# Initial Methane Production (IMP) differences between *Methanobacterium formicicum* pure culture with and without 0.5 g/L of activated carbon (AC)

Proteins only detected in the control assay in general are regarding to metabolism and cellular activity (transcription, translation, ribosomal activity). Some of the proteins most detected are poorly characterized, so it is not possible to understand their role and importance to the activity of this culture.

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| **Protein names** | **Function [CC]** | **Keywords** | **Gene ontology (GO)** | **COG general functional category** | **COG functional category** | **COG protein description** | **Number of spectra detected** |
| Uncharacterized protein |  | Complete proteome |  | POORLY CHARACTERIZED | Function unknown | Uncharacterized protein conserved in archaea | 113 |
| Uncharacterized protein |  | Complete proteome |  | POORLY CHARACTERIZED | Function unknown | Uncharacterized protein conserved in archaea | 66 |
| Type 2 DNA topoisomerase 6 subunit B (EC 5.6.2.3) (Type II DNA topoisomerase VI subunit B) (TopoVI-B) | FUNCTION: Relaxes both positive and negative superturns and exhibits a strong decatenase activity. {ECO:0000256|HAMAP-Rule:MF\_00322}. | ATP-binding;Complete proteome;DNA-binding;Isomerase;Nucleotide-binding;Topoisomerase | ATP binding [GO:0005524]; DNA binding [GO:0003677]; DNA topoisomerase type II (ATP-hydrolyzing) activity [GO:0003918]; DNA topological change [GO:0006265]; DNA unwinding involved in DNA replication [GO:0006268] | INFORMATION STORAGE AND PROCESSING | Replication, recombination and repair | DNA topoisomerase VI, subunit B | 64 |
| Cell division control protein Cdc48 (Cell division cycle protein 48 homolog MJ1156) |  | Cell cycle;Cell division;Complete proteome | ATP binding [GO:0005524]; hydrolase activity [GO:0016787]; cell division [GO:0051301] | CELLULAR PROCESSES AND SIGNALING | Posttranslational modification, protein turnover, chaperones | ATPases of the AAA+ class | 62 |
| Signal recognition particle 54 kDa protein (SRP54) | FUNCTION: Involved in targeting and insertion of nascent membrane proteins into the cytoplasmic membrane. Binds to the hydrophobic signal sequence of the ribosome-nascent chain (RNC) as it emerges from the ribosomes. The SRP-RNC complex is then targeted to the cytoplasmic membrane where it interacts with the SRP receptor FtsY. {ECO:0000256|HAMAP-Rule:MF\_00306, ECO:0000256|SAAS:SAAS00871663}. | Coiled coil;Complete proteome;Cytoplasm;GTP-binding;Nucleotide-binding;RNA-binding;Ribonucleoprotein;Signal recognition particle | signal recognition particle [GO:0048500]; 7S RNA binding [GO:0008312]; GTP binding [GO:0005525]; GTPase activity [GO:0003924]; SRP-dependent cotranslational protein targeting to membrane [GO:0006614] | CELLULAR PROCESSES AND SIGNALING | Intracellular trafficking, secretion, and vesicular transport | Signal recognition particle GTPase | 51 |
| Uncharacterized protein |  | Coiled coil;Complete proteome |  | POORLY CHARACTERIZED | Function unknown | Uncharacterized protein conserved in archaea | 49 |
| dTDP-glucose 4,6-dehydratase-like protein |  | Complete proteome | catalytic activity [GO:0003824]; coenzyme binding [GO:0050662] | CELLULAR PROCESSES AND SIGNALING | Cell wall/membrane/envelope biogenesis | Nucleoside-diphosphate-sugar epimerases | 47 |
| Nucleotidyl transferase |  | Coiled coil;Complete proteome;Transferase | nucleotidyltransferase activity [GO:0016779]; biosynthetic process [GO:0009058]; polysaccharide metabolic process [GO:0005976] | CELLULAR PROCESSES AND SIGNALING | Cell wall/membrane/envelope biogenesis | Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation initiation factor 2B, gamma/epsilon subunits (eIF-2Bgamma/eIF-2Bepsilon) | 46 |
| UPF0288 protein BRM9\_0509 |  | Complete proteome |  | CELLULAR PROCESSES AND SIGNALING | Posttranslational modification, protein turnover, chaperones | Predicted peptidyl-prolyl cis-trans isomerase (rotamase), cyclophilin family | 35 |
| Putative pantothenate synthetase |  | Complete proteome |  | POORLY CHARACTERIZED | Function unknown | Uncharacterized protein conserved in archaea | 33 |
| NAD(FAD)-dependent dehydrogenase |  | Complete proteome;Membrane;Transmembrane;Transmembrane helix | integral component of membrane [GO:0016021] | POORLY CHARACTERIZED | Function unknown | Uncharacterized conserved protein | 27 |
| Pleiotropic regulatory protein |  | Complete proteome;Pyridoxal phosphate | catalytic activity [GO:0003824] | CELLULAR PROCESSES AND SIGNALING | Cell wall/membrane/envelope biogenesis | Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis | 20 |
| Putative membrane protein |  | Coiled coil;Complete proteome;Membrane;Transmembrane;Transmembrane helix | integral component of membrane [GO:0016021] | POORLY CHARACTERIZED | Function unknown | Uncharacterized conserved protein | 17 |
| Cell wall biosynthesis protein Mur ligase family (UDP-N-acetylmuramoyl-L-alanine-D-glutamateligase) (EC 6.3.2.9) |  | Complete proteome;Ligase | ATP binding [GO:0005524]; UDP-N-acetylmuramoylalanine-D-glutamate ligase activity [GO:0008764]; biosynthetic process [GO:0009058] | CELLULAR PROCESSES AND SIGNALING | Cell wall/membrane/envelope biogenesis | UDP-N-acetylmuramoylalanine-D-glutamate ligase | 15 |
| Peptidase C60 sortase A and B |  | Complete proteome | extrinsic component of membrane [GO:0019898]; photosystem II oxygen evolving complex [GO:0009654]; calcium ion binding [GO:0005509]; photosynthesis [GO:0015979] | CELLULAR PROCESSES AND SIGNALING | Cell wall/membrane/envelope biogenesis | Sortase (surface protein transpeptidase) | 13 |
| ABC transporter ATP-binding protein (Putative ABC transporter ATP-binding protein TM\_0352) |  | ATP-binding;Complete proteome;Nucleotide-binding | ATP binding [GO:0005524]; ATPase activity [GO:0016887] | CELLULAR PROCESSES AND SIGNALING | Defense mechanisms | ABC-type antimicrobial peptide transport system, ATPase component | 13 |
| ABC transporter permease protein |  | Complete proteome;Membrane;Transmembrane;Transmembrane helix | integral component of membrane [GO:0016021] | CELLULAR PROCESSES AND SIGNALING | Cell wall/membrane/envelope biogenesis | ABC-type transport system, involved in lipoprotein release, permease component | 12 |
| Uncharacterized protein |  | Complete proteome | thiamine-phosphate kinase activity [GO:0009030]; thiamine biosynthetic process [GO:0009228] | CELLULAR PROCESSES AND SIGNALING | Posttranslational modification, protein turnover, chaperones | Hydrogenase maturation factor | 12 |
| Putative secreted protein |  | Complete proteome |  | CELLULAR PROCESSES AND SIGNALING | Cell wall/membrane/envelope biogenesis | Predicted outer membrane protein | 7 |
| Formate/nitrite transporter FdhC (Putative formate transporter) |  | Complete proteome;Membrane;Transmembrane;Transmembrane helix | integral component of membrane [GO:0016021]; transmembrane transporter activity [GO:0022857] | METABOLISM | Inorganic ion transport and metabolism | Formate/nitrite family of transporters | 4 |

Proteins only detected in the assay with AC:

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| **Protein names** | **Function [CC]** | **Pathway** | **Keywords** | **Gene ontology (GO)** | **COG general functional category** | **COG functional category** | **COG protein description** | **sample4\_9** |
| Putative ATP-dependent helicase MTH\_1802 (EC 3.6.4.-) |  |  | ATP-binding;Complete proteome;Helicase;Hydrolase;Nucleotide-binding | ATP binding [GO:0005524]; helicase activity [GO:0004386]; nucleic acid binding [GO:0003676] | POORLY CHARACTERIZED | General function prediction only | Lhr-like helicases | 99 |
| ATP-dependent DNA helicase (Helicase c2) |  |  | ATP-binding;Complete proteome;Helicase;Hydrolase;Nucleotide-binding | ATP binding [GO:0005524]; ATP-dependent helicase activity [GO:0008026]; DNA binding [GO:0003677]; nucleobase-containing compound metabolic process [GO:0006139] | INFORMATION STORAGE AND PROCESSING | Transcription | Rad3-related DNA helicases | 94 |
| Coenzyme F390 synthetase FtsA2 (Phenylacetate-coenzyme A ligase) (EC 6.2.1.30) |  |  | Complete proteome;Ligase | phenylacetate-CoA ligase activity [GO:0047475]; phenylacetate catabolic process [GO:0010124] | METABOLISM | Coenzyme transport and metabolism | Coenzyme F390 synthetase | 89 |
| DNA polymerase II large subunit (Pol II) (EC 2.7.7.7) (Exodeoxyribonuclease large subunit) (EC 3.1.11.1) | FUNCTION: Possesses two activities: a DNA synthesis (polymerase) and an exonucleolytic activity that degrades single-stranded DNA in the 3'- to 5'-direction. Has a template-primer preference which is characteristic of a replicative DNA polymerase. {ECO:0000256|HAMAP-Rule:MF\_00324}. |  | Complete proteome;DNA replication;DNA-binding;DNA-directed DNA polymerase;Exonuclease;Hydrolase;Multifunctional enzyme;Nuclease;Nucleotidyltransferase;Transferase | 3'-5' exonuclease activity [GO:0008408]; DNA binding [GO:0003677]; DNA-directed DNA polymerase activity [GO:0003887]; exodeoxyribonuclease I activity [GO:0008852]; DNA catabolic process, exonucleolytic [GO:0000738]; DNA-dependent DNA replication [GO:0006261] | INFORMATION STORAGE AND PROCESSING | Replication, recombination and repair | Archaeal DNA polymerase II, large subunit | 81 |
| Uncharacterized protein |  |  | Complete proteome;Membrane;Transmembrane;Transmembrane helix | integral component of membrane [GO:0016021] | POORLY CHARACTERIZED | Function unknown | Predicted membrane protein | 70 |
| Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2) (Anaerobic ribonucleoside-triphosphate reductase NrdD) |  |  | ATP-binding;Complete proteome;Nucleotide-binding;Oxidoreductase | ATP binding [GO:0005524]; ribonucleoside-triphosphate reductase activity [GO:0008998]; DNA replication [GO:0006260] | METABOLISM | Nucleotide transport and metabolism | Oxygen-sensitive ribonucleoside-triphosphate reductase | 64 |
| Uncharacterized protein |  |  | Complete proteome |  | CELLULAR PROCESSES AND SIGNALING | Posttranslational modification, protein turnover, chaperones | La protein, small RNA-binding pol III transcript stabilizing protein and related La-motif-containing proteins involved in translation | 58 |
| PAS/PAC sensor protein (Putative PAS/PAC sensor protein) (Response regulator/PAS domain-containing protein) |  |  | Coiled coil;Complete proteome;Phosphoprotein | phosphorelay signal transduction system [GO:0000160] | CELLULAR PROCESSES AND SIGNALING | Signal transduction mechanisms | FOG: CheY-like receiver | 46 |
| Pyruvate carboxylase subunit A (EC 6.4.1.1) (Pyruvate carboxylase subunit A PycA) |  |  | ATP-binding;Complete proteome;Ligase;Nucleotide-binding;Pyruvate | ATP binding [GO:0005524]; metal ion binding [GO:0046872]; pyruvate carboxylase activity [GO:0004736] | METABOLISM | Lipid transport and metabolism | Acetyl/propionyl-CoA carboxylase, alpha subunit | 41 |
| RNA-metabolising metallo-beta-lactamase |  |  | Complete proteome | nucleic acid binding [GO:0003676] | POORLY CHARACTERIZED | General function prediction only | Predicted metal-dependent RNase, consists of a metallo-beta-lactamase domain and an RNA-binding KH domain | 41 |
| Putative secreted protein |  |  | Complete proteome;Membrane;Transmembrane;Transmembrane helix | integral component of membrane [GO:0016021]; biosynthetic process [GO:0009058] | METABOLISM | Coenzyme transport and metabolism | Cobalamin biosynthesis protein CobN and related Mg-chelatases | 37 |
| F420H2 oxidase FprA (Type A flavoprotein FprA) (EC 1.-.-.-) |  |  | Complete proteome;Oxidoreductase | electron transfer activity [GO:0009055]; FMN binding [GO:0010181]; metal ion binding [GO:0046872] | METABOLISM | Energy production and conversion | Uncharacterized flavoproteins | 27 |
| 5'-deoxyadenosine deaminase (5'-dA deaminase) (EC 3.5.4.41) (5'-methylthioadenosine deaminase) (MTA deaminase) (EC 3.5.4.31) (Adenosine deaminase) (EC 3.5.4.4) (S-adenosylhomocysteine deaminase) (SAH deaminase) (EC 3.5.4.28) | FUNCTION: Catalyzes the deamination of three SAM-derived enzymatic products, namely 5'-deoxyadenosine, S-adenosyl-L-homocysteine, and 5'-methylthioadenosine, to produce the inosine analogs. Can also deaminate adenosine. The preferred substrate for this enzyme is 5'-deoxyadenosine, but all these substrates are efficiently deaminated. Likely functions in a S-adenosyl-L-methionine (SAM) recycling pathway from S-adenosyl-L-homocysteine (SAH) produced from SAM-dependent methylation reactions. May also be involved in the recycling of 5'-deoxyadenosine, whereupon the 5'-deoxyribose moiety of 5'-deoxyinosine is further metabolized to deoxyhexoses used for the biosynthesis of aromatic amino acids in methanogens. {ECO:0000256|HAMAP-Rule:MF\_01281}. | PATHWAY: Amino-acid biosynthesis; S-adenosyl-L-methionine biosynthesis. {ECO:0000256|HAMAP-Rule:MF\_01281}. | Complete proteome;Hydrolase;Metal-binding;Zinc | 5'-deoxyadenosine deaminase activity [GO:0090613]; adenosine deaminase activity [GO:0004000]; metal ion binding [GO:0046872]; S-adenosylhomocysteine deaminase activity [GO:0050270]; S-adenosylmethionine biosynthetic process [GO:0006556] | METABOLISM | Nucleotide transport and metabolism | Cytosine deaminase and related metal-dependent hydrolases | 24 |
| Uncharacterized protein |  |  | Complete proteome |  | POORLY CHARACTERIZED | Function unknown | Uncharacterized protein conserved in archaea | 20 |
| Putative aminopeptidase MJ0555 (EC 3.4.11.-) |  |  | Aminopeptidase;Complete proteome;Hydrolase;Metal-binding;Protease | aminopeptidase activity [GO:0004177]; metal ion binding [GO:0046872] | METABOLISM | Carbohydrate transport and metabolism | Cellulase M and related proteins | 19 |
| Uncharacterized protein |  |  | Complete proteome;Membrane;Transmembrane;Transmembrane helix | integral component of membrane [GO:0016021] | POORLY CHARACTERIZED | Function unknown | Predicted membrane protein | 14 |
| Putative secreted protein |  |  | Complete proteome |  | METABOLISM | Inorganic ion transport and metabolism | ABC-type Mn2+/Zn2+ transport systems, permease components | 13 |
| Uncharacterized protein |  |  | Complete proteome;Membrane;Transmembrane;Transmembrane helix | integral component of membrane [GO:0016021] | CELLULAR PROCESSES AND SIGNALING | Cell wall/membrane/envelope biogenesis | Uncharacterized protein potentially involved in peptidoglycan biosynthesis | 13 |
| MotA/TolQ/ExbB proton channel family protein |  |  | Complete proteome;Membrane;Protein transport;Transmembrane;Transmembrane helix;Transport | integral component of membrane [GO:0016021]; protein transport [GO:0015031] | CELLULAR PROCESSES AND SIGNALING | Intracellular trafficking, secretion, and vesicular transport | Biopolymer transport proteins | 8 |
| 50S ribosomal protein L7Ae (Ribosomal protein L8e) | FUNCTION: Multifunctional RNA-binding protein that recognizes the K-turn motif in ribosomal RNA, the RNA component of RNase P, box H/ACA, box C/D and box C'/D' sRNAs. {ECO:0000256|HAMAP-Rule:MF\_00326}. |  | Complete proteome;Cytoplasm;RNA-binding;Ribonucleoprotein;Ribosomal protein;rRNA-binding;tRNA processing | ribosome [GO:0005840]; ribonuclease P activity [GO:0004526]; rRNA binding [GO:0019843]; structural constituent of ribosome [GO:0003735]; translation [GO:0006412]; tRNA 5'-leader removal [GO:0001682] | INFORMATION STORAGE AND PROCESSING | Translation, ribosomal structure and biogenesis | Ribosomal protein HS6-type (S12/L30/L7a) | 8 |