synthetase OS=Methanobac METFO	3
443	4.19	4.22	15 tr A0A090I2L4 A0A090I2L4_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	3

Amostra 2

444	4.15	4.32	4.5 tr A0A090I1C7 A0A090I1C7_METFO	Oxidoreductase domain-containing protein OS=Methanoba METFO	2
445	4.14	4.31	14.8 tr A0A090I6Y3 A0A090I6Y3_METFO	S-adenosyl-L-methionine-dependent tRNA 4-demethylwyo METFO	3
446	4.13	4.26	11.4 tr A0A0S4FMW1 A0A0S4FMW1_METFO	Putative deoxyhypusine synthase OS=Methanobacterium f METFO	3
447	4.13	4.15	9.5 tr A0A089ZA94 A0A089ZA94_METFO	CobQ/CobB/MinD/ParA nucleotide binding domain-contain METFO	2
448	4.12	4.14	15.9 tr A0A090IAL7 A0A090IAL7_METFO	Uncharacterized protein OS=Methanobacterium formicicur METFO	3
449	4.11	4.25	20 tr A0A090I3X8 A0A090I3X8_METFO	Formylmethanofuran dehydrogenase, subunit E region OS: METFO	3
450	4.11	4.13	24.9 tr K2RTG9 K2RTG9_METFP	Archaeoflavoprotein AfpA OS=Methanobacterium formicicu METFP	5
451	4.1	4.11	14.9 tr A0A090I8I8 A0A090I8I8_METFO	GHMP kinase OS=Methanobacterium formicicum OX=216: METFO	3
452	4.09	4.14	7.5 tr A0A090I806 A0A090I806_METFO	Putative pantothenate synthetase OS=Methanobacterium f METFO	2
453	4.08	4.09	5.9 tr A0A089ZFA3 A0A089ZFA3_METFO	Acetyl-CoA decarbonylase/synthase complex subunit delta METFO	4
454	4.06	4.39	23.7 tr A0A090I182 A0A090I182_METFO	Uncharacterized protein OS=Methanobacterium formicicur METFO	3
455	4.05	4.06	12.5 tr A0A090I810 A0A090I810_METFO	Dihydroorotate dehydrogenase OS=Methanobacterium forr METFO	3
456	4.03	4.04	13 tr A0A089ZBW3 A0A089ZBW3_METFO	Glutamate synthase beta subunit GltB1 OS=Methanobacte METFO	3
457	4.02	4.02	15.3 tr A0A090I751 A0A090I751_METFO	tRNA intron endonuclease EndA OS=Methanobacterium fo METFO	2
458	4.02	4.02	16.6 tr A0A090I3G5 A0A090I3G5_METFO	3-isopropylmalate dehydratase small subunit OS=Methano METFO	2
459	4.01	4.02	7.4 tr A0A090I1U9 A0A090I1U9_METFO	2-aminoadipate transaminase OS=Methanobacterium form METFO	3
460	4.01	4.01	17.5 tr A0A090I4F8 A0A090I4F8_METFO	Iron-sulfur flavoprotein MJ1083 OS=Methanobacterium for METFO	3
461	4.01	4.01	10.6 tr A0A089ZC18 A0A089ZC18_METFO	Methanogenesis marker protein 7 OS=Methanobacterium f METFO	2
462	4.01	4.01	11.7 tr A0A090I368 A0A090I368_METFO	Formylmethanofuran dehydrogenase subunit E OS=Metha METFO	2
463	4.01	4.01	7.3 tr A0A089ZI47 A0A089ZI47_METFO	PAS/PAC sensor protein OS=Methanobacterium formicicur METFO	2
464	4.01	4.01	19.2 tr A0A089ZE55 A0A089ZE55_METFO	RNA-binding protein OS=Methanobacterium formicicum O METFO	4
465	4.01	4.01	11.2 tr K2RAP2 K2RAP2_METFP	Tetrahydromethanopterin S-methyltransferase subunit E O METFP	12
466	4.01	4.01	14.9 tr A0A090JVQ8 A0A090JVQ8_METFO	Regulatory protein MarR OS=Methanobacterium formicicur METFO	2
467	4.01	4.01	6.8 tr A0A090I4E1 A0A090I4E1_METFO	Histidinol dehydrogenase OS=Methanobacterium formicicu METFO	2
468	4.01	4.01	22.8 tr A0A089ZER4 A0A089ZER4_METFO	ACT domain-containing protein OS=Methanobacterium for METFO	2
469	4	34.46	44.6 tr K2QYM4 K2QYM4_METFP	Methyl-coenzyme M reductase subunit alpha OS=Methano METFP	120
470	4	4.01	17.2 tr K2QYV5 K2QYV5_METFP	Nucleoside diphosphate kinase OS=Methanobacterium for METFP	2
471	4	4.01	8.2 tr A0A089ZI83 A0A089ZI83_METFO	Cobalt-precorrin-5B C(1)-methyltransferase OS=Methanob METFO	2
472	4	4	6.6 tr A0A090I4T1 A0A090I4T1_METFO	Aspartate-semialdehyde dehydrogenase OS=Methanobact METFO	3
473	4	4	7.6 tr A0A089ZE18 A0A089ZE18_METFO	Uncharacterized protein OS=Methanobacterium formicicur METFO	2
474	4	4	10.6 tr A0A090I6K4 A0A090I6K4_METFO	TetR family transcriptional regulator OS=Methanobacteriun METFO	2
475	4	4	10.7 tr A0A0S4FN24 A0A0S4FN24_METFO	Orotidine 5'-phosphate decarboxylase OS=Methanobacteri METFO	2
476	4	4	18 tr A0A090JY14 A0A090JY14_METFO	Phenylacetic acid degradation-like protein OS=Methanoba METFO	3

Amostra 2

477	4	4	11.2	tr A0A090IAS5 A0A090IAS5_METFO	Oxidoreductase MW2403 OS=Methanobacterium formicicu METFO	2
478	4	4	26.3	tr A0A090IAI0 A0A090IAI0_METFO	Putative secreted protein OS=Methanobacterium formicicu METFO	2
479	4	4	12.6	tr A0A090I4U7 A0A090I4U7_METFO	Indolepyruvate ferredoxin oxidoreductase beta subunit lorB METFO	2
480	4	4	19.6	tr A0A089Z9L4 A0A089Z9L4_METFO	Nitrogen regulatory protein P-II GlnK1 OS=Methanobacterii METFO	2
481	4	4	27.1	tr A0A090I852 A0A090I852_METFO	Cupin OS=Methanobacterium formicicum OX=2162 GN=BI METFO	3
482	4	4	21.9	tr A0A090I838 A0A090I838_METFO	Putative secreted protein OS=Methanobacterium formicicu METFO	3
483	4	4	14.4	tr A0A090I6P0 A0A090I6P0_METFO	3-hexulose-6-phosphate isomerase HxIB1 OS=Methanoba METFO	2
484	4	4	22.7	tr A0A090I4X6 A0A090I4X6_METFO	Phosphoribosyl-AMP cyclohydrolase OS=Methanobacteriu METFO	2
485	4	4	17.2	tr A0A090I4H1 A0A090I4H1_METFO	Putative secreted protein OS=Methanobacterium formicicu METFO	2
486	4	4	14.8	tr A0A090I2X5 A0A090I2X5_METFO	Nitroreductase OS=Methanobacterium formicicum OX=216 METFO	2
487	4	4	49.1	tr A0A090I260 A0A090I260_METFO	50S ribosomal protein L24e OS=Methanobacterium formici METFO	2
488	4	4	12	tr A0A090I1G0 A0A090I1G0_METFO	DNA-directed RNA polymerase subunit D OS=Methanobac METFO	2
489	4	4	16	tr A0A089ZVX2 A0A089ZVX2_METFO	Putative membrane protein OS=Methanobacterium formicicu METFO	2
490	4	4	7.5	tr A0A089ZG19 A0A089ZG19_METFO	Formate/nitrite transporter FdhC OS=Methanobacterium fo METFO	2
491	4	4	15.9	tr A0A089Z7Q8 A0A089Z7Q8_METFO	TetR family transcriptional regulator OS=Methanobacteriun METFO	2
492	3.94	4.02	15.6	tr A0A090JUC2 A0A090JUC2_METFO	Translation initiation factor 2 subunit beta OS=Methanobac METFO	2
493	3.89	4.17	10.2	tr A0A090I3H5 A0A090I3H5_METFO	Adenylosuccinate lyase OS=Methanobacterium formicicum METFO	4
494	3.83	3.96	14.6	tr A0A090I618 A0A090I618_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	3
495	3.82	4.08	7.6	tr A0A090I564 A0A090I564_METFO	DEAD-box ATP-dependent RNA helicase CshA OS=Metha METFO	3
496	3.82	3.92	26.1	tr A0A089Z9R7 A0A089Z9R7_METFO	Putative secreted protein OS=Methanobacterium formicicu METFO	2
497	3.81	4.07	8.6	tr A0A090I0P2 A0A090I0P2_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	3
498	3.78	3.91	15.4	tr A0A090JX27 A0A090JX27_METFO	Amino acid-binding ACT domain-containing protein OS=Me METFO	3
499	3.74	3.91	11.4	tr A0A0S4FN48 A0A0S4FN48_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	2
500	3.66	3.83	8	tr A0A090I6X8 A0A090I6X8_METFO	2-oxoglutarate ferredoxin oxidoreductase subunit beta KorE METFO	2
501	3.66	3.81	11	tr A0A090I8I5 A0A090I8I5_METFO	Uroporphyrinogen-III C-methyltransferase OS=Methanobac METFO	2
502	3.63	3.93	32.6	tr A0A090I4J8 A0A090I4J8_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	4
503	3.62	3.74	8.1	tr A0A090I626 A0A090I626_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	2
504	3.6	3.81	12.1	tr A0A090I4P9 A0A090I4P9_METFO	Glucose-methanol-choline oxidoreductase OS=Methanoba METFO	3
505	3.6	3.78	4.4	tr A0A090JV74 A0A090JV74_METFO	Homoserine dehydrogenase OS=Methanobacterium formic METFO	2
506	3.6	3.72	7.7	tr A0A090I9I5 A0A090I9I5_METFO	5'-deoxyadenosine deaminase OS=Methanobacterium forn METFO	2
507	3.51	3.66	5.2	tr A0A090I5F2 A0A090I5F2_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	2
508	3.51	3.64	16.4	tr K2QXI5 K2QXI5_METFP	Putative nickel-responsive regulator OS=Methanobacteriun METFP	2
509	3.48	3.66	10.2	tr A0A090I4F5 A0A090I4F5_METFO	Putative cobalt-precorrin-4 C(11)-methyltransferase OS=M METFO	2

Amostra 2

510	3.41	3.59	1.8 tr A0A0S4FL46 A0A0S4FL46_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
511	3.35	3.47	4.9 tr A0A090JX53 A0A090JX53_METFO	Cell wall biosynthesis protein Mur ligase family OS=Methar METFO	4
512	3.29	3.4	11.5 tr A0A090I1A0 A0A090I1A0_METFO	Anthranilate phosphoribosyltransferase OS=Methanobacte METFO	2
513	3.24	3.38	8.4 tr A0A090I3D2 A0A090I3D2_METFO	PQQ repeat-containing cell surface protein OS=Methanoba METFO	4
514	3.21	3.32	5.5 tr A0A090I9R3 A0A090I9R3_METFO	Arginine biosynthesis bifunctional protein ArgJ OS=Methan METFO	2
515	3.1	3.2	14.5 tr A0A090I472 A0A090I472_METFO	Putative secreted protein OS=Methanobacterium formicicu METFO	2
516	3.06	3.16	12.2 tr A0A090I1S6 A0A090I1S6_METFO	Succinate--CoA ligase [ADP-forming] subunit alpha OS=M METFO	3
517	3.04	3.14	18.3 tr A0A089ZV16 A0A089ZV16_METFO	A1A0 archaeal ATP synthase subunit H AhaH OS=Methan METFO	2
518	3.02	3.17	13 tr A0A090I609 A0A090I609_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
519	3.01	3.38	16.1 tr A0A090I673 A0A090I673_METFO	Homoserine O-acetyltransferase OS=Methanobacterium fo METFO	3
520	3.01	3.11	16.6 tr A0A090JSW7 A0A090JSW7_METFO	CBS domain-containing membrane protein OS=Methanoba METFO	2
521	2.98	3.09	4.1 tr A0A090I744 A0A090I744_METFO	3-phosphoshikimate 1-carboxyvinyltransferase OS=Methar METFO	2
522	2.97	3.08	3.3 tr A0A089ZHQ2 A0A089ZHQ2_METFO	tRNA-guanine(15) transglycosylase OS=Methanobacterium METFO	2
523	2.91	4.03	22.7 tr A0A090I9F1 A0A090I9F1_METFO	Tetrahydromethanopterin S-methyltransferase subunit A O METFO	4
524	2.9	2.99	21.8 tr A0A089ZGN8 A0A089ZGN8_METFO	PRC-barrel domain-containing protein OS=Methanobacteri METFO	2
525	2.87	3.01	4.9 tr A0A090JSK7 A0A090JSK7_METFO	Bifunctional protein GlmU OS=Methanobacterium formicicu METFO	2
526	2.79	3.03	4.3 tr A0A090I8J8 A0A090I8J8_METFO	ATPase AAA OS=Methanobacterium formicicum OX=2162 METFO	2
527	2.79	2.88	11.4 tr A0A089ZUW8 A0A089ZUW8_METFO	UPF0278 protein BRM9_0586 OS=Methanobacterium forr METFO	2
528	2.74	2.85	17.1 tr A0A090I449 A0A090I449_METFO	Molybdopterin biosynthesis MoaE protein OS=Methanobac METFO	2
529	2.73	2.94	6.3 tr A0A090I0W7 A0A090I0W7_METFO	Oxidoreductase GFO/IDH/MOCA family OS=Methanobacte METFO	2
530	2.73	2.8	10.2 tr A0A0S4FP84 A0A0S4FP84_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
531	2.67	2.74	10.7 tr A0A090JYR8 A0A090JYR8_METFO	Trk system potassium uptake protein TrkA homolog OS=M METFO	2
532	2.65	2.72	7.3 tr A0A090I4S4 A0A090I4S4_METFO	Family 2 glycosyl transferase OS=Methanobacterium formi METFO	2
533	2.61	2.84	4.7 tr A0A090JUS4 A0A090JUS4_METFO	Type-2 serine-tRNA ligase OS=Methanobacterium formicic METFO	2
534	2.57	2.61	8.7 tr A0A090IAE3 A0A090IAE3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
535	2.56	2.6	35.2 tr A0A089ZV40 A0A089ZV40_METFO	TRAM domain-containing protein OS=Methanobacterium fc METFO	2
536	2.54	2.59	8.9 tr A0A090JYF6 A0A090JYF6_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
537	2.5	2.53	5.8 tr A0A090I2H7 A0A090I2H7_METFO	Glutamate decarboxylase OS=Methanobacterium formicicu METFO	2
538	2.49	2.53	4.2 tr A0A090JX92 A0A090JX92_METFO	Methylase involved in ubiquinone/menaquinone biosynthes METFO	1
539	2.48	2.57	8.8 tr A0A089ZE26 A0A089ZE26_METFO	Methionine aminopeptidase OS=Methanobacterium formici METFO	2
540	2.48	2.52	2.5 tr A0A0S4FMD8 A0A0S4FMD8_METFO	Alanine--tRNA ligase OS=Methanobacterium formicicum O METFO	2
541	2.45	2.48	7.1 tr A0A090I0S7 A0A090I0S7_METFO	O-phospho-L-seryl-tRNA:Cys-tRNA synthase OS=Methanc METFO	2
542	2.44	2.47	8.4 tr A0A0S4FLN1 A0A0S4FLN1_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2

Amostra 2

543	2.43	2.48	24.7 tr K2RRP8 K2RRP8_METFP	Uncharacterized protein OS=Methanobacterium formicicum METFP	2
544	2.42	2.45	9.2 tr A0A090I3E9 A0A090I3E9_METFO	Calcium-gated potassium channel MthK OS=Methanobacterium formicicum METFO	2
545	2.39	4.01	11.3 tr A0A0S4FLN4 A0A0S4FLN4_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
546	2.36	2.39	31.8 tr K2R0W5 K2R0W5_METFP	30S ribosomal protein S17e OS=Methanobacterium formicicum METFP	2
547	2.35	2.38	4 tr A0A089ZF54 A0A089ZF54_METFO	Oligosaccharyl transferase OS=Methanobacterium formicicum METFO	2
548	2.35	2.38	4.3 tr A0A090I5E4 A0A090I5E4_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
549	2.34	2.37	2.8 tr A0A0S4FLU0 A0A0S4FLU0_METFO	Dihydrolipoyl dehydrogenase OS=Methanobacterium formicicum METFO	1
550	2.33	2.35	2.9 tr A0A090IB35 A0A090IB35_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
551	2.29	2.32	3.7 tr A0A090I1C1 A0A090I1C1_METFO	GTP-binding protein OS=Methanobacterium formicicum OX=2 METFO	1
552	2.27	2.3	7.4 tr A0A089Z8R0 A0A089Z8R0_METFO	Cytidylate kinase OS=Methanobacterium formicicum OX=2 METFO	1
553	2.26	12.63	16.7 tr A0A090IAA4 A0A090IAA4_METFO	Pyridoxal 5'-phosphate synthase subunit PdxS OS=Methanobacterium formicicum METFO	8
554	2.25	2.33	2.4 tr A0A090I4N0 A0A090I4N0_METFO	2,3-bisphosphoglycerate-independent phosphoglycerate m METFO	1
555	2.22	2.24	2.5 tr A0A090I357 A0A090I357_METFO	Molybdenum cofactor synthesis domain-containing protein METFO	1
556	2.18	2.2	2.7 tr A0A090I1F1 A0A090I1F1_METFO	Glutamate--tRNA ligase OS=Methanobacterium formicicum METFO	1
557	2.17	2.23	5.4 tr A0A090I385 A0A090I385_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
558	2.15	2.23	7.3 tr A0A0S4FLC5 A0A0S4FLC5_METFO	Sulfur carrier protein FdhD OS=Methanobacterium formicicum METFO	2
559	2.15	2.22	6.9 tr A0A090I4P8 A0A090I4P8_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
560	2.13	2.15	5.6 tr A0A090JUH2 A0A090JUH2_METFO	Phosphohydrolase OS=Methanobacterium formicicum OX=2 METFO	1
561	2.12	2.13	8.8 tr K2QD45 K2QD45_METFP	50S ribosomal protein L19e OS=Methanobacterium formicicum METFP	1
562	2.12	2.13	2.2 tr A0A0S4FMB9 A0A0S4FMB9_METFO	UDP-N-acetylmuramoyl-L-alanine-D-glutamate ligase OS=Methanobacterium formicicum METFO	1
563	2.11	2.22	7.3 tr A0A090IAX7 A0A090IAX7_METFO	Phosphoribosylaminoimidazole-succinocarboxamide synthase METFO	2
564	2.11	2.12	37.4 tr A0A089ZES5 A0A089ZES5_METFO	Roadblock/LC7 domain-containing protein OS=Methanobacterium formicicum METFO	4
565	2.1	2.12	1.6 tr A0A090I3Q1 A0A090I3Q1_METFO	Putative FAD-dependent oxidoreductase MJ0033 OS=Methanobacterium formicicum METFO	1
566	2.1	2.11	15 tr A0A089ZVK3 A0A089ZVK3_METFO	CBS domain-containing protein OS=Methanobacterium formicicum METFO	1
567	2.1	2.11	6.3 tr A0A090I290 A0A090I290_METFO	Digeranylgeranyl glycerophospholipid reductase OS=Methanobacterium formicicum METFO	2
568	2.09	2.11	4.7 tr A0A090I2K2 A0A090I2K2_METFO	PBS lyase HEAT domain-containing protein OS=Methanobacterium formicicum METFO	2
569	2.08	2.09	3.2 tr A0A090I6W1 A0A090I6W1_METFO	ABC transporter ATP-binding protein OS=Methanobacterium formicicum METFO	1
570	2.08	2.08	7 tr A0A090I5Q4 A0A090I5Q4_METFO	CBS domain-containing protein OS=Methanobacterium formicicum METFO	1
571	2.07	2.23	6 tr A0A089ZBK5 A0A089ZBK5_METFO	Roadblock/LC7 domain-containing protein OS=Methanobacterium formicicum METFO	4
572	2.07	2.09	2.6 tr A0A090I669 A0A090I669_METFO	Putative NADH oxidase OS=Methanobacterium formicicum METFO	1
573	2.07	2.08	1.4 tr A0A090I495 A0A090I495_METFO	Restriction endonuclease OS=Methanobacterium formicicum METFO	1
574	2.07	2.08	6.7 tr A0A090I311 A0A090I311_METFO	Prephenate dehydratase PheA OS=Methanobacterium formicicum METFO	1
575	2.07	2.07	1.4 tr A0A090JU28 A0A090JU28_METFO	Probable translation initiation factor IF-2 OS=Methanobacterium formicicum METFO	1

Amostra 2

576	2.07	2.07	2.9	tr A0A090I405 A0A090I405_METFO	Ketoisovalerate oxidoreductase subunit VorA OS=Methano METFO	1
577	2.06	2.07	3.1	tr A0A0S4FPM9 A0A0S4FPM9_METFO	Phosphomethylpyrimidine synthase OS=Methanobacterium METFO	1
578	2.06	2.07	4.3	tr A0A090I5J7 A0A090I5J7_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
579	2.06	2.06	6.8	tr A0A089ZII9 A0A089ZII9_METFO	MotA/TolQ/ExbB proton channel family protein OS=Methan METFO	1
580	2.05	2.06	4.1	tr A0A090I8S7 A0A090I8S7_METFO	tRNA (Adenine(57)-N(1)/adenine(58)-N(1))-methyltransferase METFO	1
581	2.05	2.06	9.3	tr A0A090JVR4 A0A090JVR4_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
582	2.05	2.05	3.3	tr A0A090I7D4 A0A090I7D4_METFO	Metal dependent phosphohydrolase OS=Methanobacterium METFO	1
583	2.04	2.05	7.6	tr A0A090JTT8 A0A090JTT8_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
584	2.03	2.06	3.5	tr A0A090I3N5 A0A090I3N5_METFO	2-isopropylmalate synthase LeuA OS=Methanobacterium formicicum METFO	1
585	2.03	2.04	1.3	tr A0A090I5P5 A0A090I5P5_METFO	Type I restriction-modification enzyme, subunit R OS=Methanobacterium METFO	1
586	2.03	2.04	8.2	tr A0A090I8M0 A0A090I8M0_METFO	Archaeoflavoprotein AfpA3 OS=Methanobacterium formicicum METFO	1
587	2.03	2.03	3.8	tr A0A0S4FN28 A0A0S4FN28_METFO	5-amino-6-(D-ribitylamino)uracil--L-tyrosine 4-hydroxyphenyl METFO	2
588	2.03	2.03	3.3	tr A0A090JVR9 A0A090JVR9_METFO	Sulfate-transporting ATPase OS=Methanobacterium formicicum METFO	1
589	2.03	2.03	7.9	tr A0A090I6P3 A0A090I6P3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
590	2.02	2.03	8.1	tr A0A090I628 A0A090I628_METFO	Putative membrane protein OS=Methanobacterium formicicum METFO	1
591	2.02	2.03	4.3	tr A0A089ZDX7 A0A089ZDX7_METFO	Iron ABC transporter ATP-binding protein OS=Methanobacterium METFO	1
592	2.02	2.02	2.1	tr A0A089Z9I0 A0A089Z9I0_METFO	Argininosuccinate lyase OS=Methanobacterium formicicum METFO	1
593	2.02	2.02	1.8	tr A0A090I8E3 A0A090I8E3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
594	2.02	2.02	3.6	tr A0A090I4W2 A0A090I4W2_METFO	Putative cysteine desulfurase OS=Methanobacterium formicicum METFO	1
595	2.02	2.02	3	tr A0A090I1R3 A0A090I1R3_METFO	Replication factor C large subunit OS=Methanobacterium formicicum METFO	1
596	2.02	2.02	13.4	tr K2RAZ5 K2RAZ5_METFP	Transcription factor CBF/NF-Y/histone domain-containing protein METFP	1
597	2.02	2.02	5.3	tr A0A090I233 A0A090I233_METFO	Ribosomal RNA large subunit methyltransferase E OS=Methanobacterium METFO	1
598	2.01	10.94	12.1	tr K2RD45 K2RD45_METFP	Phosphoserine phosphatase SerB OS=Methanobacterium METFP	6
599	2.01	2.03	3.2	tr A0A090I4J3 A0A090I4J3_METFO	4Fe-4S ferredoxin OS=Methanobacterium formicicum OX= METFO	1
600	2.01	2.02	4.4	tr A0A090I5M7 A0A090I5M7_METFO	Fibrillarin-like rRNA/tRNA 2'-O-methyltransferase OS=Methanobacterium METFO	1
601	2.01	2.01	1.2	tr A0A090I5J4 A0A090I5J4_METFO	Cation transport ATPase OS=Methanobacterium formicicum METFO	1
602	2.01	2.01	11.4	tr A0A090I174 A0A090I174_METFO	Adenylate kinase OS=Methanobacterium formicicum OX=2 METFO	1
603	2.01	2.01	9.7	tr A0A0S4FLM0 A0A0S4FLM0_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
604	2.01	2.01	8.6	tr A0A090I0V7 A0A090I0V7_METFO	Nuclease domain-containing protein OS=Methanobacterium METFO	1
605	2.01	2.01	2.4	tr A0A089ZVM8 A0A089ZVM8_METFO	Peptide chain release factor subunit 1 OS=Methanobacterium METFO	1
606	2.01	2.01	12.6	tr A0A089Z8B7 A0A089Z8B7_METFO	Energy-converting hydrogenase B subunit A EhbA OS=Methanobacterium METFO	1
607	2.01	2.01	4.6	tr K2R544 K2R544_METFP	Geranylgeranyl reductase OS=Methanobacterium formicicum METFP	1
608	2.01	2.01	2.6	tr K2R2L5 K2R2L5_METFP	Chaperone protein DnaJ OS=Methanobacterium formicicum METFP	1

Amostra 2

609	2.01	2.01	11.9	tr K2R290 K2R290_METFP	Amino acid-binding ACT domain-containing protein OS=Methanobacterium formicicum METFP	1
610	2.01	2.01	1.6	tr A0A090JWS6 A0A090JWS6_METFO	Signal transduction histidine kinase OS=Methanobacterium formicicum METFO	1
611	2.01	2.01	2.1	tr A0A090I5I9 A0A090I5I9_METFO	Mur ligase middle domain-containing protein OS=Methanobacterium formicicum METFO	1
612	2.01	2.01	7	tr A0A090I5C4 A0A090I5C4_METFO	LemA family protein OS=Methanobacterium formicicum METFO	1
613	2.01	2.01	13.4	tr A0A090I646 A0A090I646_METFO	50S ribosomal protein L21e OS=Methanobacterium formicicum METFO	1
614	2.01	2.01	4	tr A0A090I4L3 A0A090I4L3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
615	2.01	2.01	3.7	tr A0A090I129 A0A090I129_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
616	2.01	2.01	11	tr A0A089ZH81 A0A089ZH81_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
617	2	6.01	7.7	tr K2RDN6 K2RDN6_METFP	Proline--tRNA ligase OS=Methanobacterium formicicum METFP	3
618	2	6	38.4	tr K2R0A1 K2R0A1_METFP	50S ribosomal protein L23 OS=Methanobacterium formicicum METFP	6
619	2	4.54	8	tr K2RFA3 K2RFA3_METFP	Lysine--tRNA ligase OS=Methanobacterium formicicum METFP	3
620	2	4.18	4.8	tr K2RPK7 K2RPK7_METFP	Phenylacetate--CoA ligase OS=Methanobacterium formicicum METFP	3
621	2	2.02	1.8	tr A0A0S4FPW4 A0A0S4FPW4_METFO	CoA-binding domain-containing protein OS=Methanobacterium formicicum METFO	1
622	2	2.01	5.3	tr A0A090I4E3 A0A090I4E3_METFO	Peroxiredoxin OS=Methanobacterium formicicum METFO	1
623	2	2.01	12.6	tr A0A0S4FQ17 A0A0S4FQ17_METFO	Fe-S type, tartrate/fumarate subfamily hydro-lyase subunit OS=Methanobacterium formicicum METFO	1
624	2	2.01	5.8	tr A0A090I5V7 A0A090I5V7_METFO	NADPH-dependent FMN reductase OS=Methanobacterium formicicum METFO	1
625	2	2.01	4.9	tr A0A090I302 A0A090I302_METFO	Putative membrane protein OS=Methanobacterium formicicum METFO	1
626	2	2	7.8	tr A0A089ZC90 A0A089ZC90_METFO	V-type ATP synthase subunit D OS=Methanobacterium formicicum METFO	6
627	2	2	1.9	tr A0A0S4FN73 A0A0S4FN73_METFO	PHP domain-containing protein OS=Methanobacterium formicicum METFO	1
628	2	2	4.9	tr K2R2N0 K2R2N0_METFP	PBS lyase HEAT domain-containing protein OS=Methanobacterium formicicum METFP	1
629	2	2	2.5	tr A0A090JYG5 A0A090JYG5_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
630	2	2	12	tr A0A090I9U1 A0A090I9U1_METFO	Putative secreted protein OS=Methanobacterium formicicum METFO	1
631	2	2	5.2	tr A0A090I4W9 A0A090I4W9_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
632	2	2	3.8	tr A0A090I4W1 A0A090I4W1_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
633	2	2	5.7	tr A0A090I2J4 A0A090I2J4_METFO	Phosphate-specific transport system accessory protein Phc OS=Methanobacterium formicicum METFO	2
634	2	2	5.9	tr A0A090I288 A0A090I288_METFO	HEAT repeat-containing protein OS=Methanobacterium formicicum METFO	1
635	2	2	2.2	tr A0A089ZGJ2 A0A089ZGJ2_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
636	2	2	8.4	tr K2RWB9 K2RWB9_METFP	Uncharacterized protein OS=Methanobacterium formicicum METFP	1
637	2	2	9.6	tr K2RW50 K2RW50_METFP	DNA/RNA-binding protein Alba OS=Methanobacterium formicicum METFP	3
638	2	2	1.9	tr K2RCV2 K2RCV2_METFP	Putative sensor histidine kinase OS=Methanobacterium formicicum METFP	1
639	2	2	1.8	tr K2R8N9 K2R8N9_METFP	Succinate dehydrogenase/fumarate reductase iron-sulfur subunit OS=Methanobacterium formicicum METFP	1
640	2	2	8.6	tr K2R5U5 K2R5U5_METFP	Uncharacterized protein OS=Methanobacterium formicicum METFP	1
641	2	2	3.8	tr K2QZG7 K2QZG7_METFP	Uroporphyrinogen-III synthase OS=Methanobacterium formicicum METFP	1

Amostra 2

642	2	2	2.3 tr A0A0S4FSH9 A0A0S4FSH9_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
643	2	2	2.8 tr A0A0S4FPH6 A0A0S4FPH6_METFO	Putative membrane protein OS=Methanobacterium formicicum METFO	1
644	2	2	8 tr A0A0S4FP85 A0A0S4FP85_METFO	Putative secreted protein OS=Methanobacterium formicicum METFO	2
645	2	2	4.1 tr A0A0S4FNH5 A0A0S4FNH5_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
646	2	2	2.6 tr A0A0S4FMP8 A0A0S4FMP8_METFO	ABC-type transport system, permease protein OS=Methanobacterium formicicum METFO	1
647	2	2	4.1 tr A0A0S4FLJ8 A0A0S4FLJ8_METFO	Peptidase C60 sortase A and B OS=Methanobacterium formicicum METFO	1
648	2	2	17.1 tr A0A0S4FLG1 A0A0S4FLG1_METFO	Signal transduction protein with CBS domains OS=Methanobacterium formicicum METFO	1
649	2	2	4.5 tr A0A090JUW9 A0A090JUW9_METFO	2-phosphosulfolactate phosphatase OS=Methanobacterium formicicum METFO	1
650	2	2	13.6 tr A0A090IB32 A0A090IB32_METFO	Pyridoxamine 5'-phosphate oxidase family protein OS=Methanobacterium formicicum METFO	2
651	2	2	3.5 tr A0A090I6L6 A0A090I6L6_METFO	Putative membrane protein OS=Methanobacterium formicicum METFO	1
652	2	2	12.2 tr A0A090I6E5 A0A090I6E5_METFO	Putative membrane protein OS=Methanobacterium formicicum METFO	2
653	2	2	3.5 tr A0A090I5E2 A0A090I5E2_METFO	Hydrolase HAD superfamily OS=Methanobacterium formicicum METFO	1
654	2	2	6.9 tr A0A090I5D6 A0A090I5D6_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
655	2	2	15 tr A0A090I4N4 A0A090I4N4_METFO	Putative membrane protein OS=Methanobacterium formicicum METFO	2
656	2	2	7.6 tr A0A090I492 A0A090I492_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
657	2	2	5.7 tr A0A090I0P3 A0A090I0P3_METFO	Inositol-1-monophosphatase OS=Methanobacterium formicicum METFO	1
658	2	2	5.4 tr A0A089ZGT2 A0A089ZGT2_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
659	2	2	20.7 tr K2REJ5 K2REJ5_METFP	30S ribosomal protein S27e OS=Methanobacterium formicicum METFP	1
660	2	2	13 tr K2RAP6 K2RAP6_METFP	Tetrahydromethanopterin S-methyltransferase subunit F O: METFP	1
661	2	2	4.3 tr K2R3C0 K2R3C0_METFP	Uncharacterized protein OS=Methanobacterium formicicum METFP	1
662	2	2	3.2 tr K2R2E1 K2R2E1_METFP	VWA containing CoxE family protein OS=Methanobacterium formicicum METFP	1
663	2	2	2.1 tr K2QCC1 K2QCC1_METFP	Iron-containing alcohol dehydrogenase OS=Methanobacterium formicicum METFP	1
664	2	2	4.3 tr A0A0S4FNA9 A0A0S4FNA9_METFO	Deoxyribose-phosphate aldolase OS=Methanobacterium formicicum METFO	1
665	2	2	5.6 tr A0A0S4FLC3 A0A0S4FLC3_METFO	Trimethylamine-N-oxide reductase (Cytochrome c) OS=Methanobacterium formicicum METFO	1
666	2	2	3.3 tr A0A090JUV1 A0A090JUV1_METFO	Tetrahydromethanopterin S-methyltransferase subunit D O METFO	1
667	2	2	1.6 tr A0A090IAX4 A0A090IAX4_METFO	Acyl-CoA synthetase OS=Methanobacterium formicicum O METFO	1
668	2	2	5.4 tr A0A090I857 A0A090I857_METFO	Carboxymuconolactone decarboxylase OS=Methanobacterium formicicum METFO	1
669	2	2	6.8 tr A0A090I809 A0A090I809_METFO	Putative membrane protein OS=Methanobacterium formicicum METFO	1
670	2	2	10.4 tr A0A090I800 A0A090I800_METFO	Sulfofpyruvate decarboxylase subunit beta OS=Methanobacterium formicicum METFO	1
671	2	2	5.6 tr A0A090I5I0 A0A090I5I0_METFO	Tetrahydromethanopterin S-methyltransferase subunit C O METFO	2
672	2	2	4.8 tr A0A090I4Y2 A0A090I4Y2_METFO	Putative membrane protein OS=Methanobacterium formicicum METFO	1
673	2	2	2.9 tr A0A090I4T2 A0A090I4T2_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
674	2	2	4.3 tr A0A090I4Q2 A0A090I4Q2_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1

Amostra 2

675	2	2	9.1	tr A0A090I4I3 A0A090I4I3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
676	2	2	4.8	tr A0A090I4D9 A0A090I4D9_METFO	Phosphomethylpyrimidine kinase OS=Methanobacterium formicicum METFO	1
677	2	2	3.5	tr A0A090I2B0 A0A090I2B0_METFO	tRNA(Ile2) 2-azmatinylcytidine synthetase TiaS OS=Methanobacterium formicicum METFO	1
678	2	2	5	tr A0A090I1S2 A0A090I1S2_METFO	Protease HtpX homolog OS=Methanobacterium formicicum METFO	1
679	2	2	2.2	tr A0A090I0P8 A0A090I0P8_METFO	Adenine deaminase OS=Methanobacterium formicicum METFO	1
680	2	2	3.8	tr A0A089ZV44 A0A089ZV44_METFO	GTP cyclohydrolase MptA OS=Methanobacterium formicicum METFO	1
681	2	2	8.8	tr A0A089ZJ52 A0A089ZJ52_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
682	2	2	5.1	tr A0A089ZH31 A0A089ZH31_METFO	Cobalamin biosynthesis protein CbiM3 OS=Methanobacterium formicicum METFO	2
683	2	2	4	tr A0A089ZDB2 A0A089ZDB2_METFO	Cell wall biosynthesis protein UDP-glycosyltransferase fam METFO	1
684	2	2	3	tr A0A089Z847 A0A089Z847_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
685	1.9	2.06	7.8	tr A0A0S4FPI8 A0A0S4FPI8_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
686	1.89	2	4.4	tr A0A0S4FNJ7 A0A0S4FNJ7_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
687	1.89	2	10.6	tr A0A090I4X2 A0A090I4X2_METFO	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylidene]thymine synthase METFO	2
688	1.88	2.12	27.5	tr K2RD75 K2RD75_METFP	Putative snRNP Sm-like protein OS=Methanobacterium formicicum METFP	2
689	1.84	6.22	4.4	tr A0A090I4D4 A0A090I4D4_METFO	Acetyl-coenzyme A synthetase OS=Methanobacterium formicicum METFO	4
690	1.82	2.1	12.4	tr A0A090I6H9 A0A090I6H9_METFO	3,4-dihydroxy-2-butanone 4-phosphate synthase OS=Methanobacterium formicicum METFO	2
691	1.8	1.93	9	tr A0A089ZH64 A0A089ZH64_METFO	HTH domain-containing protein OS=Methanobacterium formicicum METFO	1
692	1.8	1.92	7	tr A0A090JSV7 A0A090JSV7_METFO	RNA-binding protein OS=Methanobacterium formicicum METFO	1
693	1.8	1.92	12.6	tr A0A090I6Q6 A0A090I6Q6_METFO	Putative membrane protein OS=Methanobacterium formicicum METFO	1
694	1.78	2.02	22.1	tr A0A090I188 A0A090I188_METFO	30S ribosomal protein S19P OS=Methanobacterium formicicum METFO	2
695	1.76	1.97	5.6	tr A0A0S4FMY6 A0A0S4FMY6_METFO	NADPH-dependent FMN reductase OS=Methanobacterium formicicum METFO	1
696	1.7	1.82	24.3	tr K2REM2 K2REM2_METFP	6,7-dimethyl-8-ribityllumazine synthase OS=Methanobacterium formicicum METFP	1
697	1.67	1.81	4.9	tr A0A0S4FPR7 A0A0S4FPR7_METFO	Mevalonate kinase OS=Methanobacterium formicicum METFO	1
698	1.64	1.78	3.5	tr A0A089ZIQ0 A0A089ZIQ0_METFO	Metallophosphoesterase OS=Methanobacterium formicicum METFO	1
699	1.63	1.81	4.7	tr A0A090I5K2 A0A090I5K2_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
700	1.62	1.82	7.1	tr A0A090I8N7 A0A090I8N7_METFO	Precorrin-2 C20-methyltransferase OS=Methanobacterium formicicum METFO	1
701	1.59	1.72	3.9	tr K2QC11 K2QC11_METFP	Shikimate dehydrogenase (NADP(+)) OS=Methanobacterium formicicum METFP	1
702	1.55	1.77	2.2	tr A0A0S4FMS9 A0A0S4FMS9_METFO	Archaeal glutamate synthase [NADPH] OS=Methanobacterium formicicum METFO	1
703	1.52	1.8	4.6	tr A0A090I8U6 A0A090I8U6_METFO	Arginine--tRNA ligase OS=Methanobacterium formicicum METFO	2
704	1.5	1.66	3	tr A0A090JU62 A0A090JU62_METFO	Glutamine amidotransferase OS=Methanobacterium formicicum METFO	1
705	1.44	1.61	4.3	tr A0A089ZAI2 A0A089ZAI2_METFO	Molybdate transport system regulatory protein ModE OS=Methanobacterium formicicum METFO	1
706	1.44	1.57	8.2	tr A0A090I9J6 A0A090I9J6_METFO	Protein-export membrane protein SecF OS=Methanobacterium formicicum METFO	1
707	1.41	1.54	3.7	tr A0A0S4FPL3 A0A0S4FPL3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1

Amostra 2

708	1.4	1.63	17 tr A0A089ZUW3 A0A089ZUW3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
709	1.4	1.54	4.1 tr A0A090JW59 A0A090JW59_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
710	1.38	1.52	8.1 tr A0A090IB44 A0A090IB44_METFO	Universal stress protein UspA4 OS=Methanobacterium formicicum METFO	1
711	1.37	48.95	50.2 tr K2RBU1 K2RBU1_METFP	V-type ATP synthase alpha chain OS=Methanobacterium formicicum METFP	68
712	1.32	1.54	3.8 tr A0A090I0Y8 A0A090I0Y8_METFO	Putative (R)-citramalate synthase CimA OS=Methanobacterium formicicum METFO	2
713	1.32	1.46	8.6 tr K2RRQ3 K2RRQ3_METFP	50S ribosomal protein L31e OS=Methanobacterium formicicum METFP	1
714	1.31	1.44	1.4 tr A0A090JUA7 A0A090JUA7_METFO	DNA topoisomerase 1 OS=Methanobacterium formicicum METFO	1

Amostra 2



ID statistics table

Unused (Conf) Cutoff	Proteins Detected	Proteins Before Grouping	Distinct Peptides	Spectra Identified	% Total Spectra
>2.0 (99)	617	1314	11879	43689	24
>1.3 (95)	714	1586	12101	44158	24.2
>0.47 (66)	777	1734	12285	44476	24.4
Cutoff Applied: >0.05 (10%)	919	2062	12586	44889	24.6

Amostra 3

1) Z:\Projects\UniMS2019_95 MALves\Data\CS3_9uL.wiff

Sample Type: Identification
Cys. Alkylation: Iodoacetamide
Digestion: Trypsin
Instrument: TripleTOF 6600
Special Factors: Gel-based ID
Species:
ID Focus: Biological modifications
 Amino acid substitutions
Database: 20190624_uniprot_methanobacterium+formicicum_6903entries.fasta
Search Effort: Thorough
FDR Analysis: Yes
User Modified Parameter Files: Yes



Proteins detected table

N	Unused	Total	% Cov (95	Accession #	Name	Species	Peptides(95%)
1	69.16	69.16	24	tr A0A090I3J2 A0A090I3J2_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO		81
2	66.57	66.57	80.8	tr A0A090IAH6 A0A090IAH6_METFO	Thermosome subunit OS=Methanobacterium formicicum C METFO		155
3	63.57	63.57	69.8	tr A0A090I2T3 A0A090I2T3_METFO	Methyl-coenzyme M reductase subunit beta OS=Methanob METFO		301
4	55.25	55.25	32.9	tr A0A090I2R3 A0A090I2R3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO		39
5	54.52	54.58	41.1	tr A0A090I8L6 A0A090I8L6_METFO	Replication factor-A domain-containing protein OS=Methan METFO		32
6	52.04	52.04	46.5	tr A0A090I3A9 A0A090I3A9_METFO	Chaperone protein DnaK OS=Methanobacterium formicicu METFO		48
7	48.42	48.42	96.6	tr A0A090I573 A0A090I573_METFO	5,10-methylenetetrahydromethanopterin reductase OS=Me METFO		147
8	47.23	47.45	53.6	tr A0A090I2M3 A0A090I2M3_METFO	V-type ATP synthase alpha chain OS=Methanobacterium f METFO		37
9	44.97	44.97	63.2	tr A0A090I7W3 A0A090I7W3_METFO	Methyl-coenzyme M reductase subunit beta OS=Methanob METFO		65
10	42.53	42.53	30.4	tr A0A089ZH29 A0A089ZH29_METFO	Putative secreted protein OS=Methanobacterium formicicu METFO		37
11	41.6	41.64	54.4	tr A0A090I2G6 A0A090I2G6_METFO	Methyl-coenzyme M reductase subunit alpha OS=Methano METFO		52
12	40.16	40.16	29.4	tr A0A090I151 A0A090I151_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO		44
13	37.65	37.65	11.5	tr A0A090I3E3 A0A090I3E3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO		18
14	36.88	36.89	54.5	tr A0A090I2R9 A0A090I2R9_METFO	F420-non-reducing hydrogenase subunit A OS=Methanoba METFO		23

Amostra 3

15	34.08	34.08	33.9	tr A0A090I3G7 A0A090I3G7_METFO	CoB--CoM heterodisulfide reductase subunit A HdrA2 OS=Methanobacterium formicicum METFO	25
16	33.77	33.79	51.8	tr A0A0S4FR78 A0A0S4FR78_METFO	V-type ATP synthase beta chain OS=Methanobacterium formicicum METFO	43
17	32.88	32.92	49.4	tr A0A089ZDH4 A0A089ZDH4_METFO	Elongation factor 1-alpha OS=Methanobacterium formicicum METFO	33
18	31.91	31.91	48.3	tr A0A090I9A6 A0A090I9A6_METFO	Hydroxylamine reductase OS=Methanobacterium formicicum METFO	23
19	30.94	43.25	60.4	tr A0A090IA40 A0A090IA40_METFO	Thermosome subunit OS=Methanobacterium formicicum C METFO	63
20	28.87	28.87	26.4	tr A0A090I7T4 A0A090I7T4_METFO	Phosphoenolpyruvate synthase OS=Methanobacterium formicicum METFO	16
21	28.53	28.53	44.2	tr A0A090I7U6 A0A090I7U6_METFO	GDP-mannose 4,6-dehydratase OS=Methanobacterium formicicum METFO	17
22	28.25	28.25	44.8	tr A0A090I8W8 A0A090I8W8_METFO	Bifunctional enzyme Fae/Hps OS=Methanobacterium formicicum METFO	28
23	27.95	27.99	64.5	tr A0A090I842 A0A090I842_METFO	CBS domain-containing membrane protein OS=Methanobacterium formicicum METFO	29
24	26.71	26.75	62.6	tr A0A089ZAX5 A0A089ZAX5_METFO	30S ribosomal protein S2 OS=Methanobacterium formicicum METFO	18
25	26.61	26.67	52.7	tr A0A090I6W9 A0A090I6W9_METFO	Cell shape determining protein MreB/Mrl OS=Methanobacterium formicicum METFO	32
26	26.01	26.04	40.9	tr A0A090JVC3 A0A090JVC3_METFO	Methyl-coenzyme M reductase subunit alpha OS=Methanobacterium formicicum METFO	30
27	25.92	26.71	41.3	tr A0A090I4W3 A0A090I4W3_METFO	F420-non-reducing hydrogenase vhc subunit A OS=Methanobacterium formicicum METFO	17
28	25.65	25.71	54.7	tr A0A089ZVL0 A0A089ZVL0_METFO	Cell division protein FtsZ OS=Methanobacterium formicicum METFO	17
29	25.6	25.74	46.6	tr A0A090I210 A0A090I210_METFO	Putative aminotransferase MJ0959 OS=Methanobacterium formicicum METFO	22
30	24.72	24.81	38	tr A0A090I2P0 A0A090I2P0_METFO	CBS domain-containing protein OS=Methanobacterium formicicum METFO	18
31	23.45	23.47	26.7	tr A0A090I2L6 A0A090I2L6_METFO	D-3-phosphoglycerate dehydrogenase OS=Methanobacterium formicicum METFO	12
32	22.98	22.99	45	tr A0A090I5H3 A0A090I5H3_METFO	Methenyltetrahydromethanopterin cyclohydrolase OS=Methanobacterium formicicum METFO	14
33	22.37	22.39	54.3	tr A0A089ZEV2 A0A089ZEV2_METFO	CBS domain-containing protein OS=Methanobacterium formicicum METFO	14
34	22.1	22.11	72.8	tr A0A090I4G9 A0A090I4G9_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	100
35	20.98	21.06	62.4	tr A0A090I2W9 A0A090I2W9_METFO	Proteasome subunit beta OS=Methanobacterium formicicum METFO	24
36	20.65	20.68	42.4	tr A0A089ZG02 A0A089ZG02_METFO	DNA repair and recombination protein RadA OS=Methanobacterium formicicum METFO	12
37	20.62	20.83	16	tr A0A090I3T1 A0A090I3T1_METFO	Elongation factor 2 OS=Methanobacterium formicicum OX= METFO	11
38	20.37	20.41	37	tr A0A089ZBS9 A0A089ZBS9_METFO	Acetyl-CoA acetyltransferase OS=Methanobacterium formicicum METFO	12
39	20.17	20.21	49.3	tr A0A090I5T3 A0A090I5T3_METFO	Methyl-coenzyme M reductase subunit gamma OS=Methanobacterium formicicum METFO	12
40	20.07	20.11	49.4	tr A0A090I5U4 A0A090I5U4_METFO	SPFH domain/Band 7 family protein OS=Methanobacterium formicicum METFO	12
41	19.84	19.87	29.2	tr A0A090JXN7 A0A090JXN7_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	24
42	19.74	19.8	33.8	tr A0A090I281 A0A090I281_METFO	Pyruvate synthase subunit PorA OS=Methanobacterium formicicum METFO	19
43	18.95	18.98	46.4	tr A0A090I5W3 A0A090I5W3_METFO	30S ribosomal protein S3Ae OS=Methanobacterium formicicum METFO	12
44	18.9	18.93	41.9	tr A0A090I1H9 A0A090I1H9_METFO	30S ribosomal protein S4e OS=Methanobacterium formicicum METFO	15
45	18.5	18.55	44.4	tr A0A090JUK8 A0A090JUK8_METFO	V-type proton ATPase subunit E OS=Methanobacterium formicicum METFO	12
46	18.48	18.51	61.6	tr A0A090I219 A0A090I219_METFO	Translation initiation factor 6 OS=Methanobacterium formicicum METFO	11
47	18.42	18.69	31.9	tr A0A090I514 A0A090I514_METFO	UPF0219 protein DSM1535_2142 OS=Methanobacterium formicicum METFO	14

Amostra 3

48	18.35	18.37	35.7	tr A0A090I3I6 A0A090I3I6_METFO	Putative lipoprotein MJ0085 OS=Methanobacterium formicic METFO	15
49	17.54	17.56	29.3	tr A0A090I428 A0A090I428_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	11
50	17.25	17.32	18.6	tr A0A090I904 A0A090I904_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	9
51	16.6	16.6	37.1	tr A0A090I613 A0A090I613_METFO	Coenzyme F420 hydrogenase subunit beta OS=Methanobacterium formicicun METFO	12
52	16.42	16.46	35.1	tr A0A089ZIP7 A0A089ZIP7_METFO	DNA primase DnaG OS=Methanobacterium formicicun METFO	12
53	16.4	18	50	tr A0A090I9S3 A0A090I9S3_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	24
54	16.16	16.17	22.5	tr A0A090I7L2 A0A090I7L2_METFO	Acetyl-CoA decarboxylase/synthase complex subunit gamma METFO	9
55	16.01	16.01	37.3	tr A0A090I4Y4 A0A090I4Y4_METFO	Circadian clock protein KaiC OS=Methanobacterium formicicun METFO	10
56	15.98	16.05	39.9	tr A0A090I8V8 A0A090I8V8_METFO	F420-dependent methylenetetrahydromethanopterin dehydrogenase METFO	11
57	15.86	15.98	32.9	tr A0A090JXT2 A0A090JXT2_METFO	O-acetylhomoserine (Thiol)-lyase OS=Methanobacterium formicicun METFO	9
58	15.85	15.85	31.2	tr A0A090I0T1 A0A090I0T1_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	12
59	15.79	15.84	37.6	tr A0A090I958 A0A090I958_METFO	Extracellular solute-binding protein OS=Methanobacterium formicicun METFO	19
60	15.78	15.83	34.2	tr A0A090I345 A0A090I345_METFO	3-isopropylmalate dehydrogenase OS=Methanobacterium formicicun METFO	11
61	15.54	15.57	36.3	tr A0A090I5H7 A0A090I5H7_METFO	Tetrahydromethanopterin S-methyltransferase subunit H OS=Methanobacterium formicicun METFO	15
62	15.35	15.53	39.8	tr A0A090IB20 A0A090IB20_METFO	Proteasome subunit alpha OS=Methanobacterium formicicun METFO	8
63	15.3	15.45	36.7	tr A0A089Z979 A0A089Z979_METFO	Site-determining protein OS=Methanobacterium formicicun METFO	8
64	14.85	15.27	24.8	tr A0A089ZVL1 A0A089ZVL1_METFO	50S ribosomal protein L10 OS=Methanobacterium formicicun METFO	8
65	14.72	14.75	41.2	tr A0A090JW64 A0A090JW64_METFO	LemA family protein OS=Methanobacterium formicicun METFO	12
66	14.62	14.65	38.4	tr A0A090JTE0 A0A090JTE0_METFO	50S ribosomal protein L6 OS=Methanobacterium formicicun METFO	9
67	14.5	14.52	22.1	tr A0A090JTX8 A0A090JTX8_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	8
68	14.18	14.19	47.5	tr A0A090JWN0 A0A090JWN0_METFO	Putative secreted protein OS=Methanobacterium formicicun METFO	40
69	14.03	14.41	21.7	tr A0A090I3S6 A0A090I3S6_METFO	DNA-directed RNA polymerase subunit A' OS=Methanobacterium formicicun METFO	10
70	14	14.11	26.6	tr A0A090I9D3 A0A090I9D3_METFO	Succinate--CoA ligase [ADP-forming] subunit beta OS=Methanobacterium formicicun METFO	8
71	14	14	61.7	tr A0A089ZUS9 A0A089ZUS9_METFO	50S ribosomal protein L18 OS=Methanobacterium formicicun METFO	8
72	13.85	13.97	38.7	tr A0A090I7T8 A0A090I7T8_METFO	Peptidyl-prolyl cis-trans isomerase OS=Methanobacterium formicicun METFO	8
73	13.61	13.65	52.4	tr A0A089ZCU1 A0A089ZCU1_METFO	Transcription elongation factor Spt5 OS=Methanobacterium formicicun METFO	7
74	13.6	13.64	40	tr A0A090I424 A0A090I424_METFO	Translation initiation factor 5A OS=Methanobacterium formicicun METFO	13
75	13.54	13.67	39.4	tr A0A090I6Q2 A0A090I6Q2_METFO	Formylmethanofuran dehydrogenase subunit C FwdC OS=Methanobacterium formicicun METFO	11
76	13.52	13.68	18.8	tr A0A089ZGQ5 A0A089ZGQ5_METFO	Peptidase U62 family OS=Methanobacterium formicicun METFO	7
77	13.42	13.54	45.2	tr A0A090I0N7 A0A090I0N7_METFO	PyrE-like protein OS=Methanobacterium formicicun METFO	9
78	13.33	13.39	26.5	tr A0A090JV64 A0A090JV64_METFO	CBS domain-containing membrane protein OS=Methanobacterium formicicun METFO	8
79	13.2	13.35	28.9	tr A0A089ZUT3 A0A089ZUT3_METFO	50S ribosomal protein L3 OS=Methanobacterium formicicun METFO	10
80	13.17	13.25	15.6	tr A0A089ZAI4 A0A089ZAI4_METFO	Formylmethanofuran dehydrogenase subunit A FwdA OS=Methanobacterium formicicun METFO	7

Amostra 3

81	13.1	13.27	21.6	tr A0A090I781 A0A090I781_METFO	Fructose-1,6-bisphosphate aldolase/phosphatase OS=Methanobacterium formicicum METFO	7
82	12.65	12.92	24	tr A0A090I3H9 A0A090I3H9_METFO	5-formaminoimidazole-4-carboxamide-1-(beta)-D-ribofuran METFO	8
83	12.54	21.97	18.7	tr A0A090IAQ7 A0A090IAQ7_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	14
84	12.46	12.48	21.6	tr A0A090I1P7 A0A090I1P7_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	7
85	12.38	12.48	33.9	tr A0A090I1I9 A0A090I1I9_METFO	CoB-CoM heterodisulfide reductase iron-sulfur subunit C O METFO	13
86	12.16	12.19	37.6	tr A0A090I170 A0A090I170_METFO	TATA-box-binding protein OS=Methanobacterium formicicum METFO	6
87	12.13	12.13	19.1	tr A0A090I3J1 A0A090I3J1_METFO	Formate dehydrogenase beta subunit FdhB OS=Methanobacterium formicicum METFO	6
88	12.02	12.03	35.8	tr A0A089ZGF9 A0A089ZGF9_METFO	30S ribosomal protein S5 OS=Methanobacterium formicicum METFO	8
89	12.01	12.01	58.3	tr A0A089ZGG4 A0A089ZGG4_METFO	50S ribosomal protein L14 OS=Methanobacterium formicicum METFO	8
90	12	12.01	39.9	tr A0A090I180 A0A090I180_METFO	50S ribosomal protein L5 OS=Methanobacterium formicicum METFO	9
91	11.87	11.96	17.6	tr A0A090JTE7 A0A090JTE7_METFO	30S ribosomal protein S3 OS=Methanobacterium formicicum METFO	6
92	11.85	11.95	22.2	tr A0A090JXJ6 A0A090JXJ6_METFO	3-dehydroquinate synthase OS=Methanobacterium formicicum METFO	7
93	11.62	11.66	18.3	tr A0A090JWH2 A0A090JWH2_METFO	Phosphoglucosamine mutase GlmM2 OS=Methanobacterium formicicum METFO	6
94	11.57	11.63	23.2	tr A0A090IAD3 A0A090IAD3_METFO	Homoserine dehydrogenase OS=Methanobacterium formicicum METFO	6
95	11.49	11.55	18.2	tr A0A090I7B6 A0A090I7B6_METFO	Inosine-5'-monophosphate dehydrogenase OS=Methanobacterium formicicum METFO	7
96	11.49	11.52	31.3	tr A0A090JUG7 A0A090JUG7_METFO	Phosphate binding protein OS=Methanobacterium formicicum METFO	6
97	11.32	11.42	28.3	tr A0A089ZAG5 A0A089ZAG5_METFO	Transcriptional regulator with CBS domains OS=Methanobacterium formicicum METFO	8
98	11.31	11.36	22.4	tr A0A090JW72 A0A090JW72_METFO	Arsenite-activated ATPase ArsA OS=Methanobacterium formicicum METFO	7
99	11.26	11.47	11	tr A0A090I3V1 A0A090I3V1_METFO	Formate dehydrogenase alpha subunit FdhA OS=Methanobacterium formicicum METFO	7
100	11.25	11.38	27.3	tr A0A090JVV9 A0A090JVV9_METFO	Aspartate carbamoyltransferase OS=Methanobacterium formicicum METFO	7
101	11.09	11.16	19.4	tr A0A090I6I2 A0A090I6I2_METFO	Adenylosuccinate synthetase OS=Methanobacterium formicicum METFO	6
102	11	11.04	31.7	tr A0A090I5G8 A0A090I5G8_METFO	F420-non-reducing hydrogenase subunit G OS=Methanobacterium formicicum METFO	8
103	10.94	10.98	18.8	tr A0A090I518 A0A090I518_METFO	Digeranylgeranyl glycerophospholipid reductase OS=Methanobacterium formicicum METFO	6
104	10.9	11.01	29.1	tr A0A089ZER7 A0A089ZER7_METFO	Exosome complex component Rrp4 OS=Methanobacterium formicicum METFO	6
105	10.69	10.74	27.7	tr A0A089ZE87 A0A089ZE87_METFO	ABC transporter ATP-binding protein OS=Methanobacterium formicicum METFO	8
106	10.5	10.52	42.3	tr A0A090I2G3 A0A090I2G3_METFO	Tetrahydromethanopterin S-methyltransferase subunit A O METFO	20
107	10.17	10.18	24.9	tr A0A090I897 A0A090I897_METFO	Formylmethanofuran--tetrahydromethanopterin formyltransferase METFO	8
108	10.08	10.09	12.2	tr K2QBS7 K2QBS7_METFP	ABC transporter subunit Ycf24 OS=Methanobacterium formicicum METFP	6
109	10.03	10.09	20.2	tr A0A090I166 A0A090I166_METFO	Enolase OS=Methanobacterium formicicum OX=2162 GN= METFO	5
110	9.95	10.03	37.3	tr A0A089ZAY7 A0A089ZAY7_METFO	30S ribosomal protein S4 OS=Methanobacterium formicicum METFO	6
111	9.83	9.89	5.4	tr A0A090I4M6 A0A090I4M6_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	5
112	9.77	9.89	27.1	tr A0A090I560 A0A090I560_METFO	Putative hydrogenase nickel incorporation protein HypB OS=Methanobacterium formicicum METFO	5
113	9.76	9.85	23.3	tr A0A090I494 A0A090I494_METFO	Short-chain dehydrogenase family protein OS=Methanobacterium formicicum METFO	5

Amostra 3

114	9.74	9.87	15.1	tr A0A089ZCR8 A0A089ZCR8_METFO	Proteasome-activating nucleotidase OS=Methanobacterium METFO	5
115	9.72	9.79	10.1	tr A0A089ZHH5 A0A089ZHH5_METFO	Phosphoserine phosphatase SerB OS=Methanobacterium METFO	5
116	9.71	9.85	12.1	tr A0A089ZUL5 A0A089ZUL5_METFO	Tryptophan synthase beta chain OS=Methanobacterium formicicum METFO	5
117	9.7	9.78	14.7	tr A0A090JUQ9 A0A090JUQ9_METFO	Putative nickel insertion protein OS=Methanobacterium formicicum METFO	5
118	9.68	9.73	58.1	tr K2QX04 K2QX04_METFP	Deoxyribonuclease/rho motif-related TRAM OS=Methanobacterium formicicum METFP	7
119	9.51	9.55	33	tr A0A090JWL2 A0A090JWL2_METFO	IMP cyclohydrolase OS=Methanobacterium formicicum OX=21 METFO	6
120	9.5	9.54	21.7	tr A0A090JYU9 A0A090JYU9_METFO	Phosphosulfolactate synthase OS=Methanobacterium formicicum METFO	5
121	9.47	9.55	9.8	tr A0A089ZHQ4 A0A089ZHQ4_METFO	Methyl-coenzyme M reductase component A2 AtwA3 OS=Methanobacterium formicicum METFO	5
122	9.47	9.52	18.4	tr A0A090I246 A0A090I246_METFO	3-hydroxy-3-methylglutaryl coenzyme A reductase OS=Methanobacterium formicicum METFO	6
123	9.4	9.44	61.9	tr A0A089ZBS5 A0A089ZBS5_METFO	30S ribosomal protein S6e OS=Methanobacterium formicicum METFO	6
124	9.33	9.46	21.6	tr A0A090I7U4 A0A090I7U4_METFO	ABC transporter OS=Methanobacterium formicicum OX=21 METFO	5
125	9.31	9.39	37.1	tr A0A089Z8Q6 A0A089Z8Q6_METFO	30S ribosomal protein S11 OS=Methanobacterium formicicum METFO	10
126	9.16	9.23	9	tr A0A090JW16 A0A090JW16_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	11
127	9.1	9.17	24.6	tr A0A089ZI64 A0A089ZI64_METFO	ATP phosphoribosyltransferase OS=Methanobacterium formicicum METFO	6
128	8.97	9.11	14	tr A0A090JY31 A0A090JY31_METFO	Aspartokinase OS=Methanobacterium formicicum OX=216 METFO	5
129	8.91	9.01	20.6	tr A0A089ZGG9 A0A089ZGG9_METFO	50S ribosomal protein L4 OS=Methanobacterium formicicum METFO	6
130	8.79	9.03	30.4	tr A0A089ZCQ3 A0A089ZCQ3_METFO	Putative rubrerythrin OS=Methanobacterium formicicum OX=21 METFO	5
131	8.76	9.08	14.6	tr A0A090I4Q7 A0A090I4Q7_METFO	Aspartate--tRNA(Asp/Asn) ligase OS=Methanobacterium formicicum METFO	6
132	8.76	8.87	29.4	tr A0A090I7Y5 A0A090I7Y5_METFO	AsnC family transcriptional regulator OS=Methanobacterium formicicum METFO	5
133	8.73	8.85	22.6	tr A0A090I1Q2 A0A090I1Q2_METFO	Nicotinate-nucleotide pyrophosphorylase [carboxylating] OX=21 METFO	6
134	8.71	8.91	53.3	tr A0A090I6K9 A0A090I6K9_METFO	30S ribosomal protein S17 OS=Methanobacterium formicicum METFO	5
135	8.67	8.82	49.6	tr A0A090JTC3 A0A090JTC3_METFO	30S ribosomal protein S9 OS=Methanobacterium formicicum METFO	8
136	8.67	8.72	15.3	tr A0A089ZGS2 A0A089ZGS2_METFO	Replication factor C small subunit OS=Methanobacterium formicicum METFO	5
137	8.48	8.87	19.3	tr A0A090I305 A0A090I305_METFO	Coenzyme F420 hydrogenase alpha subunit FrhA OS=Methanobacterium formicicum METFO	8
138	8.33	8.43	12.2	tr A0A090I5S8 A0A090I5S8_METFO	Argininosuccinate synthase OS=Methanobacterium formicicum METFO	4
139	8.31	8.43	23.6	tr A0A090I622 A0A090I622_METFO	Translation initiation factor 2 subunit alpha OS=Methanobacterium formicicum METFO	5
140	8.26	8.29	11.3	tr A0A090I6T0 A0A090I6T0_METFO	Glutamine synthetase OS=Methanobacterium formicicum METFO	4
141	8.22	8.34	15.3	tr A0A090JW43 A0A090JW43_METFO	Glutamyl-tRNA(Gln) amidotransferase subunit A OS=Methanobacterium formicicum METFO	5
142	8.17	8.19	35.3	tr A0A090I579 A0A090I579_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	5
143	8.11	16.01	37.9	tr A0A090I7S6 A0A090I7S6_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	22
144	8.01	8.01	26.9	tr A0A090I8J3 A0A090I8J3_METFO	Cobalt-precorrin-8X methylmutase OS=Methanobacterium formicicum METFO	4
145	8.01	8.01	33.8	tr A0A089ZFP6 A0A089ZFP6_METFO	Peptidase S26B, signal peptidase OS=Methanobacterium formicicum METFO	4
146	8	8	44.1	tr A0A089ZGZ1 A0A089ZGZ1_METFO	30S ribosomal protein S8e OS=Methanobacterium formicicum METFO	7

Amostra 3

147	8	8	12 tr A0A089ZH78 A0A089ZH78_METFO	V-type ATP synthase subunit C OS=Methanobacterium fori	METFO	4
148	8	8	30.1 tr A0A090I4T3 A0A090I4T3_METFO	Orotate phosphoribosyltransferase OS=Methanobacterium	METFO	4
149	7.9	8.01	15.2 tr A0A090I409 A0A090I409_METFO	Glutamyl-tRNA(Gln) amidotransferase subunit D OS=Meth:	METFO	5
150	7.89	7.93	39.2 tr A0A089ZHN5 A0A089ZHN5_METFO	Probable transcription termination protein NusA OS=Metha	METFO	4
151	7.85	8.05	12.7 tr A0A090I4G3 A0A090I4G3_METFO	LL-diaminopimelate aminotransferase OS=Methanobacteri	METFO	6
152	7.78	7.83	32.4 tr K2QDP1 K2QDP1_METFP	30S ribosomal protein S10 OS=Methanobacterium formicic	METFP	4
153	7.73	7.81	26.6 tr A0A090JSP3 A0A090JSP3_METFO	Uridylate kinase OS=Methanobacterium formicicum OX=21	METFO	6
154	7.69	7.8	9.9 tr A0A090I3Y0 A0A090I3Y0_METFO	Phenylalanine--tRNA ligase beta subunit OS=Methanobact	METFO	4
155	7.66	7.7	9 tr A0A089ZGX6 A0A089ZGX6_METFO	Uncharacterized protein OS=Methanobacterium formicicun	METFO	4
156	7.63	7.73	13.7 tr A0A090I796 A0A090I796_METFO	Pyridoxal 5'-phosphate synthase subunit PdxS OS=Methan	METFO	5
157	7.55	7.66	21 tr A0A0S4FSE6 A0A0S4FSE6_METFO	Putative ABC transporter ATP-binding protein MJ0089 OS=	METFO	4
158	7.5	8.7	21.3 tr A0A089ZJ55 A0A089ZJ55_METFO	DNA polymerase sliding clamp OS=Methanobacterium forr	METFO	5
159	7.45	7.56	16.7 tr A0A089ZGM2 A0A089ZGM2_METFO	CoB--CoM heterodisulfide reductase subunit B HdrB1 OS=	METFO	5
160	7.37	7.42	20.8 tr A0A090I4X8 A0A090I4X8_METFO	F420-dependent NADP reductase OS=Methanobacterium i	METFO	4
161	7.27	7.43	13.7 tr A0A090I582 A0A090I582_METFO	50S ribosomal protein L1 OS=Methanobacterium formicicu	METFO	6
162	7.22	7.41	32.7 tr A0A089ZDW1 A0A089ZDW1_METFO	Methyl-coenzyme M reductase II D subunit MrtD OS=Meth:	METFO	4
163	7.06	7.11	40.7 tr A0A089ZGF2 A0A089ZGF2_METFO	50S ribosomal protein L13 OS=Methanobacterium formicic	METFO	7
164	7.02	7.08	18.3 tr A0A090I314 A0A090I314_METFO	CBS domain-containing protein OS=Methanobacterium fori	METFO	4
165	6.98	7.15	8.5 tr A0A090I6C9 A0A090I6C9_METFO	Ketol-acid reductoisomerase (NADP(+)) OS=Methanobact	METFO	4
166	6.95	7.01	12.9 tr A0A089ZHE0 A0A089ZHE0_METFO	Molybdenum cofactor synthesis domain-containing protein	METFO	4
167	6.89	6.94	27.6 tr A0A090JUF5 A0A090JUF5_METFO	Pyruvate synthase subunit PorC OS=Methanobacterium fo	METFO	4
168	6.86	6.98	15.4 tr A0A090I672 A0A090I672_METFO	dTDP-glucose 4,6-dehydratase OS=Methanobacterium fori	METFO	4
169	6.86	6.92	25.1 tr A0A089ZGF5 A0A089ZGF5_METFO	CBS domain-containing protein OS=Methanobacterium fori	METFO	4
170	6.85	6.9	10.8 tr A0A090I100 A0A090I100_METFO	S-inosyl-L-homocysteine hydrolase OS=Methanobacterium	METFO	4
171	6.83	6.89	54.7 tr A0A089ZB18 A0A089ZB18_METFO	50S ribosomal protein L23 OS=Methanobacterium formicic	METFO	9
172	6.82	6.88	16.4 tr A0A090I3D2 A0A090I3D2_METFO	PQQ repeat-containing cell surface protein OS=Methanob:	METFO	5
173	6.78	6.84	29.5 tr A0A090JV59 A0A090JV59_METFO	Transcription elongation factor NusA-like protein OS=Meth:	METFO	4
174	6.67	6.81	15.9 tr A0A089ZG23 A0A089ZG23_METFO	Formylmethanofuran dehydrogenase subunit F FwdF1 OS=	METFO	4
175	6.65	6.75	6.5 tr A0A089ZCC0 A0A089ZCC0_METFO	Pyruvate carboxylase subunit B PycB OS=Methanobacteri	METFO	3
176	6.65	6.71	18.2 tr A0A090JUT3 A0A090JUT3_METFO	F420-non-reducing hydrogenase iron-sulfur subunit D OS=	METFO	3
177	6.57	6.62	20.6 tr A0A090I6D3 A0A090I6D3_METFO	Ornithine carbamoyltransferase OS=Methanobacterium for	METFO	4
178	6.56	6.62	16.1 tr A0A089ZF65 A0A089ZF65_METFO	PRC-barrel domain-containing protein OS=Methanobacteri	METFO	3
179	6.45	6.6	5 tr A0A0S4FL46 A0A0S4FL46_METFO	Uncharacterized protein OS=Methanobacterium formicicun	METFO	4

Amostra 3

180	6.41	6.59	11.4	tr A0A090I2F4 A0A090I2F4_METFO	Polyferredoxin protein MvhB OS=Methanobacterium formic METFO	4
181	6.4	6.55	9.4	tr A0A090I599 A0A090I599_METFO	Acetyl-CoA decarbonylase/synthase complex subunit beta METFO	4
182	6.34	6.47	32.6	tr A0A090I4J8 A0A090I4J8_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	4
183	6.31	6.35	23.1	tr A0A089ZC51 A0A089ZC51_METFO	Extracellular phosphate-binding protein OS=Methanobacte METFO	5
184	6.16	6.18	27.4	tr A0A089ZA11 A0A089ZA11_METFO	UPF0145 protein BRM9_0823 OS=Methanobacterium forr METFO	4
185	6.1	6.12	54.8	tr A0A090JUJ7 A0A090JUJ7_METFO	Tetrahydromethanopterin S-methyltransferase subunit G O METFO	9
186	6.1	6.12	9.2	tr A0A090I471 A0A090I471_METFO	GDP-mannose 4,6-dehydratase OS=Methanobacterium for METFO	3
187	6.1	6.11	14.2	tr A0A090I5U3 A0A090I5U3_METFO	Geranylgeranylglyceryl phosphate synthase OS=Methanob METFO	3
188	6.08	6.09	23.7	tr A0A090JWM7 A0A090JWM7_METFO	2-oxoglutarate synthase subunit KorC OS=Methanobacteri METFO	3
189	6.05	6.06	10.3	tr A0A090I938 A0A090I938_METFO	Phosphomethylpyrimidine synthase OS=Methanobacteriur METFO	3
190	6.05	6.05	18.4	tr K2RRA6 K2RRA6_METFP	Uncharacterized protein OS=Methanobacterium formicicun METFP	3
191	6.04	6.05	12	tr A0A089ZDP0 A0A089ZDP0_METFO	Thiamine thiazole synthase OS=Methanobacterium formici METFO	3
192	6	6.02	15.5	tr A0A090I9B3 A0A090I9B3_METFO	GTP cyclohydrolase III OS=Methanobacterium formicicum METFO	3
193	6	6	28.2	tr A0A089ZCA7 A0A089ZCA7_METFO	Thioesterase OS=Methanobacterium formicicum OX=2162 METFO	3
194	6	6	11.4	tr A0A090I689 A0A090I689_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	3
195	6	6	14.6	tr A0A090I3Q7 A0A090I3Q7_METFO	Nucleotidyl transferase OS=Methanobacterium formicicum METFO	3
196	6	6	22	tr A0A089ZVR0 A0A089ZVR0_METFO	30S ribosomal protein S12 OS=Methanobacterium formicic METFO	4
197	6	6	17.3	tr A0A090JX40 A0A090JX40_METFO	(5-formylfuran-3-yl)methyl phosphate synthase OS=Methar METFO	3
198	5.94	6.03	19.1	tr A0A089ZEW4 A0A089ZEW4_METFO	50S ribosomal protein L11 OS=Methanobacterium formicic METFO	3
199	5.75	5.9	12.4	tr A0A090I5G4 A0A090I5G4_METFO	Exosome complex component Rrp41 OS=Methanobacteriu METFO	3
200	5.73	5.9	8.9	tr A0A090I8R6 A0A090I8R6_METFO	Acetylornithine aminotransferase OS=Methanobacterium fc METFO	3
201	5.72	5.83	21.1	tr K2REW5 K2REW5_METFP	30S ribosomal protein S15 OS=Methanobacterium formicic METFP	3
202	5.69	5.88	29.6	tr A0A090I640 A0A090I640_METFO	Exosome complex component Csl4 OS=Methanobacteriur METFO	6
203	5.62	5.7	21.9	tr A0A090JU72 A0A090JU72_METFO	Putative secreted protein OS=Methanobacterium formicicu METFO	3
204	5.49	5.62	27.9	tr A0A090I1Y5 A0A090I1Y5_METFO	Molybdenum cofactor synthesis domain-containing protein METFO	3
205	5.44	5.55	27.2	tr A0A089ZV28 A0A089ZV28_METFO	Heat shock protein Hsp20 OS=Methanobacterium formicici METFO	3
206	5.35	5.42	9	tr K2RRX2 K2RRX2_METFP	Threonine synthase OS=Methanobacterium formicicum (sti METFP	3
207	5.32	5.62	8.8	tr A0A090I433 A0A090I433_METFO	GMP synthase [glutamine-hydrolyzing] subunit B OS=Meth METFO	3
208	5.32	5.41	12.8	tr A0A090IB52 A0A090IB52_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	5
209	5.3	5.45	7.7	tr A0A090I4J0 A0A090I4J0_METFO	Pyruvate carboxylase subunit A OS=Methanobacterium for METFO	3
210	5.29	5.42	7.6	tr A0A090I4R4 A0A090I4R4_METFO	Type A flavoprotein FprA OS=Methanobacterium formicicu METFO	3
211	5.27	5.34	23.6	tr A0A089ZEU2 A0A089ZEU2_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	3
212	5.25	5.53	13.5	tr A0A090JTT4 A0A090JTT4_METFO	Methanogenesis marker protein 15 OS=Methanobacterium METFO	4

Amostra 3

213	5.15	5.31	5 tr A0A090I2M9 A0A090I2M9_METFO	Catalase-peroxidase OS=Methanobacterium formicicum O METFO	3
214	5.15	5.22	17.9 tr A0A090I552 A0A090I552_METFO	Exosome complex component Rrp42 OS=Methanobacteriu METFO	4
215	5.12	5.46	8.1 tr A0A090I3U3 A0A090I3U3_METFO	Peptidase U62 modulator of DNA gyrase OS=Methanobacti METFO	4
216	5.07	5.21	19.1 tr A0A090JU33 A0A090JU33_METFO	DNA-directed RNA polymerase OS=Methanobacterium fori METFO	4
217	4.99	5.2	16.2 tr A0A090I2K0 A0A090I2K0_METFO	Phosphoribosylformylglycinamidine cyclo-ligase OS=Metha METFO	4
218	4.93	5.21	5.2 tr A0A090I4P0 A0A090I4P0_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	3
219	4.91	4.98	35.6 tr A0A089ZGN8 A0A089ZGN8_METFO	PRC-barrel domain-containing protein OS=Methanobacteri METFO	3
220	4.87	4.94	8.6 tr A0A090I0P2 A0A090I0P2_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	3
221	4.82	4.89	35.9 tr A0A089ZG55 A0A089ZG55_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	7
222	4.74	4.92	3.6 tr A0A090I9E0 A0A090I9E0_METFO	DNA-directed RNA polymerase subunit OS=Methanobacte METFO	3
223	4.71	4.91	12.5 tr A0A090I3P4 A0A090I3P4_METFO	Alanine dehydrogenase OS=Methanobacterium formicicun METFO	3
224	4.66	4.73	16 tr A0A090I9D6 A0A090I9D6_METFO	Triosephosphate isomerase OS=Methanobacterium formic METFO	3
225	4.61	5.26	14.6 tr A0A0S4FLD6 A0A0S4FLD6_METFO	ABC transporter substrate-binding protein OS=Methanobac METFO	4
226	4.59	4.63	15 tr A0A090I9E4 A0A090I9E4_METFO	30S ribosomal protein S7 OS=Methanobacterium formicicu METFO	2
227	4.53	4.58	7.6 tr A0A089ZGW2 A0A089ZGW2_METFO	Translation initiation factor 2 subunit gamma OS=Methanol METFO	3
228	4.51	4.63	27.3 tr A0A090I2G1 A0A090I2G1_METFO	Universal stress protein MTBMA_c15380 OS=Methanobac METFO	3
229	4.5	4.53	9 tr A0A090I3S2 A0A090I3S2_METFO	Phosphoglycerate kinase OS=Methanobacterium formicicu METFO	2
230	4.48	4.59	38.8 tr A0A090I442 A0A090I442_METFO	50S ribosomal protein L30e OS=Methanobacterium formici METFO	4
231	4.44	4.55	10.3 tr A0A090IB58 A0A090IB58_METFO	Carbamoyl-phosphate synthase small chain OS=Methanob METFO	3
232	4.29	4.39	14.2 tr A0A090I8S1 A0A090I8S1_METFO	Universal stress protein UspA5 OS=Methanobacterium forr METFO	2
233	4.19	4.27	7.9 tr A0A090JUJ4 A0A090JUJ4_METFO	Probable L-aspartate dehydrogenase OS=Methanobacteri METFO	2
234	4.15	4.17	4.7 tr A0A089ZHM6 A0A089ZHM6_METFO	Methyl-coenzyme M reductase component A2 AtwA2 OS=M METFO	2
235	4.13	4.15	7.7 tr A0A090I6I6 A0A090I6I6_METFO	Isopentenyl-diphosphate delta-isomerase OS=Methanobac METFO	2
236	4.13	4.15	6.8 tr A0A090I135 A0A090I135_METFO	UTP--glucose-1-phosphate uridylyltransferase OS=Methan METFO	2
237	4.11	4.21	2.8 tr A0A0S4FQI5 A0A0S4FQI5_METFO	Cell division cycle protein 48 homolog MJ1156 OS=Methan METFO	2
238	4.09	4.11	11.5 tr A0A090JVY8 A0A090JVY8_METFO	Putative acetolactate synthase small subunit OS=Methanol METFO	3
239	4.09	4.1	18.6 tr A0A090I7B8 A0A090I7B8_METFO	30S ribosomal protein S19e OS=Methanobacterium formici METFO	2
240	4.07	4.08	7.2 tr A0A090I2K4 A0A090I2K4_METFO	Putative ATP-binding protein MJ0685 OS=Methanobacteri METFO	2
241	4.05	4.06	20.7 tr A0A090I168 A0A090I168_METFO	50S ribosomal protein L18e OS=Methanobacterium formici METFO	2
242	4.04	4.05	12.8 tr A0A090I192 A0A090I192_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	3
243	4.04	4.04	7.7 tr A0A0S4FMQ4 A0A0S4FMQ4_METFO	Putative hydrogenase expression/formation protein MJ067 METFO	2
244	4.03	4.04	18 tr A0A090JTD5 A0A090JTD5_METFO	50S ribosomal protein L30 OS=Methanobacterium formicic METFO	2
245	4.03	4.03	11.5 tr K2R511 K2R511_METFP	TOPRIM domain-containing protein OS=Methanobacteriur METFP	3

Amostra 3

246	4.02	4.03	10.7	tr A0A089ZI49 A0A089ZI49_METFO	Sensory transduction histidine kinase OS=Methanobacteriu	METFO	2
247	4.02	4.02	30.2	tr A0A089ZA06 A0A089ZA06_METFO	PRC-barrel domain-containing protein OS=Methanobacteri	METFO	4
248	4.01	4.02	5.9	tr A0A089ZFA3 A0A089ZFA3_METFO	Acetyl-CoA decarbonylase/synthase complex subunit delta	METFO	2
249	4.01	4.02	5.5	tr A0A090I731 A0A090I731_METFO	Glucose-1-phosphate thymidyltransferase OS=Methanob.	METFO	2
250	4.01	4.01	6.5	tr A0A090I391 A0A090I391_METFO	Daunorubicin resistance ABC transporter ATPase subunit (METFO	2
251	4.01	4.01	7.8	tr A0A0S4FLK3 A0A0S4FLK3_METFO	Coenzyme F420:L-glutamate ligase OS=Methanobacterium	METFO	2
252	4.01	4.01	24.2	tr A0A090I340 A0A090I340_METFO	Uncharacterized protein OS=Methanobacterium formicicu	METFO	2
253	4	4.01	6.2	tr K2R1B6 K2R1B6_METFP	Glyceraldehyde-3-phosphate dehydrogenase OS=Methanc	METFP	2
254	4	4	10.9	tr K2RAP2 K2RAP2_METFP	Tetrahydromethanopterin S-methyltransferase subunit E O	METFP	5
255	4	4	9.1	tr A0A090I1X5 A0A090I1X5_METFO	3-isopropylmalate dehydrogenase OS=Methanobacterium	METFO	2
256	4	4	4.8	tr A0A0S4FS90 A0A0S4FS90_METFO	Putative secreted protein OS=Methanobacterium formicicu	METFO	2
257	4	4	11.7	tr A0A090IAZ4 A0A090IAZ4_METFO	LmbE family protein OS=Methanobacterium formicicum O>	METFO	2
258	4	4	7.5	tr A0A090I806 A0A090I806_METFO	Putative pantothenate synthetase OS=Methanobacterium f	METFO	2
259	4	4	8.3	tr A0A090I5J7 A0A090I5J7_METFO	Uncharacterized protein OS=Methanobacterium formicicu	METFO	2
260	4	4	7.7	tr A0A090I4Y2 A0A090I4Y2_METFO	Putative membrane protein OS=Methanobacterium formici	METFO	2
261	4	4	17.2	tr A0A090I4H1 A0A090I4H1_METFO	Putative secreted protein OS=Methanobacterium formicicu	METFO	2
262	4	4	11.7	tr A0A090I4F4 A0A090I4F4_METFO	Uncharacterized protein OS=Methanobacterium formicicu	METFO	2
263	4	4	7.5	tr A0A089ZG19 A0A089ZG19_METFO	Formate/nitrite transporter FdhC OS=Methanobacterium fo	METFO	2
264	4	4	19.6	tr A0A089Z9L4 A0A089Z9L4_METFO	Nitrogen regulatory protein P-II GlnK1 OS=Methanobacteri	METFO	2
265	3.83	3.98	11.7	tr A0A090IAE6 A0A090IAE6_METFO	Putative aminopeptidase MJ0555 OS=Methanobacterium f	METFO	3
266	3.81	4.49	21.3	tr A0A090I521 A0A090I521_METFO	4-hydroxy-tetrahydrodipicolinate reductase OS=Methanoba	METFO	5
267	3.78	3.87	9.1	tr A0A090I4G2 A0A090I4G2_METFO	Bifunctional short chain isoprenyl diphosphate synthase Ids	METFO	2
268	3.76	3.89	17.7	tr A0A090I3M8 A0A090I3M8_METFO	Imidazoleglycerol-phosphate dehydratase OS=Methanobac	METFO	2
269	3.7	3.85	24.3	tr A0A090I489 A0A090I489_METFO	GTP-binding protein Rab-like protein OS=Methanobacteriu	METFO	3
270	3.7	3.84	22.2	tr A0A090JX27 A0A090JX27_METFO	Amino acid-binding ACT domain-containing protein OS=Me	METFO	3
271	3.63	3.78	8.4	tr A0A090I8I5 A0A090I8I5_METFO	Uroporphyrinogen-III C-methyltransferase OS=Methanobac	METFO	2
272	3.54	3.62	18	tr A0A090JY14 A0A090JY14_METFO	Phenylacetic acid degradation-like protein OS=Methanobac	METFO	2
273	3.47	3.55	10.4	tr A0A089ZII9 A0A089ZII9_METFO	MotA/TolQ/ExbB proton channel family protein OS=Methan	METFO	2
274	3.37	3.52	11.7	tr A0A090I2T7 A0A090I2T7_METFO	Methyl-coenzyme M reductase subunit gamma OS=Methar	METFO	2
275	3.29	3.42	7.3	tr A0A090I3J9 A0A090I3J9_METFO	Tungsten-containing formylmethanofuran dehydrogenase 2	METFO	3
276	3.27	3.35	12.4	tr A0A090I5C4 A0A090I5C4_METFO	LemA family protein OS=Methanobacterium formicicum O>	METFO	2
277	3.21	3.35	7.6	tr A0A090JSM8 A0A090JSM8_METFO	Transcription initiation factor IIB OS=Methanobacterium fo	METFO	2
278	3.19	3.32	5.8	tr A0A090JYL6 A0A090JYL6_METFO	Peptidase C60 sortase A and B OS=Methanobacterium fo	METFO	2

Amostra 3

279	3.17	3.25	3.5 tr A0A0S4FQD8 A0A0S4FQD8_METFO	Putative ABC transporter ATP-binding protein MJ0719 OS=Methanobacterium formicicum METFO	2
280	3.16	3.27	6.8 tr A0A090JWV3 A0A090JWV3_METFO	Acetylglutamate kinase OS=Methanobacterium formicicum METFO	2
281	3.14	3.22	5.6 tr A0A090I431 A0A090I431_METFO	2-oxoglutarate synthase subunit KorA OS=Methanobacterium formicicum METFO	2
282	3.13	3.21	14 tr A0A089ZGF4 A0A089ZGF4_METFO	30S ribosomal protein S13 OS=Methanobacterium formicicum METFO	2
283	3.12	3.22	2 tr A0A090I544 A0A090I544_METFO	Putative secreted protein OS=Methanobacterium formicicum METFO	2
284	3.06	3.14	7.3 tr A0A090JW77 A0A090JW77_METFO	ATP phosphoribosyltransferase OS=Methanobacterium formicicum METFO	2
285	3.06	3.13	12.5 tr A0A090I465 A0A090I465_METFO	Spore coat polysaccharide biosynthesis protein SpsK OS=Methanobacterium formicicum METFO	2
286	3.03	3.1	5 tr A0A090JVR0 A0A090JVR0_METFO	Serine hydroxymethyltransferase OS=Methanobacterium formicicum METFO	2
287	2.96	3.07	6.7 tr A0A090I8M3 A0A090I8M3_METFO	S-adenosylmethionine synthase OS=Methanobacterium formicicum METFO	2
288	2.96	3.05	7.1 tr A0A090I2L0 A0A090I2L0_METFO	CBS domain-containing protein OS=Methanobacterium formicicum METFO	2
289	2.92	3.01	8.8 tr A0A090I7Z4 A0A090I7Z4_METFO	O-acetylserine sulfhydrylase OS=Methanobacterium formicicum METFO	2
290	2.91	2.99	3.4 tr K2QDN1 K2QDN1_METFP	DNA-directed RNA polymerase subunit B OS=Methanobacterium formicicum METFP	2
291	2.91	2.99	12.8 tr A0A089ZC90 A0A089ZC90_METFO	V-type ATP synthase subunit D OS=Methanobacterium formicicum METFO	2
292	2.87	2.96	5.8 tr A0A090JTB4 A0A090JTB4_METFO	Ribonuclease J OS=Methanobacterium formicicum OX=21 METFO	2
293	2.87	2.95	9.1 tr A0A090IAU5 A0A090IAU5_METFO	Choloylglycine hydrolase OS=Methanobacterium formicicum METFO	2
294	2.82	3	5.9 tr A0A090I929 A0A090I929_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
295	2.81	6.09	9.7 tr A0A090I2C6 A0A090I2C6_METFO	Methyl-coenzyme M reductase component A2 AtwA1 OS=Methanobacterium formicicum METFO	4
296	2.75	2.87	13.7 tr A0A0S4FN48 A0A0S4FN48_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
297	2.74	3	6 tr A0A090J TZ4 A0A090J TZ4_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
298	2.7	2.78	7.6 tr A0A0S4FLM0 A0A0S4FLM0_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
299	2.65	2.72	4.9 tr K2RR54 K2RR54_METFP	Glucosamine-1-phosphate N-acetyltransferase OS=Methanobacterium formicicum METFP	2
300	2.54	2.59	5.2 tr A0A0S4FLN1 A0A0S4FLN1_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
301	2.53	2.81	7.1 tr A0A089ZBE1 A0A089ZBE1_METFO	UPF0288 protein BRM9_0509 OS=Methanobacterium formicicum METFO	3
302	2.52	2.56	5.8 tr A0A0S4FPN3 A0A0S4FPN3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
303	2.51	2.56	6.4 tr K2REI5 K2REI5_METFP	Coenzyme F420 hydrogenase subunit gamma OS=Methanobacterium formicicum METFP	1
304	2.49	2.54	4.3 tr A0A090JYP3 A0A090JYP3_METFO	Exosome subunit OS=Methanobacterium formicicum OX=2 METFO	1
305	2.43	2.47	17.2 tr A0A090I4H6 A0A090I4H6_METFO	50S ribosomal protein L15 OS=Methanobacterium formicicum METFO	2
306	2.39	2.42	8.2 tr A0A090I567 A0A090I567_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
307	2.35	2.38	3.4 tr A0A090JXZ1 A0A090JXZ1_METFO	Delta-aminolevulinic acid dehydratase OS=Methanobacterium formicicum METFO	1
308	2.32	2.46	8.5 tr A0A090I443 A0A090I443_METFO	Superoxide dismutase OS=Methanobacterium formicicum METFO	2
309	2.26	2.29	4.4 tr A0A089ZH87 A0A089ZH87_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
310	2.25	2.36	0.8 tr A0A090JUS9 A0A090JUS9_METFO	Putative secreted protein OS=Methanobacterium formicicum METFO	2
311	2.25	2.28	3.4 tr A0A0S4FM80 A0A0S4FM80_METFO	2,3-bisphosphoglycerate-independent phosphoglycerate m METFO	1

Amostra 3

312	2.23	2.25	2.3 tr A0A090I5F2 A0A090I5F2_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
313	2.22	2.25	3.7 tr A0A090IA48 A0A090IA48_METFO	Nitrite reductase (NAD(P)H) OS=Methanobacterium formicicum METFO	1
314	2.17	2.19	6.8 tr A0A090I3I4 A0A090I3I4_METFO	Putative secreted protein OS=Methanobacterium formicicum METFO	1
315	2.15	2.3	8.4 tr A0A090I7K3 A0A090I7K3_METFO	Phosphate import ATP-binding protein PstB OS=Methanobacterium formicicum METFO	2
316	2.14	2.16	2.3 tr A0A090JV74 A0A090JV74_METFO	Homoserine dehydrogenase OS=Methanobacterium formicicum METFO	1
317	2.13	2.15	3.8 tr A0A090JWL7 A0A090JWL7_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
318	2.13	2.15	5.4 tr A0A090I385 A0A090I385_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
319	2.11	2.12	3.3 tr A0A090JY2 A0A090JY2_METFO	Branched-chain-amino-acid aminotransferase OS=Methanobacterium formicicum METFO	1
320	2.1	2.22	27.5 tr K2RRN0 K2RRN0_METFP	Uncharacterized protein OS=Methanobacterium formicicum METFP	2
321	2.1	2.11	6.8 tr A0A090I8N8 A0A090I8N8_METFO	Putative thymidylate synthase OS=Methanobacterium formicicum METFO	1
322	2.08	2.1	4.4 tr A0A090I6E5 A0A090I6E5_METFO	Putative membrane protein OS=Methanobacterium formicicum METFO	1
323	2.07	2.1	5.4 tr A0A090JTX4 A0A090JTX4_METFO	dCTP deaminase, dUMP-forming OS=Methanobacterium formicicum METFO	1
324	2.07	2.09	5.7 tr A0A090JSW7 A0A090JSW7_METFO	CBS domain-containing membrane protein OS=Methanobacterium formicicum METFO	1
325	2.07	2.08	2.2 tr A0A090I8U4 A0A090I8U4_METFO	Acetolactate synthase OS=Methanobacterium formicicum METFO	1
326	2.06	2.12	3.6 tr A0A090I7X7 A0A090I7X7_METFO	Glutamine-scyllo-inositol transaminase OS=Methanobacterium formicicum METFO	1
327	2.06	2.07	4.2 tr K2QDZ9 K2QDZ9_METFP	RNA-processing protein OS=Methanobacterium formicicum METFP	1
328	2.06	2.07	7.1 tr A0A089ZVX2 A0A089ZVX2_METFO	Putative membrane protein OS=Methanobacterium formicicum METFO	1
329	2.05	2.06	3.4 tr A0A090I4Y9 A0A090I4Y9_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
330	2.05	2.06	15 tr A0A089ZVK3 A0A089ZVK3_METFO	CBS domain-containing protein OS=Methanobacterium formicicum METFO	1
331	2.04	2.05	1.9 tr A0A089ZBN0 A0A089ZBN0_METFO	PIN domain-containing protein OS=Methanobacterium formicicum METFO	1
332	2.04	2.05	15 tr A0A090IAI0 A0A090IAI0_METFO	Putative secreted protein OS=Methanobacterium formicicum METFO	1
333	2.04	2.04	7.6 tr A0A089ZV26 A0A089ZV26_METFO	Inositol-3-phosphate synthase OS=Methanobacterium formicicum METFO	2
334	2.04	2.04	4.6 tr K2R423 K2R423_METFP	50S ribosomal protein L2 OS=Methanobacterium formicicum METFP	1
335	2.03	2.05	4.5 tr A0A090JUW9 A0A090JUW9_METFO	2-phosphosulfolactate phosphatase OS=Methanobacterium formicicum METFO	1
336	2.03	2.04	2.2 tr A0A0S4FMB9 A0A0S4FMB9_METFO	UDP-N-acetylmuramoyl-L-alanine-D-glutamate ligase OS=Methanobacterium formicicum METFO	1
337	2.03	2.04	0.9 tr A0A090I571 A0A090I571_METFO	Carbamoyl-phosphate synthase large chain OS=Methanobacterium formicicum METFO	1
338	2.03	2.04	3.9 tr A0A090I4P4 A0A090I4P4_METFO	Endonuclease NucS OS=Methanobacterium formicicum METFO	1
339	2.03	2.04	8.8 tr A0A089ZED6 A0A089ZED6_METFO	50S ribosomal protein L19e OS=Methanobacterium formicicum METFO	1
340	2.03	2.04	3.3 tr A0A0S4FLL3 A0A0S4FLL3_METFO	Exodeoxyribonuclease III OS=Methanobacterium formicicum METFO	1
341	2.03	2.03	7.4 tr A0A090I8C8 A0A090I8C8_METFO	Flavodoxin/nitric oxide synthase OS=Methanobacterium formicicum METFO	1
342	2.03	2.03	4.2 tr A0A090I3L5 A0A090I3L5_METFO	UPF0285 protein DSM1535_1340 OS=Methanobacterium formicicum METFO	1
343	2.02	2.03	2.6 tr K2RUG1 K2RUG1_METFP	UDP-glucose 4-epimerase OS=Methanobacterium formicicum METFP	1
344	2.02	2.03	3 tr A0A090I574 A0A090I574_METFO	Glutamine-fructose-6-phosphate transaminase OS=Methanobacterium formicicum METFO	1

Amostra 3

345	2.02	2.02	1.5 tr A0A089Z9Y9 A0A089Z9Y9_METFO	Type II secretion system protein E GspE OS=Methanobact	METFO	1
346	2.02	2.02	5.4 tr A0A090I368 A0A090I368_METFO	Formylmethanofuran dehydrogenase subunit E OS=Metha	METFO	1
347	2.01	2.02	14.7 tr K2R2P0 K2R2P0_METFP	Transcription factor CBF/NF-Y/histone domain-containing p	METFP	1
348	2.01	2.02	2.6 tr A0A089ZA17 A0A089ZA17_METFO	Peptidase U32 family OS=Methanobacterium formicicum C	METFO	1
349	2.01	2.01	6.9 tr A0A090I5D6 A0A090I5D6_METFO	Uncharacterized protein OS=Methanobacterium formicicu	METFO	1
350	2.01	2.01	5 tr A0A090I503 A0A090I503_METFO	Malate dehydrogenase OS=Methanobacterium formicicum	METFO	1
351	2.01	2.01	2.2 tr K2RWA6 K2RWA6_METFP	Adenylosuccinate lyase OS=Methanobacterium formicicum	METFP	1
352	2.01	2.01	1.3 tr K2R8Z5 K2R8Z5_METFP	WD40-like repeat protein OS=Methanobacterium formicicu	METFP	1
353	2.01	2.01	9.3 tr K2QYV5 K2QYV5_METFP	Nucleoside diphosphate kinase OS=Methanobacterium fori	METFP	1
354	2.01	2.01	8.2 tr A0A090JSW3 A0A090JSW3_METFO	Uncharacterized protein OS=Methanobacterium formicicu	METFO	1
355	2.01	2.01	2.5 tr A0A090I7C8 A0A090I7C8_METFO	Uncharacterized protein OS=Methanobacterium formicicu	METFO	1
356	2.01	2.01	11.8 tr A0A089ZUR3 A0A089ZUR3_METFO	Uncharacterized protein OS=Methanobacterium formicicu	METFO	1
357	2.01	2.01	11 tr A0A089ZER4 A0A089ZER4_METFO	ACT domain-containing protein OS=Methanobacterium fori	METFO	1
358	2.01	2.01	3.9 tr A0A089Z928 A0A089Z928_METFO	Nitrogenase cofactor biosynthesis protein NifB OS=Methan	METFO	1
359	2	2.82	11.1 tr A0A090I9F1 A0A090I9F1_METFO	Tetrahydromethanopterin S-methyltransferase subunit A O	METFO	2
360	2	2.23	0.8 tr A0A089ZGE0 A0A089ZGE0_METFO	Adhesin-like protein with PMBR domains OS=Methanobact	METFO	2
361	2	2.1	2 tr A0A0S4FN62 A0A0S4FN62_METFO	UDP-N-acetylglucosamine 2-epimerase OS=Methanobacte	METFO	1
362	2	2.01	3 tr A0A090I9R3 A0A090I9R3_METFO	Arginine biosynthesis bifunctional protein ArgJ OS=Methan	METFO	1
363	2	2.01	3.8 tr A0A090I4Z6 A0A090I4Z6_METFO	Aminotransferase OS=Methanobacterium formicicum OX=:	METFO	1
364	2	2.01	4.7 tr A0A0S4FP84 A0A0S4FP84_METFO	Uncharacterized protein OS=Methanobacterium formicicu	METFO	1
365	2	2	8.5 tr K2RTG9 K2RTG9_METFP	Archaeoflavoprotein AfpA OS=Methanobacterium formicicu	METFP	1
366	2	2	1.6 tr K2RRP5 K2RRP5_METFP	Oligosaccharyl transferase STT3 subunit OS=Methanobaci	METFP	1
367	2	2	1.3 tr K2RPE1 K2RPE1_METFP	DNA-binding protein MutS2 OS=Methanobacterium formici	METFP	1
368	2	2	13.6 tr A0A090IB32 A0A090IB32_METFO	Pyridoxamine 5'-phosphate oxidase family protein OS=Met	METFO	1
369	2	2	4.7 tr A0A090IA01 A0A090IA01_METFO	Beta-lactamase domain protein OS=Methanobacterium fori	METFO	1
370	2	2	3.8 tr A0A090I666 A0A090I666_METFO	Nitrogenase iron protein 2 OS=Methanobacterium formicicu	METFO	1
371	2	2	3 tr A0A090I4S4 A0A090I4S4_METFO	Family 2 glycosyl transferase OS=Methanobacterium formi	METFO	1
372	2	2	7.9 tr A0A090I3X8 A0A090I3X8_METFO	Formylmethanofuran dehydrogenase, subunit E region OS:	METFO	1
373	2	2	4 tr A0A090I342 A0A090I342_METFO	N5-carboxyaminoimidazole ribonucleotide mutase OS=Met	METFO	1
374	2	2	5.1 tr A0A089ZH31 A0A089ZH31_METFO	Cobalamin biosynthesis protein CbiM3 OS=Methanobacter	METFO	1
375	2	2	8.2 tr A0A089Z7Q8 A0A089Z7Q8_METFO	TetR family transcriptional regulator OS=Methanobacteriu	METFO	1
376	2	2	8 tr K2REV5 K2REV5_METFP	Uncharacterized protein OS=Methanobacterium formicicu	METFP	1
377	2	2	6.9 tr K2RE49 K2RE49_METFP	Uncharacterized protein OS=Methanobacterium formicicu	METFP	1

Amostra 3

378	2	2	10.6	tr K2RB04 K2RB04_METFP	Phosphoribosyl-AMP cyclohydrolase OS=Methanobacterium formicicum METFP	1
379	2	2	10.4	tr K2R8M5 K2R8M5_METFP	Roadblock/LC7 family protein OS=Methanobacterium formicicum METFP	3
380	2	2	3.8	tr K2R118 K2R118_METFP	H4MPT-linked C1 transfer pathway protein OS=Methanobacterium formicicum METFP	1
381	2	2	8	tr A0A0S4FP85 A0A0S4FP85_METFO	Putative secreted protein OS=Methanobacterium formicicum METFO	1
382	2	2	4.3	tr A0A0S4FNA9 A0A0S4FNA9_METFO	Deoxyribose-phosphate aldolase OS=Methanobacterium formicicum METFO	1
383	2	2	3.3	tr A0A090JUV1 A0A090JUV1_METFO	Tetrahydromethanopterin S-methyltransferase subunit D OS=Methanobacterium formicicum METFO	1
384	2	2	5	tr A0A090JSL9 A0A090JSL9_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
385	2	2	3.1	tr A0A090IAI9 A0A090IAI9_METFO	Cobalt-precorrin-5B C(1)-methyltransferase OS=Methanobacterium formicicum METFO	1
386	2	2	3.8	tr A0A090I8F0 A0A090I8F0_METFO	Putative membrane protein OS=Methanobacterium formicicum METFO	1
387	2	2	2.9	tr A0A090I871 A0A090I871_METFO	Signal peptide peptidase SppA, 36K type OS=Methanobacterium formicicum METFO	1
388	2	2	2.6	tr A0A090I669 A0A090I669_METFO	Putative NADH oxidase OS=Methanobacterium formicicum METFO	1
389	2	2	4.3	tr A0A090I4Q2 A0A090I4Q2_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
390	2	2	15	tr A0A090I4N4 A0A090I4N4_METFO	Putative membrane protein OS=Methanobacterium formicicum METFO	1
391	2	2	1.3	tr A0A090I4B6 A0A090I4B6_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
392	2	2	8.8	tr A0A089ZJ52 A0A089ZJ52_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
393	2	2	7.4	tr A0A089ZBW3 A0A089ZBW3_METFO	Glutamate synthase beta subunit GltB1 OS=Methanobacterium formicicum METFO	1
394	2	2	4.3	tr A0A089ZAI2 A0A089ZAI2_METFO	Molybdate transport system regulatory protein ModE OS=Methanobacterium formicicum METFO	1
395	1.96	2	3.3	tr A0A090I6Y3 A0A090I6Y3_METFO	S-adenosyl-L-methionine-dependent tRNA 4-demethylase OS=Methanobacterium formicicum METFO	1
396	1.92	2	9.1	tr A0A090I4I3 A0A090I4I3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
397	1.8	2.09	4.3	tr A0A090I6D0 A0A090I6D0_METFO	Tryptophan synthase beta chain OS=Methanobacterium formicicum METFO	2
398	1.72	1.86	5.7	tr K2R1L9 K2R1L9_METFP	Aspartate carbamoyltransferase regulatory chain OS=Methanobacterium formicicum METFP	1
399	1.61	1.8	14.2	tr K2R2B6 K2R2B6_METFP	NADH ubiquinone oxidoreductase 20 kDa subunit OS=Methanobacterium formicicum METFP	2
400	1.61	1.77	7.1	tr A0A090I4U7 A0A090I4U7_METFO	Indolepyruvate ferredoxin oxidoreductase beta subunit OS=Methanobacterium formicicum METFO	1
401	1.59	1.7	9.6	tr K2RW50 K2RW50_METFP	DNA/RNA-binding protein Alba OS=Methanobacterium formicicum METFP	2
402	1.55	1.68	3.7	tr A0A0S4FPL3 A0A0S4FPL3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
403	1.51	1.62	3.1	tr A0A090I3K4 A0A090I3K4_METFO	Diaminopimelate epimerase OS=Methanobacterium formicicum METFO	1
404	1.51	1.62	2.6	tr A0A090I915 A0A090I915_METFO	5'-deoxyadenosine deaminase OS=Methanobacterium formicicum METFO	1
405	1.51	1.62	1.8	tr A0A090I8E3 A0A090I8E3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
406	1.47	1.68	10	tr A0A0S4FPQ0 A0A0S4FPQ0_METFO	Family 2 glycosyl transferase OS=Methanobacterium formicicum METFO	2
407	1.45	29.99	40.4	tr K2QYM4 K2QYM4_METFP	Methyl-coenzyme M reductase subunit alpha OS=Methanobacterium formicicum METFP	45
408	1.44	1.57	3.4	tr A0A090IAE3 A0A090IAE3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
409	1.43	1.6	6	tr A0A090I609 A0A090I609_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
410	1.43	1.55	5.6	tr A0A090I1G0 A0A090I1G0_METFO	DNA-directed RNA polymerase subunit D OS=Methanobacterium formicicum METFO	1

Amostra 3

411	1.41	1.52	2.1 tr A0A090I744 A0A090I744_METFO	3-phosphoshikimate 1-carboxyvinyltransferase OS=Methar METFO	1
412	1.4	1.51	4.6 tr K2R2N5 K2R2N5_METFP	Uncharacterized protein OS=Methanobacterium formicicun METFP	1
413	1.38	1.65	2.2 tr A0A090I657 A0A090I657_METFO	3-isopropylmalate dehydratase large subunit OS=Methanol METFO	1
414	1.37	1.55	4.7 tr A0A090I751 A0A090I751_METFO	tRNA intron endonuclease EndA OS=Methanobacterium fo METFO	1
415	1.34	1.53	2 tr A0A090I298 A0A090I298_METFO	Archaeal glutamate synthase [NADPH] OS=Methanobacteri NADPH	1

Amostra 3



ID statistics table

Unused (Conf) Cutoff	Proteins Detected	Proteins Before Grouping	Distinct Peptides	Spectra Identified	% Total Spectra
>2.0 (99)	358	747	5040	19078	14.8
>1.3 (95)	415	911	5153	19319	15
>0.47 (66)	466	1026	5278	19537	15.2
Cutoff Applied: >0.05 (10%)	591	1336	5523	19940	15.5

Amostra 4

1) Z:\Projects\UniMS2019_95 MALves\Data\CS4_9uL.wiff

Sample Type: Identification
Cys. Alkylation: Iodoacetamide
Digestion: Trypsin
Instrument: TripleTOF 6600
Special Factors: Gel-based ID
Species:
ID Focus: Biological modifications
 Amino acid substitutions
Database: 20190624_uniprot_methanobacterium+formicicum_6903entries.fasta
Search Effort: Thorough
FDR Analysis: Yes
User Modified Parameter Files: Yes



Proteins detected table

N	Unused	Total	% Cov (95	Accession #	Name	Species	Peptides(95%)
1	75.91	75.91	58.3	tr A0A090I8L6 A0A090I8L6_METFO	Replication factor-A domain-containing protein OS=Methan	METFO	52
2	66.4	66.4	78	tr A0A090IAH6 A0A090IAH6_METFO	Thermosome subunit OS=Methanobacterium formicicum C	METFO	193
3	65.3	65.36	64	tr A0A090I2M3 A0A090I2M3_METFO	V-type ATP synthase alpha chain OS=Methanobacterium f	METFO	58
4	61.3	61.3	55.3	tr A0A090I3A9 A0A090I3A9_METFO	Chaperone protein DnaK OS=Methanobacterium formicicu	METFO	46
5	59.7	59.7	77.9	tr A0A090I2T3 A0A090I2T3_METFO	Methyl-coenzyme M reductase subunit beta OS=Methanob	METFO	422
6	58.48	58.96	78.2	tr A0A090I2R9 A0A090I2R9_METFO	F420-non-reducing hydrogenase subunit A OS=Methanob	METFO	52
7	54.88	54.88	56.7	tr A0A090I3G7 A0A090I3G7_METFO	CoB--CoM heterodisulfide reductase subunit A HdrA2 OS=	METFO	56
8	54.15	54.15	74.5	tr A0A090I7W3 A0A090I7W3_METFO	Methyl-coenzyme M reductase subunit beta OS=Methanob	METFO	120
9	52.68	52.68	91	tr A0A090I573 A0A090I573_METFO	5,10-methylenetetrahydromethanopterin reductase OS=Me	METFO	182
10	48.04	48.04	55.1	tr A0A090I2G6 A0A090I2G6_METFO	Methyl-coenzyme M reductase subunit alpha OS=Methano	METFO	97
11	46.17	46.17	38.4	tr A0A090I7T4 A0A090I7T4_METFO	Phosphoenolpyruvate synthase OS=Methanobacterium for	METFO	33
12	42.76	42.76	14.4	tr A0A090I3J2 A0A090I3J2_METFO	Uncharacterized protein OS=Methanobacterium formicicu	METFO	32
13	42.12	42.13	31.1	tr A0A090I5F3 A0A090I5F3_METFO	Putative secreted protein OS=Methanobacterium formicicu	METFO	31
14	36.71	36.71	50	tr A0A090JVC3 A0A090JVC3_METFO	Methyl-coenzyme M reductase subunit alpha OS=Methano	METFO	60

Amostra 4

15	35.7	37.76	49.8 tr A0A090I4W3 A0A090I4W3_METFO	F420-non-reducing hydrogenase vhc subunit A OS=Methanobacterium formicicum METFO	27
16	34.65	34.66	52.5 tr A0A090I8W8 A0A090I8W8_METFO	Bifunctional enzyme Fae/Hps OS=Methanobacterium formicicum METFO	37
17	33.48	45.57	61.5 tr A0A090IA40 A0A090IA40_METFO	Thermosome subunit OS=Methanobacterium formicicum CMETFO	105
18	33.18	33.22	30 tr A0A090I3T1 A0A090I3T1_METFO	Elongation factor 2 OS=Methanobacterium formicicum OX= METFO	24
19	32.95	33.06	41.4 tr A0A089ZDH4 A0A089ZDH4_METFO	Elongation factor 1-alpha OS=Methanobacterium formicicum METFO	25
20	32.35	32.37	50.5 tr A0A090I7U6 A0A090I7U6_METFO	GDP-mannose 4,6-dehydratase OS=Methanobacterium formicicum METFO	29
21	31.93	32	48.5 tr A0A090I9A6 A0A090I9A6_METFO	Hydroxylamine reductase OS=Methanobacterium formicicum METFO	21
22	31.77	31.82	57.9 tr A0A0S4FR78 A0A0S4FR78_METFO	V-type ATP synthase beta chain OS=Methanobacterium formicicum METFO	52
23	27.52	27.52	68.4 tr A0A090I5H3 A0A090I5H3_METFO	Methenyltetrahydromethanopterin cyclohydrolase OS=Methanobacterium formicicum METFO	32
24	26.07	26.07	43.7 tr A0A090I210 A0A090I210_METFO	Putative aminotransferase MJ0959 OS=Methanobacterium formicicum METFO	27
25	24.91	24.92	50.4 tr A0A090I5T3 A0A090I5T3_METFO	Methyl-coenzyme M reductase subunit gamma OS=Methanobacterium formicicum METFO	16
26	24.48	24.49	29.1 tr A0A090I2L6 A0A090I2L6_METFO	D-3-phosphoglycerate dehydrogenase OS=Methanobacterium formicicum METFO	19
27	22.9	22.9	45.3 tr A0A090I281 A0A090I281_METFO	Pyruvate synthase subunit PorA OS=Methanobacterium formicicum METFO	18
28	22.61	22.61	48 tr A0A090I6Q2 A0A090I6Q2_METFO	Formylmethanofuran dehydrogenase subunit C FwdC OS=Methanobacterium formicicum METFO	17
29	22.55	22.6	54.8 tr A0A090I842 A0A090I842_METFO	CBS domain-containing membrane protein OS=Methanobacterium formicicum METFO	18
30	21.91	21.97	33.6 tr A0A090I6W9 A0A090I6W9_METFO	Cell shape determining protein MreB/Mrl OS=Methanobacterium formicicum METFO	14
31	21.54	21.62	28.3 tr A0A089ZAI4 A0A089ZAI4_METFO	Formylmethanofuran dehydrogenase subunit A FwdA OS=Methanobacterium formicicum METFO	12
32	21.43	21.62	38.8 tr A0A089ZIP7 A0A089ZIP7_METFO	DNA primase DnaG OS=Methanobacterium formicicum OX= METFO	12
33	20.52	20.54	50 tr A0A089ZAX5 A0A089ZAX5_METFO	30S ribosomal protein S2 OS=Methanobacterium formicicum METFO	15
34	20.36	20.41	51.7 tr A0A090I613 A0A090I613_METFO	Coenzyme F420 hydrogenase subunit beta OS=Methanobacterium formicicum METFO	20
35	20.17	20.18	17.1 tr A0A090I3V1 A0A090I3V1_METFO	Formate dehydrogenase alpha subunit FdhA OS=Methanobacterium formicicum METFO	13
36	19.92	19.94	48.9 tr A0A089ZEV2 A0A089ZEV2_METFO	CBS domain-containing protein OS=Methanobacterium formicicum METFO	17
37	19.72	19.75	53.9 tr A0A090I5H7 A0A090I5H7_METFO	Tetrahydromethanopterin S-methyltransferase subunit H OX= METFO	23
38	18.68	20.28	39.8 tr A0A090I305 A0A090I305_METFO	Coenzyme F420 hydrogenase alpha subunit FrhA OS=Methanobacterium formicicum METFO	19
39	18.49	18.53	54.2 tr A0A090IB20 A0A090IB20_METFO	Proteasome subunit alpha OS=Methanobacterium formicicum METFO	11
40	18.25	18.27	36.7 tr A0A089ZBS9 A0A089ZBS9_METFO	Acetyl-CoA acetyltransferase OS=Methanobacterium formicicum METFO	16
41	18.08	18.09	39.8 tr A0A089ZVL0 A0A089ZVL0_METFO	Cell division protein FtsZ OS=Methanobacterium formicicum METFO	13
42	17.86	17.96	32.1 tr A0A090I781 A0A090I781_METFO	Fructose-1,6-bisphosphate aldolase/phosphatase OS=Methanobacterium formicicum METFO	11
43	17.51	17.58	43.4 tr A0A089ZG02 A0A089ZG02_METFO	DNA repair and recombination protein RadA OS=Methanobacterium formicicum METFO	11
44	17.45	17.53	40.1 tr A0A090I1I9 A0A090I1I9_METFO	CoB-CoM heterodisulfide reductase iron-sulfur subunit C OX= METFO	15
45	17.16	17.2	28.5 tr A0A090I7L2 A0A090I7L2_METFO	Acetyl-CoA decarbonylase/synthase complex subunit gamr OS=Methanobacterium formicicum METFO	10
46	17.12	17.25	24.2 tr A0A089ZUL5 A0A089ZUL5_METFO	Tryptophan synthase beta chain OS=Methanobacterium formicicum METFO	8
47	17.06	17.14	22.3 tr A0A089ZGQ5 A0A089ZGQ5_METFO	Peptidase U62 family OS=Methanobacterium formicicum CMETFO	11

Amostra 4

48	16.88	16.96	32 tr A0A090I3I6 A0A090I3I6_METFO	Putative lipoprotein MJ0085 OS=Methanobacterium formici METFO	9
49	16.74	16.76	24.9 tr A0A090I2P0 A0A090I2P0_METFO	CBS domain-containing protein OS=Methanobacterium fori METFO	10
50	16.66	16.73	28.8 tr A0A090I6I2 A0A090I6I2_METFO	Adenylosuccinate synthetase OS=Methanobacterium formi METFO	8
51	16.63	16.73	30 tr A0A090I360 A0A090I360_METFO	F420H2 oxidase FprA OS=Methanobacterium formicicum (METFO	9
52	16.32	16.43	26.5 tr A0A090JTT4 A0A090JTT4_METFO	Methanogenesis marker protein 15 OS=Methanobacterium METFO	8
53	16.05	16.09	15.1 tr A0A090I0Y6 A0A090I0Y6_METFO	Phosphoserine phosphatase SerB OS=Methanobacterium METFO	8
54	16.02	16.02	25.7 tr A0A090JXJ6 A0A090JXJ6_METFO	3-dehydroquinate synthase OS=Methanobacterium formici METFO	8
55	16	16	48 tr A0A090JTE0 A0A090JTE0_METFO	50S ribosomal protein L6 OS=Methanobacterium formicicu METFO	11
56	15.91	16.03	23.6 tr A0A090I3J1 A0A090I3J1_METFO	Formate dehydrogenase beta subunit FdhB OS=Methanob METFO	9
57	15.66	15.73	17.4 tr A0A090I2I6 A0A090I2I6_METFO	Archaeal glutamate synthase [NADPH] OS=Methanobacteri NADPH	8
58	15.59	15.6	67.4 tr A0A090I170 A0A090I170_METFO	TATA-box-binding protein OS=Methanobacterium formicicu METFO	9
59	15.2	15.26	38.1 tr A0A090I345 A0A090I345_METFO	3-isopropylmalate dehydrogenase OS=Methanobacterium i METFO	10
60	15.08	15.16	28.6 tr A0A089ZI64 A0A089ZI64_METFO	ATP phosphoribosyltransferase OS=Methanobacterium for METFO	7
61	14.88	14.91	20.3 tr A0A090I3H2 A0A090I3H2_METFO	Phosphoribosylformylglycinamide synthase subunit PurL METFO	12
62	14.64	14.82	27 tr A0A089ZFS2 A0A089ZFS2_METFO	Argininosuccinate synthase OS=Methanobacterium formici METFO	9
63	14.58	14.64	40.6 tr A0A090I4Y4 A0A090I4Y4_METFO	Circadian clock protein KaiC OS=Methanobacterium formic METFO	12
64	14.41	14.54	22.3 tr A0A090I3H9 A0A090I3H9_METFO	5-formaminoimidazole-4-carboxamide-1-(beta)-D-ribofuran METFO	8
65	14.05	14.11	45.2 tr A0A090I2W9 A0A090I2W9_METFO	Proteasome subunit beta OS=Methanobacterium formicicu METFO	13
66	14.05	14.06	47.1 tr A0A090I8V8 A0A090I8V8_METFO	F420-dependent methylenetetrahydromethanopterin dehyd METFO	17
67	13.92	13.92	40.9 tr A0A089ZGF9 A0A089ZGF9_METFO	30S ribosomal protein S5 OS=Methanobacterium formicicu METFO	10
68	13.79	13.85	23.1 tr A0A090I938 A0A090I938_METFO	Phosphomethylpyrimidine synthase OS=Methanobacteriun METFO	9
69	13.77	13.79	61.7 tr A0A089ZUS9 A0A089ZUS9_METFO	50S ribosomal protein L18 OS=Methanobacterium formicic METFO	7
70	13.75	13.88	25.6 tr A0A089ZCR8 A0A089ZCR8_METFO	Proteasome-activating nucleotidase OS=Methanobacteriun METFO	8
71	13.73	13.96	22.7 tr A0A090I2C6 A0A090I2C6_METFO	Methyl-coenzyme M reductase component A2 AtwA1 OS=M METFO	9
72	13.39	13.43	66.7 tr A0A089ZCU1 A0A089ZCU1_METFO	Transcription elongation factor Spt5 OS=Methanobacteriun METFO	7
73	13.35	13.4	33.6 tr A0A089Z979 A0A089Z979_METFO	Site-determining protein OS=Methanobacterium formicicun METFO	7
74	13.28	13.35	35.3 tr A0A090I166 A0A090I166_METFO	Enolase OS=Methanobacterium formicicum OX=2162 GN= METFO	12
75	13.14	13.17	41.2 tr A0A090JW64 A0A090JW64_METFO	LemA family protein OS=Methanobacterium formicicum O METFO	9
76	12.86	12.89	35.7 tr A0A090I0N7 A0A090I0N7_METFO	PyrE-like protein OS=Methanobacterium formicicum OX=2 METFO	7
77	12.81	12.91	33.3 tr A0A090JUK8 A0A090JUK8_METFO	V-type proton ATPase subunit E OS=Methanobacterium fo METFO	7
78	12.74	12.88	18.3 tr A0A089ZV33 A0A089ZV33_METFO	FeS assembly protein SufBD OS=Methanobacterium formi METFO	8
79	12.57	12.6	27.5 tr A0A090I0T1 A0A090I0T1_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	11
80	12.52	12.61	46 tr A0A090I2I9 A0A090I2I9_METFO	Translation initiation factor 6 OS=Methanobacterium formic METFO	10

Amostra 4

81	12.16	12.35	20.9	tr A0A090I4G3 A0A090I4G3_METFO	LL-diaminopimelate aminotransferase OS=Methanobacteri METFO	8
82	11.99	12.1	8.7	tr A0A090I151 A0A090I151_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO	7
83	11.82	11.95	25.3	tr A0A090I1P7 A0A090I1P7_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO	6
84	11.82	11.88	16.1	tr A0A090JTE7 A0A090JTE7_METFO	30S ribosomal protein S3 OS=Methanobacterium formicicu METFO	9
85	11.77	11.8	24.6	tr A0A0S4FRT9 A0A0S4FRT9_METFO	Formylmethanofuran--tetrahydromethanopterin formyltrans METFO	22
86	11.72	11.77	39.9	tr A0A090I180 A0A090I180_METFO	50S ribosomal protein L5 OS=Methanobacterium formicicu METFO	6
87	11.3	11.33	31.7	tr A0A090I5G8 A0A090I5G8_METFO	F420-non-reducing hydrogenase subunit G OS=Methanob METFO	9
88	11.21	11.24	17.9	tr A0A090I9D3 A0A090I9D3_METFO	Succinate--CoA ligase [ADP-forming] subunit beta OS=MetADP-formin	6
89	11.16	11.27	38.2	tr A0A090I1H9 A0A090I1H9_METFO	30S ribosomal protein S4e OS=Methanobacterium formicic METFO	8
90	11.16	11.2	27.2	tr A0A090I7T8 A0A090I7T8_METFO	Peptidyl-prolyl cis-trans isomerase OS=Methanobacterium METFO	6
91	11.08	11.28	17.6	tr A0A090I3Y0 A0A090I3Y0_METFO	Phenylalanine--tRNA ligase beta subunit OS=Methanobact METFO	8
92	11.05	11.09	31.3	tr A0A090I4G9 A0A090I4G9_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO	7
93	10.91	11.03	29.5	tr A0A090I494 A0A090I494_METFO	Short-chain dehydrogenase family protein OS=Methanoba METFO	6
94	10.82	10.95	20.1	tr A0A090I6T0 A0A090I6T0_METFO	Glutamine synthetase OS=Methanobacterium formicicum (METFO	8
95	10.2	10.28	21.7	tr A0A090JV64 A0A090JV64_METFO	CBS domain-containing membrane protein OS=Methanoba METFO	8
96	10.11	10.11	34.1	tr A0A089ZGG4 A0A089ZGG4_METFO	50S ribosomal protein L14 OS=Methanobacterium formicic METFO	5
97	10.01	10.01	12.6	tr A0A090JXN7 A0A090JXN7_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO	5
98	9.94	12.46	16.8	tr A0A0S4FLI0 A0A0S4FLI0_METFO	Putative ABC transporter ATP-binding protein MJ1242 OS= METFO	8
99	9.91	9.98	22.2	tr A0A090I6V8 A0A090I6V8_METFO	CoB-CoM heterodisulfide reductase subunit B OS=Methan METFO	7
100	9.88	9.97	25	tr A0A089ZUT3 A0A089ZUT3_METFO	50S ribosomal protein L3 OS=Methanobacterium formicicu METFO	5
101	9.78	9.83	23.1	tr A0A090I471 A0A090I471_METFO	GDP-mannose 4,6-dehydratase OS=Methanobacterium fo METFO	7
102	9.74	9.81	28.9	tr A0A090I2T7 A0A090I2T7_METFO	Methyl-coenzyme M reductase subunit gamma OS=Methar METFO	5
103	9.56	9.68	13.6	tr A0A090I2F4 A0A090I2F4_METFO	Polyferredoxin protein MvhB OS=Methanobacterium formic METFO	5
104	9.52	9.67	18	tr A0A090I8M3 A0A090I8M3_METFO	S-adenosylmethionine synthase OS=Methanobacterium fo METFO	6
105	9.39	9.43	17.4	tr A0A090I796 A0A090I796_METFO	Pyridoxal 5'-phosphate synthase subunit PdxS OS=Methan METFO	5
106	9.37	9.41	19.5	tr A0A089ZAG5 A0A089ZAG5_METFO	Transcriptional regulator with CBS domains OS=Methanob. METFO	5
107	9.29	9.33	25.8	tr A0A089ZER7 A0A089ZER7_METFO	Exosome complex component Rrp4 OS=Methanobacteriun METFO	5
108	9.07	9.11	13.7	tr A0A090I7B6 A0A090I7B6_METFO	Inosine-5'-monophosphate dehydrogenase OS=Methanoba METFO	5
109	9.04	9.11	20.9	tr A0A090JVT4 A0A090JVT4_METFO	Putative ABC transporter ATP-binding protein MJ0089 OS= METFO	5
110	8.89	8.94	36.8	tr A0A090I2G3 A0A090I2G3_METFO	Tetrahydromethanopterin S-methyltransferase subunit A O. METFO	7
111	8.75	8.86	15.8	tr A0A090I518 A0A090I518_METFO	Digeranylglycerolglycerophospholipid reductase OS=Metha METFO	5
112	8.69	8.86	4.3	tr A0A090I571 A0A090I571_METFO	Carbamoyl-phosphate synthase large chain OS=Methanob METFO	5
113	8.65	8.82	23.4	tr A0A089ZJ55 A0A089ZJ55_METFO	DNA polymerase sliding clamp OS=Methanobacterium forr METFO	6

Amostra 4

114	8.58	8.71	29.1	tr A0A090I5W3 A0A090I5W3_METFO	30S ribosomal protein S3Ae OS=Methanobacterium formic METFO	5
115	8.53	8.64	22.2	tr A0A0S4FPQ4 A0A0S4FPQ4_METFO	Putative rubrerythrin OS=Methanobacterium formicicum O METFO	5
116	8.48	8.66	15.6	tr A0A090JXT2 A0A090JXT2_METFO	O-acetylhomoserine (Thiol)-lyase OS=Methanobacterium f METFO	5
117	8.42	8.61	22.4	tr A0A090I3J9 A0A090I3J9_METFO	Tungsten-containing formylmethanofuran dehydrogenase 2 METFO	7
118	8.31	8.34	13.8	tr A0A090I4Y0 A0A090I4Y0_METFO	Threonine synthase OS=Methanobacterium formicicum OX METFO	4
119	8.21	8.23	17.9	tr A0A090I552 A0A090I552_METFO	Exosome complex component Rrp42 OS=Methanobacteriu METFO	4
120	8.19	8.29	20.2	tr A0A090I7U4 A0A090I7U4_METFO	ABC transporter OS=Methanobacterium formicicum OX=21 METFO	5
121	8.18	8.4	19.2	tr A0A089ZI25 A0A089ZI25_METFO	Serine hydroxymethyltransferase OS=Methanobacterium fc METFO	7
122	8.07	8.25	19.1	tr A0A090I3S6 A0A090I3S6_METFO	DNA-directed RNA polymerase subunit A' OS=Methanoba METFO	6
123	8.03	8.24	41.7	tr A0A089ZF65 A0A089ZF65_METFO	PRC-barrel domain-containing protein OS=Methanobacteri METFO	5
124	8	8	27	tr A0A090JUT3 A0A090JUT3_METFO	F420-non-reducing hydrogenase iron-sulfur subunit D OS= METFO	5
125	7.98	8.09	22.4	tr A0A090I622 A0A090I622_METFO	Translation initiation factor 2 subunit alpha OS=Methanoba METFO	4
126	7.73	7.81	15.1	tr A0A090I8R6 A0A090I8R6_METFO	Acetylornithine aminotransferase OS=Methanobacterium fc METFO	4
127	7.66	7.72	17.4	tr A0A090I958 A0A090I958_METFO	Extracellular solute-binding protein OS=Methanobacterium METFO	6
128	7.65	7.74	32.3	tr A0A089ZGZ1 A0A089ZGZ1_METFO	30S ribosomal protein S8e OS=Methanobacterium formicic METFO	6
129	7.58	7.65	3.4	tr A0A090I2R3 A0A090I2R3_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	5
130	7.55	7.74	18.4	tr A0A090I246 A0A090I246_METFO	3-hydroxy-3-methylglutaryl coenzyme A reductase OS=Met METFO	5
131	7.53	7.68	14.6	tr A0A090I433 A0A090I433_METFO	GMP synthase [glutamine-hydrolyzing] subunit B OS=Meth METFO	4
132	7.51	7.59	20	tr A0A090I7Q9 A0A090I7Q9_METFO	2-amino-3,7-dideoxy-D-threo-hept-6-ulosonate synthase O METFO	4
133	7.43	7.49	20.8	tr A0A090I4X8 A0A090I4X8_METFO	F420-dependent NADP reductase OS=Methanobacterium i METFO	4
134	7.33	7.45	31.4	tr A0A090I9S3 A0A090I9S3_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	5
135	7.13	7.29	24.6	tr A0A090I424 A0A090I424_METFO	Translation initiation factor 5A OS=Methanobacterium form METFO	6
136	7.09	8.4	11.8	tr K2R140 K2R140_METFP	AAA ATPase OS=Methanobacterium formicicum (strain D METFP	7
137	7.02	7.21	19.9	tr A0A090JTX8 A0A090JTX8_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	6
138	6.91	7.07	38.9	tr A0A089ZDW1 A0A089ZDW1_METFO	Methyl-coenzyme M reductase II D subunit MrtD OS=Meth METFO	9
139	6.9	6.98	12.3	tr A0A090I8R0 A0A090I8R0_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	4
140	6.8	6.93	9.8	tr A0A089ZGX6 A0A089ZGX6_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	4
141	6.78	6.94	14	tr A0A090JWH2 A0A090JWH2_METFO	Phosphoglucosamine mutase GImM2 OS=Methanobacteriu METFO	5
142	6.77	6.85	6.4	tr A0A090I599 A0A090I599_METFO	Acetyl-CoA decarbonylase/synthase complex subunit beta METFO	3
143	6.77	6.84	17.6	tr A0A090I5U4 A0A090I5U4_METFO	SPFH domain/Band 7 family protein OS=Methanobacteriun METFO	4
144	6.6	6.63	46	tr A0A089ZBS5 A0A089ZBS5_METFO	30S ribosomal protein S6e OS=Methanobacterium formicic METFO	4
145	6.56	6.66	8.2	tr A0A090I298 A0A090I298_METFO	Archaeal glutamate synthase [NADPH] OS=Methanobacteri NADPH	4
146	6.52	6.7	35.5	tr A0A090JWL2 A0A090JWL2_METFO	IMP cyclohydrolase OS=Methanobacterium formicicum OX METFO	6

Amostra 4

147	6.45	6.49	7.9 tr A0A090JY31 A0A090JY31_METFO	Aspartokinase OS=Methanobacterium formicicum OX=216 METFO	3
148	6.43	6.57	4.6 tr A0A090I9E0 A0A090I9E0_METFO	DNA-directed RNA polymerase subunit OS=Methanobacte METFO	4
149	6.28	6.38	12.5 tr A0A089ZGS2 A0A089ZGS2_METFO	Replication factor C small subunit OS=Methanobacterium f METFO	5
150	6.28	6.31	12.5 tr A0A090JW72 A0A090JW72_METFO	Arsenite-activated ATPase ArsA OS=Methanobacterium fo METFO	4
151	6.27	6.3	21.6 tr A0A090JWN0 A0A090JWN0_METFO	Putative secreted protein OS=Methanobacterium formicicu METFO	8
152	6.24	6.39	13.9 tr A0A0S4FMQ4 A0A0S4FMQ4_METFO	Putative hydrogenase expression/formation protein MJ067 METFO	4
153	6.17	6.29	15 tr A0A090IAD3 A0A090IAD3_METFO	Homoserine dehydrogenase OS=Methanobacterium formic METFO	4
154	6.13	6.19	6.3 tr A0A0S4FN19 A0A0S4FN19_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO	3
155	6.11	6.29	13.6 tr A0A089ZG23 A0A089ZG23_METFO	Formylmethanofuran dehydrogenase subunit F FwdF1 OS= METFO	3
156	6.11	6.13	9.4 tr A0A090I657 A0A090I657_METFO	3-isopropylmalate dehydratase large subunit OS=Methanol METFO	4
157	6.09	6.22	18.3 tr A0A090I314 A0A090I314_METFO	CBS domain-containing protein OS=Methanobacterium for METFO	4
158	6.07	6.09	14.6 tr A0A090I3Q7 A0A090I3Q7_METFO	Nucleotidyl transferase OS=Methanobacterium formicicum METFO	3
159	6.05	6.06	32.6 tr A0A089Z8Q6 A0A089Z8Q6_METFO	30S ribosomal protein S11 OS=Methanobacterium formicic METFO	3
160	6.02	6.18	15 tr A0A090JUJ4 A0A090JUJ4_METFO	Probable L-aspartate dehydrogenase OS=Methanobacteriu METFO	4
161	6.01	6.01	42.9 tr A0A090JUU7 A0A090JUU7_METFO	Tetrahydromethanopterin S-methyltransferase subunit G O METFO	3
162	6.01	6.01	13.7 tr A0A089ZGG9 A0A089ZGG9_METFO	50S ribosomal protein L4 OS=Methanobacterium formicicu METFO	3
163	6	6	15.5 tr K2R0Q6 K2R0Q6_METFP	GTP cyclohydrolase III OS=Methanobacterium formicicum METFP	3
164	6	6	13.4 tr A0A089ZV26 A0A089ZV26_METFO	Inositol-3-phosphate synthase OS=Methanobacterium forr METFO	3
165	6	6	36.1 tr A0A089ZB18 A0A089ZB18_METFO	50S ribosomal protein L23 OS=Methanobacterium formicic METFO	3
166	5.92	6	14.1 tr A0A090JU62 A0A090JU62_METFO	Glutamine amidotransferase OS=Methanobacterium formic METFO	3
167	5.55	5.64	13.5 tr A0A090JUG7 A0A090JUG7_METFO	Phosphate binding protein OS=Methanobacterium formicic METFO	3
168	5.47	5.54	11.8 tr A0A0S4FNG0 A0A0S4FNG0_METFO	Formylmethanofuran-tetrahydromethanopterin formyltransf METFO	3
169	5.34	5.45	23 tr A0A090JSP3 A0A090JSP3_METFO	Uridylate kinase OS=Methanobacterium formicicum OX=21 METFO	6
170	5.28	5.39	10.1 tr A0A090I5E9 A0A090I5E9_METFO	Pyruvate carboxylase subunit B OS=Methanobacterium for METFO	6
171	5.27	5.36	8.8 tr A0A090I409 A0A090I409_METFO	Glutamyl-tRNA(Gln) amidotransferase subunit D OS=Meth METFO	3
172	5.15	5.43	14.8 tr A0A090I672 A0A090I672_METFO	dTDP-glucose 4,6-dehydratase OS=Methanobacterium forr METFO	4
173	5.06	5.12	20.3 tr A0A090I8S1 A0A090I8S1_METFO	Universal stress protein UspA5 OS=Methanobacterium forr METFO	3
174	4.91	5.31	12.2 tr A0A090I3P4 A0A090I3P4_METFO	Alanine dehydrogenase OS=Methanobacterium formicicu METFO	3
175	4.87	4.92	23.7 tr A0A090JWM7 A0A090JWM7_METFO	2-oxoglutarate synthase subunit KorC OS=Methanobacteriu METFO	3
176	4.75	4.91	11.9 tr A0A090I6C9 A0A090I6C9_METFO	Ketol-acid reductoisomerase (NADP(+)) OS=Methanobacte METFO	4
177	4.73	4.78	4.3 tr A0A090I8V0 A0A090I8V0_METFO	Threonine--tRNA ligase OS=Methanobacterium formicicum METFO	3
178	4.69	4.73	7.7 tr A0A090I4J0 A0A090I4J0_METFO	Pyruvate carboxylase subunit A OS=Methanobacterium for METFO	3
179	4.65	4.79	35.9 tr A0A089ZG55 A0A089ZG55_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO	5

Amostra 4

180	4.6	4.63	7.8 tr A0A090JYU9 A0A090JYU9_METFO	Phosphosulfolactate synthase OS=Methanobacterium form METFO	2
181	4.55	4.57	12.8 tr A0A090I3K4 A0A090I3K4_METFO	Diaminopimelate epimerase OS=Methanobacterium formic METFO	3
182	4.53	4.6	20.3 tr A0A090JTX4 A0A090JTX4_METFO	dCTP deaminase, dUMP-forming OS=Methanobacterium f METFO	4
183	4.41	4.43	5.2 tr A0A090I5F2 A0A090I5F2_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	2
184	4.4	4.42	10.2 tr K2REI5 K2REI5_METFP	Coenzyme F420 hydrogenase subunit gamma OS=Methan METFP	2
185	4.4	4.42	13.1 tr A0A089ZC51 A0A089ZC51_METFO	Extracellular phosphate-binding protein OS=Methanobacte METFO	2
186	4.37	4.44	14 tr A0A090I521 A0A090I521_METFO	4-hydroxy-tetrahydrodipicolinate reductase OS=Methanoba METFO	4
187	4.33	4.42	18.4 tr A0A089ZE87 A0A089ZE87_METFO	ABC transporter ATP-binding protein OS=Methanobacteriu METFO	3
188	4.32	4.45	17.8 tr A0A090I8S8 A0A090I8S8_METFO	ABC transporter ATP-binding protein OS=Methanobacteriu METFO	3
189	4.31	4.34	13 tr A0A089ZEW4 A0A089ZEW4_METFO	50S ribosomal protein L11 OS=Methanobacterium formicic METFO	2
190	4.3	4.38	8.7 tr A0A090I4Y9 A0A090I4Y9_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	3
191	4.28	4.34	7.1 tr A0A090I514 A0A090I514_METFO	UPF0219 protein DSM1535_2142 OS=Methanobacterium i METFO	2
192	4.23	4.25	15.7 tr A0A089ZV28 A0A089ZV28_METFO	Heat shock protein Hsp20 OS=Methanobacterium formicici METFO	2
193	4.18	4.27	7.4 tr A0A090I428 A0A090I428_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	3
194	4.16	4.18	28.6 tr A0A090I442 A0A090I442_METFO	50S ribosomal protein L30e OS=Methanobacterium formici METFO	2
195	4.14	4.16	7.6 tr A0A090I2K4 A0A090I2K4_METFO	Putative ATP-binding protein MJ0685 OS=Methanobacteriu METFO	2
196	4.07	4.08	6.8 tr A0A090I135 A0A090I135_METFO	UTP--glucose-1-phosphate uridylyltransferase OS=Methan METFO	2
197	4.07	4.08	4.4 tr A0A089ZGW2 A0A089ZGW2_METFO	Translation initiation factor 2 subunit gamma OS=Methanol METFO	2
198	4.07	4.08	4.6 tr A0A090I8U6 A0A090I8U6_METFO	Arginine--tRNA ligase OS=Methanobacterium formicicum C METFO	2
199	4.05	4.06	5.6 tr A0A090I431 A0A090I431_METFO	2-oxoglutarate synthase subunit KorA OS=Methanobacteriu METFO	2
200	4.04	4.04	19.6 tr A0A090I6K9 A0A090I6K9_METFO	30S ribosomal protein S17 OS=Methanobacterium formicic METFO	2
201	4.03	4.06	7.3 tr A0A090JW77 A0A090JW77_METFO	ATP phosphoribosyltransferase OS=Methanobacterium for METFO	2
202	4.01	4.13	21.8 tr A0A090JUF5 A0A090JUF5_METFO	Pyruvate synthase subunit PorC OS=Methanobacterium fo METFO	3
203	4.01	4.02	22.9 tr A0A089ZGF2 A0A089ZGF2_METFO	50S ribosomal protein L13 OS=Methanobacterium formicic METFO	3
204	4.01	4.01	6.2 tr K2R1B6 K2R1B6_METFP	Glyceraldehyde-3-phosphate dehydrogenase OS=Methanc METFP	2
205	4	4.01	9 tr K2RRA6 K2RRA6_METFP	Uncharacterized protein OS=Methanobacterium formicicun METFP	2
206	4	4	36.5 tr A0A090JYF1 A0A090JYF1_METFO	TRAM domain-containing protein OS=Methanobacterium fc METFO	2
207	4	4	10.9 tr K2RAP2 K2RAP2_METFP	Tetrahydromethanopterin S-methyltransferase subunit E O METFP	4
208	4	4	17.7 tr K2QZS6 K2QZS6_METFP	UPF0145 protein A994_06900 OS=Methanobacterium forn METFP	2
209	4	4	15.1 tr A0A090I489 A0A090I489_METFO	GTP-binding protein Rab-like protein OS=Methanobacteriu METFO	2
210	4	4	22.4 tr A0A089ZHN5 A0A089ZHN5_METFO	Probable transcription termination protein NusA OS=Metha METFO	2
211	4	4	22.6 tr K2QDP1 K2QDP1_METFP	30S ribosomal protein S10 OS=Methanobacterium formicic METFP	2
212	4	4	7.1 tr A0A0S4FM93 A0A0S4FM93_METFO	Histidinol-phosphate aminotransferase OS=Methanobacter METFO	2

Amostra 4

213	4	4	11.5	tr A0A090JVV8 A0A090JVV8_METFO	Putative acetolactate synthase small subunit OS=Methanobacterium formicicum METFO	2
214	4	4	16.6	tr A0A090I6A2 A0A090I6A2_METFO	Cyclophilin type peptidyl-prolyl cis-trans isomerase OS=Methanobacterium formicicum METFO	2
215	4	4	7.5	tr A0A089ZG19 A0A089ZG19_METFO	Formate/nitrite transporter FdhC OS=Methanobacterium formicicum METFO	2
216	3.81	3.97	16.9	tr A0A090I465 A0A090I465_METFO	Spore coat polysaccharide biosynthesis protein SpsK OS=Methanobacterium formicicum METFO	3
217	3.79	4.05	18.4	tr A0A090I684 A0A090I684_METFO	Formylmethanofuran dehydrogenase subunit E OS=Methanobacterium formicicum METFO	3
218	3.77	3.92	11.9	tr A0A090IAU5 A0A090IAU5_METFO	Choloylglycine hydrolase OS=Methanobacterium formicicum METFO	3
219	3.71	3.97	11.4	tr A0A090I8Z8 A0A090I8Z8_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
220	3.62	3.7	12.1	tr A0A090I308 A0A090I308_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
221	3.59	3.73	7.6	tr A0A090I4R4 A0A090I4R4_METFO	Type A flavoprotein FprA OS=Methanobacterium formicicum METFO	3
222	3.58	3.73	12.6	tr A0A090JWV3 A0A090JWV3_METFO	Acetylglutamate kinase OS=Methanobacterium formicicum METFO	3
223	3.57	3.66	3.3	tr A0A090I8E3 A0A090I8E3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
224	3.48	3.58	11.8	tr A0A090JX40 A0A090JX40_METFO	(5-formylfuran-3-yl)methyl phosphate synthase OS=Methanobacterium formicicum METFO	2
225	3.46	3.55	24.1	tr A0A090JTC3 A0A090JTC3_METFO	30S ribosomal protein S9 OS=Methanobacterium formicicum METFO	2
226	3.42	3.69	5.8	tr A0A0S4FPN3 A0A0S4FPN3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
227	3.38	3.5	5.5	tr A0A090I3Q1 A0A090I3Q1_METFO	Putative FAD-dependent oxidoreductase MJ0033 OS=Methanobacterium formicicum METFO	3
228	3.28	3.39	9.2	tr A0A090I5G4 A0A090I5G4_METFO	Exosome complex component Rrp41 OS=Methanobacterium formicicum METFO	2
229	3.27	3.41	3.7	tr A0A090JW16 A0A090JW16_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
230	3.26	3.37	6.3	tr A0A090I496 A0A090I496_METFO	N-acetyl-gamma-glutamyl-phosphate reductase OS=Methanobacterium formicicum METFO	2
231	3.25	3.45	9.2	tr A0A089ZHM6 A0A089ZHM6_METFO	Methyl-coenzyme M reductase component A2 AtwA2 OS=Methanobacterium formicicum METFO	3
232	3.22	3.31	14.4	tr A0A090JU33 A0A090JU33_METFO	DNA-directed RNA polymerase OS=Methanobacterium formicicum METFO	4
233	3.19	3.3	6	tr A0A090I100 A0A090I100_METFO	S-inosyl-L-homocysteine hydrolase OS=Methanobacterium formicicum METFO	2
234	3.15	3.24	4.8	tr A0A0S4FS90 A0A0S4FS90_METFO	Putative secreted protein OS=Methanobacterium formicicum METFO	2
235	3.14	3.27	13.8	tr A0A090I3I7 A0A090I3I7_METFO	Putative sugar kinase MTH_1544 OS=Methanobacterium formicicum METFO	2
236	3.14	3.26	10.8	tr A0A090I2L4 A0A090I2L4_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
237	3.12	3.22	9.8	tr A0A090I5U3 A0A090I5U3_METFO	Geranylgeranyl glyceryl phosphate synthase OS=Methanobacterium formicicum METFO	2
238	3.11	3.21	5.9	tr A0A089ZFA3 A0A089ZFA3_METFO	Acetyl-CoA decarbonylase/synthase complex subunit delta OS=Methanobacterium formicicum METFO	2
239	3.02	3.19	12.3	tr A0A090I653 A0A090I653_METFO	Methanogenesis marker protein 11 OS=Methanobacterium formicicum METFO	5
240	2.98	3.1	3.1	tr A0A090I2M9 A0A090I2M9_METFO	Catalase-peroxidase OS=Methanobacterium formicicum METFO	2
241	2.97	3.07	7.1	tr A0A090I2K0 A0A090I2K0_METFO	Phosphoribosylformylglycinamide cyclo-ligase OS=Methanobacterium formicicum METFO	2
242	2.96	3.05	14.3	tr A0A089ZA12 A0A089ZA12_METFO	30S ribosomal protein S15 OS=Methanobacterium formicicum METFO	2
243	2.94	3.06	7.8	tr A0A090IB58 A0A090IB58_METFO	Carbamoyl-phosphate synthase small chain OS=Methanobacterium formicicum METFO	2
244	2.92	3.05	4	tr A0A090I0Z8 A0A090I0Z8_METFO	Type 2 DNA topoisomerase 6 subunit B OS=Methanobacterium formicicum METFO	2
245	2.91	3.7	9.9	tr A0A0S4FLD6 A0A0S4FLD6_METFO	ABC transporter substrate-binding protein OS=Methanobacterium formicicum METFO	3

Amostra 4

246	2.87	2.96	18.6	tr A0A090I7B8 A0A090I7B8_METFO	30S ribosomal protein S19e OS=Methanobacterium formicic METFO	2
247	2.85	2.96	2.5	tr A0A090I8M1 A0A090I8M1_METFO	Lon protease OS=Methanobacterium formicicum OX=2162 METFO	2
248	2.83	2.97	9.8	tr A0A089ZH87 A0A089ZH87_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
249	2.8	2.93	3.6	tr A0A089Z9Y9 A0A089Z9Y9_METFO	Type II secretion system protein E GspE OS=Methanobact METFO	2
250	2.78	2.93	2.1	tr A0A090I4Q7 A0A090I4Q7_METFO	Aspartate--tRNA(Asp/Asn) ligase OS=Methanobacterium fc METFO	1
251	2.78	2.88	12.7	tr A0A090JV59 A0A090JV59_METFO	Transcription elongation factor NusA-like protein OS=Meth METFO	2
252	2.76	2.86	3.7	tr A0A090JXV9 A0A090JXV9_METFO	CTP synthase OS=Methanobacterium formicicum OX=216 METFO	2
253	2.75	2.85	9.8	tr A0A090I443 A0A090I443_METFO	Superoxide dismutase OS=Methanobacterium formicicum METFO	2
254	2.75	2.84	7.1	tr A0A089Z928 A0A089Z928_METFO	Nitrogenase cofactor biosynthesis protein NifB OS=Methan METFO	2
255	2.73	2.95	18.7	tr A0A090I579 A0A090I579_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
256	2.72	2.81	10.4	tr A0A089ZII9 A0A089ZII9_METFO	MotA/TolQ/ExbB proton channel family protein OS=Methan METFO	2
257	2.71	2.8	3.7	tr A0A090I8Q5 A0A090I8Q5_METFO	Probable cobalamin synthase OS=Methanobacterium form METFO	2
258	2.71	2.8	15.6	tr A0A089ZVR0 A0A089ZVR0_METFO	30S ribosomal protein S12 OS=Methanobacterium formicic METFO	2
259	2.65	2.86	4.1	tr A0A090I524 A0A090I524_METFO	tRNA-splicing ligase RtcB OS=Methanobacterium formicicu METFO	2
260	2.6	2.72	1.9	tr A0A090I383 A0A090I383_METFO	Diaminopimelate decarboxylase OS=Methanobacterium fo METFO	1
261	2.6	2.66	6.6	tr A0A089ZDP9 A0A089ZDP9_METFO	Methanogenesis marker protein 13 OS=Methanobacterium METFO	2
262	2.59	2.67	14.8	tr A0A089ZCA7 A0A089ZCA7_METFO	Thioesterase OS=Methanobacterium formicicum OX=2162 METFO	2
263	2.58	2.91	6	tr A0A090JTZ4 A0A090JTZ4_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
264	2.58	2.65	9	tr A0A090I3S2 A0A090I3S2_METFO	Phosphoglycerate kinase OS=Methanobacterium formicicu METFO	2
265	2.55	2.64	4.4	tr A0A090I7K3 A0A090I7K3_METFO	Phosphate import ATP-binding protein PstB OS=Methanob METFO	1
266	2.47	2.73	7.2	tr A0A089ZVL1 A0A089ZVL1_METFO	50S ribosomal protein L10 OS=Methanobacterium formicic METFO	2
267	2.44	2.52	10.2	tr A0A090I9E4 A0A090I9E4_METFO	30S ribosomal protein S7 OS=Methanobacterium formicicu METFO	1
268	2.39	2.44	9.4	tr K2RR02 K2RR02_METFP	50S ribosomal protein L1 OS=Methanobacterium formicicu METFP	3
269	2.35	2.41	4.8	tr A0A090I192 A0A090I192_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
270	2.35	2.41	2.6	tr A0A090I4H9 A0A090I4H9_METFO	UDP-glucose 4-epimerase OS=Methanobacterium formicic METFO	1
271	2.29	2.53	9.5	tr A0A089ZDP0 A0A089ZDP0_METFO	Thiamine thiazole synthase OS=Methanobacterium formici METFO	2
272	2.29	2.35	4.3	tr A0A090I904 A0A090I904_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
273	2.26	2.31	3.2	tr A0A090I4T1 A0A090I4T1_METFO	Aspartate-semialdehyde dehydrogenase OS=Methanobact METFO	1
274	2.25	2.29	9.4	tr A0A090I455 A0A090I455_METFO	Type 2 DNA topoisomerase 6 subunit A OS=Methanobacte METFO	2
275	2.23	2.27	2.2	tr A0A090I8U4 A0A090I8U4_METFO	Acetolactate synthase OS=Methanobacterium formicicum METFO	1
276	2.22	2.41	5.6	tr A0A090JUQ9 A0A090JUQ9_METFO	Putative nickel insertion protein OS=Methanobacterium form METFO	2
277	2.17	2.21	4.4	tr A0A090I368 A0A090I368_METFO	Formylmethanofuran dehydrogenase subunit E OS=Metha METFO	1
278	2.17	2.2	4.3	tr A0A090I679 A0A090I679_METFO	UDP-glucose 4-epimerase OS=Methanobacterium formicic METFO	1

Amostra 4

279	2.16	3.37	5.2 tr K2R4C2 K2R4C2_METFP	Flavodoxin/nitric oxide synthase OS=Methanobacterium formicicum METFP	2
280	2.15	2.18	5.7 tr A0A090JU20 A0A090JU20_METFO	3-hexulose-6-phosphate isomerase HxIB2 OS=Methanobacterium formicicum METFO	1
281	2.14	2.17	2.4 tr A0A090I5M1 A0A090I5M1_METFO	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit METFO	1
282	2.13	2.16	0.9 tr A0A090I4M6 A0A090I4M6_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
283	2.12	2.15	9.4 tr A0A090JX27 A0A090JX27_METFO	Amino acid-binding ACT domain-containing protein OS=Methanobacterium formicicum METFO	1
284	2.12	2.14	4.1 tr K2QEU7 K2QEU7_METFP	Coenzyme A biosynthesis bifunctional protein CoaBC OS=Methanobacterium formicicum METFP	1
285	2.09	2.11	5 tr A0A089ZA94 A0A089ZA94_METFO	CobQ/CobB/MinD/ParA nucleotide binding domain-containing protein METFO	1
286	2.07	2.09	2.7 tr A0A090I3A4 A0A090I3A4_METFO	Phosphoribosylamine--glycine ligase OS=Methanobacterium formicicum METFO	1
287	2.06	2.08	4.3 tr A0A090JYQ2 A0A090JYQ2_METFO	Vitamin-B12 independent methionine synthase OS=Methanobacterium formicicum METFO	1
288	2.05	2.24	4.6 tr A0A089ZHE0 A0A089ZHE0_METFO	Molybdenum cofactor synthesis domain-containing protein METFO	2
289	2.05	2.07	2 tr A0A0S4FN62 A0A0S4FN62_METFO	UDP-N-acetylglucosamine 2-epimerase OS=Methanobacterium formicicum METFO	1
290	2.05	2.07	2 tr A0A090I2S7 A0A090I2S7_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
291	2.05	2.06	3.6 tr A0A090I3D2 A0A090I3D2_METFO	PQQ repeat-containing cell surface protein OS=Methanobacterium formicicum METFO	1
292	2.04	2.05	2.1 tr A0A090I583 A0A090I583_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
293	2.04	2.05	2.3 tr K2RTW1 K2RTW1_METFP	Tryptophan synthase beta chain OS=Methanobacterium formicicum METFP	1
294	2.04	2.05	0.6 tr A0A090I544 A0A090I544_METFO	Putative secreted protein OS=Methanobacterium formicicum METFO	1
295	2.04	2.04	2.1 tr K2QCN1 K2QCN1_METFP	V-type ATP synthase subunit C OS=Methanobacterium formicicum METFP	1
296	2.03	2.04	1.7 tr A0A090JW98 A0A090JW98_METFO	Anaerobic ribonucleoside-triphosphate reductase OS=Methanobacterium formicicum METFO	1
297	2.03	2.04	3.7 tr A0A090I1N1 A0A090I1N1_METFO	Coenzyme F390 synthetase FtsA2 OS=Methanobacterium formicicum METFO	1
298	2.03	2.04	2 tr A0A089ZAR5 A0A089ZAR5_METFO	Divergent AAA domain-containing protein OS=Methanobacterium formicicum METFO	1
299	2.02	2.03	1.6 tr A0A0S4FSQ1 A0A0S4FSQ1_METFO	Acetyl-coenzyme A synthetase OS=Methanobacterium formicicum METFO	1
300	2.02	2.03	3.5 tr A0A090JXI6 A0A090JXI6_METFO	Cyclic 2,3-diphosphoglycerate synthetase OS=Methanobacterium formicicum METFO	1
301	2.02	2.02	4.9 tr A0A089ZDD2 A0A089ZDD2_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
302	2.01	2.01	3.7 tr A0A090I866 A0A090I866_METFO	4-hydroxy-tetrahydrodipicolinate synthase OS=Methanobacterium formicicum METFO	1
303	2	36.07	41.1 tr K2QYM4 K2QYM4_METFP	Methyl-coenzyme M reductase subunit alpha OS=Methanobacterium formicicum METFP	78
304	2	6.21	8.5 tr A0A090IAA4 A0A090IAA4_METFO	Pyridoxal 5'-phosphate synthase subunit PdxS OS=Methanobacterium formicicum METFO	3
305	2	4	12.1 tr K2QD49 K2QD49_METFP	50S ribosomal protein L5 OS=Methanobacterium formicicum METFP	2
306	2	4	13.6 tr K2Q9U8 K2Q9U8_METFP	LemA family protein OS=Methanobacterium formicicum (strain L) METFP	4
307	2	2.02	4.5 tr A0A090JUW9 A0A090JUW9_METFO	2-phosphosulfolactate phosphatase OS=Methanobacterium formicicum METFO	1
308	2	2.01	3.2 tr K2RR15 K2RR15_METFP	Peptidase U62 OS=Methanobacterium formicicum (strain L) METFP	2
309	2	2	2.6 tr A0A090I669 A0A090I669_METFO	Putative NADH oxidase OS=Methanobacterium formicicum METFO	1
310	2	2	3.4 tr K2R6Y5 K2R6Y5_METFP	Cobyrinic acid ac-diamide synthase OS=Methanobacterium formicicum METFP	1
311	2	2	4.8 tr K2QBL8 K2QBL8_METFP	Uncharacterized protein OS=Methanobacterium formicicum METFP	1

Amostra 4

312	2	2	2.9 tr A0A090JSM8 A0A090JSM8_METFO	Transcription initiation factor IIB OS=Methanobacterium for METFO	1
313	2	2	3 tr A0A090I6D3 A0A090I6D3_METFO	Ornithine carbamoyltransferase OS=Methanobacterium for METFO	1
314	2	2	11.4 tr A0A090I340 A0A090I340_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
315	2	2	4.2 tr K2RW75 K2RW75_METFP	Sugar fermentation stimulation protein homolog OS=Metha METFP	1
316	2	2	2.5 tr K2RDR1 K2RDR1_METFP	Lactate utilization protein B/C OS=Methanobacterium formi METFP	1
317	2	2	5.3 tr A0A090I9D6 A0A090I9D6_METFO	Triosephosphate isomerase OS=Methanobacterium formic METFO	1
318	2	2	3.1 tr A0A090I731 A0A090I731_METFO	Glucose-1-phosphate thymidyltransferase OS=Methanob. METFO	1
319	2	2	2.7 tr A0A090I4G2 A0A090I4G2_METFO	Bifunctional short chain isoprenyl diphosphate synthase Ids METFO	1
320	2	2	3 tr A0A090I4E1 A0A090I4E1_METFO	Histidinol dehydrogenase OS=Methanobacterium formicicu METFO	1
321	2	2	3.4 tr A0A090I385 A0A090I385_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
322	2	2	8.8 tr A0A089ZJ52 A0A089ZJ52_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
323	2	2	4.2 tr K2RTL1 K2RTL1_METFP	Uncharacterized protein OS=Methanobacterium formicicun METFP	1
324	2	2	13 tr K2RAP6 K2RAP6_METFP	Tetrahydromethanopterin S-methyltransferase subunit F O: METFP	1
325	2	2	4.4 tr K2R714 K2R714_METFP	3,4-dihydroxy-2-butanone 4-phosphate synthase OS=Meth. METFP	1
326	2	2	5.4 tr K2R2J6 K2R2J6_METFP	Thiamine thiazole synthase OS=Methanobacterium formici METFP	1
327	2	2	5.4 tr K2R2B6 K2R2B6_METFP	NADH ubiquinone oxidoreductase 20 kDa subunit OS=Met METFP	1
328	2	2	1.4 tr K2R1G9 K2R1G9_METFP	Archaeal glutamate synthase [NADPH] OS=Methanobacteri NADPH	1
329	2	2	3.8 tr K2QZG7 K2QZG7_METFP	Uroporphyrinogen-III synthase OS=Methanobacterium forr METFP	1
330	2	2	1 tr A0A0S4FSW2 A0A0S4FSW2_METFO	Putative secreted protein OS=Methanobacterium formicicu METFO	1
331	2	2	5.6 tr A0A0S4FMY6 A0A0S4FMY6_METFO	NADPH-dependent FMN reductase OS=Methanobacteriun METFO	1
332	2	2	5.5 tr A0A0S4FLN4 A0A0S4FLN4_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
333	2	2	0.8 tr A0A0S4FL46 A0A0S4FL46_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
334	2	2	3.8 tr A0A090JWL7 A0A090JWL7_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
335	2	2	1.7 tr A0A090JVX7 A0A090JVX7_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
336	2	2	3.3 tr A0A090JUV1 A0A090JUV1_METFO	Tetrahydromethanopterin S-methyltransferase subunit D O METFO	1
337	2	2	3.4 tr A0A090I9V8 A0A090I9V8_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
338	2	2	3.3 tr A0A090I6Y3 A0A090I6Y3_METFO	S-adenosyl-L-methionine-dependent tRNA 4-demethylwyo: METFO	1
339	2	2	5.6 tr A0A090I5I0 A0A090I5I0_METFO	Tetrahydromethanopterin S-methyltransferase subunit C O METFO	2
340	2	2	8 tr A0A089ZHC6 A0A089ZHC6_METFO	Tetrahydromethanopterin S-methyltransferase subunit B O: METFO	1
341	2	2	5.1 tr A0A089ZH31 A0A089ZH31_METFO	Cobalamin biosynthesis protein CbiM3 OS=Methanobacter METFO	1
342	2	2	4.1 tr A0A089ZGT2 A0A089ZGT2_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
343	2	2	6.2 tr A0A089ZGF5 A0A089ZGF5_METFO	CBS domain-containing protein OS=Methanobacterium for METFO	1
344	2	2	15.3 tr A0A089ZCI4 A0A089ZCI4_METFO	Dinitrogenase iron-molybdenum cofactor biosynthesis prot METFO	1

Amostra 4

345	1.89	2.09	5.9 tr A0A090JVV9 A0A090JVV9_METFO	Aspartate carbamoyltransferase OS=Methanobacterium fo	METFO	1
346	1.87	2.02	2 tr K2RAX3 K2RAX3_METFP	ATPase RIL OS=Methanobacterium formicicum (strain DS	METFP	1
347	1.83	2.01	6 tr A0A090I1A0 A0A090I1A0_METFO	Anthranilate phosphoribosyltransferase OS=Methanobacte	METFO	1
348	1.62	1.98	5.6 tr A0A090JYJ5 A0A090JYJ5_METFO	Glutamine--fructose-6-phosphate aminotransferase [isome	METFO	3
349	1.48	1.6	2.8 tr A0A0S4FLU0 A0A0S4FLU0_METFO	Dihydrolipoyl dehydrogenase OS=Methanobacterium formi	METFO	1
350	1.45	1.57	4.2 tr K2QDZ9 K2QDZ9_METFP	RNA-processing protein OS=Methanobacterium formicicu	METFP	1
351	1.42	1.54	9.6 tr K2RW50 K2RW50_METFP	DNA/RNA-binding protein Alba OS=Methanobacterium forr	METFP	1
352	1.35	1.47	4.7 tr A0A089ZAY7 A0A089ZAY7_METFO	30S ribosomal protein S4 OS=Methanobacterium formicicu	METFO	1

Amostra 4



ID statistics table

Unused (Conf) Cutoff	Proteins Detected	Proteins Before Grouping	Distinct Peptides	Spectra Identified	% Total Spectra
>2.0 (99)	302	647	4582	16330	12.6
>1.3 (95)	352	775	4694	16520	12.7
>0.47 (66)	384	856	4766	16647	12.8
Cutoff Applied: >0.05 (10%)	489	1127	4958	17021	13.1

Amostra 5

1) Z:\Projects\UniMS2019_95 MALves\Data\CS5_9uL.wiff



Sample Type: Identification
Cys. Alkylation: Iodoacetamide
Digestion: Trypsin
Instrument: TripleTOF 6600
Special Factors: Gel-based ID
Species:
ID Focus: Biological modifications
Amino acid substitutions
Database: 20190624_uniprot_methanobacterium+formicicum_6903entries.fasta
Search Effort: Thorough
FDR Analysis: Yes
User Modified Parameter Files: Yes

Proteins detected table

N	Unused	Total	% Cov (95	Accession #	Name	Species	Peptides(95%)
1	59.39	59.39	42.7	tr A0A090I8L6 A0A090I8L6_METFO	Replication factor-A domain-containing protein OS=Methan	METFO	32
2	59.35	59.38	59.9	tr A0A090I2M3 A0A090I2M3_METFO	V-type ATP synthase alpha chain OS=Methanobacterium fr	METFO	52
3	57.62	57.62	74.5	tr A0A090IAH6 A0A090IAH6_METFO	Thermosome subunit OS=Methanobacterium formicicum C	METFO	161
4	52.39	52.39	49.8	tr A0A090I3A9 A0A090I3A9_METFO	Chaperone protein DnaK OS=Methanobacterium formicicu	METFO	38
5	50.21	50.21	94.7	tr A0A090I573 A0A090I573_METFO	5,10-methylenetetrahydromethanopterin reductase OS=Me	METFO	182
6	49.89	50.16	67.6	tr A0A090I2R9 A0A090I2R9_METFO	F420-non-reducing hydrogenase subunit A OS=Methanoba	METFO	44
7	47.31	47.31	53.8	tr A0A090I2G6 A0A090I2G6_METFO	Methyl-coenzyme M reductase subunit alpha OS=Methano	METFO	86
8	46.16	46.27	59.4	tr A0A090I7W3 A0A090I7W3_METFO	Methyl-coenzyme M reductase subunit beta OS=Methanob	METFO	68
9	44.69	44.69	45.1	tr A0A090I3G7 A0A090I3G7_METFO	CoB--CoM heterodisulfide reductase subunit A HdrA2 OS=	METFO	50
10	43.01	43.47	68.2	tr A0A090I2T3 A0A090I2T3_METFO	Methyl-coenzyme M reductase subunit beta OS=Methanob	METFO	230
11	40.88	40.88	37.2	tr A0A090I7T4 A0A090I7T4_METFO	Phosphoenolpyruvate synthase OS=Methanobacterium for	METFO	29
12	38.26	38.26	30	tr A0A090I5F3 A0A090I5F3_METFO	Putative secreted protein OS=Methanobacterium formicicu	METFO	33
13	37.61	37.77	32.3	tr A0A090I3T1 A0A090I3T1_METFO	Elongation factor 2 OS=Methanobacterium formicicum OX-	METFO	22
14	36.92	37.02	48.7	tr A0A090JVC3 A0A090JVC3_METFO	Methyl-coenzyme M reductase subunit alpha OS=Methano	METFO	77

Amostra 5

15	28.63	28.63	41.9 tr A0A090I9A6 A0A090I9A6_METFO	Hydroxylamine reductase OS=Methanobacterium formicicu METFO	18
16	27.85	27.92	7 tr A0A090I3J2 A0A090I3J2_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO	18
17	27.02	27.53	41.3 tr A0A090I4W3 A0A090I4W3_METFO	F420-non-reducing hydrogenase vhc subunit A OS=Metha METFO	17
18	26.98	36.23	57.3 tr A0A090IA40 A0A090IA40_METFO	Thermosome subunit OS=Methanobacterium formicicum C METFO	88
19	26.07	26.12	42 tr A0A090I7U6 A0A090I7U6_METFO	GDP-mannose 4,6-dehydratase OS=Methanobacterium fo METFO	17
20	23.5	23.5	35.8 tr A0A089ZDH4 A0A089ZDH4_METFO	Elongation factor 1-alpha OS=Methanobacterium formicicu METFO	22
21	22.61	22.63	34.5 tr A0A090I8W8 A0A090I8W8_METFO	Bifunctional enzyme Fae/Hps OS=Methanobacterium formi METFO	17
22	21.79	21.82	25 tr A0A090I2L6 A0A090I2L6_METFO	D-3-phosphoglycerate dehydrogenase OS=Methanobacter METFO	11
23	20.64	20.65	37.4 tr A0A090I5C2 A0A090I5C2_METFO	V-type ATP synthase beta chain OS=Methanobacterium fo METFO	29
24	19.71	19.74	31.6 tr A0A089ZAI4 A0A089ZAI4_METFO	Formylmethanofuran dehydrogenase subunit A FwdA OS= METFO	12
25	18.63	18.64	41 tr A0A090I5T3 A0A090I5T3_METFO	Methyl-coenzyme M reductase subunit gamma OS=Methar METFO	12
26	18.45	18.46	38.8 tr A0A090I5H3 A0A090I5H3_METFO	Methenyltetrahydromethanopterin cyclohydrolase OS=Met METFO	9
27	17.61	17.64	15.6 tr A0A090I3V1 A0A090I3V1_METFO	Formate dehydrogenase alpha subunit FdhA OS=Methano METFO	10
28	17.2	17.21	53.3 tr A0A090I5H7 A0A090I5H7_METFO	Tetrahydromethanopterin S-methyltransferase subunit H O METFO	25
29	16.81	16.84	38.9 tr A0A089ZEV2 A0A089ZEV2_METFO	CBS domain-containing protein OS=Methanobacterium fo METFO	9
30	16.41	16.43	42.2 tr A0A090I6I3 A0A090I6I3_METFO	Coenzyme F420 hydrogenase subunit beta OS=Methanoba METFO	15
31	16.03	16.04	34.6 tr A0A0S4FQL4 A0A0S4FQL4_METFO	Putative aminotransferase MJ0959 OS=Methanobacterium METFO	12
32	15.94	15.98	31.1 tr A0A090I3I6 A0A090I3I6_METFO	Putative lipoprotein MJ0085 OS=Methanobacterium formici METFO	10
33	15.7	15.78	25.4 tr A0A090I281 A0A090I281_METFO	Pyruvate synthase subunit PorA OS=Methanobacterium fo METFO	10
34	15.3	15.35	38.4 tr A0A090I842 A0A090I842_METFO	CBS domain-containing membrane protein OS=Methanoba METFO	10
35	15.19	15.26	33.3 tr A0A089ZVL0 A0A089ZVL0_METFO	Cell division protein FtsZ OS=Methanobacterium formicicu METFO	8
36	14.25	14.28	20.4 tr A0A089ZIP7 A0A089ZIP7_METFO	DNA primase DnaG OS=Methanobacterium formicicum O METFO	6
37	13.91	13.94	30.5 tr A0A089ZUL5 A0A089ZUL5_METFO	Tryptophan synthase beta chain OS=Methanobacterium fo METFO	8
38	13.64	13.67	37.2 tr A0A090I6Q2 A0A090I6Q2_METFO	Formylmethanofuran dehydrogenase subunit C FwdC OS= METFO	11
39	13.61	13.64	33.9 tr A0A090IB20 A0A090IB20_METFO	Proteasome subunit alpha OS=Methanobacterium formicic METFO	7
40	13.29	13.32	26.2 tr A0A090I2P0 A0A090I2P0_METFO	CBS domain-containing protein OS=Methanobacterium fo METFO	11
41	13.1	13.42	26.2 tr A0A090I3H9 A0A090I3H9_METFO	5-formaminoimidazole-4-carboxamide-1-(beta)-D-ribofuran METFO	7
42	12.35	12.36	25.3 tr A0A089ZBS9 A0A089ZBS9_METFO	Acetyl-CoA acetyltransferase OS=Methanobacterium formi METFO	7
43	12.23	12.26	21.6 tr A0A090I781 A0A090I781_METFO	Fructose-1,6-bisphosphate aldolase/phosphatase OS=Met METFO	6
44	12.18	12.22	38.4 tr A0A090JTE0 A0A090JTE0_METFO	50S ribosomal protein L6 OS=Methanobacterium formicicu METFO	8
45	11.7	11.89	24 tr A0A090I305 A0A090I305_METFO	Coenzyme F420 hydrogenase alpha subunit FrhA OS=Met METFO	11
46	11.68	11.75	34.4 tr A0A090I8V8 A0A090I8V8_METFO	F420-dependent methylenetetrahydromethanopterin dehyd METFO	8
47	11.63	11.74	37.2 tr A0A089ZUU9 A0A089ZUU9_METFO	CoB--CoM heterodisulfide reductase subunit C HdrC1 OS= METFO	10

Amostra 5

48	11.52	11.55	20.8	tr A0A090I938 A0A090I938_METFO	Phosphomethylpyrimidine synthase OS=Methanobacterium METFO	7
49	11.41	11.56	5.1	tr A0A090I571 A0A090I571_METFO	Carbamoyl-phosphate synthase large chain OS=Methanobacterium METFO	6
50	11.17	11.26	47	tr A0A090I170 A0A090I170_METFO	TATA-box-binding protein OS=Methanobacterium formicicum METFO	7
51	11.13	11.27	16.3	tr A0A090JXJ6 A0A090JXJ6_METFO	3-dehydroquinate synthase OS=Methanobacterium formicicum METFO	5
52	10.95	11.05	24.4	tr A0A089ZG02 A0A089ZG02_METFO	DNA repair and recombination protein RadA OS=Methanobacterium METFO	6
53	10.67	10.78	29.5	tr A0A090I494 A0A090I494_METFO	Short-chain dehydrogenase family protein OS=Methanobacterium METFO	6
54	10.57	10.6	15.1	tr A0A090JTE7 A0A090JTE7_METFO	30S ribosomal protein S3 OS=Methanobacterium formicicum METFO	5
55	10.53	10.57	16.2	tr A0A090I7L2 A0A090I7L2_METFO	Acetyl-CoA decarbonylase/synthase complex subunit gamma OS=Methanobacterium METFO	5
56	10.35	10.58	19.4	tr A0A090I6I2 A0A090I6I2_METFO	Adenylosuccinate synthetase OS=Methanobacterium formicicum METFO	6
57	10.21	10.22	15.3	tr A0A089ZV33 A0A089ZV33_METFO	FeS assembly protein SufBD OS=Methanobacterium formicicum METFO	5
58	10.19	10.25	41.2	tr A0A090JW64 A0A090JW64_METFO	LemA family protein OS=Methanobacterium formicicum OS=Methanobacterium METFO	8
59	9.93	10.02	24.6	tr A0A089ZI64 A0A089ZI64_METFO	ATP phosphoribosyltransferase OS=Methanobacterium formicicum METFO	5
60	9.92	10	34.1	tr A0A0S4FSE6 A0A0S4FSE6_METFO	Putative ABC transporter ATP-binding protein MJ0089 OS=Methanobacterium METFO	6
61	9.8	9.88	36.1	tr A0A089ZCQ3 A0A089ZCQ3_METFO	Putative rubrerythrin OS=Methanobacterium formicicum OS=Methanobacterium METFO	6
62	9.54	9.62	29.3	tr A0A090I2T7 A0A090I2T7_METFO	Methyl-coenzyme M reductase subunit gamma OS=Methanobacterium METFO	5
63	9.3	9.41	11.7	tr A0A0S4FLI0 A0A0S4FLI0_METFO	Putative ABC transporter ATP-binding protein MJ1242 OS=Methanobacterium METFO	5
64	9.27	9.43	6	tr K2R140 K2R140_METFP	AAA ATPase OS=Methanobacterium formicicum (strain D5) METFP	4
65	9.16	9.27	16.3	tr A0A090I5S8 A0A090I5S8_METFO	Argininosuccinate synthase OS=Methanobacterium formicicum METFO	5
66	9.11	9.19	14.9	tr A0A090JTT4 A0A090JTT4_METFO	Methanogenesis marker protein 15 OS=Methanobacterium METFO	5
67	9.06	9.17	16.8	tr A0A0S4FLJ3 A0A0S4FLJ3_METFO	Cell shape determining protein MreB/Mrl OS=Methanobacterium METFO	5
68	8.99	9.02	25.8	tr A0A089ZER7 A0A089ZER7_METFO	Exosome complex component Rrp4 OS=Methanobacterium METFO	5
69	8.63	8.66	32.4	tr A0A090I180 A0A090I180_METFO	50S ribosomal protein L5 OS=Methanobacterium formicicum METFO	5
70	8.55	8.64	11.6	tr A0A090I2I6 A0A090I2I6_METFO	Archaeal glutamate synthase [NADPH] OS=Methanobacterium formicicum METFO	5
71	8.46	8.52	22.2	tr A0A089ZAX5 A0A089ZAX5_METFO	30S ribosomal protein S2 OS=Methanobacterium formicicum METFO	6
72	8.4	8.46	11.1	tr A0A090I6T0 A0A090I6T0_METFO	Glutamine synthetase OS=Methanobacterium formicicum METFO	4
73	8.15	8.16	21.7	tr A0A090JUK8 A0A090JUK8_METFO	V-type proton ATPase subunit E OS=Methanobacterium formicicum METFO	4
74	8.08	8.16	5.6	tr A0A090I151 A0A090I151_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	5
75	8	8	17.6	tr A0A090I2G3 A0A090I2G3_METFO	Tetrahydromethanopterin S-methyltransferase subunit A OS=Methanobacterium METFO	6
76	7.93	8.02	17.4	tr A0A090I958 A0A090I958_METFO	Extracellular solute-binding protein OS=Methanobacterium METFO	8
77	7.83	7.89	40	tr A0A090I2W9 A0A090I2W9_METFO	Proteasome subunit beta OS=Methanobacterium formicicum METFO	5
78	7.72	7.77	17.9	tr A0A090I3Q7 A0A090I3Q7_METFO	Nucleotidyl transferase OS=Methanobacterium formicicum METFO	4
79	7.71	7.78	25.9	tr A0A090I219 A0A090I219_METFO	Translation initiation factor 6 OS=Methanobacterium formicicum METFO	4
80	7.62	7.68	27	tr A0A090JUT3 A0A090JUT3_METFO	F420-non-reducing hydrogenase iron-sulfur subunit D OS=Methanobacterium METFO	5

Amostra 5

81	7.51	7.69	10.9	tr A0A089ZHH5 A0A089ZHH5_METFO	Phosphoserine phosphatase SerB OS=Methanobacterium METFO	5
82	7.26	7.33	14.9	tr K2QF40 K2QF40_METFP	Uncharacterized protein OS=Methanobacterium formicicun METFP	4
83	6.97	7.01	9.8	tr A0A089ZGX6 A0A089ZGX6_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	4
84	6.92	7.05	22.4	tr A0A090I622 A0A090I622_METFO	Translation initiation factor 2 subunit alpha OS=Methanoba METFO	4
85	6.84	6.99	13	tr A0A090I9D3 A0A090I9D3_METFO	Succinate--CoA ligase [ADP-forming] subunit beta OS=MelADP-formin	4
86	6.82	6.89	15.1	tr A0A090JV64 A0A090JV64_METFO	CBS domain-containing membrane protein OS=Methanoba METFO	4
87	6.73	6.78	30.7	tr A0A089ZGF9 A0A089ZGF9_METFO	30S ribosomal protein S5 OS=Methanobacterium formicicu METFO	4
88	6.69	6.82	26.5	tr A0A089ZGG4 A0A089ZGG4_METFO	50S ribosomal protein L14 OS=Methanobacterium formicic METFO	4
89	6.66	6.76	26.4	tr A0A089ZUS9 A0A089ZUS9_METFO	50S ribosomal protein L18 OS=Methanobacterium formicic METFO	4
90	6.47	6.63	30.6	tr A0A089ZCU1 A0A089ZCU1_METFO	Transcription elongation factor Spt5 OS=Methanobacteriun METFO	4
91	6.47	6.58	27.1	tr A0A090I0N7 A0A090I0N7_METFO	PyrE-like protein OS=Methanobacterium formicicum OX=2 METFO	4
92	6.41	6.44	10.2	tr A0A090I8M3 A0A090I8M3_METFO	S-adenosylmethionine synthase OS=Methanobacterium fo METFO	3
93	6.36	6.5	17.9	tr A0A090I552 A0A090I552_METFO	Exosome complex component Rrp42 OS=Methanobacteriu METFO	5
94	6.33	6.35	33	tr A0A090JWL2 A0A090JWL2_METFO	IMP cyclohydrolase OS=Methanobacterium formicicum OX METFO	5
95	6.27	6.38	12.5	tr A0A090I360 A0A090I360_METFO	F420H2 oxidase FprA OS=Methanobacterium formicicum (METFO	3
96	6.27	6.29	12.1	tr A0A0S4FRT9 A0A0S4FRT9_METFO	Formylmethanofuran--tetrahydromethanopterin formyltrans METFO	5
97	6.24	6.27	35.9	tr A0A089ZG55 A0A089ZG55_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	5
98	6.03	6.17	10	tr A0A090I3H2 A0A090I3H2_METFO	Phosphoribosylformylglycinamide synthase subunit PurL METFO	4
99	6.03	6.03	13	tr A0A090I0T1 A0A090I0T1_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	6
100	6.01	6.01	9.2	tr A0A090I518 A0A090I518_METFO	Digeranylgeranylglycerophospholipid reductase OS=Metha METFO	3
101	6	6	12.5	tr A0A090JW72 A0A090JW72_METFO	Arsenite-activated ATPase ArsA OS=Methanobacterium fo METFO	3
102	5.9	6.1	9.9	tr A0A0S4FPE3 A0A0S4FPE3_METFO	Phenylalanine--tRNA ligase beta subunit OS=Methanobact METFO	4
103	5.82	5.98	13.2	tr A0A090I7K3 A0A090I7K3_METFO	Phosphate import ATP-binding protein PstB OS=Methanob METFO	3
104	5.79	5.89	16.1	tr A0A089ZF65 A0A089ZF65_METFO	PRC-barrel domain-containing protein OS=Methanobacteri METFO	3
105	5.75	5.85	15.5	tr A0A090I5G8 A0A090I5G8_METFO	F420-non-reducing hydrogenase subunit G OS=Methanoba METFO	7
106	5.65	5.75	12.3	tr A0A090I7B6 A0A090I7B6_METFO	Inosine-5'-monophosphate dehydrogenase OS=Methanoba METFO	5
107	5.46	5.52	36.5	tr A0A089ZBS5 A0A089ZBS5_METFO	30S ribosomal protein S6e OS=Methanobacterium formicic METFO	3
108	5.31	5.42	15.5	tr A0A090I4X8 A0A090I4X8_METFO	F420-dependent NADP reductase OS=Methanobacterium METFO	3
109	5.18	5.55	14.3	tr A0A089ZGS2 A0A089ZGS2_METFO	Replication factor C small subunit OS=Methanobacterium f METFO	4
110	5.11	5.3	12.2	tr A0A090I6C9 A0A090I6C9_METFO	Ketol-acid reductoisomerase (NADP(+)) OS=Methanobacte METFO	4
111	5.11	5.21	7.4	tr A0A090JTX8 A0A090JTX8_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	3
112	4.96	5.2	13.9	tr A0A089ZJ55 A0A089ZJ55_METFO	DNA polymerase sliding clamp OS=Methanobacterium forr METFO	6
113	4.96	5.04	12.5	tr A0A090I3P4 A0A090I3P4_METFO	Alanine dehydrogenase OS=Methanobacterium formicicun METFO	3

Amostra 5

114	4.88	4.98	24.1	tr A0A090I4G9 A0A090I4G9_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	4
115	4.85	4.9	36.1	tr A0A089ZB18 A0A089ZB18_METFO	50S ribosomal protein L23 OS=Methanobacterium formicicum METFO	3
116	4.83	5.02	6.7	tr A0A090JWH2 A0A090JWH2_METFO	Phosphoglucosamine mutase GlmM2 OS=Methanobacterium formicicum METFO	2
117	4.76	4.94	9.3	tr A0A090I4R4 A0A090I4R4_METFO	Type A flavoprotein FprA OS=Methanobacterium formicicum METFO	3
118	4.76	4.88	18.4	tr A0A090I7T8 A0A090I7T8_METFO	Peptidyl-prolyl cis-trans isomerase OS=Methanobacterium formicicum METFO	3
119	4.71	4.98	20.5	tr A0A090I4Y4 A0A090I4Y4_METFO	Circadian clock protein KaiC OS=Methanobacterium formicicum METFO	4
120	4.67	4.82	8.1	tr A0A090JXN7 A0A090JXN7_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	4
121	4.63	4.87	9.4	tr A0A089ZGQ5 A0A089ZGQ5_METFO	Peptidase U62 family OS=Methanobacterium formicicum METFO	3
122	4.38	4.42	3.5	tr A0A090I5E9 A0A090I5E9_METFO	Pyruvate carboxylase subunit B OS=Methanobacterium formicicum METFO	2
123	4.1	4.58	6.1	tr A0A089ZCR8 A0A089ZCR8_METFO	Proteasome-activating nucleotidase OS=Methanobacterium formicicum METFO	2
124	4.08	4.09	8.4	tr A0A090I5E6 A0A090I5E6_METFO	Inositol-3-phosphate synthase OS=Methanobacterium formicicum METFO	2
125	4.03	4.08	8.6	tr A0A090JWN0 A0A090JWN0_METFO	Putative secreted protein OS=Methanobacterium formicicum METFO	2
126	4.02	4.03	7	tr A0A090I4Y0 A0A090I4Y0_METFO	Threonine synthase OS=Methanobacterium formicicum METFO	2
127	4.01	4.01	5.3	tr A0A090I0Z8 A0A090I0Z8_METFO	Type 2 DNA topoisomerase 6 subunit B OS=Methanobacterium formicicum METFO	2
128	4.01	4.01	6.2	tr K2R1B6 K2R1B6_METFP	Glyceraldehyde-3-phosphate dehydrogenase OS=Methanobacterium formicicum METFP	2
129	4	4	16.2	tr A0A090I424 A0A090I424_METFO	Translation initiation factor 5A OS=Methanobacterium formicicum METFO	2
130	4	4	7.8	tr A0A0S4FLK3 A0A0S4FLK3_METFO	Coenzyme F420:L-glutamate ligase OS=Methanobacterium formicicum METFO	2
131	4	4	7.5	tr A0A090I657 A0A090I657_METFO	3-isopropylmalate dehydratase large subunit OS=Methanobacterium formicicum METFO	2
132	4	4	22.9	tr A0A089ZGF2 A0A089ZGF2_METFO	50S ribosomal protein L13 OS=Methanobacterium formicicum METFO	2
133	4	4	10.9	tr K2RAP2 K2RAP2_METFP	Tetrahydromethanopterin S-methyltransferase subunit E OS=Methanobacterium formicicum METFP	3
134	4	4	17.7	tr K2QZS6 K2QZS6_METFP	UPF0145 protein A994_06900 OS=Methanobacterium formicicum METFP	2
135	4	4	6.7	tr A0A090JXT2 A0A090JXT2_METFO	O-acetylhomoserine (Thiol)-lyase OS=Methanobacterium formicicum METFO	2
136	4	4	2.1	tr A0A090I4M6 A0A090I4M6_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
137	3.92	4	29.8	tr A0A090JUU7 A0A090JUU7_METFO	Tetrahydromethanopterin S-methyltransferase subunit G OS=Methanobacterium formicicum METFO	2
138	3.77	3.86	7.7	tr A0A0S4FMQ4 A0A0S4FMQ4_METFO	Putative hydrogenase expression/formation protein MJ067 OS=Methanobacterium formicicum METFO	2
139	3.73	3.88	13.6	tr A0A090I7Q9 A0A090I7Q9_METFO	2-amino-3,7-dideoxy-D-threo-hept-6-ulosonate synthase OS=Methanobacterium formicicum METFO	3
140	3.69	3.96	16.5	tr A0A090I653 A0A090I653_METFO	Methanogenesis marker protein 11 OS=Methanobacterium formicicum METFO	6
141	3.62	3.7	6.6	tr A0A090JU62 A0A090JU62_METFO	Glutamine amidotransferase OS=Methanobacterium formicicum METFO	2
142	3.6	3.81	5.9	tr A0A090JYJ5 A0A090JYJ5_METFO	Glutamine--fructose-6-phosphate aminotransferase [isozyme 1] OS=Methanobacterium formicicum METFO	2
143	3.54	3.69	9.5	tr A0A090I345 A0A090I345_METFO	3-isopropylmalate dehydrogenase OS=Methanobacterium formicicum METFO	2
144	3.48	3.61	7.3	tr A0A090I6V8 A0A090I6V8_METFO	CoB-CoM heterodisulfide reductase subunit B OS=Methanobacterium formicicum METFO	2
145	3.41	3.49	24.5	tr A0A090I442 A0A090I442_METFO	50S ribosomal protein L30e OS=Methanobacterium formicicum METFO	2
146	3.29	3.44	9.5	tr A0A090I1H9 A0A090I1H9_METFO	30S ribosomal protein S4e OS=Methanobacterium formicicum METFO	2

Amostra 5

147	3.28	3.43	6.4	tr A0A090JVX7 A0A090JVX7_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
148	3.26	3.4	6.8	tr A0A090I8Z8 A0A090I8Z8_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
149	3.18	3.26	6.9	tr A0A090I3A4 A0A090I3A4_METFO	Phosphoribosylamine--glycine ligase OS=Methanobacterium formicicum METFO	2
150	3.15	3.22	4.8	tr A0A0S4FS90 A0A0S4FS90_METFO	Putative secreted protein OS=Methanobacterium formicicum METFO	2
151	3.1	3.68	27.1	tr A0A090I6K9 A0A090I6K9_METFO	30S ribosomal protein S17 OS=Methanobacterium formicicum METFO	3
152	3.06	3.14	8.7	tr A0A090I314 A0A090I314_METFO	CBS domain-containing protein OS=Methanobacterium formicicum METFO	2
153	3.02	3.1	9.7	tr A0A089ZE87 A0A089ZE87_METFO	ABC transporter ATP-binding protein OS=Methanobacterium formicicum METFO	2
154	2.97	3.1	8.4	tr A0A090I1P7 A0A090I1P7_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
155	2.92	3.08	12.8	tr A0A090JSP3 A0A090JSP3_METFO	Uridylate kinase OS=Methanobacterium formicicum OX=21 METFO	2
156	2.9	2.98	24.2	tr A0A090I340 A0A090I340_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
157	2.88	2.99	7.1	tr A0A089ZAG5 A0A089ZAG5_METFO	Transcriptional regulator with CBS domains OS=Methanobacterium formicicum METFO	2
158	2.75	2.87	2.5	tr A0A090I246 A0A090I246_METFO	3-hydroxy-3-methylglutaryl coenzyme A reductase OS=Methanobacterium formicicum METFO	1
159	2.73	2.98	7.7	tr A0A090I4J0 A0A090I4J0_METFO	Pyruvate carboxylase subunit A OS=Methanobacterium formicicum METFO	3
160	2.72	2.81	5.2	tr A0A090I1J8 A0A090I1J8_METFO	Putative methylthioribose-1-phosphate isomerase OS=Methanobacterium formicicum METFO	2
161	2.69	3.47	11.1	tr A0A089ZG23 A0A089ZG23_METFO	Formylmethanofuran dehydrogenase subunit F FwdF1 OS=Methanobacterium formicicum METFO	3
162	2.68	2.93	8	tr A0A090I471 A0A090I471_METFO	GDP-mannose 4,6-dehydratase OS=Methanobacterium formicicum METFO	2
163	2.58	2.64	6	tr K2RCU3 K2RCU3_METFP	DNA-directed RNA polymerase subunit A' OS=Methanobacterium formicicum METFP	2
164	2.57	2.82	26.5	tr A0A089ZDW1 A0A089ZDW1_METFO	Methyl-coenzyme M reductase II D subunit MtrD OS=Methanobacterium formicicum METFO	3
165	2.53	2.6	3.9	tr A0A090I135 A0A090I135_METFO	UTP--glucose-1-phosphate uridylyltransferase OS=Methanobacterium formicicum METFO	1
166	2.41	2.46	8.1	tr A0A090I8S1 A0A090I8S1_METFO	Universal stress protein UspA5 OS=Methanobacterium formicicum METFO	1
167	2.4	2.48	2.1	tr A0A090I4Q7 A0A090I4Q7_METFO	Aspartate--tRNA(Asp/Asn) ligase OS=Methanobacterium formicicum METFO	1
168	2.34	2.37	7.5	tr A0A089ZV28 A0A089ZV28_METFO	Heat shock protein Hsp20 OS=Methanobacterium formicicum METFO	1
169	2.25	2.28	2.7	tr A0A090I574 A0A090I574_METFO	Glutamine-fructose-6-phosphate transaminase OS=Methanobacterium formicicum METFO	1
170	2.24	2.27	4.4	tr A0A089ZH87 A0A089ZH87_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
171	2.24	2.27	3.7	tr A0A090I5U3 A0A090I5U3_METFO	Geranylgeranyl glyceryl phosphate synthase OS=Methanobacterium formicicum METFO	1
172	2.22	2.25	1.5	tr A0A090I3L9 A0A090I3L9_METFO	Dihydroxy-acid dehydratase OS=Methanobacterium formicicum METFO	1
173	2.22	2.24	5.7	tr K2R3V7 K2R3V7_METFP	Pyruvate ferredoxin oxidoreductase subunit gamma/delta C METFP	1
174	2.18	2.2	2.3	tr A0A090I2R3 A0A090I2R3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
175	2.13	2.15	2.3	tr A0A090I5F2 A0A090I5F2_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
176	2.1	2.12	1.9	tr A0A090I8R0 A0A090I8R0_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
177	2.09	2.1	5.1	tr A0A090I796 A0A090I796_METFO	Pyridoxal 5'-phosphate synthase subunit PdxS OS=Methanobacterium formicicum METFO	1
178	2.06	2.07	2.3	tr A0A090I409 A0A090I409_METFO	Glutamyl-tRNA(Gln) amidotransferase subunit D OS=Methanobacterium formicicum METFO	1
179	2.06	2.06	15.8	tr A0A089ZGZ1 A0A089ZGZ1_METFO	30S ribosomal protein S8e OS=Methanobacterium formicicum METFO	1

Amostra 5

180	2.05	2.06	10.2 tr A0A090I9E4 A0A090I9E4_METFO	30S ribosomal protein S7 OS=Methanobacterium formicicu	METFO	1
181	2.05	2.06	2.7 tr A0A090I2F4 A0A090I2F4_METFO	Polyferredoxin protein MvhB OS=Methanobacterium formic	METFO	1
182	2.04	2.05	8.8 tr K2QDP1 K2QDP1_METFP	30S ribosomal protein S10 OS=Methanobacterium formicic	METFP	1
183	2.04	2.05	1.1 tr K2QC73 K2QC73_METFP	Lon protease OS=Methanobacterium formicicum (strain D5	METFP	1
184	2.02	2.03	9.8 tr A0A089Z9L4 A0A089Z9L4_METFO	Nitrogen regulatory protein P-II GlnK1 OS=Methanobacteriu	METFO	1
185	2.02	2.02	10.3 tr A0A090JU33 A0A090JU33_METFO	DNA-directed RNA polymerase OS=Methanobacterium fori	METFO	1
186	2.02	2.02	7.8 tr A0A089ZVR0 A0A089ZVR0_METFO	30S ribosomal protein S12 OS=Methanobacterium formicic	METFO	1
187	2.01	6.27	7.3 tr A0A090I2C6 A0A090I2C6_METFO	Methyl-coenzyme M reductase component A2 AtwA1 OS=M	METFO	3
188	2.01	2.02	4 tr A0A090I514 A0A090I514_METFO	UPF0219 protein DSM1535_2142 OS=Methanobacterium i	METFO	1
189	2.01	2.01	5.6 tr A0A090I5G4 A0A090I5G4_METFO	Exosome complex component Rrp41 OS=Methanobacteriu	METFO	1
190	2.01	2.01	4.2 tr K2RR02 K2RR02_METFP	50S ribosomal protein L1 OS=Methanobacterium formicicu	METFP	1
191	2.01	2.01	8.3 tr K2R401 K2R401_METFP	30S ribosomal protein S11 OS=Methanobacterium formicic	METFP	1
192	2.01	2.01	2.1 tr A0A089ZHW9 A0A089ZHW9_METFO	ABC transporter permease protein OS=Methanobacterium	METFO	1
193	2.01	2.01	7.4 tr A0A089ZBW3 A0A089ZBW3_METFO	Glutamate synthase beta subunit GltB1 OS=Methanobacte	METFO	1
194	2	36.47	40 tr K2QYM4 K2QYM4_METFP	Methyl-coenzyme M reductase subunit alpha OS=Methano	METFP	66
195	2	2.01	4.1 tr A0A090JV79 A0A090JV79_METFO	Formamidopyrimidine-DNA glycosylase OS=Methanobacte	METFO	1
196	2	2	2.2 tr K2R3P6 K2R3P6_METFP	Acetyl-CoA decarbonylase/synthase complex subunit beta	METFP	1
197	2	2	5.6 tr K2QZX7 K2QZX7_METFP	Extracellular phosphate-binding protein OS=Methanobacte	METFP	1
198	2	2	1.6 tr K2QDN1 K2QDN1_METFP	DNA-directed RNA polymerase subunit B OS=Methanobac	METFP	1
199	2	2	4 tr A0A090IAU5 A0A090IAU5_METFO	Choloylglycine hydrolase OS=Methanobacterium formicicu	METFO	1
200	2	2	5.2 tr A0A090I9B3 A0A090I9B3_METFO	GTP cyclohydrolase III OS=Methanobacterium formicicum	METFO	1
201	2	2	2 tr K2RWD7 K2RWD7_METFP	Nitrogenase MoFe cofactor biosynthesis protein NifE OS=M	METFP	1
202	2	2	4.2 tr K2RTL1 K2RTL1_METFP	Uncharacterized protein OS=Methanobacterium formicicu	METFP	1
203	2	2	3.4 tr K2R5G7 K2R5G7_METFP	Superoxide dismutase OS=Methanobacterium formicicum	METFP	1
204	2	2	5.7 tr K2R1L9 K2R1L9_METFP	Aspartate carbamoyltransferase regulatory chain OS=Meth	METFP	1
205	2	2	4 tr K2QXG4 K2QXG4_METFP	Glucose-methanol-choline oxidoreductase OS=Methanoba	METFP	1
206	2	2	2.1 tr K2QCN1 K2QCN1_METFP	V-type ATP synthase subunit C OS=Methanobacterium fori	METFP	1
207	2	2	2.8 tr A0A090JX53 A0A090JX53_METFO	Cell wall biosynthesis protein Mur ligase family OS=Methar	METFO	1
208	2	2	3.3 tr A0A090JUV1 A0A090JUV1_METFO	Tetrahydromethanopterin S-methyltransferase subunit D O	METFO	1
209	2	2	6.9 tr A0A090JU72 A0A090JU72_METFO	Putative secreted protein OS=Methanobacterium formicicu	METFO	1
210	2	2	6.7 tr A0A090I9D6 A0A090I9D6_METFO	Triosephosphate isomerase OS=Methanobacterium formic	METFO	1
211	2	2	7.2 tr A0A090I489 A0A090I489_METFO	GTP-binding protein Rab-like protein OS=Methanobacteriu	METFO	1
212	2	2	2.5 tr A0A090I3U3 A0A090I3U3_METFO	Peptidase U62 modulator of DNA gyrase OS=Methanobact	METFO	1

Amostra 5

213	2	2	15	tr A0A089ZVK3 A0A089ZVK3_METFO	CBS domain-containing protein OS=Methanobacterium formicicum METFO	1
214	2	2	3.1	tr A0A089ZIC5 A0A089ZIC5_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
215	2	2	5.1	tr A0A089ZH31 A0A089ZH31_METFO	Cobalamin biosynthesis protein CbiM3 OS=Methanobacterium formicicum METFO	2
216	2	2	6.7	tr A0A089ZGY8 A0A089ZGY8_METFO	Putative membrane protein OS=Methanobacterium formicicum METFO	1
217	2	2	6.1	tr A0A089ZDB1 A0A089ZDB1_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
218	2	2	3.9	tr A0A089Z928 A0A089Z928_METFO	Nitrogenase cofactor biosynthesis protein NifB OS=Methanobacterium formicicum METFO	1
219	1.93	2.01	4.4	tr A0A090I171 A0A090I171_METFO	Probable tRNA pseudouridine synthase B OS=Methanobacterium formicicum METFO	1
220	1.91	2.13	6.1	tr A0A090JXI6 A0A090JXI6_METFO	Cyclic 2,3-diphosphoglycerate synthetase OS=Methanobacterium formicicum METFO	2
221	1.88	2.16	8.5	tr A0A089Z979 A0A089Z979_METFO	Site-determining protein OS=Methanobacterium formicicum METFO	2
222	1.73	1.87	2.9	tr A0A090I166 A0A090I166_METFO	Enolase OS=Methanobacterium formicicum OX=2162 GN= METFO	1
223	1.62	1.77	2.2	tr A0A089ZGW2 A0A089ZGW2_METFO	Translation initiation factor 2 subunit gamma OS=Methanobacterium formicicum METFO	1
224	1.6	1.72	7.6	tr K2R4J0 K2R4J0_METFP	2-oxoglutarate ferredoxin oxidoreductase subunit gamma C METFP	1
225	1.57	1.83	8.7	tr A0A090I672 A0A090I672_METFO	dTDP-glucose 4,6-dehydratase OS=Methanobacterium formicicum METFO	2
226	1.5	1.65	3.3	tr A0A090I3J1 A0A090I3J1_METFO	Formate dehydrogenase beta subunit FdhB OS=Methanobacterium formicicum METFO	1
227	1.4	1.57	3.6	tr A0A089ZH50 A0A089ZH50_METFO	Phosphate ABC transporter phosphate-binding protein PstA METFO	1
228	1.38	1.6	5	tr A0A090JTX4 A0A090JTX4_METFO	dCTP deaminase, dUMP-forming OS=Methanobacterium formicicum METFO	1
229	1.38	1.49	12.6	tr A0A090I6Q6 A0A090I6Q6_METFO	Putative membrane protein OS=Methanobacterium formicicum METFO	1
230	1.36	1.47	9.6	tr K2RW50 K2RW50_METFP	DNA/RNA-binding protein Alba OS=Methanobacterium formicicum METFP	1
231	1.34	1.55	4.8	tr A0A090I8U4 A0A090I8U4_METFO	Acetolactate synthase OS=Methanobacterium formicicum METFO	2

Amostra 5



ID statistics table

Unused (Conf) Cutoff	Proteins Detected	Proteins Before Grouping	Distinct Peptides	Spectra Identified	% Total Spectra
>2.0 (99)	193	383	2727	9609	14.1
>1.3 (95)	231	495	2803	9775	14.4
>0.47 (66)	265	568	2876	9888	14.6
Cutoff Applied: >0.05 (10%)	360	816	3028	10113	14.9

Amostra 6

1) Z:\Projects\UniMS2019_95 MALves\Data\CS6_9uL.wiff

Sample Type: Identification
Cys. Alkylation: Iodoacetamide
Digestion: Trypsin
Instrument: TripleTOF 6600
Special Factors: Gel-based ID
Species:
ID Focus: Biological modifications
 Amino acid substitutions
Database: 20190624_uniprot_methanobacterium+formicum_6903entries.fasta
Search Effort: Thorough
FDR Analysis: Yes
User Modified Parameter Files: Yes



Proteins detected table

N	Unused	Total	% Cov (95	Accession #	Name	Species	Peptides(95%)
1	96.54	96.54	69.7	tr A0A090I8L6 A0A090I8L6_METFO	Replication factor-A domain-containing protein OS=Methan	METFO	89
2	87.97	87.97	36.2	tr A0A090I3J2 A0A090I3J2_METFO	Uncharacterized protein OS=Methanobacterium formicicum	METFO	127
3	76.45	76.45	84.1	tr A0A090I2R9 A0A090I2R9_METFO	F420-non-reducing hydrogenase subunit A OS=Methanob	METFO	109
4	71.84	71.84	70.2	tr A0A090I3G7 A0A090I3G7_METFO	CoB--CoM heterodisulfide reductase subunit A HdrA2 OS=	METFO	99
5	71.78	71.8	62.9	tr A0A090I3T1 A0A090I3T1_METFO	Elongation factor 2 OS=Methanobacterium formicum OX-	METFO	68
6	68.69	68.7	77.3	tr A0A090IAH6 A0A090IAH6_METFO	Thermosome subunit OS=Methanobacterium formicum C	METFO	207
7	67.51	67.52	65.6	tr A0A090I2M3 A0A090I2M3_METFO	V-type ATP synthase alpha chain OS=Methanobacterium f	METFO	72
8	66.57	66.67	91.9	tr A0A090I7W3 A0A090I7W3_METFO	Methyl-coenzyme M reductase subunit beta OS=Methanob	METFO	192
9	65.93	66.06	60.9	tr A0A090I3A9 A0A090I3A9_METFO	Chaperone protein DnaK OS=Methanobacterium formicicu	METFO	48
10	64.32	64.32	72.5	tr A0A090I2T3 A0A090I2T3_METFO	Methyl-coenzyme M reductase subunit beta OS=Methanob	METFO	262
11	63.74	63.78	56.8	tr A0A090I7T4 A0A090I7T4_METFO	Phosphoenolpyruvate synthase OS=Methanobacterium for	METFO	57
12	56.52	56.52	71.3	tr A0A090I2G6 A0A090I2G6_METFO	Methyl-coenzyme M reductase subunit alpha OS=Methano	METFO	148
13	53.62	53.62	72.5	tr A0A090I9A6 A0A090I9A6_METFO	Hydroxylamine reductase OS=Methanobacterium formicicu	METFO	58
14	51.81	51.81	92.8	tr A0A090I573 A0A090I573_METFO	5,10-methylenetetrahydromethanopterin reductase OS=Me	METFO	235

Amostra 6

15	49.63	49.63	24.3	tr A0A090I8K7 A0A090I8K7_METFO	Cobalamin biosynthesis protein CobN OS=Methanobacteri METFO	31
16	47	47	33	tr A0A090I5F3 A0A090I5F3_METFO	Putative secreted protein OS=Methanobacterium formicicu METFO	76
17	43.01	43.01	70.9	tr A0A090JVC3 A0A090JVC3_METFO	Methyl-coenzyme M reductase subunit alpha OS=Methano METFO	109
18	42.77	42.85	58.4	tr A0A089ZDH4 A0A089ZDH4_METFO	Elongation factor 1-alpha OS=Methanobacterium formicicu METFO	34
19	41.84	42.03	20	tr A0A090I544 A0A090I544_METFO	Putative secreted protein OS=Methanobacterium formicicu METFO	28
20	40.74	40.74	34.2	tr A0A090I151 A0A090I151_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO	34
21	40.7	40.72	35.4	tr A0A089ZDA2 A0A089ZDA2_METFO	Cell division control protein Cdc48 OS=Methanobacterium METFO	22
22	39.86	39.88	49.9	tr A0A089ZAI4 A0A089ZAI4_METFO	Formylmethanofuran dehydrogenase subunit A FwdA OS= METFO	40
23	38.02	40	49.6	tr A0A090I4W3 A0A090I4W3_METFO	F420-non-reducing hydrogenase vhc subunit A OS=Metha METFO	30
24	36.89	36.9	58.8	tr A0A090I7U6 A0A090I7U6_METFO	GDP-mannose 4,6-dehydratase OS=Methanobacterium fo METFO	29
25	34.51	45.8	61.5	tr A0A090IA40 A0A090IA40_METFO	Thermosome subunit OS=Methanobacterium formicicum C METFO	88
26	33.42	33.43	37.4	tr A0A090I2L6 A0A090I2L6_METFO	D-3-phosphoglycerate dehydrogenase OS=Methanobacter METFO	17
27	32.98	34.79	21.4	tr A0A090I2R3 A0A090I2R3_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO	22
28	32.5	32.5	51.8	tr A0A0S4FR78 A0A0S4FR78_METFO	V-type ATP synthase beta chain OS=Methanobacterium fo METFO	61
29	31.25	31.28	49.9	tr A0A089ZUL5 A0A089ZUL5_METFO	Tryptophan synthase beta chain OS=Methanobacterium fo METFO	21
30	29.59	29.59	40.6	tr A0A090I8W8 A0A090I8W8_METFO	Bifunctional enzyme Fae/Hps OS=Methanobacterium formi METFO	24
31	29.52	29.55	80.8	tr A0A089ZAX5 A0A089ZAX5_METFO	30S ribosomal protein S2 OS=Methanobacterium formicicu METFO	20
32	29.35	29.43	15.9	tr A0A090I571 A0A090I571_METFO	Carbamoyl-phosphate synthase large chain OS=Methanob METFO	16
33	28.86	28.89	52.1	tr A0A090I2P0 A0A090I2P0_METFO	CBS domain-containing protein OS=Methanobacterium fo METFO	20
34	26.62	26.62	44.5	tr A0A090I360 A0A090I360_METFO	F420H2 oxidase FprA OS=Methanobacterium formicicum (METFO	21
35	26.42	26.44	58.7	tr A0A090I6Q2 A0A090I6Q2_METFO	Formylmethanofuran dehydrogenase subunit C FwdC OS= METFO	25
36	26.17	26.22	33.3	tr A0A090I2C6 A0A090I2C6_METFO	Methyl-coenzyme M reductase component A2 AtwA1 OS= METFO	14
37	26.12	26.19	44.4	tr A0A090I781 A0A090I781_METFO	Fructose-1,6-bisphosphate aldolase/phosphatase OS=Met METFO	29
38	26.04	26.04	64.3	tr A0A089ZG02 A0A089ZG02_METFO	DNA repair and recombination protein RadA OS=Methano METFO	19
39	26	26	54.9	tr A0A090I5T3 A0A090I5T3_METFO	Methyl-coenzyme M reductase subunit gamma OS=Methar METFO	16
40	25.52	25.73	11.6	tr A0A090I3E3 A0A090I3E3_METFO	Uncharacterized protein OS=Methanobacterium formicicu METFO	16
41	25.33	25.46	27.3	tr A0A090JYJ5 A0A090JYJ5_METFO	Glutamine--fructose-6-phosphate aminotransferase [isome METFO	13
42	25.22	25.37	40.3	tr A0A090I6W9 A0A090I6W9_METFO	Cell shape determining protein MreB/Mrl OS=Methanobact METFO	14
43	25.07	25.1	52.9	tr A0A090I281 A0A090I281_METFO	Pyruvate synthase subunit PorA OS=Methanobacterium fo METFO	26
44	24.9	25.02	43.4	tr A0A090JTT4 A0A090JTT4_METFO	Methanogenesis marker protein 15 OS=Methanobacterium METFO	12
45	24.69	24.8	22.6	tr A0A090I5E9 A0A090I5E9_METFO	Pyruvate carboxylase subunit B OS=Methanobacterium fo METFO	14
46	24.67	24.76	39.5	tr A0A089ZIP7 A0A089ZIP7_METFO	DNA primase DnaG OS=Methanobacterium formicicum O METFO	13
47	23.91	23.94	55.2	tr A0A090I842 A0A090I842_METFO	CBS domain-containing membrane protein OS=Methanoba METFO	25

Amostra 6

48	22.93	22.93	20.8	tr A0A089ZHH5 A0A089ZHH5_METFO	Phosphoserine phosphatase SerB OS=Methanobacterium METFO	12
49	22.92	22.98	56.9	tr A0A090I5H3 A0A090I5H3_METFO	Methenyltetrahydromethanopterin cyclohydrolase OS=Metf METFO	18
50	22.12	22.15	19.3	tr A0A089ZGB0 A0A089ZGB0_METFO	Catalase-peroxidase OS=Methanobacterium formicicum O METFO	11
51	21.83	21.86	33.7	tr A0A090I3J9 A0A090I3J9_METFO	Tungsten-containing formylmethanofuran dehydrogenase 2 METFO	16
52	21.79	21.79	41.9	tr A0A089ZGX6 A0A089ZGX6_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	20
53	21.75	21.78	39.3	tr A0A089ZBS9 A0A089ZBS9_METFO	Acetyl-CoA acetyltransferase OS=Methanobacterium formi METFO	11
54	21.52	21.54	18.6	tr A0A090I3V1 A0A090I3V1_METFO	Formate dehydrogenase alpha subunit FdhA OS=Methano METFO	18
55	21.39	21.41	46.1	tr A0A089ZVL0 A0A089ZVL0_METFO	Cell division protein FtsZ OS=Methanobacterium formicicum METFO	15
56	21.06	21.11	27.4	tr A0A0S4FMY2 A0A0S4FMY2_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	11
57	20.76	20.83	40	tr A0A090I6I2 A0A090I6I2_METFO	Adenylosuccinate synthetase OS=Methanobacterium formi METFO	13
58	20.56	20.62	25.6	tr A0A090JWH2 A0A090JWH2_METFO	Phosphoglucosamine mutase GlmM2 OS=Methanobacteri METFO	10
59	20.38	20.44	55.4	tr A0A090I8V8 A0A090I8V8_METFO	F420-dependent methylenetetrahydromethanopterin dehyd METFO	21
60	20.33	20.38	33.3	tr A0A090JXN7 A0A090JXN7_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	22
61	20.25	20.27	57.9	tr A0A089ZEV2 A0A089ZEV2_METFO	CBS domain-containing protein OS=Methanobacterium for METFO	16
62	20.25	20.26	38	tr A0A090I2I0 A0A090I2I0_METFO	Putative aminotransferase MJ0959 OS=Methanobacterium METFO	22
63	20.23	20.28	51.7	tr A0A090I6I3 A0A090I6I3_METFO	Coenzyme F420 hydrogenase subunit beta OS=Methanoba METFO	15
64	20.17	20.26	27.1	tr A0A090I4Q7 A0A090I4Q7_METFO	Aspartate--tRNA(Asp/Asn) ligase OS=Methanobacterium fc METFO	11
65	20.1	20.11	38.6	tr A0A090I3I6 A0A090I3I6_METFO	Putative lipoprotein MJ0085 OS=Methanobacterium formici METFO	12
66	20.08	20.08	62.8	tr A0A090I5H7 A0A090I5H7_METFO	Tetrahydromethanopterin S-methyltransferase subunit H O METFO	21
67	20.06	20.06	53	tr A0A090IB20 A0A090IB20_METFO	Proteasome subunit alpha OS=Methanobacterium formicic METFO	12
68	19.54	19.59	16.2	tr A0A090I8V0 A0A090I8V0_METFO	Threonine--tRNA ligase OS=Methanobacterium formicicum METFO	10
69	19.2	19.27	50.2	tr A0A090I2T7 A0A090I2T7_METFO	Methyl-coenzyme M reductase subunit gamma OS=Methar METFO	10
70	19.1	19.2	31.7	tr A0A090I8M3 A0A090I8M3_METFO	S-adenosylmethionine synthase OS=Methanobacterium fo METFO	10
71	19.02	20.53	36.8	tr A0A090I305 A0A090I305_METFO	Coenzyme F420 hydrogenase alpha subunit FrhA OS=Met METFO	23
72	18.71	18.71	29.9	tr A0A090I5S8 A0A090I5S8_METFO	Argininosuccinate synthase OS=Methanobacterium formici METFO	11
73	18.57	18.63	26.5	tr A0A090I4R4 A0A090I4R4_METFO	Type A flavoprotein FprA OS=Methanobacterium formicicu METFO	9
74	18.22	18.23	44.7	tr A0A090I443 A0A090I443_METFO	Superoxide dismutase OS=Methanobacterium formicicum METFO	15
75	18.08	19.32	24.6	tr A0A0S4FN19 A0A0S4FN19_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	12
76	18.03	18.03	29	tr A0A089ZV33 A0A089ZV33_METFO	FeS assembly protein SufBD OS=Methanobacterium formi METFO	11
77	17.73	17.75	54.6	tr A0A089ZCQ3 A0A089ZCQ3_METFO	Putative rubrerythrin OS=Methanobacterium formicicum O METFO	9
78	17.64	17.67	31.8	tr A0A090I5I8 A0A090I5I8_METFO	Digeranylglycerolglycerophospholipid reductase OS=Metha METFO	24
79	17.62	17.64	49	tr A0A090I1I9 A0A090I1I9_METFO	CoB-CoM heterodisulfide reductase iron-sulfur subunit C O METFO	14
80	17.33	17.35	39.2	tr A0A089ZI64 A0A089ZI64_METFO	ATP phosphoribosyltransferase OS=Methanobacterium for METFO	11

Amostra 6

81	17.05	17.07	44.9 tr A0A090JVT4 A0A090JVT4_METFO	Putative ABC transporter ATP-binding protein MJ0089 OS=Methanobacterium formicicum METFO	10
82	16.79	16.83	43.7 tr A0A090I5U4 A0A090I5U4_METFO	SPFH domain/Band 7 family protein OS=Methanobacterium formicicum METFO	9
83	16.68	16.74	12.2 tr A0A0S4FQI5 A0A0S4FQI5_METFO	Cell division cycle protein 48 homolog MJ1156 OS=Methanobacterium formicicum METFO	8
84	16.65	16.67	27 tr A0A090JXJ6 A0A090JXJ6_METFO	3-dehydroquinate synthase OS=Methanobacterium formicicum METFO	11
85	16.39	16.4	24 tr A0A090JW43 A0A090JW43_METFO	Glutamyl-tRNA(Gln) amidotransferase subunit A OS=Methanobacterium formicicum METFO	8
86	16.34	16.38	30.7 tr A0A090I9D3 A0A090I9D3_METFO	Succinate--CoA ligase [ADP-forming] subunit beta OS=Methanobacterium formicicum METFO	9
87	16.31	16.35	21.1 tr A0A089ZHM6 A0A089ZHM6_METFO	Methyl-coenzyme M reductase component A2 AtwA2 OS=Methanobacterium formicicum METFO	8
88	16.24	16.25	34.3 tr A0A089ZGS2 A0A089ZGS2_METFO	Replication factor C small subunit OS=Methanobacterium formicicum METFO	8
89	16.21	16.27	37.8 tr A0A089Z979 A0A089Z979_METFO	Site-determining protein OS=Methanobacterium formicicum METFO	9
90	16.08	16.13	31.3 tr A0A090JV64 A0A090JV64_METFO	CBS domain-containing membrane protein OS=Methanobacterium formicicum METFO	12
91	16.03	16.04	48 tr A0A090JTE0 A0A090JTE0_METFO	50S ribosomal protein L6 OS=Methanobacterium formicicum METFO	10
92	16.03	16.03	26.6 tr A0A090I7L2 A0A090I7L2_METFO	Acetyl-CoA decarbonylase/synthase complex subunit gamr OS=Methanobacterium formicicum METFO	8
93	15.9	15.95	49.8 tr A0A090I1H9 A0A090I1H9_METFO	30S ribosomal protein S4e OS=Methanobacterium formicicum METFO	11
94	15.8	15.89	35.3 tr A0A090I0T1 A0A090I0T1_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	10
95	15.79	15.9	23.1 tr A0A0S4FSL7 A0A0S4FSL7_METFO	Diaminopimelate decarboxylase OS=Methanobacterium formicicum METFO	8
96	15.63	15.71	41.1 tr A0A090JUK8 A0A090JUK8_METFO	V-type proton ATPase subunit E OS=Methanobacterium formicicum METFO	12
97	15.58	15.61	34.2 tr A0A090I345 A0A090I345_METFO	3-isopropylmalate dehydrogenase OS=Methanobacterium formicicum METFO	10
98	15.37	15.45	15.6 tr A0A090I904 A0A090I904_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	8
99	15.26	24.65	29.9 tr A0A089ZHQ4 A0A089ZHQ4_METFO	Methyl-coenzyme M reductase component A2 AtwA3 OS=Methanobacterium formicicum METFO	13
100	15.22	15.3	25.1 tr A0A090JTE7 A0A090JTE7_METFO	30S ribosomal protein S3 OS=Methanobacterium formicicum METFO	8
101	15.21	15.29	25.8 tr A0A090JVX7 A0A090JVX7_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	8
102	15.16	15.23	62.4 tr A0A090I2W9 A0A090I2W9_METFO	Proteasome subunit beta OS=Methanobacterium formicicum METFO	34
103	15.02	15.08	32.2 tr A0A089ZVL1 A0A089ZVL1_METFO	50S ribosomal protein L10 OS=Methanobacterium formicicum METFO	9
104	15	15.18	11.7 tr A0A090I9E0 A0A090I9E0_METFO	DNA-directed RNA polymerase subunit OS=Methanobacterium formicicum METFO	11
105	14.96	15.07	30.1 tr A0A090I938 A0A090I938_METFO	Phosphomethylpyrimidine synthase OS=Methanobacterium formicicum METFO	9
106	14.87	14.99	33.7 tr A0A090I1P7 A0A090I1P7_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	12
107	14.73	16.94	23.7 tr A0A089ZCR8 A0A089ZCR8_METFO	Proteasome-activating nucleotidase OS=Methanobacterium formicicum METFO	8
108	14.65	14.76	22.3 tr A0A089ZI25 A0A089ZI25_METFO	Serine hydroxymethyltransferase OS=Methanobacterium formicicum METFO	7
109	14.42	14.5	20.3 tr A0A090I3H2 A0A090I3H2_METFO	Phosphoribosylformylglycinamide synthase subunit PurL OS=Methanobacterium formicicum METFO	11
110	14.19	14.24	36.5 tr A0A090I4Y4 A0A090I4Y4_METFO	Circadian clock protein KaiC OS=Methanobacterium formicicum METFO	8
111	14.12	19.93	19.3 tr A0A090IAQ7 A0A090IAQ7_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	16
112	14.09	14.09	16.4 tr A0A089ZV53 A0A089ZV53_METFO	Phenylalanine--tRNA ligase beta subunit OS=Methanobacterium formicicum METFO	7
113	14.07	14.14	23 tr A0A090I4J0 A0A090I4J0_METFO	Pyruvate carboxylase subunit A OS=Methanobacterium formicicum METFO	8

Amostra 6

114	14.07	14.08	34.3	tr A0A090I897 A0A090I897_METFO	Formylmethanofuran--tetrahydromethanopterin formyltrans METFO	19
115	14	14	20.8	tr A0A090I7B6 A0A090I7B6_METFO	Inosine-5'-monophosphate dehydrogenase OS=Methanobacterium formicicum METFO	8
116	13.74	13.77	41.2	tr A0A090JW64 A0A090JW64_METFO	LemA family protein OS=Methanobacterium formicicum OX=2162 GN= METFO	7
117	13.7	13.74	40.7	tr A0A090I4X8 A0A090I4X8_METFO	F420-dependent NADP reductase OS=Methanobacterium formicicum METFO	8
118	13.62	13.7	23.9	tr A0A090I3Q7 A0A090I3Q7_METFO	Nucleotidyl transferase OS=Methanobacterium formicicum METFO	8
119	13.59	13.63	66.7	tr A0A089ZCU1 A0A089ZCU1_METFO	Transcription elongation factor Spt5 OS=Methanobacterium formicicum METFO	7
120	13.59	13.62	61.7	tr A0A089ZUS9 A0A089ZUS9_METFO	50S ribosomal protein L18 OS=Methanobacterium formicicum METFO	7
121	13.56	13.6	35.7	tr A0A090I0N7 A0A090I0N7_METFO	PyrE-like protein OS=Methanobacterium formicicum OX=2162 GN= METFO	7
122	13.39	13.42	47	tr A0A089ZGG4 A0A089ZGG4_METFO	50S ribosomal protein L14 OS=Methanobacterium formicicum METFO	7
123	13.25	13.49	41	tr A0A090I653 A0A090I653_METFO	Methanogenesis marker protein 11 OS=Methanobacterium formicicum METFO	14
124	13.22	13.27	28.1	tr A0A090I166 A0A090I166_METFO	Enolase OS=Methanobacterium formicicum OX=2162 GN= METFO	8
125	13.09	13.23	39.8	tr A0A090I5W3 A0A090I5W3_METFO	30S ribosomal protein S3Ae OS=Methanobacterium formicicum METFO	7
126	13.08	13.12	25.4	tr A0A090I672 A0A090I672_METFO	dTDP-glucose 4,6-dehydratase OS=Methanobacterium formicicum METFO	7
127	13.07	13.24	15.5	tr A0A090I2I6 A0A090I2I6_METFO	Archaeal glutamate synthase [NADPH] OS=Methanobacterium formicicum METFO	7
128	12.92	13.03	35.2	tr A0A090JUG7 A0A090JUG7_METFO	Phosphate binding protein OS=Methanobacterium formicicum METFO	9
129	12.63	13.02	15.5	tr A0A090I5M1 A0A090I5M1_METFO	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit METFO	7
130	12.62	12.75	11.2	tr A0A090JW98 A0A090JW98_METFO	Anaerobic ribonucleoside-triphosphate reductase OS=Methanobacterium formicicum METFO	8
131	12.59	12.73	29.4	tr A0A090I7Q9 A0A090I7Q9_METFO	2-amino-3,7-dideoxy-D-threo-hept-6-ulosonate synthase OX=2162 GN= METFO	7
132	12.57	12.64	19.1	tr A0A090JX53 A0A090JX53_METFO	Cell wall biosynthesis protein Mur ligase family OS=Methanobacterium formicicum METFO	7
133	12.54	13.03	27.8	tr A0A090I3H9 A0A090I3H9_METFO	5-formaminoimidazole-4-carboxamide-1-(beta)-D-ribofuran METFO	13
134	12.49	12.56	23.1	tr A0A090I135 A0A090I135_METFO	UTP--glucose-1-phosphate uridylyltransferase OS=Methanobacterium formicicum METFO	6
135	12.47	12.59	35.9	tr A0A090I7K3 A0A090I7K3_METFO	Phosphate import ATP-binding protein PstB OS=Methanobacterium formicicum METFO	7
136	12.43	12.47	53.4	tr A0A090I9S3 A0A090I9S3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	13
137	12.42	12.57	67.4	tr A0A090I170 A0A090I170_METFO	TATA-box-binding protein OS=Methanobacterium formicicum METFO	9
138	12.39	12.47	34.6	tr A0A089ZE87 A0A089ZE87_METFO	ABC transporter ATP-binding protein OS=Methanobacterium formicicum METFO	10
139	12.38	12.42	19.1	tr A0A090JTX8 A0A090JTX8_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	7
140	12.22	12.41	21.2	tr A0A090I3S6 A0A090I3S6_METFO	DNA-directed RNA polymerase subunit A' OS=Methanobacterium formicicum METFO	9
141	12.18	12.2	37.7	tr A0A090I2G3 A0A090I2G3_METFO	Tetrahydromethanopterin S-methyltransferase subunit A OX=2162 GN= METFO	13
142	12.1	12.16	12.2	tr A0A089Z9Y9 A0A089Z9Y9_METFO	Type II secretion system protein E GspE OS=Methanobacterium formicicum METFO	7
143	12.04	12.18	18.3	tr A0A090I8U4 A0A090I8U4_METFO	Acetolactate synthase OS=Methanobacterium formicicum METFO	7
144	12	12	47.5	tr A0A089ZDW1 A0A089ZDW1_METFO	Methyl-coenzyme M reductase II D subunit MrtD OS=Methanobacterium formicicum METFO	8
145	12	12	25.3	tr A0A089ZAG5 A0A089ZAG5_METFO	Transcriptional regulator with CBS domains OS=Methanobacterium formicicum METFO	9
146	12	12	31.7	tr A0A090I5G8 A0A090I5G8_METFO	F420-non-reducing hydrogenase subunit G OS=Methanobacterium formicicum METFO	8

Amostra 6

147	11.92	11.99	47.1	tr A0A090JWN0 A0A090JWN0_METFO	Putative secreted protein OS=Methanobacterium formicicum METFO	37
148	11.89	11.96	22.9	tr A0A090I3P4 A0A090I3P4_METFO	Alanine dehydrogenase OS=Methanobacterium formicicum METFO	6
149	11.64	11.7	22.4	tr A0A090JW72 A0A090JW72_METFO	Arsenite-activated ATPase ArsA OS=Methanobacterium formicicum METFO	6
150	11.59	11.64	29.5	tr A0A090I494 A0A090I494_METFO	Short-chain dehydrogenase family protein OS=Methanobacterium formicicum METFO	7
151	11.5	11.57	31.3	tr A0A090I4G9 A0A090I4G9_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	9
152	11.44	11.51	28.4	tr A0A090I0T5 A0A090I0T5_METFO	Toprim domain-containing protein OS=Methanobacterium formicicum METFO	8
153	11.34	11.44	66.2	tr A0A090JUT3 A0A090JUT3_METFO	F420-non-reducing hydrogenase iron-sulfur subunit D OS=Methanobacterium formicicum METFO	7
154	11.25	11.31	29.5	tr A0A090I740 A0A090I740_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	7
155	11.2	11.52	16.2	tr A0A090JXV9 A0A090JXV9_METFO	CTP synthase OS=Methanobacterium formicicum OX=216 METFO	7
156	11.2	11.29	47	tr A0A089ZF65 A0A089ZF65_METFO	PRC-barrel domain-containing protein OS=Methanobacterium formicicum METFO	6
157	11.14	11.4	9.6	tr A0A090I4D4 A0A090I4D4_METFO	Acetyl-coenzyme A synthetase OS=Methanobacterium formicicum METFO	7
158	11.03	11.08	14.5	tr A0A090JY31 A0A090JY31_METFO	Aspartokinase OS=Methanobacterium formicicum OX=216 METFO	7
159	10.98	11.22	22.4	tr A0A090I433 A0A090I433_METFO	GMP synthase [glutamine-hydrolyzing] subunit B OS=Methanobacterium formicicum METFO	7
160	10.9	11.29	37.5	tr A0A090I6C9 A0A090I6C9_METFO	Ketol-acid reductoisomerase (NADP(+)) OS=Methanobacterium formicicum METFO	10
161	10.88	11	18.9	tr A0A090JUQ9 A0A090JUQ9_METFO	Putative nickel insertion protein OS=Methanobacterium formicicum METFO	6
162	10.8	10.85	17.1	tr A0A090I8E3 A0A090I8E3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	6
163	10.76	10.88	18.8	tr A0A090I428 A0A090I428_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	6
164	10.73	10.79	19.1	tr A0A090I796 A0A090I796_METFO	Pyridoxal 5'-phosphate synthase subunit PdxS OS=Methanobacterium formicicum METFO	6
165	10.71	10.88	23	tr A0A089ZC17 A0A089ZC17_METFO	Glutamine synthetase GlnA2 OS=Methanobacterium formicicum METFO	8
166	10.7	10.86	29.9	tr A0A089ZJ55 A0A089ZJ55_METFO	DNA polymerase sliding clamp OS=Methanobacterium formicicum METFO	9
167	10.65	10.82	17.6	tr A0A090I5F2 A0A090I5F2_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	6
168	10.57	10.77	15.8	tr A0A090I4G3 A0A090I4G3_METFO	LL-diaminopimelate aminotransferase OS=Methanobacterium formicicum METFO	7
169	10.52	10.64	22.1	tr A0A090I0K3 A0A090I0K3_METFO	Histidinol-phosphate aminotransferase OS=Methanobacterium formicicum METFO	6
170	10.45	10.59	13.3	tr A0A090I0Z8 A0A090I0Z8_METFO	Type 2 DNA topoisomerase 6 subunit B OS=Methanobacterium formicicum METFO	6
171	10.44	10.54	34.4	tr A0A090I622 A0A090I622_METFO	Translation initiation factor 2 subunit alpha OS=Methanobacterium formicicum METFO	9
172	10.4	10.49	14.5	tr A0A090I6T0 A0A090I6T0_METFO	Glutamine synthetase OS=Methanobacterium formicicum METFO	5
173	10.26	10.29	21.3	tr A0A090I314 A0A090I314_METFO	CBS domain-containing protein OS=Methanobacterium formicicum METFO	5
174	10.26	10.28	5.4	tr A0A090I4M6 A0A090I4M6_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	6
175	10.19	10.22	46	tr A0A090JWL2 A0A090JWL2_METFO	IMP cyclohydrolase OS=Methanobacterium formicicum OX=216 METFO	11
176	10.18	12.21	31.6	tr A0A089ZER7 A0A089ZER7_METFO	Exosome complex component Rrp4 OS=Methanobacterium formicicum METFO	9
177	10.15	10.17	19.4	tr A0A090I4Z6 A0A090I4Z6_METFO	Aminotransferase OS=Methanobacterium formicicum OX=216 METFO	5
178	10.08	10.14	9.8	tr A0A0S4FR34 A0A0S4FR34_METFO	Acetyl-CoA decarbonylase/synthase complex subunit alpha OS=Methanobacterium formicicum METFO	5
179	10.02	10.03	32.4	tr A0A090I180 A0A090I180_METFO	50S ribosomal protein L5 OS=Methanobacterium formicicum METFO	5

Amostra 6

180	9.98	10.09	20.4	tr A0A090I8R6 A0A090I8R6_METFO	Acetylornithine aminotransferase OS=Methanobacterium fc METFO	9
181	9.89	10.06	12.8	tr A0A089ZGW2 A0A089ZGW2_METFO	Translation initiation factor 2 subunit gamma OS=Methanol METFO	5
182	9.82	9.9	35.8	tr A0A089ZGF9 A0A089ZGF9_METFO	30S ribosomal protein S5 OS=Methanobacterium formicicu METFO	5
183	9.75	9.88	8.5	tr A0A090I6Y8 A0A090I6Y8_METFO	DNA-directed RNA polymerase subunit B OS=Methanobac METFO	5
184	9.74	9.96	16.9	tr A0A090I246 A0A090I246_METFO	3-hydroxy-3-methylglutaryl coenzyme A reductase OS=Met METFO	5
185	9.67	9.77	19.4	tr A0A090I4Y0 A0A090I4Y0_METFO	Threonine synthase OS=Methanobacterium formicicum OX METFO	5
186	9.66	9.72	28.9	tr A0A090I2J1 A0A090I2J1_METFO	Pyruvate ferredoxin oxidoreductase beta subunit PorB OS= METFO	6
187	9.6	9.67	13.7	tr A0A089ZHI2 A0A089ZHI2_METFO	S-inosyl-L-homocysteine hydrolase OS=Methanobacterium METFO	6
188	9.41	9.53	19.4	tr A0A089Z928 A0A089Z928_METFO	Nitrogenase cofactor biosynthesis protein NifB OS=Methan METFO	6
189	9.4	9.44	46.5	tr A0A089ZGZ1 A0A089ZGZ1_METFO	30S ribosomal protein S8e OS=Methanobacterium formicic METFO	9
190	9.36	9.46	27.3	tr A0A090I471 A0A090I471_METFO	GDP-mannose 4,6-dehydratase OS=Methanobacterium for METFO	8
191	9.35	9.4	24.3	tr A0A090JTX4 A0A090JTX4_METFO	dCTP deaminase, dUMP-forming OS=Methanobacterium f METFO	5
192	9.3	9.46	18.9	tr A0A090IAD3 A0A090IAD3_METFO	Homoserine dehydrogenase OS=Methanobacterium formic METFO	5
193	9.15	9.19	26.6	tr A0A090JSP3 A0A090JSP3_METFO	Uridylate kinase OS=Methanobacterium formicicum OX=21 METFO	5
194	9.02	9.16	23	tr A0A090I3I7 A0A090I3I7_METFO	Putative sugar kinase MTH_1544 OS=Methanobacterium f METFO	5
195	8.98	9.02	19.9	tr A0A089ZAD0 A0A089ZAD0_METFO	Hydrogenase expression/formation protein HypE1 OS=Met METFO	5
196	8.97	9.1	24.3	tr A0A090JVV9 A0A090JVV9_METFO	Aspartate carbamoyltransferase OS=Methanobacterium fo METFO	6
197	8.95	16.57	31.1	tr A0A090I7S6 A0A090I7S6_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	14
198	8.9	8.94	23	tr A0A090I7T8 A0A090I7T8_METFO	Peptidyl-prolyl cis-trans isomerase OS=Methanobacterium METFO	5
199	8.88	9.01	25.4	tr A0A090I424 A0A090I424_METFO	Translation initiation factor 5A OS=Methanobacterium form METFO	8
200	8.86	9.11	18.2	tr A0A089ZBE1 A0A089ZBE1_METFO	UPF0288 protein BRM9_0509 OS=Methanobacterium forr METFO	7
201	8.79	8.91	17.7	tr A0A090I514 A0A090I514_METFO	UPF0219 protein DSM1535_2142 OS=Methanobacterium METFO	5
202	8.69	8.78	10	tr A0A090I3L9 A0A090I3L9_METFO	Dihydroxy-acid dehydratase OS=Methanobacterium formic METFO	5
203	8.68	8.78	18.1	tr A0A090I409 A0A090I409_METFO	Glutamyl-tRNA(Gln) amidotransferase subunit D OS=Meth: METFO	6
204	8.67	8.8	18	tr A0A090JXT2 A0A090JXT2_METFO	O-acetylhomoserine (Thiol)-lyase OS=Methanobacterium f METFO	6
205	8.58	8.73	11	tr A0A090JWN5 A0A090JWN5_METFO	DNA-directed RNA polymerase subunit beta OS=Methanol METFO	6
206	8.53	8.67	26.9	tr A0A090I552 A0A090I552_METFO	Exosome complex component Rrp42 OS=Methanobacteriu METFO	7
207	8.46	8.49	22.8	tr A0A090I455 A0A090I455_METFO	Type 2 DNA topoisomerase 6 subunit A OS=Methanobacte METFO	5
208	8.38	8.57	19.3	tr A0A090I6D3 A0A090I6D3_METFO	Ornithine carbamoyltransferase OS=Methanobacterium for METFO	5
209	8.38	8.53	14.8	tr A0A0S4FN62 A0A0S4FN62_METFO	UDP-N-acetylglucosamine 2-epimerase OS=Methanobacte METFO	5
210	8.33	8.4	12	tr A0A090I599 A0A090I599_METFO	Acetyl-CoA decarbonylase/synthase complex subunit beta METFO	6
211	8.3	8.33	6.9	tr A0A0S4FQD8 A0A0S4FQD8_METFO	Putative ABC transporter ATP-binding protein MJ0719 OS= METFO	4
212	8.27	8.42	11.5	tr A0A090I4Y9 A0A090I4Y9_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	4

Amostra 6

213	8.15	8.27	10 tr A0A090I298 A0A090I298_METFO	Archaeal glutamate synthase [NADPH] OS=Methanobacteri	NADPH	6
214	8.05	8.15	25.9 tr A0A090I219 A0A090I219_METFO	Translation initiation factor 6 OS=Methanobacterium formic	METFO	4
215	8.05	8.06	27.6 tr A0A090JUF5 A0A090JUF5_METFO	Pyruvate synthase subunit PorC OS=Methanobacterium fo	METFO	4
216	8.01	8.02	12 tr A0A089ZH78 A0A089ZH78_METFO	V-type ATP synthase subunit C OS=Methanobacterium fori	METFO	4
217	8	8	15.3 tr A0A090I574 A0A090I574_METFO	Glutamine-fructose-6-phosphate transaminase OS=Methar	METFO	4
218	8	8	19.1 tr A0A090I5E6 A0A090I5E6_METFO	Inositol-3-phosphate synthase OS=Methanobacterium form	METFO	5
219	7.98	8.24	16.2 tr A0A090I3N5 A0A090I3N5_METFO	2-isopropylmalate synthase LeuA OS=Methanobacterium fi	METFO	4
220	7.75	7.82	23.2 tr A0A090I3S2 A0A090I3S2_METFO	Phosphoglycerate kinase OS=Methanobacterium formicicu	METFO	7
221	7.72	7.79	15.3 tr A0A090JXZ1 A0A090JXZ1_METFO	Delta-aminolevulinic acid dehydratase OS=Methanobacteri	METFO	4
222	7.7	7.8	12.5 tr A0A090I8R0 A0A090I8R0_METFO	Uncharacterized protein OS=Methanobacterium formicicu	METFO	5
223	7.61	7.69	40.6 tr A0A090I579 A0A090I579_METFO	Uncharacterized protein OS=Methanobacterium formicicu	METFO	4
224	7.48	7.55	15 tr A0A090JUJ4 A0A090JUJ4_METFO	Probable L-aspartate dehydrogenase OS=Methanobacteriu	METFO	4
225	7.44	7.48	17.4 tr A0A090I958 A0A090I958_METFO	Extracellular solute-binding protein OS=Methanobacterium	METFO	4
226	7.41	7.6	21.5 tr A0A090I6V8 A0A090I6V8_METFO	CoB-CoM heterodisulfide reductase subunit B OS=Methan	METFO	5
227	7.3	7.36	9 tr A0A090I2S7 A0A090I2S7_METFO	Uncharacterized protein OS=Methanobacterium formicicu	METFO	4
228	7.28	7.41	20.9 tr A0A089ZGF5 A0A089ZGF5_METFO	CBS domain-containing protein OS=Methanobacterium fori	METFO	4
229	7.27	7.39	13.7 tr A0A090JSU7 A0A090JSU7_METFO	Glyceraldehyde-3-phosphate dehydrogenase OS=Methanc	METFO	5
230	7.14	7.19	14.6 tr A0A0S4FLD6 A0A0S4FLD6_METFO	ABC transporter substrate-binding protein OS=Methanobac	METFO	4
231	7.11	7.29	28.8 tr A0A090I7Y5 A0A090I7Y5_METFO	AsnC family transcriptional regulator OS=Methanobacteriur	METFO	4
232	7.07	7.11	17.6 tr A0A090I5G4 A0A090I5G4_METFO	Exosome complex component Rrp41 OS=Methanobacteriu	METFO	4
233	7.05	7.17	8.5 tr A0A090JUS4 A0A090JUS4_METFO	Type-2 serine-tRNA ligase OS=Methanobacterium formicic	METFO	4
234	7.01	7.22	16.4 tr A0A090I689 A0A090I689_METFO	Uncharacterized protein OS=Methanobacterium formicicu	METFO	5
235	6.98	7.03	10.5 tr A0A090I3H5 A0A090I3H5_METFO	Adenylosuccinate lyase OS=Methanobacterium formicicum	METFO	4
236	6.92	6.95	12.9 tr A0A090I5T7 A0A090I5T7_METFO	Multifunctional fusion protein OS=Methanobacterium formic	METFO	4
237	6.91	6.94	36.4 tr A0A089ZA06 A0A089ZA06_METFO	PRC-barrel domain-containing protein OS=Methanobacteri	METFO	5
238	6.88	6.96	32.4 tr K2QDP1 K2QDP1_METFP	30S ribosomal protein S10 OS=Methanobacterium formicic	METFP	4
239	6.8	6.84	35.9 tr A0A089ZG55 A0A089ZG55_METFO	Uncharacterized protein OS=Methanobacterium formicicu	METFO	9
240	6.75	6.86	9.9 tr A0A090I1C7 A0A090I1C7_METFO	Oxidoreductase domain-containing protein OS=Methanoba	METFO	4
241	6.69	6.79	14.7 tr A0A090I431 A0A090I431_METFO	2-oxoglutarate synthase subunit KorA OS=Methanobacteri	METFO	5
242	6.66	6.76	50.5 tr A0A090I6K9 A0A090I6K9_METFO	30S ribosomal protein S17 OS=Methanobacterium formicic	METFO	5
243	6.62	6.8	17.8 tr A0A089ZGH1 A0A089ZGH1_METFO	Bifunctional biotin operon repressor/biotin-acetyl-CoA-carb	METFO	6
244	6.59	7.62	13.1 tr A0A090I3X2 A0A090I3X2_METFO	Probable phosphoglucosamine mutase OS=Methanobacte	METFO	5
245	6.57	6.6	11.4 tr A0A090I2F4 A0A090I2F4_METFO	Polyferredoxin protein MvhB OS=Methanobacterium formic	METFO	4

Amostra 6

246	6.44	6.61	25.4	tr A0A090I148 A0A090I148_METFO	dTDP-glucose 4,6-dehydratase-like protein OS=Methanobac METFO	5
247	6.38	6.59	9.6	tr A0A090I4F2 A0A090I4F2_METFO	Methionine--tRNA ligase OS=Methanobacterium formicicur METFO	5
248	6.34	6.45	20.3	tr A0A090I8S1 A0A090I8S1_METFO	Universal stress protein UspA5 OS=Methanobacterium form METFO	3
249	6.32	6.42	16.8	tr A0A089ZGG9 A0A089ZGG9_METFO	50S ribosomal protein L4 OS=Methanobacterium formicicu METFO	4
250	6.32	6.35	12.2	tr A0A090I306 A0A090I306_METFO	Restriction endonuclease OS=Methanobacterium formicicu METFO	3
251	6.28	6.36	22	tr A0A090I7U4 A0A090I7U4_METFO	ABC transporter OS=Methanobacterium formicicum OX=21 METFO	5
252	6.22	6.29	46	tr A0A089ZBS5 A0A089ZBS5_METFO	30S ribosomal protein S6e OS=Methanobacterium formicic METFO	4
253	6.16	6.27	12.2	tr A0A090I524 A0A090I524_METFO	tRNA-splicing ligase RtcB OS=Methanobacterium formicicu METFO	4
254	6.11	6.12	8.3	tr A0A090JXI6 A0A090JXI6_METFO	Cyclic 2,3-diphosphoglycerate synthetase OS=Methanobac METFO	4
255	6.03	6.03	36.1	tr A0A089ZB18 A0A089ZB18_METFO	50S ribosomal protein L23 OS=Methanobacterium formicic METFO	3
256	6.02	6.03	7.4	tr A0A090I583 A0A090I583_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	3
257	6.01	6.01	29.4	tr A0A089ZHN5 A0A089ZHN5_METFO	Probable transcription termination protein NusA OS=Metha METFO	3
258	6.01	6.01	7	tr A0A0S4FM80 A0A0S4FM80_METFO	2,3-bisphosphoglycerate-independent phosphoglycerate m METFO	3
259	6	6	9.7	tr A0A0S4FPJ4 A0A0S4FPJ4_METFO	N-acetyl-gamma-glutamyl-phosphate reductase OS=Metha METFO	3
260	6	6	48.7	tr A0A090JYF1 A0A090JYF1_METFO	TRAM domain-containing protein OS=Methanobacterium fc METFO	3
261	6	6	42.9	tr A0A090JUU7 A0A090JUU7_METFO	Tetrahydromethanopterin S-methyltransferase subunit G O METFO	3
262	6	6	9	tr A0A090I731 A0A090I731_METFO	Glucose-1-phosphate thymidyltransferase OS=Methanob. METFO	3
263	6	6	18.5	tr A0A090I368 A0A090I368_METFO	Formylmethanofuran dehydrogenase subunit E OS=Metha METFO	3
264	6	6	15	tr A0A090I2L4 A0A090I2L4_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	3
265	5.97	6.1	18.8	tr A0A090I521 A0A090I521_METFO	4-hydroxy-tetrahydrodipicolinate reductase OS=Methanoba METFO	4
266	5.85	5.92	10.2	tr A0A090IAE6 A0A090IAE6_METFO	Putative aminopeptidase MJ0555 OS=Methanobacterium fi METFO	3
267	5.83	6.06	6.3	tr A0A089ZAV8 A0A089ZAV8_METFO	RNA-metabolising metallo-beta-lactamase OS=Methanoba METFO	4
268	5.76	5.87	10.9	tr A0A090JYG5 A0A090JYG5_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	4
269	5.75	5.8	20.3	tr A0A090I9E4 A0A090I9E4_METFO	30S ribosomal protein S7 OS=Methanobacterium formicicu METFO	3
270	5.74	5.82	13	tr A0A090JWV3 A0A090JWV3_METFO	Acetylglutamate kinase OS=Methanobacterium formicicum METFO	3
271	5.72	5.8	9	tr A0A090I1N1 A0A090I1N1_METFO	Coenzyme F390 synthetase FtsA2 OS=Methanobacterium METFO	4
272	5.68	5.94	14.4	tr A0A089ZUP9 A0A089ZUP9_METFO	Energy-converting hydrogenase B subunit N EhbN OS=Me METFO	5
273	5.58	5.69	15.9	tr A0A089ZG23 A0A089ZG23_METFO	Formylmethanofuran dehydrogenase subunit F FwdF1 OS= METFO	4
274	5.57	5.67	11.9	tr A0A089ZUT3 A0A089ZUT3_METFO	50S ribosomal protein L3 OS=Methanobacterium formicicu METFO	3
275	5.55	5.7	17.1	tr A0A090I8N8 A0A090I8N8_METFO	Putative thymidylate synthase OS=Methanobacterium form METFO	4
276	5.49	5.64	9.5	tr A0A090I4K5 A0A090I4K5_METFO	Glutamate dehydrogenase OS=Methanobacterium formicic METFO	3
277	5.47	5.58	9	tr A0A090I4N0 A0A090I4N0_METFO	2,3-bisphosphoglycerate-independent phosphoglycerate m METFO	4
278	5.43	5.52	26.7	tr A0A090I4J8 A0A090I4J8_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	3

Amostra 6

279	5.37	5.49	11 tr A0A090I3A4 A0A090I3A4_METFO	Phosphoribosylamine--glycine ligase OS=Methanobacteriu METFO	4
280	5.35	5.46	16 tr A0A090JYQ2 A0A090JYQ2_METFO	Vitamin-B12 independent methionine synthase OS=Methar METFO	4
281	5.33	5.46	9.4 tr A0A090I657 A0A090I657_METFO	3-isopropylmalate dehydratase large subunit OS=Methanol METFO	3
282	5.33	5.39	21.7 tr A0A090JV59 A0A090JV59_METFO	Transcription elongation factor NusA-like protein OS=Meth METFO	3
283	5.31	5.41	16.6 tr A0A090I3K4 A0A090I3K4_METFO	Diaminopimelate epimerase OS=Methanobacterium formic METFO	4
284	5.27	5.33	27.3 tr A0A090I2G1 A0A090I2G1_METFO	Universal stress protein MTBMA_c15380 OS=Methanobac METFO	3
285	5.23	5.33	18.4 tr A0A090I729 A0A090I729_METFO	TrkA domain-containing protein OS=Methanobacterium for METFO	3
286	5.21	5.31	34.6 tr A0A090JTC3 A0A090JTC3_METFO	30S ribosomal protein S9 OS=Methanobacterium formicicu METFO	3
287	5.19	5.25	14.5 tr A0A089ZA94 A0A089ZA94_METFO	CobQ/CobB/MinD/ParA nucleotide binding domain-containi METFO	3
288	5.15	5.21	8.5 tr A0A090I9P2 A0A090I9P2_METFO	Phenylacetate-coenzyme A ligase OS=Methanobacterium 1 METFO	3
289	5.13	5.2	8.8 tr A0A090JY2 A0A090JY2_METFO	Branched-chain-amino-acid aminotransferase OS=Methan METFO	3
290	5.12	5.18	38.8 tr A0A090I442 A0A090I442_METFO	50S ribosomal protein L30e OS=Methanobacterium formici METFO	3
291	5.08	5.23	8.8 tr A0A090I116 A0A090I116_METFO	Amidophosphoribosyltransferase OS=Methanobacterium fc METFO	3
292	5.06	5.41	4.2 tr A0A090JWU4 A0A090JWU4_METFO	Valine--tRNA ligase OS=Methanobacterium formicicum OX METFO	4
293	5.03	5.17	7.2 tr A0A090JWG4 A0A090JWG4_METFO	DNA ligase OS=Methanobacterium formicicum OX=2162 C METFO	3
294	4.97	5.05	15.7 tr A0A089ZV28 A0A089ZV28_METFO	Heat shock protein Hsp20 OS=Methanobacterium formicici METFO	3
295	4.93	5.04	4.8 tr A0A090JW16 A0A090JW16_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	8
296	4.92	5.07	21.1 tr K2REW5 K2REW5_METFP	30S ribosomal protein S15 OS=Methanobacterium formicic METFP	3
297	4.89	5.07	15.3 tr A0A090I3I4 A0A090I3I4_METFO	Putative secreted protein OS=Methanobacterium formicicu METFO	3
298	4.83	4.89	19.1 tr A0A090JU33 A0A090JU33_METFO	DNA-directed RNA polymerase OS=Methanobacterium for METFO	3
299	4.81	4.95	10 tr A0A090I6B3 A0A090I6B3_METFO	Homocitrate synthase AksA OS=Methanobacterium formici METFO	3
300	4.67	4.75	7.3 tr A0A090I410 A0A090I410_METFO	CRISPR-associated negative autoregulator, DevR family O METFO	2
301	4.65	4.82	6.6 tr A0A090I6D0 A0A090I6D0_METFO	Tryptophan synthase beta chain OS=Methanobacterium fo METFO	3
302	4.63	4.67	17.4 tr A0A090I684 A0A090I684_METFO	Formylmethanofuran dehydrogenase subunit E OS=Metha METFO	3
303	4.61	4.66	6.5 tr A0A090I391 A0A090I391_METFO	Daunorubicin resistance ABC transporter ATPase subunit (METFO	2
304	4.61	4.65	27.4 tr K2QZS6 K2QZS6_METFP	UPF0145 protein A994_06900 OS=Methanobacterium forn METFP	3
305	4.58	4.75	9.8 tr A0A090I3J1 A0A090I3J1_METFO	Formate dehydrogenase beta subunit FdhB OS=Methanob METFO	3
306	4.55	4.67	12.9 tr K2REI5 K2REI5_METFP	Coenzyme F420 hydrogenase subunit gamma OS=Methan METFP	3
307	4.48	4.62	8 tr A0A090I5D7 A0A090I5D7_METFO	Glutamate-1-semialdehyde 2,1-aminomutase OS=Methanc METFO	3
308	4.44	4.55	13.1 tr A0A090I6I6 A0A090I6I6_METFO	Isopentenyl-diphosphate delta-isomerase OS=Methanobac METFO	3
309	4.36	4.39	22 tr A0A089Z8Q6 A0A089Z8Q6_METFO	30S ribosomal protein S11 OS=Methanobacterium formicic METFO	3
310	4.35	4.58	6.3 tr A0A090JWA7 A0A090JWA7_METFO	Lysine--tRNA ligase OS=Methanobacterium formicicum O METFO	3
311	4.28	4.31	24.2 tr A0A090I340 A0A090I340_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	2

Amostra 6

312	4.27	4.38	19.3	tr A0A090I950 A0A090I950_METFO	Formylmethanofuran dehydrogenase subunit D FwdD OS=Methanobacterium formicicum METFO	3
313	4.18	4.2	9.8	tr A0A089ZH87 A0A089ZH87_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
314	4.15	4.26	4.4	tr A0A090I8R1 A0A090I8R1_METFO	UDP-N-acetylmuramoyl-L-alanine-D-glutamate ligase OS=Methanobacterium formicicum METFO	2
315	4.15	4.24	9.2	tr A0A0S4FNG0 A0A0S4FNG0_METFO	Formylmethanofuran-tetrahydromethanopterin formyltransferase OS=Methanobacterium formicicum METFO	2
316	4.12	4.13	7.5	tr A0A090I171 A0A090I171_METFO	Probable tRNA pseudouridine synthase B OS=Methanobacterium formicicum METFO	2
317	4.08	6.11	17.1	tr A0A090I9F1 A0A090I9F1_METFO	Tetrahydromethanopterin S-methyltransferase subunit A OS=Methanobacterium formicicum METFO	3
318	4.05	4.16	4.3	tr A0A090I9W6 A0A090I9W6_METFO	Adenine specific DNA methylase Mod OS=Methanobacterium formicicum METFO	3
319	4.05	4.06	17.2	tr A0A090JWM7 A0A090JWM7_METFO	2-oxoglutarate synthase subunit KorC OS=Methanobacterium formicicum METFO	2
320	4.03	4.3	6	tr A0A089ZBK5 A0A089ZBK5_METFO	Roadblock/LC7 domain-containing protein OS=Methanobacterium formicicum METFO	3
321	4.02	4.03	12	tr A0A090I8S8 A0A090I8S8_METFO	ABC transporter ATP-binding protein OS=Methanobacterium formicicum METFO	2
322	4.02	4.02	17.3	tr A0A090I174 A0A090I174_METFO	Adenylate kinase OS=Methanobacterium formicicum OX=2 METFO	2
323	4.01	4.02	25.3	tr K2RRN0 K2RRN0_METFP	Uncharacterized protein OS=Methanobacterium formicicum METFP	2
324	4.01	4.01	9.4	tr K2RR02 K2RR02_METFP	50S ribosomal protein L1 OS=Methanobacterium formicicum METFP	3
325	4.01	4.01	7.8	tr A0A090I6W5 A0A090I6W5_METFO	Coenzyme F420:L-glutamate ligase OS=Methanobacterium formicicum METFO	2
326	4.01	4.01	5.9	tr A0A089ZFA3 A0A089ZFA3_METFO	Acetyl-CoA decarbonylase/synthase complex subunit delta OS=Methanobacterium formicicum METFO	2
327	4.01	4.01	8.1	tr A0A090I503 A0A090I503_METFO	Malate dehydrogenase OS=Methanobacterium formicicum METFO	2
328	4.01	4.01	9.1	tr A0A090IAU5 A0A090IAU5_METFO	Choloylglycine hydrolase OS=Methanobacterium formicicum METFO	2
329	4.01	4.01	10.4	tr A0A089ZII9 A0A089ZII9_METFO	MotA/TolQ/ExbB proton channel family protein OS=Methanobacterium formicicum METFO	2
330	4	4	7.7	tr A0A0S4FMQ4 A0A0S4FMQ4_METFO	Putative hydrogenase expression/formation protein MJ0676 OS=Methanobacterium formicicum METFO	2
331	4	4	5.5	tr K2QE14 K2QE14_METFP	Arginine biosynthesis bifunctional protein ArgJ OS=Methanobacterium formicicum METFP	2
332	4	4	4.6	tr A0A089ZHE0 A0A089ZHE0_METFO	Molybdenum cofactor synthesis domain-containing protein OS=Methanobacterium formicicum METFO	2
333	4	4	13.7	tr A0A090JSW3 A0A090JSW3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
334	4	4	10.3	tr A0A090I192 A0A090I192_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
335	4	4	10.9	tr K2RAP2 K2RAP2_METFP	Tetrahydromethanopterin S-methyltransferase subunit E OS=Methanobacterium formicicum METFP	3
336	4	4	6.6	tr A0A0S4FSI3 A0A0S4FSI3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
337	4	4	13	tr A0A090JU20 A0A090JU20_METFO	3-hexulose-6-phosphate isomerase HxlB2 OS=Methanobacterium formicicum METFO	2
338	3.93	4.21	11.6	tr A0A0S4FPY7 A0A0S4FPY7_METFO	Aminotransferase OS=Methanobacterium formicicum OX=1 METFO	4
339	3.87	3.99	22.8	tr A0A090I8C8 A0A090I8C8_METFO	Flavodoxin/nitric oxide synthase OS=Methanobacterium formicicum METFO	3
340	3.85	3.92	9.8	tr A0A090I5U3 A0A090I5U3_METFO	Geranylgeranyl glyceryl phosphate synthase OS=Methanobacterium formicicum METFO	2
341	3.79	3.91	5.8	tr A0A090I3Q1 A0A090I3Q1_METFO	Putative FAD-dependent oxidoreductase MJ0033 OS=Methanobacterium formicicum METFO	3
342	3.78	3.91	15.6	tr A0A089ZVR0 A0A089ZVR0_METFO	30S ribosomal protein S12 OS=Methanobacterium formicicum METFO	3
343	3.77	3.86	4	tr A0A090JU38 A0A090JU38_METFO	Argininosuccinate lyase OS=Methanobacterium formicicum METFO	2
344	3.73	3.85	8.8	tr A0A090I3Z3 A0A090I3Z3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2

Amostra 6

345	3.69	3.76	6.3 tr A0A090I8Q5 A0A090I8Q5_METFO	Probable cobyric acid synthase OS=Methanobacterium formicicum METFO	2
346	3.61	3.8	7.9 tr A0A089ZV44 A0A089ZV44_METFO	GTP cyclohydrolase MptA OS=Methanobacterium formicicum METFO	2
347	3.51	3.61	6 tr A0A090JX22 A0A090JX22_METFO	Proline--tRNA ligase OS=Methanobacterium formicicum O METFO	3
348	3.49	3.54	4.3 tr A0A090IAX4 A0A090IAX4_METFO	Acyl-CoA synthetase OS=Methanobacterium formicicum O METFO	2
349	3.48	3.55	22.9 tr A0A089ZGF2 A0A089ZGF2_METFO	50S ribosomal protein L13 OS=Methanobacterium formicicum METFO	2
350	3.41	3.48	11.2 tr A0A090IAS5 A0A090IAS5_METFO	Oxidoreductase MW2403 OS=Methanobacterium formicicum METFO	2
351	3.4	3.73	6.8 tr A0A090JSM8 A0A090JSM8_METFO	Transcription initiation factor IIB OS=Methanobacterium formicicum METFO	2
352	3.35	3.55	16.9 tr A0A090I8I5 A0A090I8I5_METFO	Uroporphyrinogen-III C-methyltransferase OS=Methanobacterium formicicum METFO	3
353	3.33	3.4	5.3 tr A0A090I4Q8 A0A090I4Q8_METFO	Phenylalanine--tRNA ligase alpha subunit OS=Methanobacterium formicicum METFO	2
354	3.29	3.43	3.4 tr A0A089ZBN0 A0A089ZBN0_METFO	PIN domain-containing protein OS=Methanobacterium formicicum METFO	2
355	3.27	3.35	16.9 tr A0A090I465 A0A090I465_METFO	Spore coat polysaccharide biosynthesis protein SpsK OS=Methanobacterium formicicum METFO	3
356	3.26	3.41	6.5 tr A0A090I679 A0A090I679_METFO	UDP-glucose 4-epimerase OS=Methanobacterium formicicum METFO	2
357	3.25	3.33	11 tr A0A090I560 A0A090I560_METFO	Putative hydrogenase nickel incorporation protein HypB OS=Methanobacterium formicicum METFO	2
358	3.24	3.34	7.7 tr A0A090I333 A0A090I333_METFO	Signal recognition particle 54 kDa protein OS=Methanobacterium formicicum METFO	3
359	3.23	3.36	7.4 tr A0A090I3U3 A0A090I3U3_METFO	Peptidase U62 modulator of DNA gyrase OS=Methanobacterium formicicum METFO	3
360	3.15	3.29	19.6 tr A0A089Z9L4 A0A089Z9L4_METFO	Nitrogen regulatory protein P-II GlnK1 OS=Methanobacterium formicicum METFO	2
361	3.15	3.21	4.8 tr A0A0S4FS90 A0A0S4FS90_METFO	Putative secreted protein OS=Methanobacterium formicicum METFO	2
362	3.12	3.19	5.1 tr A0A090I2K2 A0A090I2K2_METFO	PBS lyase HEAT domain-containing protein OS=Methanobacterium formicicum METFO	2
363	3.11	3.17	18.8 tr A0A090I5C4 A0A090I5C4_METFO	LemA family protein OS=Methanobacterium formicicum O METFO	3
364	3.05	3.16	13.1 tr A0A089ZC51 A0A089ZC51_METFO	Extracellular phosphate-binding protein OS=Methanobacterium formicicum METFO	2
365	3.03	3.15	7.3 tr A0A090JW77 A0A090JW77_METFO	ATP phosphoribosyltransferase OS=Methanobacterium formicicum METFO	2
366	3.01	3.08	8.1 tr A0A090I626 A0A090I626_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
367	2.96	3.14	5.1 tr A0A090I251 A0A090I251_METFO	Histidine--tRNA ligase OS=Methanobacterium formicicum METFO	2
368	2.92	2.98	7.2 tr A0A090I3L5 A0A090I3L5_METFO	UPF0285 protein DSM1535_1340 OS=Methanobacterium formicicum METFO	2
369	2.91	3.01	4.8 tr A0A090I3Y4 A0A090I3Y4_METFO	Transcriptional repressor of nif and glnA operons NrpR OS=Methanobacterium formicicum METFO	2
370	2.86	2.92	14 tr A0A089ZGF4 A0A089ZGF4_METFO	30S ribosomal protein S13 OS=Methanobacterium formicicum METFO	2
371	2.83	2.89	30.1 tr A0A0S4FLE4 A0A0S4FLE4_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
372	2.8	2.86	8.2 tr A0A090I4P4 A0A090I4P4_METFO	Endonuclease NucS OS=Methanobacterium formicicum O METFO	2
373	2.78	2.88	9.2 tr A0A090I5P8 A0A090I5P8_METFO	Coenzyme A biosynthesis bifunctional protein CoaBC OS=Methanobacterium formicicum METFO	3
374	2.74	2.8	7.5 tr A0A090IA04 A0A090IA04_METFO	5-amino-6-(D-ribitylamino)uracil--L-tyrosine 4-hydroxyphenyl transferase OS=Methanobacterium formicicum METFO	2
375	2.74	2.8	14.6 tr A0A090I8J3 A0A090I8J3_METFO	Cobalt-precorrin-8X methylmutase OS=Methanobacterium formicicum METFO	2
376	2.72	2.81	5.3 tr A0A090JTB4 A0A090JTB4_METFO	Ribonuclease J OS=Methanobacterium formicicum OX=21 METFO	2
377	2.72	2.78	20.1 tr A0A090I3Y5 A0A090I3Y5_METFO	Flavodoxin OS=Methanobacterium formicicum OX=2162 G METFO	2

Amostra 6

378	2.71	2.78	3.3 tr A0A090I4P0 A0A090I4P0_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
379	2.68	2.74	8.5 tr A0A090I420 A0A090I420_METFO	Probable porphobilinogen deaminase OS=Methanobacterium formicicum METFO	2
380	2.63	2.68	17.8 tr A0A089ZCA7 A0A089ZCA7_METFO	Thioesterase OS=Methanobacterium formicicum OX=2162 METFO	2
381	2.59	2.64	8.2 tr A0A089ZI47 A0A089ZI47_METFO	PAS/PAC sensor protein OS=Methanobacterium formicicum METFO	2
382	2.57	2.63	2.7 tr A0A090I1X5 A0A090I1X5_METFO	3-isopropylmalate dehydrogenase OS=Methanobacterium formicicum METFO	1
383	2.57	2.61	16.1 tr A0A090JX27 A0A090JX27_METFO	Amino acid-binding ACT domain-containing protein OS=Methanobacterium formicicum METFO	2
384	2.56	4.68	14.1 tr A0A090JU62 A0A090JU62_METFO	Glutamine amidotransferase OS=Methanobacterium formicicum METFO	3
385	2.56	2.61	4.2 tr A0A090I5I9 A0A090I5I9_METFO	Mur ligase middle domain-containing protein OS=Methanobacterium formicicum METFO	2
386	2.55	2.6	5.8 tr A0A0S4FLY1 A0A0S4FLY1_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
387	2.5	2.54	5.2 tr K2R956 K2R956_METFP	Shikimate kinase OS=Methanobacterium formicicum (strain DSM 1627) METFP	2
388	2.46	2.51	1.6 tr K2R9Y9 K2R9Y9_METFP	ATP-dependent protease Lon OS=Methanobacterium formicicum METFP	1
389	2.46	2.49	18.6 tr A0A090I7B8 A0A090I7B8_METFO	30S ribosomal protein S19e OS=Methanobacterium formicicum METFO	2
390	2.41	2.45	4 tr A0A089ZA17 A0A089ZA17_METFO	Peptidase U32 family OS=Methanobacterium formicicum C METFO	1
391	2.41	2.45	12.5 tr A0A090I810 A0A090I810_METFO	Dihydroorotate dehydrogenase OS=Methanobacterium formicicum METFO	2
392	2.36	2.49	7.3 tr A0A090I0W7 A0A090I0W7_METFO	Oxidoreductase GFO/IDH/MOCA family OS=Methanobacterium formicicum METFO	2
393	2.35	2.39	4 tr A0A090I4C0 A0A090I4C0_METFO	Indole-3-glycerol phosphate synthase OS=Methanobacterium formicicum METFO	1
394	2.34	2.37	9.8 tr A0A090I4Y2 A0A090I4Y2_METFO	Putative membrane protein OS=Methanobacterium formicicum METFO	2
395	2.32	2.35	2.8 tr A0A0S4FLU0 A0A0S4FLU0_METFO	Dihydrolipoyl dehydrogenase OS=Methanobacterium formicicum METFO	1
396	2.32	2.35	3.5 tr A0A090I8P6 A0A090I8P6_METFO	Ribose-phosphate pyrophosphokinase OS=Methanobacterium formicicum METFO	1
397	2.29	2.4	23.6 tr A0A089ZH81 A0A089ZH81_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
398	2.27	2.3	4.9 tr A0A089ZEW4 A0A089ZEW4_METFO	50S ribosomal protein L11 OS=Methanobacterium formicicum METFO	1
399	2.23	2.37	8.6 tr A0A090I0P2 A0A090I0P2_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
400	2.23	2.33	20.9 tr A0A090I1M8 A0A090I1M8_METFO	UPF0173 metal-dependent hydrolase DSM1535_0376 OS=Methanobacterium formicicum METFO	2
401	2.21	2.23	7.4 tr K2R2Q1 K2R2Q1_METFP	Exosome complex component Csl4 OS=Methanobacterium formicicum METFP	1
402	2.2	2.23	8.6 tr A0A090I1Q2 A0A090I1Q2_METFO	Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Methanobacterium formicicum METFO	4
403	2.2	2.22	3.6 tr A0A090I7X7 A0A090I7X7_METFO	Glutamine-scyllo-inositol transaminase OS=Methanobacterium formicicum METFO	1
404	2.19	2.3	4.7 tr A0A089ZAY7 A0A089ZAY7_METFO	30S ribosomal protein S4 OS=Methanobacterium formicicum METFO	1
405	2.19	2.22	5.5 tr A0A090I4B2 A0A090I4B2_METFO	Flap endonuclease 1 OS=Methanobacterium formicicum O METFO	1
406	2.18	2.21	2.6 tr A0A090I4H9 A0A090I4H9_METFO	UDP-glucose 4-epimerase OS=Methanobacterium formicicum METFO	1
407	2.15	2.18	2.2 tr A0A0S4FMB9 A0A0S4FMB9_METFO	UDP-N-acetylmuramoyl-L-alanine-D-glutamate ligase OS=Methanobacterium formicicum METFO	1
408	2.13	2.16	3.8 tr A0A090I706 A0A090I706_METFO	Glycine-tRNA ligase OS=Methanobacterium formicicum O METFO	1
409	2.12	2.14	2.4 tr A0A089ZVM8 A0A089ZVM8_METFO	Peptide chain release factor subunit 1 OS=Methanobacterium formicicum METFO	1
410	2.12	2.13	2.1 tr A0A090IB52 A0A090IB52_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1

Amostra 6

411	2.11	2.13	3.3 tr A0A090JYG2 A0A090JYG2_METFO	Putative membrane protein OS=Methanobacterium formicicum METFO	1
412	2.09	2.21	4.4 tr A0A089ZG11 A0A089ZG11_METFO	ABC transporter permease protein OS=Methanobacterium METFO	2
413	2.09	2.1	7.7 tr A0A090IAZ4 A0A090IAZ4_METFO	LmbE family protein OS=Methanobacterium formicicum O METFO	1
414	2.08	2.09	13 tr A0A089ZI49 A0A089ZI49_METFO	Sensory transduction histidine kinase OS=Methanobacteriu METFO	4
415	2.08	2.09	3.8 tr A0A090I2K0 A0A090I2K0_METFO	Phosphoribosylformylglycinamide cyclo-ligase OS=Metha METFO	1
416	2.08	2.09	3.6 tr A0A089ZUW8 A0A089ZUW8_METFO	UPF0278 protein BRM9_0586 OS=Methanobacterium forr METFO	1
417	2.07	2.1	2.8 tr A0A0S4FRZ5 A0A0S4FRZ5_METFO	Digeranylgeranylglycerophospholipid reductase OS=Metha METFO	1
418	2.07	2.08	18.6 tr A0A090I6A2 A0A090I6A2_METFO	Cyclophilin type peptidyl-prolyl cis-trans isomerase OS=Me METFO	2
419	2.06	2.07	6.9 tr A0A090JU72 A0A090JU72_METFO	Putative secreted protein OS=Methanobacterium formicicu METFO	1
420	2.06	2.07	8.5 tr K2RTG9 K2RTG9_METFP	Archaeoflavoprotein AfpA OS=Methanobacterium formicicu METFP	1
421	2.05	2.06	2.5 tr K2QAU0 K2QAU0_METFP	Thiamine thiazole synthase OS=Methanobacterium formici METFP	1
422	2.05	2.05	2.2 tr A0A090JVX2 A0A090JVX2_METFO	Phosphoesterase RecJ domain-containing protein OS=Met METFO	1
423	2.04	2.05	1.9 tr A0A090JU28 A0A090JU28_METFO	Probable translation initiation factor IF-2 OS=Methanobacte METFO	1
424	2.04	2.04	2.2 tr A0A089ZGJ2 A0A089ZGJ2_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
425	2.04	2.04	6.3 tr A0A089ZC18 A0A089ZC18_METFO	Methanogenesis marker protein 7 OS=Methanobacterium f METFO	1
426	2.02	35.29	50 tr K2QYM4 K2QYM4_METFP	Methyl-coenzyme M reductase subunit alpha OS=Methanol METFP	118
427	2.02	2.19	4 tr A0A090I0Y8 A0A090I0Y8_METFO	Putative (R)-citramalate synthase CimA OS=Methanobacte METFO	1
428	2.02	2.03	4.5 tr K2RR54 K2RR54_METFP	Glucosamine-1-phosphate N-acetyltransferase OS=Methar METFP	2
429	2.02	2.03	1.3 tr A0A0S4FMD8 A0A0S4FMD8_METFO	Alanine--tRNA ligase OS=Methanobacterium formicicum O METFO	1
430	2.02	2.02	5.5 tr A0A0S4FLN4 A0A0S4FLN4_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
431	2.01	2.02	4.5 tr A0A090JUW9 A0A090JUW9_METFO	2-phosphosulfolactate phosphatase OS=Methanobacteriun METFO	1
432	2.01	2.02	3 tr A0A090I7Y1 A0A090I7Y1_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
433	2.01	2.01	1.6 tr K2R961 K2R961_METFP	ATP-dependent DNA helicase Hel308 OS=Methanobacteri METFP	1
434	2.01	2.01	13.4 tr K2RAZ5 K2RAZ5_METFP	Transcription factor CBF/NF-Y/histone domain-containing p METFP	1
435	2.01	2.01	2.9 tr A0A090I8G0 A0A090I8G0_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
436	2.01	2.01	1.5 tr A0A090I8L0 A0A090I8L0_METFO	Ferrous iron transport protein B, FeoB OS=Methanobacteri METFO	1
437	2.01	2.01	5.1 tr A0A090I2P2 A0A090I2P2_METFO	Uncharacterized protein OS=Methanobacterium formicicun METFO	1
438	2.01	2.01	1.6 tr A0A089ZF54 A0A089ZF54_METFO	Oligosaccharyl transferase OS=Methanobacterium formicic METFO	1
439	2.01	2.01	9.3 tr K2QYV5 K2QYV5_METFP	Nucleoside diphosphate kinase OS=Methanobacterium fori METFP	1
440	2.01	2.01	8.1 tr A0A090I528 A0A090I528_METFO	Probable cyclic pyranopterin monophosphate synthase OS METFO	1
441	2.01	2.01	3.7 tr A0A090I4P9 A0A090I4P9_METFO	Glucose-methanol-choline oxidoreductase OS=Methanoba METFO	1
442	2.01	2.01	4.3 tr A0A089ZGN3 A0A089ZGN3_METFO	Deoxyribose-phosphate aldolase OS=Methanobacterium fc METFO	1
443	2	49.15	53.6 tr K2RBU1 K2RBU1_METFP	V-type ATP synthase alpha chain OS=Methanobacterium f METFP	53

Amostra 6

444	2	7.93	13.4	tr A0A090I4H2 A0A090I4H2_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	9
445	2	2.04	7.1	tr A0A090I912 A0A090I912_METFO	NH(3)-dependent NAD(+) synthetase OS=Methanobacterium formicicum METFO	2
446	2	2.01	4.1	tr A0A090I8S7 A0A090I8S7_METFO	tRNA (Adenine(57)-N(1)/adenine(58)-N(1))-methyltransferase METFO	1
447	2	2.01	7.6	tr A0A090JXC2 A0A090JXC2_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
448	2	2.01	3.3	tr A0A090I7D4 A0A090I7D4_METFO	Metal dependent phosphohydrolase OS=Methanobacterium formicicum METFO	1
449	2	2	1.1	tr K2RQD4 K2RQD4_METFP	Heavy metal translocating P-type ATPase OS=Methanobacterium formicicum METFP	1
450	2	2	3.3	tr A0A090IB07 A0A090IB07_METFO	Energy-coupling factor transporter ATP-binding protein Ecf METFO	1
451	2	2	10	tr K2RQU8 K2RQU8_METFP	Putative anti-sigma factor antagonist OS=Methanobacterium formicicum METFP	1
452	2	2	5.9	tr K2RBN6 K2RBN6_METFP	Archaeoflavoprotein AfpA OS=Methanobacterium formicicum METFP	1
453	2	2	10.4	tr K2R8M5 K2R8M5_METFP	Roadblock/LC7 family protein OS=Methanobacterium formicicum METFP	2
454	2	2	12.4	tr K2QYF6 K2QYF6_METFP	Nitroreductase OS=Methanobacterium formicicum (strain C) METFP	1
455	2	2	5	tr K2QG91 K2QG91_METFP	Nitrogenase OS=Methanobacterium formicicum (strain DSI) METFP	1
456	2	2	4.8	tr K2QBL8 K2QBL8_METFP	Uncharacterized protein OS=Methanobacterium formicicum METFP	1
457	2	2	4.1	tr A0A0S4FLM0 A0A0S4FLM0_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
458	2	2	3.8	tr A0A090JWL7 A0A090JWL7_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
459	2	2	3.3	tr A0A090JVS5 A0A090JVS5_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
460	2	2	4.5	tr A0A090JTY9 A0A090JTY9_METFO	Peptidase C60 sortase A and B OS=Methanobacterium formicicum METFO	1
461	2	2	10	tr A0A090I6P0 A0A090I6P0_METFO	3-hexulose-6-phosphate isomerase HxlB1 OS=Methanobacterium formicicum METFO	1
462	2	2	33.3	tr A0A090I4K2 A0A090I4K2_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
463	2	2	15	tr A0A089ZVK3 A0A089ZVK3_METFO	CBS domain-containing protein OS=Methanobacterium formicicum METFO	1
464	2	2	7.8	tr A0A089ZC90 A0A089ZC90_METFO	V-type ATP synthase subunit D OS=Methanobacterium formicicum METFO	1
465	2	2	9.6	tr K2RW50 K2RW50_METFP	DNA/RNA-binding protein Alba OS=Methanobacterium formicicum METFP	1
466	2	2	5.4	tr K2R2B6 K2R2B6_METFP	NADH ubiquinone oxidoreductase 20 kDa subunit OS=Methanobacterium formicicum METFP	1
467	2	2	17.9	tr K2Q9W8 K2Q9W8_METFP	Uncharacterized protein OS=Methanobacterium formicicum METFP	1
468	2	2	3.1	tr A0A0S4FSJ7 A0A0S4FSJ7_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
469	2	2	8	tr A0A0S4FP85 A0A0S4FP85_METFO	Putative secreted protein OS=Methanobacterium formicicum METFO	1
470	2	2	4.1	tr A0A0S4FLJ8 A0A0S4FLJ8_METFO	Peptidase C60 sortase A and B OS=Methanobacterium formicicum METFO	1
471	2	2	3.3	tr A0A090JUV1 A0A090JUV1_METFO	Tetrahydromethanopterin S-methyltransferase subunit D O METFO	1
472	2	2	8.4	tr A0A090I852 A0A090I852_METFO	Cupin OS=Methanobacterium formicicum OX=2162 GN=BI METFO	1
473	2	2	3.3	tr A0A090I6Y3 A0A090I6Y3_METFO	S-adenosyl-L-methionine-dependent tRNA 4-demethyltransferase METFO	1
474	2	2	5.6	tr A0A090I5I0 A0A090I5I0_METFO	Tetrahydromethanopterin S-methyltransferase subunit C O METFO	2
475	2	2	2.9	tr A0A090I4T2 A0A090I4T2_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
476	2	2	9.1	tr A0A090I4I3 A0A090I4I3_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1

Amostra 6

477	2	2	5.3	tr A0A090I4E3 A0A090I4E3_METFO	Peroxiredoxin OS=Methanobacterium formicicum OX=2162 METFO	1
478	2	2	1.3	tr A0A090I4B6 A0A090I4B6_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
479	2	2	10.9	tr A0A090I3M8 A0A090I3M8_METFO	Imidazoleglycerol-phosphate dehydratase OS=Methanobacterium formicicum METFO	1
480	2	2	4.9	tr A0A090I2A7 A0A090I2A7_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
481	2	2	2.2	tr A0A090I0P8 A0A090I0P8_METFO	Adenine deaminase OS=Methanobacterium formicicum OX=2162 METFO	1
482	2	2	7.1	tr A0A089ZVX2 A0A089ZVX2_METFO	Putative membrane protein OS=Methanobacterium formicicum METFO	1
483	2	2	16.9	tr A0A089ZV40 A0A089ZV40_METFO	TRAM domain-containing protein OS=Methanobacterium formicicum METFO	1
484	2	2	8.8	tr A0A089ZJ52 A0A089ZJ52_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
485	2	2	5.1	tr A0A089ZH31 A0A089ZH31_METFO	Cobalamin biosynthesis protein CbiM3 OS=Methanobacterium formicicum METFO	1
486	2	2	6.7	tr A0A089ZGY8 A0A089ZGY8_METFO	Putative membrane protein OS=Methanobacterium formicicum METFO	1
487	1.94	2.1	6.2	tr A0A0S4FPI2 A0A0S4FPI2_METFO	Molybdopterin biosynthesis MoaE protein OS=Methanobacterium formicicum METFO	1
488	1.92	2.01	1.8	tr A0A0S4FPZ6 A0A0S4FPZ6_METFO	Fibronectin-binding A domain-containing protein OS=Methanobacterium formicicum METFO	1
489	1.85	1.99	1.9	tr A0A0S4FLI5 A0A0S4FLI5_METFO	Signal transduction histidine kinase OS=Methanobacterium formicicum METFO	1
490	1.8	1.89	3.5	tr A0A090I6L6 A0A090I6L6_METFO	Putative membrane protein OS=Methanobacterium formicicum METFO	1
491	1.8	1.89	4	tr A0A0S4FM70 A0A0S4FM70_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
492	1.7	1.8	4.4	tr A0A090I4Q1 A0A090I4Q1_METFO	Response regulator receiver protein OS=Methanobacterium formicicum METFO	1
493	1.66	1.87	3.9	tr A0A090I744 A0A090I744_METFO	3-phosphoshikimate 1-carboxyvinyltransferase OS=Methanobacterium formicicum METFO	2
494	1.66	1.78	2.4	tr A0A090I2G9 A0A090I2G9_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
495	1.64	1.75	4.2	tr K2QDZ9 K2QDZ9_METFP	RNA-processing protein OS=Methanobacterium formicicum METFP	1
496	1.63	1.8	2.3	tr A0A090JV74 A0A090JV74_METFO	Homoserine dehydrogenase OS=Methanobacterium formicicum METFO	1
497	1.62	5.8	4.7	tr A0A0S4FSQ1 A0A0S4FSQ1_METFO	Acetyl-coenzyme A synthetase OS=Methanobacterium formicicum METFO	4
498	1.62	1.79	3.7	tr A0A090IA48 A0A090IA48_METFO	Nitrite reductase (NAD(P)H) OS=Methanobacterium formicicum METFO	1
499	1.61	1.87	14.9	tr A0A090I4G2 A0A090I4G2_METFO	Bifunctional short chain isoprenyl diphosphate synthase Ids OS=Methanobacterium formicicum METFO	3
500	1.54	1.73	13	tr A0A090I3I8 A0A090I3I8_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
501	1.52	1.64	1.1	tr A0A0S4FP58 A0A0S4FP58_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2
502	1.49	2.05	11.3	tr A0A0S4FR49 A0A0S4FR49_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	3
503	1.49	1.64	4.5	tr A0A090I666 A0A090I666_METFO	Nitrogenase iron protein 2 OS=Methanobacterium formicicum METFO	1
504	1.49	1.63	4.3	tr A0A089ZAI2 A0A089ZAI2_METFO	Molybdate transport system regulatory protein ModE OS=Methanobacterium formicicum METFO	2
505	1.49	1.61	0.8	tr A0A090I495 A0A090I495_METFO	Restriction endonuclease OS=Methanobacterium formicicum METFO	1
506	1.47	1.58	5.2	tr A0A089ZHU8 A0A089ZHU8_METFO	Response regulator domain-containing protein OS=Methanobacterium formicicum METFO	1
507	1.44	1.58	4	tr A0A090I3L4 A0A090I3L4_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
508	1.42	1.54	3.5	tr A0A090JW83 A0A090JW83_METFO	Imidazole glycerol phosphate synthase subunit HisF OS=Methanobacterium formicicum METFO	1
509	1.41	1.51	5.7	tr A0A090I2J4 A0A090I2J4_METFO	Phosphate-specific transport system accessory protein Phc OS=Methanobacterium formicicum METFO	1

Amostra 6

510	1.4	1.51	6.4 tr A0A0S4FN48 A0A0S4FN48_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	1
511	1.37	1.48	7.8 tr K2QBG9 K2QBG9_METFP	Uncharacterized protein OS=Methanobacterium formicicum METFP	1
512	1.35	1.47	1.8 tr A0A089ZHQ2 A0A089ZHQ2_METFO	tRNA-guanine(15) transglycosylase OS=Methanobacterium METFO	1
513	1.31	1.55	6.6 tr A0A090I6J2 A0A090I6J2_METFO	Uncharacterized protein OS=Methanobacterium formicicum METFO	2

Amostra 6



ID statistics table

Unused (Conf) Cutoff	Proteins Detected	Proteins Before Grouping	Distinct Peptides	Spectra Identified	% Total Spectra
>2.0 (99)	443	956	7047	25431	17.5
>1.3 (95)	513	1144	7202	25760	17.7
>0.47 (66)	585	1320	7419	26060	17.9
Cutoff Applied: >0.05 (10%)	739	1688	7744	26528	18.2

TIC chromatogram

