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Proteomic analysis of secretomes from *Bacillus* sp. AR03: characterization of enzymatic cocktails active on complex carbohydrates for xylooligosaccharides production

Johan S. Hero^{a*} , José H. Pisa^{a*}, Enzo E. Raimondo^{a,b}, and M. Alejandra Martínez^{a,c}

^aPlanta Piloto de Procesos Industriales Microbiológicos (PROIMI), CONICET, Tucumán, Argentina; ^bFacultad de Bioquímica, Química y Farmacia, Universidad Nacional de Tucumán, Tucumán, Argentina; ^cFacultad de Ciencias Exactas y Tecnología, Universidad Nacional de Tucumán, Tucumán, Argentina

ABSTRACT

Bacillus sp. AR03 have been described as an important producer of carbohydrate-active enzymes (CAZymes) when growing in a peptone-based medium supplemented with simple sugars and/or carboxymethyl cellulose (CMC) as carbon sources. This work aimed to identify the extracellular enzymatic cocktails through shotgun proteomics. The proteomic analysis showed that enzymes involved in cellulose and xylan degradation were among the most abundant proteins. These enzymes included an endo-glucanase GH5_2 and a glucuronoxylanase GH30_8, which were found in all conditions. In addition, several proteins were differentially expressed in the three evaluated culture media, indicating microbial metabolic changes due to the different supplied carbon sources, particularly, in the presence of CMC. Finally, the capability of the crude enzymatic cocktails from culture media to degrade birchwood xylan was assessed, which produced mostly xylooligosaccharides containing among 3–5 xylose units. Consequently, this work shows the potential of the extracellular enzymes from *Bacillus* sp. AR03 for producing emergent prebiotics.

KEYWORDS



Bacillus sp. AR03;
glucuronoxylanase; GH30_8;
endoglucanase; proteomics;
xylooligosaccharides


Introduction

In nature, lignocellulosic biomass constitutes the source of the most abundant renewable polysaccharides with a huge potential for their bioconversion into several value-added bioproducts. Consequently, carbohydrate-active enzymes (CAZymes) are key in a biorefinery context. Among them, cellulases and xylanases have prominent uses for the production of biofuels, food compounds with prebiotic properties, pulp paper bleaching, etc.^[1] However, the exploration of novel producers of CAZymes and the large-scale production of these enzymes are still considerable targets to develop biocatalysts with application in bio-based processes.^[2]

The dominant role of *Firmicutes* in plant biomass deconstruction in different environments has been widely reported.^[3,4] Within this phylum, members of *Bacillus* genus are considered one of the most robust and versatile enzyme producers for microbial fermentations due to their high growth rates and capability to secrete large amounts of extracellular enzymes.^[5,6] Nevertheless, physiological data supporting the role that several strains play in polysaccharide decomposition are scarce.^[7] To overcome some of these limitations, shotgun proteomic studies have provided information about the protein composition of microorganisms.^[8] Unlike genomic analyses that only allow the theoretical identification

of genes encoding potential xylanases and cellulases in microbial genomes, proteomic techniques provide evidence of the actual production of these enzymes on lignocellulose presence.^[7] For example, Větrovský et al.^[9] found that only a few environmental actinobacteria isolates decomposed lignocellulose, despite the presence of cellulolytic genes in their genomes is common.^[4] Besides, proteomic analyses are adequate to evaluate the proteins expressed in a particular set of culture conditions (strain, growth medium, carbon source, temperature, growth phase, etc.) or to compare different sets of protein mixtures corresponding to different conditions.^[8] This experimental approach was previously employed for studying mixtures of cellulases and hemicellulases in order to determine the protein composition of these mixtures, corroborating with the specific activity of the individual enzymes.^[10] Due to the above, proteomic analyses are suitable to describe the potential of *Bacillus* strains in the decomposition of lignocellulosic organic matter. In this context, Tang et al.^[11] performed secretomic studies to explore the lignocellulose-degrading potential of *Bacillus velezensis* LC1 grown in an alkali-pretreated bamboo-based medium by using liquid chromatography-tandem mass spectrometry (LC-MS/MS). The secretome analysis demonstrated the presence of a considerable number of proteins involved in lignocellulose

CONTACT Johan S. Hero  johan.hero@conicet.gov.ar  Planta Piloto de Procesos Industriales Microbiológicos (PROIMI-CONICET), Av. Belgrano y Pasaje Caseros, San Miguel de Tucumán, 4000, Tucumán, Argentina.

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*These authors contributed equally to this work.

degradation, such as cellulases, hemicellulases, and other related proteins.

Our research group has previously reported the strain AR03 that belongs to the *Bacillus subtilis* group.^[12] This strain was isolated from pulp and paper feedstock obtained from a paper mill in Argentina and selected by its significant cellulase activity when growing in a peptone-based medium supplemented with carboxymethyl cellulose (CMC) or simple sugars under submerged fermentation conditions. Moreover, Manfredi et al.^[13] reported that the combination of a simple sugar and CMC in a culture medium enhanced cellulase production by this strain. Unlike substrates derived from agroindustrial residues, the use of soluble substrates for submerged fermentations favors both operative culture conditions and downstream process. Therefore, *Bacillus* sp. AR03 is a promising candidate for the production of CAZymes; however, the identification of these enzymes remains unknown. Knowing the hydrolytic arsenal produced by this strain allows to better define the technological potential of its enzymatic cocktail. In this context, we performed a gel-free proteomic analysis of enzymatic cocktails produced by *Bacillus* sp. AR03 in three different culture media to identify their extracellular enzymes.

Materials and methods

Growth conditions, enzyme production, and protein extract preparation for proteomic analysis

Bacillus sp. AR03 was grown in 125-mL flasks containing 20 mL of modified DTSB culture medium whose composition was described by Manfredi et al.^[13] This culture medium was supplemented with different carbohydrates: 10 g L⁻¹ of glucose (condition 1); 10 g L⁻¹ of CMC (condition 2); and 10 g L⁻¹ of glucose + 10 g L⁻¹ of CMC (condition 3). Each condition was performed by three independent biological replicas. Inoculated flasks were incubated at 30 °C for 72 hr with orbital agitation (200 rpm). Samples were taken every 24 hr and cell-free supernatants were recovered by centrifugation (4 °C, 8,000 × g, 10 min) and subsequently used for protein and enzymatic activity determinations. Growth curves of *Bacillus* sp. AR03 in the different culture media were carried out using three independent biological replicas for each condition. Samples were taken every 1 h for the first 13 hr, and thereafter at 24, 48, and 72 hr. OD_{600nm} readings were measured on a microplate reader (Multiskan GO, Thermo Scientific, Waltham, MA).

Protein preparation for LC-MS/MS analysis was performed according to La Greca et al.^[14] with slight modifications. Briefly, 50 µg of protein from each condition were treated with 20 µL of reducing solution (200 mM DTT, 100 mM Tris, pH 7.8) and with alkylation solution (200 mM iodoacetamide, 100 mM Tris, pH 7.8) for 1 hr at room temperature. Then, proteins were precipitated with 10% TCA and centrifuged (4 °C, 16,000 × g, 30 min). Pellets were washed three times with pre-cooled acetone (-20 °C), resuspended in 50 mM ammonium bicarbonate (pH 8.0) at a concentration of 10 µg µL⁻¹, and digested with trypsin. Finally, the digested proteins were purified with a Zip-Tip

C18 column, freeze-dried by Speed Vac, and preserved until their MS analysis.

LC-MS/MS analysis

The LC-MS/MS of the protein extracts were carried out by means of two independent biological replicates from each condition in CEQUIBIEM – University of Buenos Aires, Argentina, according to La Greca et al.^[14], with slight modifications. Briefly, samples were dissolved in 10 µL of 0.1% formic acid and analyzed by nano HPLC coupled to a mass spectrometer with Orbitrap technology. LC was performed by using a Thermo Scientific model EASY-nLC 1000 coupled to an Easy-Spray Column PepMap RSLC (C18, 2 µm, 100 Å, 50 µm × 150 mm). Two solutions (Solution A: 0.1% (v/v) formic acid; Solution B: acetonitrile with 0.1% (v/v) formic acid) were used for peptides elution, developing a gradient from 5% to 100% of solution B for 120 min at a flow rate of 0.300 µL min⁻¹. Mass spectra were obtained by a Q-Exactive Orbitrap instrument (Thermo Fisher Scientific). The configuration of the equipment allowed the identification of peptides to be carried out at the same time that they were separated by chromatography, obtaining Full MS (resolution: 70,000) and MS/MS (resolution: 17,500). The 15 most intense peaks obtained for each MS spectrum were selected for fragmentation in MS/MS. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE^[15] partner repository with the dataset identifier PXD023035.

Data analysis and protein quantification

Peptides identification was performed through Thermo ScientificTM Proteome Discoverer version 2.1 software, Waltham, MA, USA, using the reference proteome of *B. subtilis* 168 (UP000001570) as database. The following parameters were considered as search criteria: parent ion tolerance, 10 ppm; fragment ion mass tolerance, 0.05 Da; Miscalculation, 2; Dynamic Modifications, methionine oxidation (M); static modifications, Carbamidomethylation (C). On these bases, the software qualified the detected peptides in three confidence levels: Low, Medium, and High. At least two peptides per protein were necessary to consider the presence of a protein in the sample. For area estimations of each identified protein, we only considered those peptides with a High confidence level.

The statistical analysis of data was carried out with Perseus software version 1.5.8.5, Martinsried, Germany (2016). Only those proteins identified in both replicates of each condition were considered for the analysis. Protein abundances in term of normalized area intensities (label-free quantification [LQF]) were transformed into their log₂ to compare among two conditions. Besides, proteins were considered significantly regulated when: (i) they showed an average increase higher than 2 folds in their abundance and (ii) *t*-test showed a *p* value < 0.05. Fold-changes (FCs) for up-regulated proteins were calculated as the ratio between their normalized areas for the two compared conditions.

CAZy domain and COG category assignation

Protein sequences from *B. subtilis* 168, used as reference dataset to identify the *Bacillus* sp. AR03 proteomic sequences,^[16] were submitted to dbCAN2 meta server for CAZy domain assignment (<http://bcb.unl.edu/dbCAN2>)^[17] and to WebMGA Server for COG classification (<http://weizhong-lab.ucsd.edu/webMGA>).^[18] SignalP-4.1 Server on-line tool was used to predict the presence of signal peptides.^[19]

Enzymatic activity assays and hydrolysis profile for xylan-containing substrates

Protein concentration was determined according to Bradford,^[20] by using bovine serum albumin as standard.

Endoglucanase and xylanase activities were evaluated by using CMC and birchwood xylan as substrates, respectively. Reaction mixture consisted of 450 μ L of 1% (w/v) suitable substrate in 100 mM sodium phosphate buffer (pH 6.0) and 50 μ L of sample. After incubation for 30 min at 50 °C, the released reducing sugars were measured by dinitrosalicylic acid (DNS) method.^[21] One unit of enzyme activity was defined as the enzyme amount required to release 1 μ mol of reducing sugars (as xylose or glucose) per minute.^[12,22]

The Rezex RSO-Oligosaccharide Ag⁺ 4% column, 200 \times 10 mm (Phenomenex), was used to identify oligosaccharides released from enzymatic reactions, using D-(+)-xylose (X1), 1,4- β -D-xylobiose (X2), 1,4- β -D-xilotriose (X3), 1,4- β -D-xylotetraose (X4), and 1,4- β -D-xylopentose (X5) (*Megazyme*) as standards. Employed running conditions were based on those previously published.^[23] The Chromatopac Shimadzu C-R8A data processor was used to analyze the obtained data.

All the experiments were performed in triplicate and results were reported as the arithmetic means with their corresponding standard deviations. Data were analyzed using Minitab[®] version 17.1.0 statistical software (Minitab Inc., State College, PA) by means of analysis of variance (ANOVA). Differences were significant when $p < 0.05$. Associations between variables were assessed using Tukey's HSD test ($p < 0.05$).

Results and discussion

Production of endoglucanases and xylanases by *Bacillus* sp. AR03 in the three evaluated conditions

Bacillus sp. strain AR03 was characterized as a cellulase producer in a peptone-based medium.^[13] In this work, the bacterium was able to grow in the three assessed conditions, though OD values were higher when the culture medium was supplemented with glucose (condition 1) and with glucose + CMC (condition 3) ([Supplementary Material 1](#)).

Endoglucanase production in condition 1 (Glu) did not show significant differences between 48 and 72 hr (1.30 ± 0.08 and 1.42 ± 0.14 IU mL⁻¹, respectively) ($p > 0.05$); however, these values were significantly higher than that measured at 24 hr (0.91 ± 0.06 IU mL⁻¹) ($p < 0.05$). On the other hand, the enzymatic production obtained in

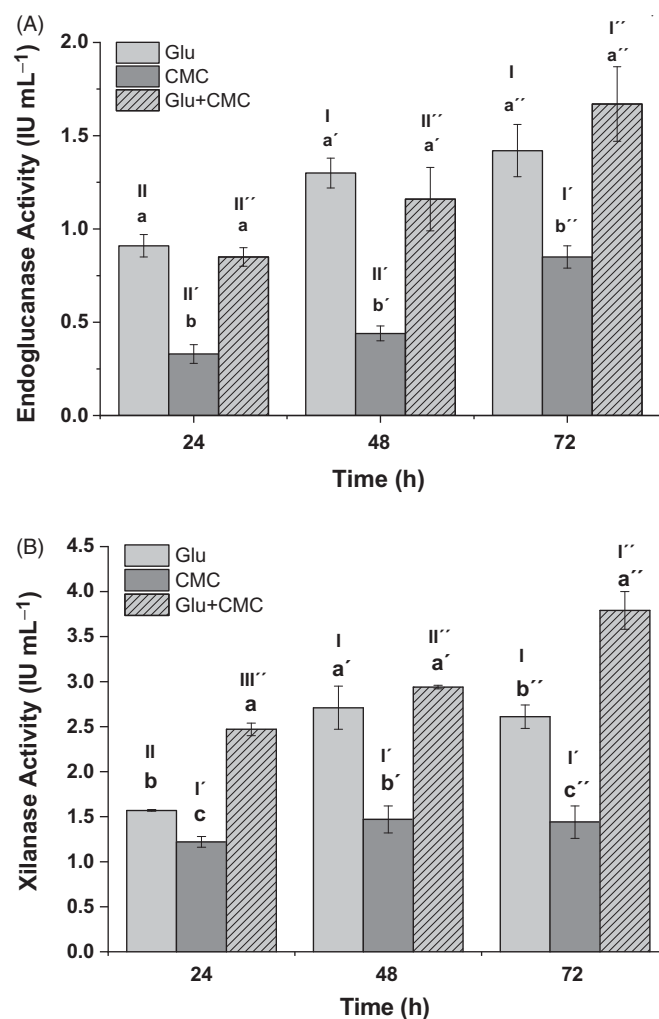


Figure 1. Endoglucanase (A) and xylanase (B) activities detected in the enzymatic cocktails from *Bacillus* sp. strain AR03 on the three evaluated conditions. Error bars represent the standard deviation calculated from three independent experiments. Different letters indicate significant differences among conditions (1, 2, and 3) for each incubation time ($p < 0.05$, Tukey test). (a, b, c), (a', b', c'), and (a'', b'', c'') were used for comparisons among conditions at 24, 48, and 72 hr, respectively. Different roman numerals indicate significant differences among incubation times (24, 48, and 72 hr) for each condition ($p < 0.05$, Tukey test). (I, II, III), (I', II', III'), and (I'', II'', III'') were used for comparisons among incubation times for condition 1, 2, and 3, respectively (see also [Supplementary Material 2](#)). Condition 1: Glu (glucose); Condition 2: CMC (carboxymethyl cellulose); Condition 3: Glu + CMC (glucose + carboxymethyl cellulose).

conditions 2 (CMC) and 3 (Glu + CMC) at 72 hr (0.85 ± 0.06 and 1.67 ± 0.20 IU mL⁻¹, respectively) was significantly higher than those obtained at the other two incubation times ($p < 0.05$) ([Fig. 1A](#), [Supplementary Material 2](#)).

Regarding the xylanolytic enzymes production, the activity values did not present significant differences between 48 and 72 hr (2.71 ± 0.24 and 2.61 ± 0.13 IU mL⁻¹, respectively) in condition 1 ($p > 0.05$), while no significant differences were observed in the activity values at all tested times in condition 2 ($p > 0.05$). However, condition 3 presented the maximum activity value at 72 hr (3.79 ± 0.21 IU mL⁻¹), with significant differences regarding the values obtained at 24 and 48 hr (2.47 ± 0.07 and 2.94 ± 0.02 IU mL⁻¹, respectively) ($p < 0.05$) ([Fig. 1B](#), [Supplementary Material 2](#)).

Additionally, the xylanolytic activity observed for the cocktail produced in glucose + CMC condition

(3.79 ± 0.21 IU mL⁻¹) was significantly higher than those observed for the cocktails produced in glucose condition (2.61 ± 0.13 IU mL⁻¹) and CMC condition (1.44 ± 0.18 IU mL⁻¹) at 72 hr of incubation ($p < 0.05$) (Fig. 1, Supplementary Material 2). Possibly, the presence of two carbon sources contributed to maintaining the metabolic state of the studied microorganism, especially by using partially degraded CMC (such as cellobiose obtained through the hydrolysis of the produced endoglucanases) in a late growth phase.^[24,25] In this sense, the medium from condition 3 contributed with more glucose or smaller oligosaccharides that supported the higher growth of *Bacillus* sp. AR03 and enzymatic production. Notably, these results are consistent with the growth studies of *Bacillus* AR03 in mono- and co-cultures previously reported,^[25] where a diauxic phenomenon was observed during the production of CAZymes. It is also remarkable the capability of this strain to produce CAZymes in absence of polymeric substrates. Similarly, other authors reported that the used carbon source significantly influenced the production of xylanases, getting the maximum values when a complex substrate^[26,27] and a monomer^[28] were added to the medium.

Considering the biotechnological potential, the production of this mixed cellulase/xylanase cocktail is useful due to the widely showed synergistic effect that these enzymes have on complex substrates.^[29]

Protein identification of enzymatic cocktails produced by *Bacillus* sp. AR03

Due to the maximum enzymatic activities were reached at 72 hr of incubation in many assessed conditions and in order to unify the times to carry out proteomic studies, the samples collected at 72 hr were used for subsequent studies.

The proteins present in the culture supernatants obtained from media supplemented with different carbon sources were scanned by shotgun proteomic analyses to describe the enzymes produced for polysaccharides utilization. Since *Bacillus* sp. AR03 was closely related to *B. subtilis* group^[13] and its genome has not yet been sequenced, the genome and protein sequences of *B. subtilis* 168 were used as an appropriate database to identify the proteins detected by the proteomic analysis.

Figure 2 shows the total number of proteins identified in each evaluated condition. Media supplemented with glucose and glucose + CMC showed similar amounts of identified proteins (172 and 167, respectively) and shared 147 proteins (85% and 88% of total proteins for glucose and glucose + CMC conditions, respectively). Furthermore, the Volcano plots denoted that some up-regulated proteins were found by comparing both media (Supplementary Material 3). Among them, only protein P02968 (flagellin) was up-regulated on glucose condition, while the proteins C0SP82 (probable oxidoreductase), P09339 (aconitate hydratase), P96579 (ribosomal N-acetyltransferase), and P04957 (β -glucanase) were up-regulated on glucose + CMC condition. On the other hand, medium containing CMC as the only carbon source presented the lowest number of proteins (147), with

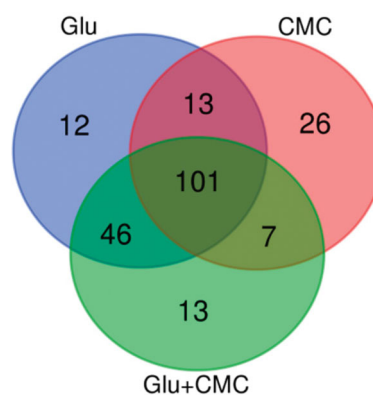


Figure 2. Venn diagram showing the total amount of proteins detected on each evaluated proteome: Glu: glucose (blue); CMC: carboxymethyl cellulose (red); Glu + CMC: glucose + carboxymethyl cellulose (green).

a higher number of unique and up-regulated proteins regarding the other two media (Fig. 2; Supplementary Material 3).

These observations are further explained by analyzing the differential proteomes obtained for each condition. A differential proteome includes proteins that are up-regulated and/or only found in a specific condition.^[30,31] Proteins constituting differential proteomes of each condition were subjected into functional categories according to COG classification (Fig. 3).

Differential proteome from condition 1 revealed that proteins associated with cell motility (N) were up-regulated, particularly those related to flagellar assembly such as a flagellin (P02968) and two flagellar hook-associated proteins (P39810 and P96501) (Fig. 3, Supplementary Table 1). Thus, the presence of CMC in culture media would negatively affect the cell motility, probably due to the high viscosity of media containing this substrate.^[32] Several reports indicated that viscosity notably affected bacterial motility, reducing the speed of motility of flagellar microorganisms and causing cell immobilization at high viscosities.^[33,34]

Differential proteome from condition 2 presented unique proteins related to cell cycle control and mitosis (D) (P07788, a putative spore coat protein), lipid transport and metabolism (I) (O34421, a putative acyl-CoA dehydrogenase), replication, recombination, and repair of DNA (L) (P54521, exodeoxyribonuclease), and cell wall/membrane/envelope biogenesis (M) (P23261 spore coat protein; Q06320 sporulation-specific N-acetylmuramoyl-L-alanine amidase) (Fig. 3, Supplementary Table 1). In addition, 13 proteins not classified into any COG category were detected in the differential proteome obtained from the medium with CMC (Supplementary Material 3). Those mainly encompass proteins associated with sporulation and protein degradation processes (Supplementary Table 1). The up-regulation of these proteins might be evidence of a stress state of *Bacillus* sp. AR03 in the medium with CMC at 72 hr of growth, and would be associated with the lower values of OD and enzymatic activities observed in this condition (Fig. 1). Previously, other researchers identified these sporulation proteins in *Bacillus* species through proteomic studies and described their importance as indicators of cellular stress

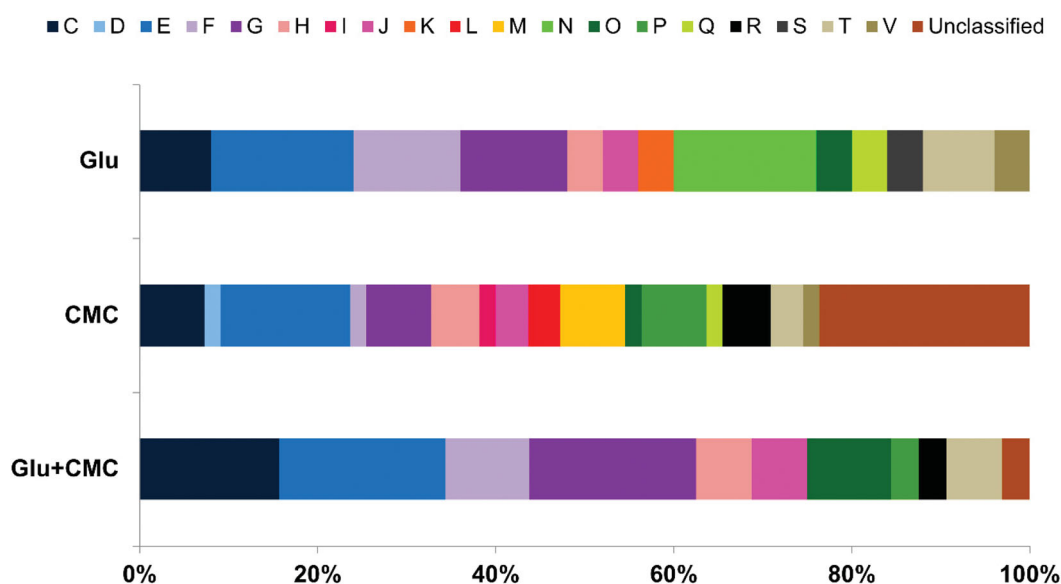


Figure 3. Functional classification of identified proteins in each condition according to COG categories. Glu: differential proteome of glucose condition; CMC: differential proteome of CMC condition; Glu + CMC: differential proteome of glucose + CMC condition. Figure references: (C) Energy production and conversion; (D) Cell cycle control and mitosis; (E) Amino Acid metabolism and transport; (F) Nucleotide metabolism and transport; (G) Carbohydrate metabolism and transport; (H) Coenzyme metabolism; (I) Lipid transport and metabolism; (J) Translation; (K) Transcription; (L) Replication and repair; (M) Cell wall/membrane/envelope biogenesis; (N) Cell motility; (O) Post-translational modification, protein turnover, chaperone functions; (P) Inorganic ion transport and metabolism; (Q) Secondary metabolites biosynthesis, transport and catabolism; (R) General functional prediction only; (S) Function Unknown; (T) Signal Transduction; (V) Defense mechanisms.

status.^[35,36] Additionally, the role of the transcriptional regulation of the gene coding for N-acetylmuramoyl-L-alanine amidase in the mother cell lysis during sporulation of *B. thuringiensis* was reported by Yang et al.^[37]

The stress condition might be related to the rheological properties of the culture media containing CMC. Viscosity is a fundamental property of liquids and plays an important role in the processes of flow, molecular diffusion, and fluid transport.^[38,39] The flow of nutrients and oxygen changes in a very viscous culture medium, leading to the accumulation of metabolites and the formation of gradients, which in turn cause differences in bacterial physiology.^[40] The decrease in dissolved oxygen and the formation of these gradients generate metabolic stress conditions that produce an increase in sporulation.^[41]

Regarding the condition 3, a significant percentage of the identified proteins (53.13%) were related to energy production (C) (15.63%), amino acid transport and metabolism (E) (18.75%), and carbohydrate transport and metabolism (G) (18.75%) (Fig. 3). This result is in concordance with the higher growth and enzymatic activities observed in this condition regarding the conditions 1 and 2 (Fig. 1B).

Proteomic analysis of CAZymes involved in cellulose and xylan degradation

Concerning the carbohydrate active enzymes, proteomes from the three conditions presented enzymes involved in the degradation of cellulose, xylan, starch, and pectin. Heat map from Fig. 4 indicates that cellulose and xylan degrading enzymes were the most abundant CAZymes. The expression of several CAZymes without an inducible substrate is not surprising because genes encoding these enzymes are generally organized in short cluster flanked by transcriptional

regulators.^[7] In this sense, 47 gene clusters encompassing sequences encoding putative CAZymes were found by analyzing the genome of *B. subtilis* 168 with dbCAN2 meta server (Supplementary Table 2).

Two extracellular β -glucan degrading enzymes were found in all conditions: P10475 and P04957. According to CAZy database, P10475 contains a GH5_2 domain associated with CBM3 domain. Experimentally characterized GH5_2 presents endoglucanase activity (EC 3.2.1.4), while CBM3 usually binds to cellulose.^[42–44] This enzyme was up-regulated in glucose condition (fold change value = 6.7) and glucose + CMC condition (fold change value = 6.1) regarding the CMC condition (Fig. 4). On the other hand, P04957 presented a GH16 domain. Enzymes from this family mainly present β -1,3(4)-glucanase activity (EC 3.2.1.6),^[45–47] but they also include β -glucosidase (EC 3.2.1.-), laminarinase (EC 3.2.1.39), and β -transglycosidase (EC 2.4.1.-) activities.^[43] P04957 was significantly up-regulated on the medium containing glucose + CMC, while no differences were found between conditions 1 and 2 (Fig. 4). Probably, these two enzymes would be the main responsible of CMCase activity observed in culture supernatants (Fig. 1A). The high abundance of these enzymes in the evaluated conditions might be related to the expression (or induction) of an entire series of enzymes involved in the degradation of cellulosic compounds present in plant biomass (including different types of endo-glucans), and promoted by the presence of a natural cellulose analog, such as CMC.^[48] In several studies, GH16 CAZymes have been expressed in presence of a great variety of cellulosic substrates, such as cellobiose, avicel, soforose, and sugarcane bagasse.^[49–51]

Notably, three putative CAZymes related to xylan degradation were also found in all conditions: a putative extracellular xylanase with a GH30_8 domain (Q45070) and two

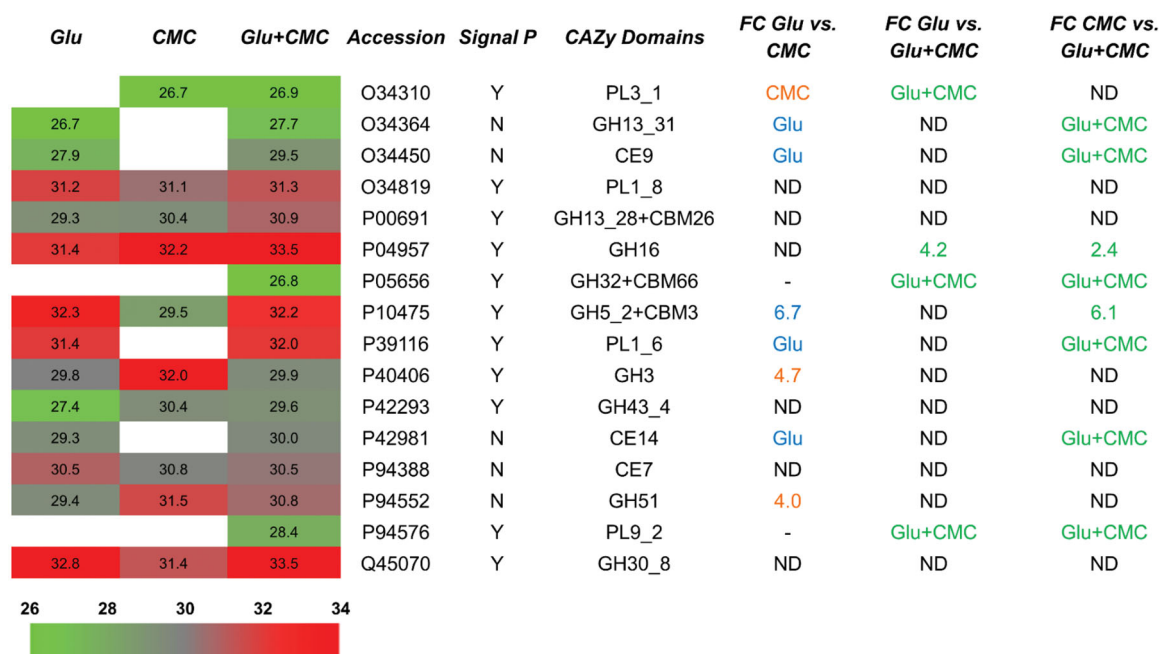


Figure 4. Proteins with a CAZy domain found in analyzed proteomes. Fold-change (FC) for a protein between two conditions was calculated as the ratio of protein abundances in each condition. ND: no significant differences; Glu: only present on Glucose condition; CMC: only present on CMC condition; Glu + CMC: only present on Glucose + CMC condition. Blue: up-regulated on Glucose condition; Orange: up-regulated on CMC condition; Green: up-regulated on Glucose + CMC condition. Heat map was drawn according to average of enzyme abundances in each condition. Scale: green indicates low abundance; red indicates high abundance.

α -arabinofuranosidases (EC 3.2.1.55) from GH43_4 (P42293) and GH51 (P94552) families. Of these enzymes, only GH51 was up-regulated in the CMC condition regarding the glucose condition, with a fold change value = 4.0 (Fig. 4). Many enzymes belonging to GH51 family were classified as α -arabinofuranosidase. However, other well-known activities of this family include endoglucanase, endo- β -1,4-xylanase (EC 3.2.1.8), and β -xylosidase (EC 3.2.1.37).^[43] It was reported that GH51 CAZymes showed endo- β -1,4-glucanase activity with CMC as substrate,^[52,53] which might explain the up-regulation of P94552 from *Bacillus* sp. AR03 in CMC condition (Fig. 4). However, additional studies are necessary to confirm the substrate specificity of this GH51 enzyme, or its ability to hydrolyze different bonds and polysaccharides.

The proteomic analysis was unable to detect any unique peptide belonging to GH11 xylanase (P18429) from *B. subtilis* 168. However, due to some peptide sequences detected through this analysis are shared by both GH11 and GH30 xylanases, the presence of a GH xylanase in enzymatic cocktails produced by *Bacillus* sp. AR03 might not be discounted.

Besides, it is important to note that genes encoding the endoglucanase GH5_2 (P10475) and the glucuronoxylanase GH30_8 (Q45070) were found to constitute a gene cluster in the genome of *B. subtilis* 168 (Supplementary Table 2). These enzymes were also detected with similar abundances in the proteomic analysis. Thus, this gene arrangement might be conserved in genome of *Bacillus* sp. AR03.

Xylan hydrolysis by enzymatic cocktails and product characterization

CAZymes from GH30_8 family were described as specific glucuronoxylan degrading enzymes (EC 3.2.1.136). These

Table 1. Xylooligosaccharides (XOS) yield obtained from birchwood xylan, treated with enzymatic cocktails produced by *Bacillus* sp. AR03 in different conditions: culture medium supplemented with glucose (Glu) (condition 1), carboxymethyl cellulose (CMC) (condition 2), and glucose and carboxymethyl cellulose (Glu + CMC) (condition 3).

Condition	Hydrolysis product (mg mL ⁻¹)				
	X5	X4	X3	X2	Total
Glu	0.37 ± 0.05	0.34 ± 0.01	0.35 ± 0.03	ND	1.06 ± 0.09
CMC	0.44 ± 0.10	0.45 ± 0.08	0.50 ± 0.07	0.24 ± 0.01	1.63 ± 0.24
Glu + CMC	0.46 ± 0.07	0.50 ± 0.07	0.58 ± 0.16	0.36 ± 0.18	1.90 ± 0.49

ND: non detected.

enzymes show very low selectivity for unsubstituted xylan, arabinoxylan, and xylooligosaccharides (XOS), which is the main difference with respect to the xylanases of the GH10 and GH11 families.^[54,55] GH30_8 xylanases showed potential in the production of XOS with prebiotic properties,^[56,57] and were previously identified in different *Bacillus* spp. species.^[58,59] Thus, it was evaluated the capability of enzymatic cocktails produced by *Bacillus* sp. AR03 in the different culture media to degrade birchwood xylan, a substrate with D-methylglucuronic acid substitutions (MeGlcAc).

XOS with polymerization degree between 3 and 5 xylose units were the main products obtained from birchwood xylan hydrolysis (Table 1). Besides, other two unknown products, U1 and U2, were also detected. Notably, xylose (X1) was not produced (Fig. 5). In contrast to a typical XOS mixture produced by GH10 enzymes,^[56] the quantity of produced xylobiose (X2) was low (0.36 and 0.24 mg mL⁻¹) for the cocktails corresponding to glucose + CMC and CMC conditions, respectively, and not detectable for the cocktail from condition with glucose (Table 1). The total XOS production was maximum (1.90 mg mL⁻¹) with the cocktail

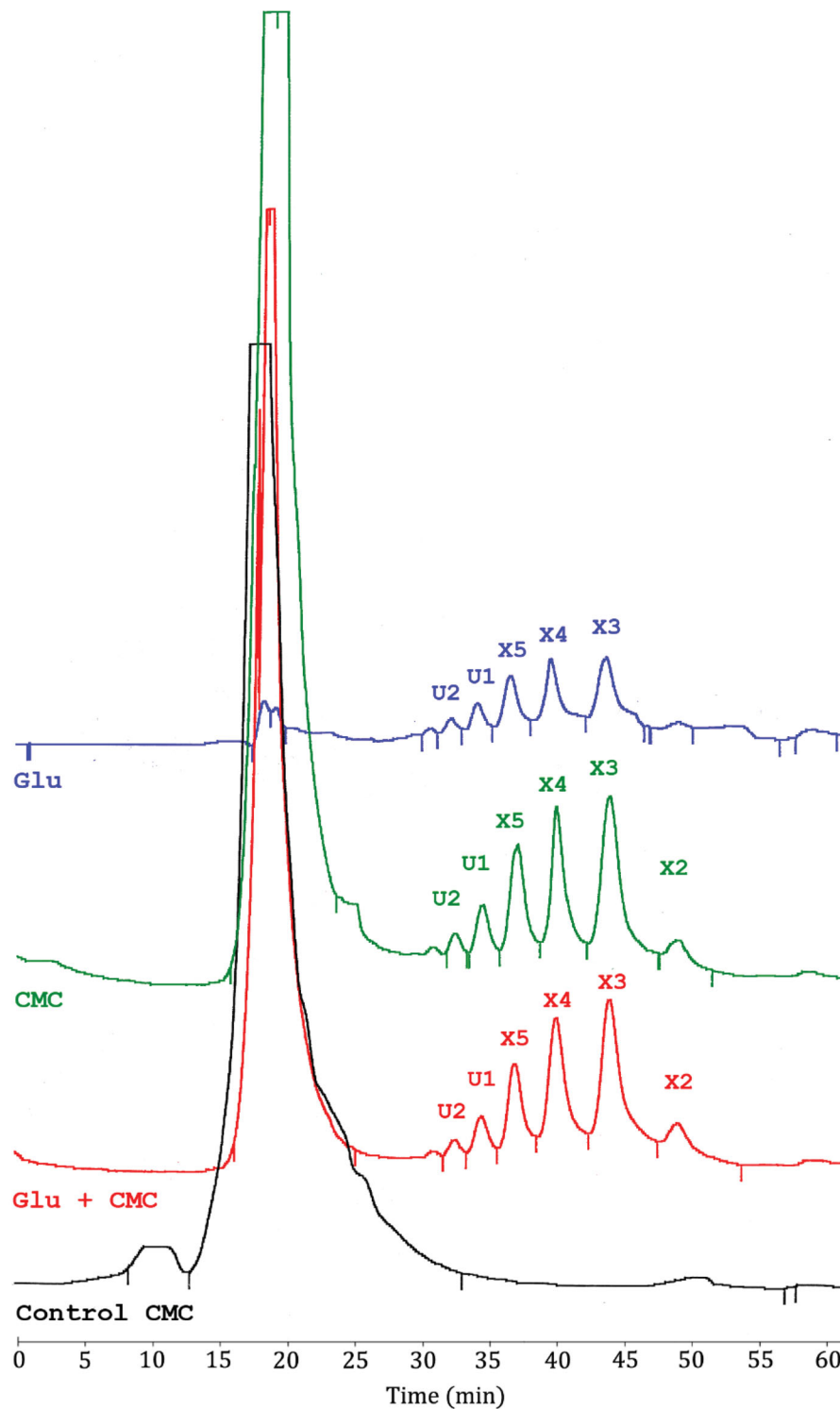


Figure 5. Products profile of birchwood xylan degradation by enzymatic cocktails produced by *Bacillus* sp. AR03 in different conditions: **condition 1** (Glu, blue line); **condition 2** (CMC, green line); and **condition 3** (Glu + CMC, red line). Control was carried out by mixing the enzymatic cocktail produced in the CMC condition, previously inactivated by heat, and the substrate (birchwood xylan) (black line). Xylotriose (X3), xylotetraose (X4), xylobiose (X2), xylopentaose (X5), unknown products (U1 and U2).

obtained in the medium supplemented with glucose + CMC (Table 1). This result corroborates the higher xylanolytic activity determined for the enzyme mixture in this medium (Fig. 1B).

The profile of products might be explained by the action mode of GH30_8, which hydrolyzes the xylan backbone near a substitution with MGlucAc.^[60] In this work, this

enzyme generated XOS without substitutions and a substituted oligosaccharide, possibly U1 and U2 (Fig. 5). As previously reported, this enzyme continues hydrolyzing until X5, generating lower molecular weight oligosaccharides, such as X2 and X3.^[61] However, this enzyme does not show activity against X3, unlike other glycoside hydrolases, such as GH10.^[62] For this reason, the enzymatic cocktails produced

by *Bacillus* sp. AR03 would not have generated xylose as a product. However, this absence of xylose between hydrolysis products is a desirable feature for prebiotic production.^[63]

Probably, the lack of activity with low molecular weight oligosaccharides is due to the presence of six highly conserved subsites for members of this family: +2, +1 (aglycone region), -1, -2a, -2b, and -3 (glycone region). The -2a and -2b designation refer to the specific subsites for xylose and MGlucAc, respectively. A high number of subsites, in addition to modifications in the residues compared to the conserved active site of GH10 xylanases, demonstrated that X4 with a group MGlucAc at position -2 was the smallest oligosaccharide capable of generating a structure with catalytic capacity.^[64] Recently, it was reported a fungal GH30_8 capable of hydrolyzing X4, generating X2 as the main product, without presenting xylosidase activity.^[65]

Conclusion

The proteomic analyses performed in this work revealed that *Bacillus* sp. AR03 produced enzymes mainly involved in the degradation of cellulose, xylan, starch, and pectin when growing in media containing glucose, CMC, or glucose + CMC as carbon sources. An endoglucanase GH5_2, a β -1,3(4)-glucanase GH16, and a glucuronoxylanase GH30_8 were found among the most abundant proteins in all evaluated conditions. The proteomic studies presented correlation with the endoglucanase and xylanase activities measured in these cocktails. Additionally, the enzymatic cocktails were effective to hydrolyze birchwood xylan, obtaining XOS from 3 to 5 xylose units. Despite the obtained cocktails exhibited similar products profiles after the substrate bioconversion, the highest xylooligomer concentrations were detected with the cocktail from glucose + CMC condition. These results show the potential application of the enzyme mixtures produced by *Bacillus* sp. AR03 for the production of emerging prebiotics.

Disclosure statement

The authors declare that they have no conflict of interest.

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ORCID

Johan S. Hero  <http://orcid.org/0000-0002-3905-3666>

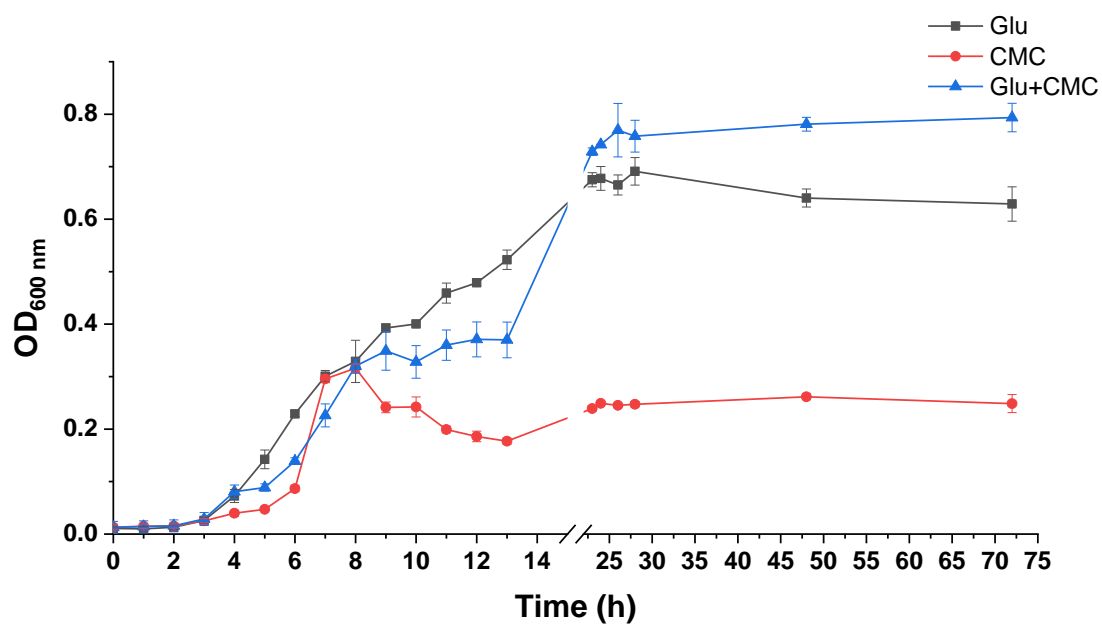
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Supplementary Material 1. Growth curves of *Bacillus* sp. AR03 in the different growth media. Condition 1: 10 g L⁻¹ glucose (**Glu**), Condition 2: 10 g L⁻¹ of CMC (**CMC**), Condition 3: 10 g L⁻¹ of glucose + 10 g L⁻¹ of CMC (**Glu+CMC**). Error bars represent the standard deviation calculated from three independent experiments.



Supplementary Material 2. One-way ANOVA test for endoglucanase (A) and xylanase (B) activity values under conditions 1 (Glu), 2 (CMC) and 3 (Glu+CMC) at different times: 24 h, 48 h, 72 h (see also Fig. 1).

A

Endoglucanase activity

Factor: Time / Values: Glu; CMC; Glu+CMC

<i>Source</i>	<i>DF</i>	<i>Adj SS</i>	<i>Adj MS</i>	<i>F-Value</i>	<i>P-Value</i>	<i>Source</i>	<i>DF</i>	<i>Adj SS</i>	<i>Adj MS</i>	<i>F-Value</i>	<i>P-Value</i>	<i>Source</i>	<i>DF</i>	<i>Adj SS</i>	<i>Adj MS</i>	<i>F-Value</i>	<i>P-Value</i>
Time 24 h	2	0.6168	0.3084	65.12	0.000	Time 48 h	2	1.3514	0.6757	60.76	0.000	Time 72 h	2	1.051	0.5259	30.5	0.001
Error	6	0.0284	0.0047			Error	6	0.0667	0.0111			Error	6	0.103	0.0172		
Total	8	0.6452				Total	8	1.4181				Total	8	1.155			

Factor: Condition / Values: 24 h; 48 h; 72 h

<i>Source</i>	<i>DF</i>	<i>Adj SS</i>	<i>Adj MS</i>	<i>F-Value</i>	<i>P-Value</i>	<i>Source</i>	<i>DF</i>	<i>Adj SS</i>	<i>Adj MS</i>	<i>F-Value</i>	<i>P-Value</i>	<i>Source</i>	<i>DF</i>	<i>Adj SS</i>	<i>Adj MS</i>	<i>F-Value</i>	<i>P-Value</i>
Condition 1	2	0.4031	0.2015	25.18	0.001	Condition 2	2	0.4453	0.2226	96.82	0.000	Condition 3	2	0.980	0.4903	21.51	0.002
Error	6	0.0480	0.0080			Error	6	0.0138	0.0023			Error	6	0.136	0.0228		
Total	8	0.4511				Total	8	0.4591				Total	8	1.117			

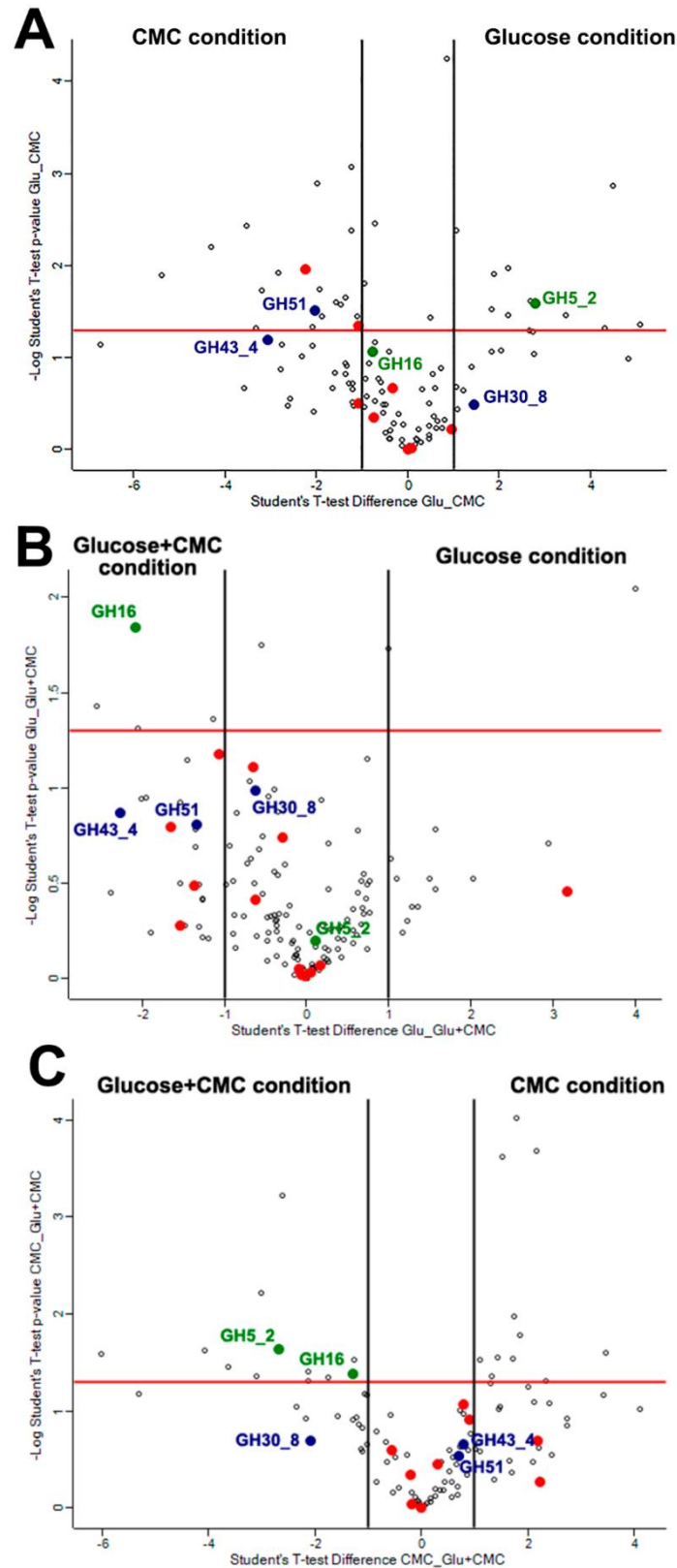
B**Xylanase activity****Factor: Time / Values: Glu; CMC; Glu+CMC**

<i>Source</i>	<i>DF</i>	<i>Adj SS</i>	<i>Adj MS</i>	<i>F-Value</i>	<i>P-Value</i>	<i>Source</i>	<i>DF</i>	<i>Adj SS</i>	<i>Adj MS</i>	<i>F-Value</i>	<i>P-Value</i>	<i>Source</i>	<i>DF</i>	<i>Adj SS</i>	<i>Adj MS</i>	<i>F-Value</i>	<i>P-Value</i>
Time 24 h	2	2.5281	1.2640	469.49	0.000	Time 48 h	2	3.7658	1.8829	68.41	0.000	Time 72 h	2	8.2872	4.1436	126.04	0.000
Error	6	0.0161	0.0026			Error	6	0.1651	0.0275			Error	6	0.1973	0.0328		
Total	8	2.5443				Total	8	3.9310				Total	8	8.4845			

Factor: Condition / Values: 24 h; 48 h; 72 h

<i>Source</i>	<i>DF</i>	<i>Adj SS</i>	<i>Adj MS</i>	<i>F-Value</i>	<i>P-Value</i>	<i>Source</i>	<i>DF</i>	<i>Adj SS</i>	<i>Adj MS</i>	<i>F-Value</i>	<i>P-Value</i>	<i>Source</i>	<i>DF</i>	<i>Adj SS</i>	<i>Adj MS</i>	<i>F-Value</i>	<i>P-Value</i>
Condition 1	2	2.3893	1.1946	47.45	0.000	Condition 2	2	0.1146	0.0572	2.81	0.138	Condition 3	2	2.6852	1.3426	76.55	0.000
Error	6	0.1511	0.0252			Error	6	0.1222	0.0203			Error	6	0.1052	0.0175		
Total	8	2.5404				Total	8	0.2368				Total	8	2.7905			

Supplementary Material 3. Volcano plots comparing the protein abundance between two conditions. Glucose vs. CMC (**A**); Glucose vs. Glucose+CMC (**B**); CMC vs. Glucose+CMC (**C**). Filled circles indicate proteins with CAZy domains. Blue circles: CAZymes related to the degradation of xylan of GH30_8 (Q45070), GH43_4 (P42293) and GH51 (P94552) families. Green circles: extracellular β -glucanases of GH5_2 (P10475) and GH16 (P04957) families. Red circles: other putative GHs, PLs and CEs.



Accession	Description	Signal P	Cazy Domain	COG Number
P37940	2-oxoisovalerate dehyd	N		COG1071
P37941	2-oxoisovalerate dehyd	N		COG0022
P54533	Dihydrolipoyl dehyd	N		COG1249
P13714	L-lactate dehydrogen	N		COG0039
P42412	Methylmalonate sen	N		COG1012
P08065	Succinate dehydrogen	N		COG1053
P09339	Aconitate hydratase	N		COG1048
P54572	Probable NAD-deper	N		COG0281
P37808	ATP synthase subuni	N		COG0056
P37809	ATP synthase subuni	N		COG0055
P37813	ATP synthase subuni	N		COG0356
P46912	Menaquinol-cytochr	N		COG1290
P46913	Menaquinol-cytochr	N		COG1290
P94424	FMN reductase [NAD	N		COG0778
O31404	Acetoin:2,6-dichloro	N		COG1071
O32224	FMN-dependent NAD	N		COG1182
O34591	Acetoin:2,6-dichloro	N		COG0022
P24469	Cytochrome c-550 O	N		COG2010
C0SP82	Probable oxidoreduc	N		COG0243
O07529	FMN-dependent NAD	N		COG0431
P42175	Nitrate reductase alp	N		COG5013
P42176	Nitrate reductase be	N		COG1140
P07788	Spore coat protein A	N		COG2132
O31669	Acireductone dioxyg	N		COG1791
P10944	Histidine ammonia-l	N		COG2986
P18186	Ornithine carbamoyl	N		COG0078
P19080	Chorismate mutase	N		COG4401
P25503	Urocanate hydratase	N		COG2987
P39138	Arginase OS=Bacillus	N		COG0010
P54420	Asparagine syntheta	N		COG0367
P54517	3-dehydroquinate de	N		COG0757
P54531	Leucine dehydrogen	N		COG0334
P04990	Threonine synthase	N		COG0498
P42318	Uncharacterized pro	N		COG0620
P94427	Probable 4-aminobu	N		COG0160
P12425	Glutamine synthetas	N		COG0174
P39148	Serine hydroxymeth	N		COG0112
O05394	Cystathionine gamm	N		COG0626
P37887	Cysteine synthase O	N		COG0031
P24141	Oligopeptide-binding	Y		COG4166
O32106	Probable cytosol am	N		COG0260
P54422	Gamma-glutamyltra	Y		COG0405
P71035	Urease subunit beta	N		COG0832
P75030	Urease subunit gam	N		COG0831
P77837	Urease subunit alph	N		COG0804
P26902	D-aminopeptidase O	N		COG2362
P39762	Aminopeptidase Am	N		COG2309
P50848	Carboxypeptidase 1	N		COG2317
P54542	Uncharacterized pro	N		COG2195

P55179	Peptidase T OS=Baci	N		COG2195
O07622	Putative Rieske 2Fe-	N		COG0665
P39790	Extracellular metallic	Y		COG3591
O07603	Putative aminopepti	N		COG1363
O34924	Putative aminopepti	N		COG1363
P94521	Putative aminopepti	N		COG1363
O07597	D-alanine aminotran	N		COG0115
Q04789	Acetolactate synthas	N		COG0028
P80862	Phosphoserine amin	N		COG1932
Q04796	4-hydroxy-tetrahydr	N		COG0329
O31776	L-threonine 3-dehyd	N		COG1063
O34788	(R,R)-butanediol deH	N		COG1063
P54535	Arginine-binding ext	Y		COG0834
O05269	GMP reductase OS=I	N		COG0516
P25995	Dihydrooorotase OS=	N		COG0044
P46354	Purine nucleoside ph	N		COG0005
P21879	Inosine-5'-monopho	N		COG0516
P94526	Sugar-phosphatase A	N		COG0647
O34313	Trifunctional nucleot	Y		COG0737
O31801	Probable deoxyuridi	N		COG0756
O31668	Methylthioribulose-3	N		COG0235
O34364	Probable oligo-1,6-g	N	GH13_31(28-376)	COG0366
O34450	N-acetylglucosamine	N	CE9(8-384)	COG1820
O34714	Oxalate decarboxyla	N		COG2140
P00691	Alpha-amylase OS=B	Y	GH13_28(58-317)+CB	COG0366
P05656	Levanase OS=Bacillu	Y	GH32(39-349)+CBM6	COG1621
P19669	Transaldolase OS=Ba	N		COG0176
P39841	Putative mannose-6-	N		COG1482
P50843	4-deoxy-L-threo-5-h	N		COG3717
P94523	L-arabinose isomera	N		COG2160
P94552	Intracellular exo-alf	N	GH51(3-492)	COG3534
P39116	Pectate lyase OS=Ba	Y	PL1_6(134-346)	COG3866
O34557	Ribulose-phosphate	N		COG0036
P39773	2,3-bisphosphoglyce	N		COG0696
P09124	Glyceraldehyde-3-ph	N		COG0057
P10475	Endoglucanase OS=E	Y	GH5_2(52-296)+CBM	COG2730
P40406	Beta-hexosaminidas	Y	GH3(112-348)	COG1472
P46353	Phosphopentomutas	N		COG1015
P36946	D-ribose pyranase O	N		COG1869
O34819	Pectin lyase OS=Baci	Y	PL1_8(83-275)	COG3866
P42293	Extracellular endo-al	Y	GH43_4(35-360)	COG3507
P42418	Protein lolH OS=Baci	N		COG1082
P42981	N-acetyl-alpha-D-glu	N	CE14(7-112)	COG2120
P04957	Beta-glucanase OS=E	Y	GH16(35-239)	COG2273
Q795U4	UPF0173 metal-depe	N		COG2220
O31676	6-carboxy-5,6,7,8-ter	N		COG0720
O34457	Molybdenum cofact	N		COG0521
O34899	Cob(I)yrinic acid a,c-	N		COG2096
O35033	Probable coenzyme	Y		COG0452
P11998	6,7-dimethyl-8-ribity	N		COG0054

P16440	Riboflavin synthase (N	COG0307
P16616	Porphobilinogen deaY	COG0181
P19465	GTP cyclohydrolase .N	COG0302
P25052	Aminopyrimidine anN	COG0819
P28823	Dihydroneopterin alN	COG1539
P39666	Probable nicotinate-N	COG0157
O31705	Molybdopterin syntN	COG0314
P52999	Aspartate 1-decarboN	COG0853
O05243	UPF0047 protein YugN	COG0432
P49786	Biotin carboxyl carriN	COG0511
O06734	AB hydrolase superfiN	COG0596
P94584	3-hydroxyacyl-[acyl-(N	COG0764
Q06756	2-C-methyl-D-erythrN	COG0245
P37967	Para-nitrobenzyl estN	COG2272
O34421	Probable acyl-CoA diN	COG1960
O34340	3-oxoacyl-[acyl-carriN	COG0304
P40397	Uncharacterized oxiaN	COG1028
O31742	50S ribosomal proteN	COG0335
O32038	Aspartate--tRNA(AspN	COG0173
O32053	Queuine tRNA-ribosyN	COG0343
P50849	Polyribonucleotide rN	COG1185
O31678	NADPH-dependent 7N	COG0780
P94462	Peptide deformylaseN	COG0242
Q45495	Peptide deformylaseN	COG0242
O07607	Probable metallo-hyN	COG1234
P96579	Putative ribosomal MN	COG1670
O31754	Regulator of sigma-VN	COG0750
P05653	DNA gyrase subunit. N	COG0188
P37455	Single-stranded DNA N	COG0629
P54521	Exodeoxyribonuclea: N	COG1570
P14192	Bifunctional protein N	COG1207
P55180	UDP-glucose 4-epim N	COG1087
P0CI73	Glutamine--fructose N	COG0449
P10725	Alanine racemase 1. N	COG0787
P94494	Alanine racemase 2. N	COG0787
Q06320	Sporulation-specific N	COG0860
Q45070	Glucuronoxylanase X Y	GH30_8(34-379) COG5520
P23261	Spore coat protein FN	COG5577
P23446	Flagellar basal-body N	COG4786
P39810	Flagellar hook-assocY	COG1256
P96501	Flagellar hook-assocN	COG1344
P02968	Flagellin OS=BacillusN	COG1344
P04189	Subtilisin E OS=BacilY	COG1404
P11018	Major intracellular sN	COG1404
P16397	Bacillopeptidase F O Y	COG4412
P29141	Minor extracellular pY	COG1404
P37476	ATP-dependent zinc N	COG0465
P54423	Cell wall-associated Y	COG1404
O31657	Protease HtpX homcN	COG0501
P25152	Aminopeptidase YwaY	COG2234

P39070	ATP-dependent prot	N	COG5405
O32218	Disulfide bond forma	Y	COG1651
O34357	Thioredoxin-like pro	N	COG0526
O34789	Uncharacterized pro	N	COG4260
P26901	Vegetative catalase	N	COG0753
P42234	Catalase-2 OS=Bacill	N	COG0753
O32167	Methionine-binding	Y	COG1464
O34385	Manganese-binding	Y	COG0803
P46338	Phosphate-binding p	Y	COG0226
P54375	Superoxide dismutas	N	COG0605
P39645	Putative heme-depe	N	COG3253
Q45538	Protein CotJC OS=Ba	N	COG3546
P37960	Metalloregulation D	N	COG0783
P94388	Cephalosporin-C dea	N	COG3458
O32210	Glyoxal reductase O	N	COG0656
P39586	Uncharacterized pro	N	COG0346
P45743	Isochorismatase OS=	N	COG1535
O31455	Putative hydrolase	Y	COG2312
O31535	Uncharacterized pro	N	COG0346
O34374	Putative cytochrome	N	COG2124
P54501	Probable metallo-hy	N	COG0491
O05408	Uncharacterized oxi	N	COG0667
O31737	Uncharacterized pro	Y	COG5266
O34355	Putative amidohydr	N	COG1574
O34696	Uncharacterized tran	N	COG0663
P37502	Probable metallo-hy	N	COG0491
P42972	Uncharacterized oxi	N	COG4989
P94533	Uncharacterized pro	N	COG2764
Q04805	Uncharacterized zin	N	COG0612
P37538	Uncharacterized pro	N	COG3870
P40407	Uncharacterized pro	Y	COG3876
O34667	S-ribosylhomocystei	N	COG1854
O31796	RNA-binding protein	N	COG1923
O34483	HPr kinase/phospho	N	COG1493
O34384	Uncharacterized pro	N	COG2310
P80875	General stress prote	N	COG2310
O34973	Putative hydrolase	Y	COG1073
P81100	Stress response prot	N	COG2310
P80242	Organic hydroperoxi	N	COG1764
P10943	Hut operon positive	N	
P19466	Transcription attenu	N	
P54507	Spore coat-associate	Y	
P70960	Uncharacterized pro	Y	
P39620	Spore coat protein	N	
Q45536	Protein CotJA OS=Ba	N	
Q45537	Protein CotJB OS=Ba	N	
O07629	Uncharacterized pro	Y	
O31436	Uncharacterized pro	Y	
O31451	Uncharacterized pro	N	
O31649	Uncharacterized pro	N	

CE7(3-312)

O31803	Uncharacterized pro	Y
O31858	Uncharacterized pro	N
O32211	Stress response prot	Y
O32245	Uncharacterized pro	N
O34310	Pectate lyase C OS=E	Y
O34365	Uncharacterized pro	N
O34882	Probable tautomer	N
P37495	Uncharacterized pro	N
P39797	Phage-like element	N
P39804	Intracellular protein	N
P42091	Protein CgeC OS=Ba	N
P54327	Phage-like element	N
P54331	Phage-like element	N
P54332	Phage-like element	N
P94409	Uncharacterized pro	N
P94576	Uncharacterized pro	Y
Q04385	Uncharacterized pro	N
Q08311	Spore coat protein	Y N
Q08312	Spore coat protein	Z N

PL3_1(30-202)

PL9_2(31-395)

COG Class	Syr COG Class	Coverage	# PSMs	# Unique Peptides
C	Energy production	82.1	58	8
C	Energy production	22.4	28	4
C	Energy production	30.5	76	3
C	Energy production	29.4	82	5
C	Energy production	31.9	14	9
C	Energy production	11.8	21	6
C	Energy production	12.2	3	3
C	Energy production	25.9	11	2
C	Energy production	45.8	584	26
C	Energy production	10.6	4	4
C	Energy production	8.2	7	4
C	Energy production	30.6	16	3
C	Energy production	47.2	256	12
C	Energy production	17.6	7	2
C	Energy production	22.4	8	6
C	Energy production	41.3	263	14
C	Energy production	3.1	5	2
C	Energy production	45.5	113	13
C	Energy production	21.6	8	5
C	Energy production	45.7	122	10
C; P	Energy production	44.1	57	3
C; P	Energy production	12.3	16	3
D; M; P	Cell cycle control, c	4.4	5	3
E	Amino acid transpo	14.5	18	2
E	Amino acid transpo	23.4	82	4
E	Amino acid transpo	46.3	153	13
E	Amino acid transpo	26.7	38	4
E	Amino acid transpo	13.8	16	3
E	Amino acid transpo	32.6	281	5
E	Amino acid transpo	34.4	108	8
E	Amino acid transpo	8.9	4	2
E	Amino acid transpo	40.0	157	4
E	Amino acid transpo	75.3	243	4
E	Amino acid transpo	7.9	2	2
E	Amino acid transpo	15.0	7	3
E	Amino acid transpo	31.2	13	3
E	Amino acid transpo	46.6	178	13
E	Amino acid transpo	78.3	86	7
E	Amino acid transpo	15.1	22	8
E	Amino acid transpo	50.6	851	19
E	Amino acid transpo	35.2	125	14
E	Amino acid transpo	34.0	29	7
E	Amino acid transpo	26.3	16	2
E	Amino acid transpo	22.7	12	5
E	Amino acid transpo	15.8	21	4
E	Amino acid transpo	40.2	36	7
E	Amino acid transpo	36.5	78	6
E	Amino acid transpo	9.9	2	2
E	Amino acid transpo	37.2	64	7

E	Amino acid transp	24.2	83	4
E	Amino acid transp	42.5	82	3
E	Amino acid transp	16.4	2	2
E; G	Amino acid transp	66.9	774	23
E; G	Amino acid transp	43.1	646	21
E; G	Amino acid transp	9.0	10	2
E; H	Amino acid transp	19.7	24	8
E; H	Amino acid transp	11.5	12	3
E; H	Amino acid transp	38.0	29	4
E; M	Amino acid transp	33.2	63	5
E; R	Amino acid transp	60.7	211	14
E; R	Amino acid transp	30.0	34	7
E; T	Amino acid transp	39.8	50	5
F	Nucleotide transp	25.4	131	7
F	Nucleotide transp	6.1	2	2
F	Nucleotide transp	31.8	31	7
F	Nucleotide transp	27.3	394	7
F	Nucleotide transp	18.7	20	9
F; V	Nucleotide transp	17.5	4	3
F; V	Nucleotide transp	21.7	10	8
G	Carbohydrate trans	25.9	9	4
G	Carbohydrate trans	23.4	20	5
G	Carbohydrate trans	43.5	478	17
G	Carbohydrate trans	24.8	106	23
G	Carbohydrate trans	9.7	13	2
G	Carbohydrate trans	26.2	171	4
G	Carbohydrate trans	63.4	212	11
G	Carbohydrate trans	54.9	73	9
G	Carbohydrate trans	38.0	280	5
G	Carbohydrate trans	73.9	247	6
G	Carbohydrate trans	22.9	19	6
G	Carbohydrate trans	34.3	151	5
G	Carbohydrate trans	4.7	3	3
G	Carbohydrate trans	44.4	87	14
G	Carbohydrate trans	6.7	2	2
G	Carbohydrate trans	16.2	22	4
G	Carbohydrate trans	14.8	12	5
G	Carbohydrate trans	63.3	813	15
G	Carbohydrate trans	72.3	424	12
G	Carbohydrate trans	14.9	15	4
G	Carbohydrate trans	19.4	57	5
G	Carbohydrate trans	44.9	238	12
G	Carbohydrate trans	16.8	6	2
G	Carbohydrate trans	27.8	11	3
G	Carbohydrate trans	84.1	1737	10
H	Coenzyme transpo	32.4	25	3
H	Coenzyme transpo	53.1	170	12
H	Coenzyme transpo	65.7	3161	18
H	Coenzyme transpo	26.1	248	14
H	Coenzyme transpo	51.5	36	5

H	Coenzyme transpo	41.9	116	6
H	Coenzyme transpo	36.3	260	8
H	Coenzyme transpo	30.0	10	4
H	Coenzyme transpo	37.8	108	11
H	Coenzyme transpo	54.9	80	7
H	Coenzyme transpo	19.8	34	8
H	Coenzyme transpo	39.0	80	9
H	Coenzyme transpo	60.1	79	7
H	Coenzyme transpo	32.0	26	5
H; I	Coenzyme transpo	59.2	188	9
H; R	Coenzyme transpo	30.9	24	9
I	Lipid transport and	38.0	232	9
I	Lipid transport and	62.0	1556	13
I	Lipid transport and	11.4	37	3
I	Lipid transport and	15.1	6	3
I; Q	Lipid transport and	21.2	82	8
I; Q; R	Lipid transport and	16.7	3	2
J	Translation, riboso	69.7	195	14
J	Translation, riboso	60.8	545	18
J	Translation, riboso	26.6	39	7
J	Translation, riboso	14.4	130	3
J	Translation, riboso	41.1	268	15
J	Translation, riboso	24.8	24	2
J	Translation, riboso	17.0	6	4
J	Translation, riboso	22.3	28	4
J; O	Translation, riboso	42.3	137	14
K; O	Transcription; Post	6.1	3	2
L	Replication, recom	40.2	242	16
L	Replication, recom	35.2	128	9
L	Replication, recom	12.6	8	3
M	Cell wall/membran	12.8	30	3
M	Cell wall/membran	44.6	28	7
M	Cell wall/membran	40.2	252	19
M	Cell wall/membran	13.8	2	2
M	Cell wall/membran	8.0	13	2
M	Cell wall/membran	6.5	13	3
M	Cell wall/membran	32.1	4	3
M	Cell wall/membran	47.2	118	6
N	Cell motility	30.1	48	4
N	Cell motility	4.0	3	2
N	Cell motility	55.9	108	10
N	Cell motility	90.1	550	13
O	Posttranslational m	13.3	4	3
O	Posttranslational m	28.8	47	3
O	Posttranslational m	83.8	1320	8
O	Posttranslational m	7.2	3	2
O	Posttranslational m	14.4	225	12
O	Posttranslational m	35.6	15	4
O	Posttranslational m	24.7	20	7
O	Posttranslational m	8.6	3	2

O	Posttranslational m	56.0	1857	19
O	Posttranslational m	32.3	46	13
O	Posttranslational m	67.5	2028	22
O	Posttranslational m	26.3	9	3
P	Inorganic ion trans	15.8	49	3
P	Inorganic ion trans	65.9	310	10
P	Inorganic ion trans	16.9	18	7
P	Inorganic ion trans	6.6	12	2
P	Inorganic ion trans	30.1	79	10
P	Inorganic ion trans	18.9	55	3
P	Inorganic ion trans	75.6	629	20
P	Inorganic ion trans	27.0	3	2
P; V	Inorganic ion trans	18.8	14	8
Q	Secondary metabo	50.0	378	6
Q	Secondary metabo	42.7	18	8
Q	Secondary metabo	45.6	45	10
Q	Secondary metabo	25.4	43	6
Q	Secondary metabo	9.9	2	2
Q	Secondary metabo	49.5	317	16
Q; V	Secondary metabo	12.9	9	3
R	General function p	15.1	21	5
R	General function p	27.8	9	3
R	General function p	26.8	51	11
R	General function p	81.0	61	5
R	General function p	29.6	45	9
R	General function p	41.4	46	9
R	General function p	35.0	87	5
R	General function p	21.8	31	5
R	General function p	10.4	2	2
S	Function unknown	74.7	295	6
S	Function unknown	26.7	5	3
T	Signal transduction	9.4	16	2
T	Signal transduction	25.0	21	4
T	Signal transduction	22.0	22	8
T	Signal transduction	13.1	8	3
T	Signal transduction	44.6	49	11
T	Signal transduction	27.5	32	2
T	Signal transduction	54.9	253	12
V	Defense mechanis	24.8	6	3
		17.0	40	2
		7.6	4	2
		27.6	13	4
		17.2	9	3
		63.9	568	19
		17.1	33	4
		23.5	12	2
		15.8	12	5
		28.1	45	7
		46.6	300	9
		39.2	151	4

		39.6	48	9
		48.4	162	6
		25.9	108	15
		52.8	405	12
		22.8	55	5
		35.9	100	12
		64.2	308	19
		20.9	5	2
		21.6	20	4
		4.9	4	2
		11.7	10	2
		53.7	50	3
		64.4	74	3
		74.1	338	9
		40.0	58	6
		28.7	15	2
		4.1	3	2
		8.5	14	2
		16.3	20	2

# AAs	MW [kDa]	calc. pI	Area Glu Prom	Area CMC Prom
145	16.6	4.7	285375157.5	-
183	21	5.9	463758562.0	-
131	15.2	8.8	4388794428.4	13011882815.8
170	18.4	5.4	8242041223.4	-
342	36.8	4.7	1017892729.4	-
705	77.4	5.2	-	280793693.4
441	49.4	9.0	134611054.0	346813720.4
116	13	7.6	1438063331.2	3778641105.9
806	85.6	6.2	138623811.7	-
396	43.6	5.0	183147469.2	-
637	70.9	6.3	-	372780835.2
160	17.8	5.1	-	392324724.3
422	47.3	8.9	656228576.1	603602392.8
262	30.1	6.4	878653246.7	-
330	36.3	5.1	-	-
499	55.3	8.5	3811744438.2	15787228086.7
649	73.8	8.7	-	-
389	43.2	8.4	2057756103.4	9728278994.8
379	40.9	5.5	195476782.6	-
352	37.4	5.5	172465813.7	-
136	14.6	5.1	506834211.2	65626105.3
333	36	5.2	181385695.1	-
664	76.1	5.2	-	3040340801.9
124	13.6	9.3	507639656.7	-
141	15.7	6.3	-	-
190	21.2	6.8	-	343832018.0
236	27.4	5.2	1717112383.8	284947466.0
312	35.1	4.8	-	993191807.7
181	19.5	6.6	3177434881.1	19390074354.3
326	36.6	6.9	155360471.8	219782863.4
257	28	9.6	3383162294.8	4653091311.3
120	13.6	4.8	235656379.5	-
73	8.5	8.5	2768226259.7	701507670.6
366	39.4	6.3	3622641467.0	1004581300.5
220	25.3	6.0	850943429.1	2002911555.1
157	17.8	5.0	15242963271.6	-
410	45.8	5.3	321708693.4	474217431.0
157	17.7	5.5	-	182999590.8
894	96.4	9.2	-	2259755421.0
500	53.6	4.8	16534327442.1	-
659	72.3	6.2	8904800727.1	22883183420.6
268	30.5	7.3	12090440375.9	418139086.7
80	9.3	7.2	582359604.4	-
396	45	5.7	912558206.5	-
380	40.9	6.2	1944089693.6	443235252.3
326	35.8	6.5	462318893.2	980811100.1
255	27.1	6.4	3323554156.7	-
181	21	4.4	6968964294.0	3330774783.0
250	26.6	9.6	8538055300.5	389550109.0

161	17.6	5.2	9548111146.6	-
127	14.5	5.9	-	328041454.4
152	17.7	4.3	-	849920386.6
444	50.2	5.2	5141245966.4	4260482273.8
545	61.5	5.8	4549734754.6	3695906163.9
279	30.3	5.7	10399401142.1	10297713875.5
508	55.6	5.5	347481347.4	932294971.0
373	40.9	5.8	643602128.4	-
171	18.8	7.1	954520790.8	731037501.4
199	21.8	5.7	3216778837.8	6918488056.4
318	35.8	5.8	643574225.8	283568294.3
487	55.4	5.4	536725916.0	-
161	17.7	8.5	-	-
347	37	6.5	337830451.4	-
377	40.6	7.2	183753346.4	-
236	26.2	6.7	10411840740.1	522440234.7
289	31.4	5.5	69900442347.2	15332940635.9
657	73.7	5.5	-	-
212	23	6.2	2607721922.0	5578256671.5
561	65.8	5.6	1286952732.5	1663988078.4
290	32.4	5.1	574893158.7	-
316	35.4	5.3	105681780.0	-
474	50.4	5.3	548583924.9	-
1228	139	6.5	8824650905.3	26174043508.4
300	31.7	5.2	733472232.1	1410849850.1
172	18.7	5.2	-	-
254	29.5	5.3	-	218907329.6
264	27.4	5.2	115491935.6	-
192	20.9	4.8	-	-
119	14.1	4.9	-	-
414	46	7.6	744212253.4	2995546365.3
274	30.1	5.4	2895217069.1	-
622	69	7.4	1163214129.3	1536138518.1
446	51.8	7.1	47146898593.0	12682193264.8
448	51	9.1	185332896.4	-
413	44	5.1	5373037920.9	802540746.9
507	54.3	4.7	938135222.7	4448855800.5
289	33.5	5.3	110294677.8	-
271	29.1	5.2	1068776447.0	2245163899.3
255	28.1	7.4	2699169008.3	3518637134.7
310	34.7	5.2	201333811.7	1452678523.5
345	38.1	9.2	3305769586.3	17113315132.9
184	20.2	6.6	684249640.2	-
115	13.4	10.8	2820642632.4	4861717023.0
227	24.8	5.4	32318799453.1	57825014245.2
105	11.4	5.2	1491290951.9	1493628780.0
439	45.9	5.2	945063070.4	1546720447.2
306	33.4	6.6	649178211.0	437138512.9
686	77.4	6.3	1377939292.8	784194595.7
165	19.4	5.2	34238211631.9	51782621680.5

215	23.5	6.3	2527765134.8	1549966274.2
314	34.8	5.4	4837264698.4	769299306.8
120	13.5	5.5	3484575065.8	8267798480.3
436	47.2	5.6	237270418.9	737561388.5
144	16.4	5.4	-	-
521	56.5	7.7	13202265708.0	2027410847.9
359	40.1	5.9	167736179.5	-
193	20.7	4.7	4635654680.3	1830927425.7
178	20.8	4.7	325266851.0	1941684130.0
184	20.6	5.8	-	3268184587.5
463	51	5.0	-	998564228.8
300	34.1	5.6	2211857690.0	1746247271.7
361	39.2	6.0	1674822902.9	1811664046.8
298	32.8	9.8	389481092.8	-
299	31.7	8.0	-	551563124.4
420	45.5	8.3	195838076.0	236550781.6
150	16.2	6.1	-	1125246459.2
290	31	5.2	199931317.6	-
385	43.5	5.4	1886071415.0	4604142040.3
346	37.3	5.1	2160313066.8	-
181	20.3	7.2	-	600164387.0
569	61.1	5.4	-	-
109	12	6.5	178923177.1	212224344.9
294	34.4	6.3	3031794000.5	11902777885.6
319	34.6	5.3	1693310335.6	1314479356.1
466	50.2	4.8	365181466.1	-
378	39.7	5.4	106287897.9	-
592	65.9	5.0	360425415.4	1395539750.1
381	43.7	6.6	644417930.0	1888447823.0
285	31.5	8.6	-	411236224.1
406	44	6.5	508002557.0	307747962.1
222	24.9	5.4	209134261.3	-
642	70.5	9.4	682700197.7	-
130	14.2	5.0	312714037.6	1822000169.7
313	33.8	8.9	-	425888073.9
584	62.8	5.6	-	3427474975.0
106	12.4	4.7	7713772277.3	3641909981.4
127	13.9	5.9	-	1179041463.5
249	27.9	5.4	2879498875.4	245034269.9
422	46.7	5.4	188909673.7	-
311	34.6	5.5	158707683.1	-
202	22.5	5.4	118917922037.1	5267383368.2
255	28.3	5.4	24028215300.8	18911085539.7
146	16.5	6.1	-	-
154	16.3	5.5	11692751726.9	8628207849.2
446	48.3	5.4	11594795667.5	12522719843.4
821	92	5.5	171914498.6	190709926.2
174	18.9	7.0	180221095.7	243686358.1
364	40	5.3	-	2127997484.0
394	43.6	9.3	23082323515.6	34688779381.1

455	49.4	7.1	1975360342.5	1310320872.0
600	65.3	5.1	-	-
511	56.3	5.6	788503321.4	428436591.5
224	25.5	7.7	465337086.0	335200529.7
158	17.1	5.8	37386273321.2	57844692108.0
211	23.3	5.4	2444895871.9	2208908457.1
586	65.1	6.2	2225970605.6	6160310072.2
211	23.2	5.2	72618007911.6	114342550002.2
469	52.6	7.6	134505396.4	1582681776.2
132	15	6.1	24779777220.7	40561297926.2
410	45.5	4.8	2346879394.5	-
148	16.5	5.5	165486793.2	11559342656.8
670	77	5.9	1898339621.2	-
242	27.3	6.9	1537570197.2	1918923410.0
335	35.8	5.4	135137998.4	266250057.7
261	28.3	5.8	548723587.4	-
489	54	5.1	-	1025676594.9
363	40.3	5.2	374523293.4	-
378	43.1	5.3	1838522218.1	2100482667.3
394	44	5.3	225132352.4	-
509	57.1	6.1	245267988.5	-
194	21.5	6.1	613598626.7	1319748639.2
570	62	5.5	703600120.3	1091329669.7
126	14.4	4.7	964632708.2	1861340147.5
415	45.5	5.9	340286671.9	-
319	33.8	4.8	67411860.8	-
120	12.8	5.6	3473299018.4	3292249719.4
285	30.8	7.5	3108587154.4	-
202	22.3	5.6	66321585.2	1317125317.6
75	8.3	7.6	1077112473.6	-
187	20.6	4.6	114405631.7	-
244	27	9.1	5345717668.2	1499223553.3
276	31.6	5.4	8773598252.5	23197648501.7
496	56.1	5.6	402671783.5	2876663992.3
275	31.1	5.5	11927940967.3	-
323	36.1	5.3	437245313.9	-
131	14.2	5.3	225641909.0	1988311055.9
357	39.2	6.1	2098471215.6	-
125	13.8	5.6	1210407933.6	-
159	17.2	4.6	-	213628852.4
353	39.6	5.6	5995728402.0	12166896193.1
203	22.4	4.5	367740752.2	1726831501.5
221	24.3	8.8	595125821.9	-
371	39.6	5.0	5620993843.4	22453724267.9
409	46	5.6	308420743.3	12071683941.5
162	17.9	5.2	-	1871035829.7
552	60.6	6.1	192255376.6	337825628.1
327	35.8	5.1	127130158.2	-
296	32.1	5.3	156693661.5	349983701.8
148	16.4	5.4	-	4489722364.8

396	42.6	5.6	625246183.1	431850894.1
217	23.3	6.1	398870544.9	252046877.0
909	99.3	5.2	1740989058.3	1247587969.4
320	34.8	5.8	4024636277.7	5947225887.5
456	49.6	6.3	-	108128709.0
487	53.4	5.4	-	684354627.2
274	30.3	8.3	227015639.5	815930665.7
148	16.2	6.4	-	547048120.9
227	24.5	8.8	339358215.3	-
224	24	5.0	794703832.7	7165594919.7
298	32.7	4.8	-	944998556.4
82	9.7	9.0	929848161.5	373615914.8
87	10.2	6.3	1845143777.9	1028874485.4
189	21.7	5.2	1325391979.3	1102995887.4
160	18.7	7.6	-	514451772.4
101	11.4	5.1	-	-
687	77	6.0	-	184517408.9
272	29.3	5.7	-	1267686103.1
80	8.8	4.6	-	206738536.6

Area Glu+CMC Prom	Log ₂ Glu Norm 1	Log ₂ Glu Norm 2
-	27.7	28.4
237773762.4	28.5	29.1
5254857220.4	32.2	31.8
19440007648.1	33.6	31.5
672271085.4	30.3	29.4
-	#VALUE!	#VALUE!
770187009.9	27.4	26.5
919143905.0	30.0	30.7
-	27.0	27.1
106319558.7	26.3	28.1
93317199.3	#VALUE!	#VALUE!
-	#VALUE!	#VALUE!
660406739.6	29.5	29.1
634627759.3	29.4	29.9
141853895.2	#VALUE!	#VALUE!
4821645297.7	31.3	32.2
113304624.3	#VALUE!	#VALUE!
3807104671.1	31.8	28.4
437803008.5	27.6	27.5
247365634.8	27.6	27.1
1146257245.5	29.5	27.9
602465393.8	28.3	24.8
-	#VALUE!	#VALUE!
490639429.2	29.8	26.1
490625087.7	#VALUE!	#VALUE!
631846048.1	#VALUE!	#VALUE!
2359163253.7	30.9	30.3
-	#VALUE!	#VALUE!
4016367575.3	32.1	30.7
158108042.8	27.0	27.4
2554701714.5	31.1	32.1
180602045.6	27.8	27.9
3179795809.1	31.6	31.0
3186221036.7	32.0	31.5
757479961.9	29.7	29.6
15897824999.1	33.9	33.7
255534337.0	27.3	28.8
-	#VALUE!	#VALUE!
-	#VALUE!	#VALUE!
27584800425.1	34.2	33.6
8789793640.4	32.8	33.2
21822249356.2	33.9	32.9
800739296.5	26.2	30.0
883953653.2	29.6	29.9
1886603633.9	30.9	30.8
810303164.2	28.4	29.1
4112231957.0	32.5	28.7
8117942081.5	32.6	32.8
10102070917.8	33.6	31.9

17312515702.6	33.9	31.6
-	#VALUE!	#VALUE!
245652638.4	#VALUE!	#VALUE!
2944409595.7	31.1	32.9
4429427781.6	32.1	32.1
11017418430.4	33.2	33.3
175046801.8	28.3	28.4
408655187.7	28.9	29.5
818346316.1	28.7	30.4
1206031459.0	30.7	32.1
1726497556.0	29.7	28.6
631525545.3	29.5	28.2
35657282.4	#VALUE!	#VALUE!
442557778.8	28.2	28.4
-	27.6	27.3
5787410913.0	32.4	33.8
68649067153.8	36.2	35.9
293748340.6	#VALUE!	#VALUE!
3195030871.6	31.4	31.2
869792110.1	30.8	29.3
797249120.9	29.5	28.6
224196397.6	26.7	26.6
738345124.9	29.9	25.9
6287803250.5	32.4	33.5
2021141277.0	30.0	28.5
121176123.2	#VALUE!	#VALUE!
-	#VALUE!	#VALUE!
-	27.0	26.6
127652219.8	#VALUE!	#VALUE!
383960833.0	#VALUE!	#VALUE!
1931699318.6	29.8	29.1
4380816312.7	31.8	30.9
1739888968.4	30.2	30.0
30724955251.9	35.2	35.6
164850499.2	28.2	25.8
4930353223.5	32.1	32.5
1311346932.7	30.0	29.6
75963152.9	26.5	26.9
1799998449.2	30.5	29.2
2632697756.4	30.6	31.8
875934544.3	28.2	26.5
5969130150.8	32.4	30.1
1064416728.8	29.2	29.5
11924887327.7	31.5	31.2
34614824578.4	34.7	35.1
3458586917.2	29.7	31.0
1267886511.2	29.8	29.8
440109940.6	29.1	29.4
-	29.2	31.0
55478881531.5	35.1	34.9

3237359403.1	31.1	31.4
3805851663.3	32.4	31.9
3145821411.5	31.7	31.7
-	27.0	28.3
718130109.2	#VALUE!	#VALUE!
16096044747.9	33.2	33.9
251690050.1	23.0	28.3
3864440459.2	31.3	32.6
422611572.0	29.0	26.5
1370082459.6	#VALUE!	#VALUE!
-	#VALUE!	#VALUE!
725015515.8	30.6	31.4
1845433772.1	30.3	30.9
1001143434.8	29.1	27.6
-	#VALUE!	#VALUE!
154810590.1	27.1	27.9
206842497.8	#VALUE!	#VALUE!
-	27.7	27.5
2008487968.1	30.4	31.1
1407218200.9	30.6	31.3
-	#VALUE!	#VALUE!
1361622417.3	#VALUE!	#VALUE!
96059005.0	27.0	27.7
2673565872.1	31.4	31.6
1856733772.1	30.8	30.5
1434495547.2	28.8	27.9
-	24.4	27.5
1038198283.2	28.4	28.4
-	26.9	30.1
-	#VALUE!	#VALUE!
591586717.0	28.3	29.4
306474487.9	27.6	27.7
301488549.8	29.6	29.1
201049212.3	25.2	29.1
-	#VALUE!	#VALUE!
-	#VALUE!	#VALUE!
11784945687.9	32.6	33.0
-	#VALUE!	#VALUE!
-	30.7	31.9
-	27.4	27.6
-	27.6	26.7
7579616913.8	36.6	36.9
39080476360.1	34.7	34.3
1143362889.8	#VALUE!	#VALUE!
7747164942.9	33.6	33.3
10041834090.5	33.5	33.3
-	27.6	27.0
-	27.0	27.8
-	#VALUE!	#VALUE!
31180924626.0	34.5	34.3

1695272031.3	30.3	31.3
496908676.6	#VALUE!	#VALUE!
590051315.7	29.2	29.8
139023708.9	27.9	29.3
46558979230.9	35.5	34.6
1683769762.4	30.4	31.7
2834314047.4	30.9	31.2
87061238033.9	35.9	36.2
151523315.5	27.1	26.9
27291036186.6	34.4	34.7
3916030257.8	31.7	30.0
-	28.2	24.7
5315301733.3	31.5	29.3
1567183526.5	30.7	30.3
155868655.2	27.2	26.8
288974771.4	29.2	28.8
282188509.6	#VALUE!	#VALUE!
656990904.1	29.0	27.6
2467952286.5	31.0	30.6
-	28.6	25.7
145038127.8	28.3	27.3
927537438.9	29.3	29.1
960991039.0	28.8	29.8
1093345665.5	29.8	29.9
59173884.4	27.5	28.9
88727548.7	24.9	26.6
2888700179.9	31.6	31.8
2801381255.7	31.9	31.0
-	26.2	25.8
-	29.4	30.4
105755286.6	27.2	26.2
4867461734.7	31.8	32.7
5427818237.7	32.7	33.3
-	28.3	28.8
12652591636.8	33.1	33.8
-	29.5	26.8
594030934.6	28.1	27.3
-	30.3	31.4
1509930330.8	30.5	29.7
-	#VALUE!	#VALUE!
5631536129.6	32.5	32.4
-	27.7	29.0
1001290477.7	28.3	29.7
1883519253.7	32.8	31.7
-	28.7	27.5
-	#VALUE!	#VALUE!
111678900.9	27.4	27.6
162965889.3	25.0	27.7
565681818.7	26.4	27.7
-	#VALUE!	#VALUE!

870366864.1	29.3	29.2
-	27.9	29.0
2846890002.0	30.7	30.7
3989019439.8	31.6	32.2
123405195.3	#VALUE!	#VALUE!
-	#VALUE!	#VALUE!
-	27.4	28.0
-	#VALUE!	#VALUE!
362681182.3	28.4	28.3
2883244639.6	30.1	28.7
-	#VALUE!	#VALUE!
552074032.5	29.6	30.0
1556363467.0	30.8	30.8
799101018.5	29.9	30.6
-	#VALUE!	#VALUE!
355579689.8	#VALUE!	#VALUE!
-	#VALUE!	#VALUE!
-	#VALUE!	#VALUE!
-	#VALUE!	#VALUE!

Log ₂ CMC Norm 1	Log ₂ CMC Norm 2	Log ₂ Glu+CMC Norm 1
#VALUE!	#VALUE!	#VALUE!
#VALUE!	#VALUE!	27.2
33.8	33.4	32.5
#VALUE!	#VALUE!	33.7
#VALUE!	#VALUE!	29.6
28.3	27.7	#VALUE!
27.9	28.7	29.8
32.4	30.8	30.6
#VALUE!	#VALUE!	#VALUE!
#VALUE!	#VALUE!	27.5
27.6	29.0	25.0
28.2	28.8	#VALUE!
28.7	29.5	30.2
#VALUE!	#VALUE!	29.8
#VALUE!	#VALUE!	26.2
33.6	34.1	32.4
#VALUE!	#VALUE!	25.8
33.9	31.5	32.6
#VALUE!	#VALUE!	28.9
#VALUE!	#VALUE!	27.9
25.6	26.3	30.5
#VALUE!	#VALUE!	29.8
31.7	31.3	#VALUE!
#VALUE!	#VALUE!	28.5
#VALUE!	#VALUE!	29.6
28.2	28.5	28.9
28.5	27.4	31.5
29.9	29.9	#VALUE!
34.4	33.9	32.4
28.2	26.9	27.4
32.0	32.2	31.6
#VALUE!	#VALUE!	26.7
29.8	28.7	32.0
30.1	29.7	32.0
30.9	30.9	29.7
#VALUE!	#VALUE!	32.2
28.6	29.0	28.2
28.0	26.6	#VALUE!
31.6	30.4	#VALUE!
#VALUE!	#VALUE!	34.3
34.5	34.3	33.4
27.3	29.3	34.3
#VALUE!	#VALUE!	29.6
#VALUE!	#VALUE!	30.3
28.3	29.1	31.1
29.0	30.4	29.7
#VALUE!	#VALUE!	32.5
31.6	31.7	33.3
29.4	26.5	33.2

#VALUE!	#VALUE!	34.0
28.5	28.0	#VALUE!
29.7	29.7	27.9
31.9	32.1	31.8
31.9	31.6	32.1
33.4	33.0	33.0
29.2	30.2	27.2
#VALUE!	#VALUE!	28.2
29.2	29.7	28.7
33.1	32.0	30.9
28.1	28.0	30.7
#VALUE!	#VALUE!	30.0
#VALUE!	#VALUE!	24.6
#VALUE!	#VALUE!	28.7
#VALUE!	#VALUE!	#VALUE!
29.5	28.1	32.4
33.7	34.0	35.5
#VALUE!	#VALUE!	28.0
32.6	32.1	31.7
30.1	31.0	29.9
#VALUE!	#VALUE!	29.6
#VALUE!	#VALUE!	27.4
#VALUE!	#VALUE!	29.6
34.1	35.0	32.3
30.0	30.7	30.9
#VALUE!	#VALUE!	27.0
28.4	26.5	#VALUE!
#VALUE!	#VALUE!	#VALUE!
#VALUE!	#VALUE!	26.8
#VALUE!	#VALUE!	28.1
31.4	31.6	31.3
#VALUE!	#VALUE!	31.6
30.6	30.4	31.1
33.5	33.6	35.0
#VALUE!	#VALUE!	27.4
29.1	29.9	32.2
32.2	31.9	31.0
#VALUE!	#VALUE!	26.7
31.1	31.0	31.2
29.7	32.5	31.3
30.5	30.4	29.2
34.0	34.0	32.5
#VALUE!	#VALUE!	29.9
32.0	32.4	33.7
36.0	35.5	35.1
29.9	30.9	31.7
30.6	30.5	29.9
29.0	28.4	29.3
29.9	29.1	#VALUE!
35.2	35.9	35.9

30.3	30.7	31.4
30.0	28.8	32.2
32.9	33.0	31.9
30.0	28.7	#VALUE!
#VALUE!	#VALUE!	29.0
31.1	30.7	33.9
#VALUE!	#VALUE!	28.6
30.5	31.0	32.3
31.6	29.1	29.4
32.4	29.3	30.9
30.5	28.7	#VALUE!
28.6	31.5	30.4
30.5	31.0	30.8
#VALUE!	#VALUE!	30.5
29.1	29.0	#VALUE!
28.4	26.8	27.0
30.3	29.8	28.3
#VALUE!	#VALUE!	#VALUE!
32.6	31.4	30.9
#VALUE!	#VALUE!	30.7
29.6	28.6	#VALUE!
#VALUE!	#VALUE!	29.9
27.7	27.7	27.3
33.5	33.4	31.3
31.0	28.8	31.1
#VALUE!	#VALUE!	30.4
#VALUE!	#VALUE!	#VALUE!
30.6	30.1	30.5
31.4	29.7	#VALUE!
29.0	28.0	#VALUE!
27.3	28.7	29.2
#VALUE!	#VALUE!	28.2
#VALUE!	#VALUE!	26.8
31.0	30.5	28.2
29.1	28.1	#VALUE!
31.6	31.8	#VALUE!
30.3	32.5	33.5
30.8	28.9	#VALUE!
28.1	27.6	#VALUE!
#VALUE!	#VALUE!	#VALUE!
#VALUE!	#VALUE!	#VALUE!
32.3	32.2	33.1
33.4	34.6	34.8
#VALUE!	#VALUE!	26.3
32.6	33.3	32.1
33.4	33.7	33.9
28.3	25.8	#VALUE!
27.8	27.9	#VALUE!
31.0	31.0	#VALUE!
34.6	35.4	35.3

29.6	30.8	31.0
#VALUE!	#VALUE!	25.6
29.3	27.6	29.7
28.9	27.4	27.1
36.4	34.4	35.1
31.8	29.4	31.0
32.7	32.3	31.4
36.4	37.0	36.2
30.3	30.8	27.6
35.4	35.1	35.1
#VALUE!	#VALUE!	32.3
34.0	32.3	#VALUE!
#VALUE!	#VALUE!	30.4
30.8	30.9	30.8
27.5	28.3	27.3
#VALUE!	#VALUE!	28.7
29.8	30.1	28.2
#VALUE!	#VALUE!	29.1
31.0	30.9	30.8
#VALUE!	#VALUE!	#VALUE!
#VALUE!	#VALUE!	27.0
30.1	30.5	29.5
30.0	30.1	29.3
30.7	30.9	29.7
#VALUE!	#VALUE!	26.6
#VALUE!	#VALUE!	26.0
30.9	32.1	31.3
#VALUE!	#VALUE!	30.8
30.6	30.0	#VALUE!
#VALUE!	#VALUE!	#VALUE!
#VALUE!	#VALUE!	26.5
30.8	30.0	32.2
34.0	34.8	32.7
31.6	31.2	#VALUE!
#VALUE!	#VALUE!	33.5
#VALUE!	#VALUE!	#VALUE!
31.1	30.7	29.1
#VALUE!	#VALUE!	#VALUE!
#VALUE!	#VALUE!	30.7
28.6	24.3	#VALUE!
32.8	34.0	32.2
30.2	31.0	#VALUE!
#VALUE!	#VALUE!	29.9
34.1	34.6	31.6
33.7	33.3	#VALUE!
30.7	30.9	#VALUE!
29.1	26.8	27.5
#VALUE!	#VALUE!	27.0
28.5	28.2	28.7
31.8	32.3	#VALUE!

28.4	28.9	29.5
27.7	28.1	#VALUE!
30.1	30.3	31.8
32.5	32.4	32.5
26.5	26.9	27.0
29.1	29.6	#VALUE!
29.4	29.8	#VALUE!
29.5	28.3	#VALUE!
#VALUE!	#VALUE!	28.3
33.0	32.5	31.6
29.6	30.0	#VALUE!
28.9	27.9	29.0
29.9	29.9	30.3
30.2	29.8	30.0
28.2	29.4	#VALUE!
#VALUE!	#VALUE!	28.6
27.4	27.5	#VALUE!
30.4	30.0	#VALUE!
27.4	27.8	#VALUE!

Log ₂ Glu+CMC Norm 2	-Log Student's T	Student's T-test	FC Glu_CMC
#VALUE!	0.0		#VALUE!
28.3	0.0		#VALUE!
32.1	1.6	-1.6	3.0
34.5	0.0		#VALUE!
29.0	0.0		#VALUE!
#VALUE!	0.0		#VALUE!
29.2	0.8	-1.4	2.6
27.7	0.5	-1.2	2.6
#VALUE!	0.0		#VALUE!
24.5	0.0		#VALUE!
27.2	0.0		#VALUE!
#VALUE!	0.0		#VALUE!
26.9	0.1	0.2	1.1
28.2	0.0		#VALUE!
27.6	0.0	0.0	#VALUE!
31.9	1.3	-2.1	4.1
27.3	0.0	0.0	#VALUE!
30.2	0.5	-2.6	4.7
28.4	0.0		#VALUE!
27.8	0.0		#VALUE!
29.4	1.0	2.8	7.7
28.0	0.0		#VALUE!
#VALUE!	0.0		#VALUE!
29.2	0.0		#VALUE!
27.2	0.0	0.0	#VALUE!
29.5	0.0		#VALUE!
30.7	1.3	2.7	6.0
#VALUE!	0.0		#VALUE!
31.1	1.1	-2.8	6.1
27.1	0.2	-0.4	1.4
30.8	0.4	-0.5	1.4
27.9	0.0		#VALUE!
30.8	1.1	2.1	3.9
30.9	1.5	1.8	3.6
29.2	3.1	-1.2	2.4
34.7	0.0		#VALUE!
27.6	0.4	-0.7	1.5
#VALUE!	0.0		#VALUE!
#VALUE!	0.0		#VALUE!
35.0	0.0		#VALUE!
32.5	1.7	-1.4	2.6
34.4	1.4	5.1	28.9
29.5	0.0		#VALUE!
28.7	0.0		#VALUE!
30.5	1.5	2.2	4.4
29.5	0.5	-1.0	2.1
31.1	0.0		#VALUE!
32.4	2.4	1.1	2.1
33.3	1.0	4.8	21.9

34.0	0.0		#VALUE!
#VALUE!	0.0		#VALUE!
27.9	0.0		#VALUE!
31.0	0.0	0.0	1.2
32.0	0.7	0.3	1.2
33.6	0.0	0.0	1.0
27.5	0.9	-1.3	2.7
28.9	0.0		#VALUE!
30.2	0.1	0.2	1.3
28.8	0.5	-1.2	2.2
30.7	0.7	1.1	2.3
27.7	0.0		#VALUE!
25.5	0.0	0.0	#VALUE!
28.8	0.0		#VALUE!
#VALUE!	0.0		#VALUE!
32.4	1.3	4.3	19.9
36.3	2.0	2.2	4.6
28.2	0.0	0.0	#VALUE!
31.5	1.3	-1.1	2.1
29.4	0.2	-0.5	1.3
29.5	0.0		#VALUE!
28.0	0.0		#VALUE!
29.3	0.0		#VALUE!
32.7	0.8	-1.6	3.0
31.0	0.5	-1.1	1.9
26.7	0.0	0.0	#VALUE!
#VALUE!	0.0		#VALUE!
#VALUE!	0.0		#VALUE!
27.1	0.0	0.0	#VALUE!
28.8	0.0	0.0	#VALUE!
30.3	1.5	-2.0	4.0
32.3	0.0		#VALUE!
30.0	1.1	-0.4	1.3
34.6	1.9	1.9	3.7
27.2	0.0		#VALUE!
32.2	1.6	2.8	6.7
28.7	2.0	-2.3	4.7
25.3	0.0		#VALUE!
30.0	0.7	-1.2	2.1
31.3	0.0	0.1	0.8
30.1	1.2	-3.1	7.2
32.5	0.9	-2.8	5.2
30.0	0.0		#VALUE!
33.3	1.1	-0.8	1.7
34.9	0.9	-0.8	1.8
31.7	0.0	-0.1	1.0
30.5	2.5	-0.7	1.6
27.7	0.7	0.6	1.5
#VALUE!	0.2	0.6	1.8
35.5	0.6	-0.6	1.5

31.8	0.9	0.7	1.6
31.3	1.3	2.7	6.3
31.0	2.4	-1.2	2.4
#VALUE!	0.7	-1.7	3.1
29.7	0.0	0.0	#VALUE!
33.9	1.6	2.7	6.5
26.5	0.0		#VALUE!
31.2	0.6	1.2	2.5
27.2	0.6	-2.6	6.0
29.5	0.0		#VALUE!
#VALUE!	0.0		#VALUE!
25.2	0.2	0.9	1.3
30.8	0.1	-0.1	1.1
29.0	0.0		#VALUE!
#VALUE!	0.0		#VALUE!
27.3	0.0	-0.1	1.2
26.3	0.0		#VALUE!
#VALUE!	0.0		#VALUE!
31.0	0.7	-1.2	2.4
29.9	0.0		#VALUE!
#VALUE!	0.0		#VALUE!
30.7	0.0	0.0	#VALUE!
24.7	0.3	-0.3	1.2
31.3	2.9	-2.0	3.9
30.4	0.2	0.7	1.3
30.4	0.0		#VALUE!
#VALUE!	0.0		#VALUE!
29.0	1.7	-1.9	3.9
#VALUE!	0.4	-2.1	2.9
#VALUE!	0.0		#VALUE!
29.1	0.3	0.8	1.7
28.2	0.0		#VALUE!
28.9	0.0		#VALUE!
26.4	0.7	-3.6	5.8
#VALUE!	0.0		#VALUE!
#VALUE!	0.0		#VALUE!
33.4	0.5	1.5	2.1
#VALUE!	0.0		#VALUE!
#VALUE!	1.5	3.5	11.8
#VALUE!	0.0		#VALUE!
#VALUE!	0.0		#VALUE!
32.4	2.9	4.5	22.6
35.5	0.3	0.5	1.3
31.0	0.0	0.0	#VALUE!
33.4	0.5	0.5	1.4
31.8	0.3	-0.1	1.1
#VALUE!	0.1	0.3	0.9
#VALUE!	0.5	-0.5	1.4
#VALUE!	0.0		#VALUE!
34.3	0.5	-0.5	1.5

30.2	0.3	0.6	1.5
29.8	0.0	0.0	#VALUE!
28.2	0.4	1.1	1.8
27.0	0.2	0.5	1.4
35.7	0.1	-0.4	1.5
30.2	0.1	0.5	1.1
31.4	1.6	-1.5	2.8
36.4	0.8	-0.6	1.6
26.6	2.4	-3.5	11.8
34.0	1.2	-0.7	1.6
31.3	0.0		#VALUE!
#VALUE!	1.1	-6.7	69.9
33.1	0.0		#VALUE!
30.3	0.7	-0.3	1.2
27.1	0.8	-0.9	2.0
27.2	0.0		#VALUE!
27.9	0.0		#VALUE!
29.4	0.0		#VALUE!
31.5	0.4	-0.2	1.1
#VALUE!	0.0		#VALUE!
27.2	0.0		#VALUE!
30.0	1.4	-1.1	2.2
30.2	0.5	-0.7	1.6
30.3	1.8	-0.9	1.9
23.9	0.0		#VALUE!
26.7	0.0		#VALUE!
31.5	0.1	0.2	1.1
31.8	0.0		#VALUE!
#VALUE!	2.2	-4.3	19.9
#VALUE!	0.0		#VALUE!
26.8	0.0		#VALUE!
32.2	1.1	1.8	3.6
31.8	0.9	-1.4	2.6
#VALUE!	1.9	-2.8	7.1
33.6	0.0		#VALUE!
#VALUE!	0.0		#VALUE!
29.2	1.7	-3.2	8.8
#VALUE!	0.0		#VALUE!
30.3	0.0		#VALUE!
#VALUE!	0.0		#VALUE!
32.6	0.6	-0.9	2.0
#VALUE!	1.0	-2.3	4.7
29.9	0.0		#VALUE!
28.9	1.1	-2.1	4.0
#VALUE!	1.9	-5.4	39.1
#VALUE!	0.0		#VALUE!
24.9	0.1	-0.4	1.8
27.5	0.0		#VALUE!
29.4	0.7	-1.3	2.2
#VALUE!	0.0		#VALUE!

29.8	0.8	0.6	1.4
#VALUE!	0.4	0.6	1.6
30.9	1.4	0.5	1.4
30.7	0.7	-0.6	1.5
26.8	0.0		#VALUE!
#VALUE!	0.0		#VALUE!
#VALUE!	1.4	-1.9	3.6
#VALUE!	0.0		#VALUE!
28.5	0.0		#VALUE!
31.2	1.3	-3.3	9.0
#VALUE!	0.0		#VALUE!
29.1	0.9	1.4	2.5
30.7	4.3	0.8	1.8
29.1	0.2	0.2	1.2
#VALUE!	0.0		#VALUE!
28.2	0.0	0.0	#VALUE!
#VALUE!	0.0		#VALUE!
#VALUE!	0.0		#VALUE!
#VALUE!	0.0		#VALUE!

-Log Student's Student's T-tesFC Glu_Glu+CI -Log Student's Student's T-tes

0.0		#VALUE!	0.0	0.0
0.6	1.0	2.0	0.0	
0.3	-0.3	1.2	1.4	1.3
0.5	-1.5	2.4	0.0	
0.4	0.6	1.5	0.0	
0.0	0.0	#VALUE!	0.0	
1.4	-2.6	5.7	0.9	-1.2
0.3	1.2	1.6	0.6	2.4
0.0		#VALUE!	0.0	0.0
0.2	1.2	1.7	0.0	
0.0		#VALUE!	0.6	2.2
0.0	0.0	#VALUE!	0.0	
0.2	0.7	1.0	0.1	0.6
0.3	0.7	1.4	0.0	
0.0		#VALUE!	0.0	
0.3	-0.4	1.3	1.5	1.7
0.0		#VALUE!	0.0	
0.2	-1.3	1.9	0.3	1.4
1.4	-1.1	2.2	0.0	
0.7	-0.5	1.4	0.0	
0.5	-1.3	2.3	1.6	-4.1
0.5	-2.4	3.3	0.0	
0.0	0.0	#VALUE!	0.0	
0.2	-0.9	1.0	0.0	
0.0		#VALUE!	0.0	
0.0		#VALUE!	0.8	-0.9
0.3	-0.4	1.4	1.4	-3.1
0.0	0.0	#VALUE!	0.0	
0.1	-0.4	1.3	1.1	2.4
0.0	0.0	1.0	0.2	0.3
0.2	0.4	1.3	0.8	0.9
0.3	0.5	1.3	0.0	
0.1	-0.1	1.1	0.9	-2.2
0.1	0.3	1.1	0.9	-1.6
0.3	0.2	1.1	1.5	1.4
0.1	0.4	1.0	0.0	
0.1	0.2	1.3	0.9	0.9
0.0	0.0	#VALUE!	0.0	
0.0	0.0	#VALUE!	0.0	
0.6	-0.7	1.7	0.0	
0.1	0.1	1.0	1.0	1.5
0.7	-0.9	1.8	1.6	-6.0
0.3	-1.5	1.4	0.0	
0.1	0.2	1.0	0.0	
0.1	0.1	1.0	1.3	-2.1
0.9	-0.8	1.8	0.1	0.1
0.2	-1.2	1.2	0.0	
0.1	-0.2	1.2	0.9	-1.2
0.2	-0.5	1.2	1.2	-5.3

0.4	-1.3	1.8	0.0	
0.0	0.0	#VALUE!	0.0	
0.0		#VALUE!	4.0	1.8
0.2	0.6	1.7	0.5	0.6
0.2	0.0	1.0	0.6	-0.3
0.1	-0.1	1.1	0.1	-0.1
1.7	1.0	2.0	1.3	2.3
0.5	0.7	1.6	0.0	
0.0	0.2	1.2	0.0	0.0
0.5	1.6	2.7	0.8	2.7
0.9	-1.5	2.7	3.2	-2.6
0.0	0.0	0.8	0.0	
0.0		#VALUE!	0.0	
1.0	-0.4	1.3	0.0	
0.0		#VALUE!	0.0	0.0
0.4	0.7	1.8	1.5	-3.6
0.1	0.1	1.0	1.4	-2.1
0.0		#VALUE!	0.0	
0.7	-0.3	1.2	1.1	0.8
0.2	0.4	1.5	0.6	0.9
0.4	-0.5	1.4	0.0	
1.2	-1.1	2.1	0.0	
0.3	-1.5	1.3	0.0	
0.3	0.4	1.4	1.3	2.0
0.8	-1.6	2.8	0.6	-0.6
0.0		#VALUE!	0.0	
0.0	0.0	#VALUE!	0.0	
0.0		#VALUE!	0.0	0.0
0.0		#VALUE!	0.0	
0.0		#VALUE!	0.0	
0.8	-1.3	2.6	0.5	0.7
0.4	-0.6	1.5	0.0	
0.3	-0.5	1.5	0.0	-0.1
0.8	0.6	1.5	1.5	-1.3
0.1	-0.3	0.9	0.0	
0.2	0.1	1.1	1.6	-2.7
0.0	-0.1	1.4	0.7	2.2
0.3	0.7	1.5	0.0	
0.3	-0.8	1.7	0.3	0.4
0.0	-0.1	1.0	0.0	-0.2
0.9	-2.3	4.4	0.7	0.8
0.4	-1.3	1.8	3.6	1.5
1.1	-0.6	1.6	0.0	
1.8	-2.1	4.2	1.4	-1.3
0.2	-0.1	1.1	1.0	0.7
0.8	-1.3	2.3	0.9	-1.3
0.6	-0.4	1.3	0.4	0.3
0.3	0.8	1.5	0.1	0.2
0.0		#VALUE!	0.0	
1.0	-0.7	1.6	0.1	-0.1

0.5	-0.4	1.3	1.2	-1.1
0.3	0.4	1.3	1.0	-2.3
0.2	0.2	1.1	1.0	1.5
0.0		#VALUE!	0.0	
0.0		#VALUE!	0.0	
0.3	-0.3	1.2	2.2	-3.0
0.2	-1.9	1.5	0.0	
0.1	0.2	1.2	0.7	-1.0
0.1	-0.5	1.3	0.5	2.1
0.0		#VALUE!	0.1	0.7
0.0	0.0	#VALUE!	0.0	
0.5	3.2	3.1	0.3	2.2
0.2	-0.2	1.1	0.1	0.0
0.5	-1.4	2.6	0.0	
0.0	0.0	#VALUE!	0.0	
0.3	0.3	1.3	0.2	0.4
0.0		#VALUE!	0.9	2.7
0.0		#VALUE!	0.0	0.0
0.1	-0.1	1.1	0.7	1.1
0.5	0.6	1.5	0.0	
0.0	0.0	#VALUE!	0.0	
0.0		#VALUE!	0.0	
0.4	1.4	1.9	0.5	1.7
0.9	0.2	1.1	3.7	2.2
0.1	-0.1	1.1	0.3	-0.9
1.3	-2.0	3.9	0.0	
0.0		#VALUE!	0.0	0.0
0.7	-1.4	2.9	0.3	0.6
0.0		#VALUE!	0.0	
0.0	0.0	#VALUE!	0.0	
0.2	-0.3	1.2	0.6	-1.1
1.7	-0.6	1.5	0.0	
0.5	1.5	2.3	0.0	
0.0	-0.2	0.6	1.2	3.4
0.0	0.0	#VALUE!	0.0	
0.0	0.0	#VALUE!	0.0	
1.0	-0.6	1.5	0.7	-2.1
0.0	0.0	#VALUE!	0.0	
0.0		#VALUE!	0.0	
0.0		#VALUE!	0.0	0.0
0.0		#VALUE!	0.0	0.0
2.0	4.0	15.7	0.5	-0.5
0.6	-0.7	1.6	0.6	-1.1
0.0		#VALUE!	0.0	
0.4	0.7	1.5	0.1	0.3
0.2	0.6	1.2	0.2	0.7
0.0		#VALUE!	0.0	
0.0		#VALUE!	0.0	
0.0	0.0	#VALUE!	0.0	
0.3	-0.4	1.4	0.1	0.2

0.1	0.2	1.2	0.2	-0.4
0.0		#VALUE!	0.0	
0.3	0.6	1.3	0.2	-0.5
0.8	1.6	3.3	0.6	1.1
0.2	-0.4	1.2	0.0	0.0
0.2	0.5	1.5	0.0	0.0
0.9	-0.4	1.3	1.5	1.1
0.6	-0.3	1.2	0.5	0.4
0.1	-0.1	1.1	1.6	3.5
0.0	0.0	1.1	0.5	0.7
0.3	-0.9	1.7	0.0	
0.0		#VALUE!	0.0	
0.3	-1.3	2.8	0.0	
0.0	0.0	1.0	0.5	0.3
0.4	-0.2	1.2	0.6	0.7
0.5	1.1	1.9	0.0	
0.0		#VALUE!	1.8	1.9
0.5	-1.0	1.8	0.0	
0.3	-0.4	1.3	0.2	-0.2
0.0		#VALUE!	0.0	0.0
0.5	0.7	1.7	0.0	
0.7	-0.6	1.5	0.6	0.5
0.2	-0.5	1.4	0.2	0.3
0.2	-0.2	1.1	1.0	0.8
0.7	2.9	5.8	0.0	
0.2	-0.6	1.3	0.0	
0.7	0.3	1.2	0.0	0.1
0.1	0.2	1.1	0.0	
0.0		#VALUE!	0.0	
0.0		#VALUE!	0.0	0.0
0.0	0.1	1.1	0.0	
0.1	0.1	1.1	1.3	-1.8
0.5	0.7	1.6	1.1	2.1
0.0		#VALUE!	0.0	
0.1	-0.1	1.1	0.0	
0.0		#VALUE!	0.0	0.0
1.1	-1.5	2.6	2.0	1.7
0.0		#VALUE!	0.0	0.0
0.3	-0.4	1.2	0.0	
0.0	0.0	#VALUE!	0.0	
0.2	0.1	1.1	0.6	1.0
0.0		#VALUE!	0.0	
0.5	-0.9	1.7	0.0	
0.5	2.0	3.0	1.0	4.1
0.0		#VALUE!	0.0	
0.0	0.0	#VALUE!	0.0	
0.4	1.3	1.7	0.4	1.7
0.2	-0.9	1.3	0.0	
1.0	-2.0	3.6	0.7	-0.7
0.0	0.0	#VALUE!	0.0	

1.0	-0.5	1.4	1.2	-1.0
0.0		#VALUE!	0.0	
0.5	-0.6	1.6	0.8	-1.1
0.1	0.3	1.0	0.3	0.9
0.0		#VALUE!	0.3	-0.2
0.0	0.0	#VALUE!	0.0	
0.0		#VALUE!	0.0	
0.0	0.0	#VALUE!	0.0	
0.3	-0.1	1.1	0.0	
0.9	-2.0	3.6	1.3	1.3
0.0	0.0	#VALUE!	0.0	
1.2	0.7	1.7	0.5	-0.6
0.5	0.3	1.2	1.0	-0.6
0.5	0.8	1.7	0.4	0.5
0.0	0.0	#VALUE!	0.0	
0.0		#VALUE!	0.0	
0.0	0.0	#VALUE!	0.0	
0.0	0.0	#VALUE!	0.0	
0.0	0.0	#VALUE!	0.0	

FC CMC_Glu+CMC

#VALUE!

#VALUE!

2.5

#VALUE!

#VALUE!

#VALUE!

2.2

4.1

#VALUE!

#VALUE!

4.0

#VALUE!

0.9

#VALUE!

#VALUE!

3.3

#VALUE!

2.6

#VALUE!

#VALUE!

17.5

#VALUE!

#VALUE!

#VALUE!

#VALUE!

1.8

8.3

#VALUE!

4.8

1.4

1.8

#VALUE!

4.5

3.2

2.6

#VALUE!

1.9

#VALUE!

#VALUE!

#VALUE!

2.6

52.2

#VALUE!

#VALUE!

4.3

1.2

#VALUE!

2.4

25.9

#VALUE!
#VALUE!
3.5
1.4
1.2
1.1
5.3
#VALUE!
1.1
5.7
6.1
#VALUE!
#VALUE!
#VALUE!
#VALUE!
11.1
4.5
#VALUE!
1.7
1.9
#VALUE!
#VALUE!
#VALUE!
4.2
1.4
#VALUE!
#VALUE!
#VALUE!
#VALUE!
#VALUE!
1.6
#VALUE!
1.1
2.4
#VALUE!
6.1
3.4
#VALUE!
1.2
0.7
1.7
2.9
#VALUE!
2.5
1.7
2.3
1.2
1.0
#VALUE!
1.1

2.1
4.9
2.6
#VALUE!
#VALUE!
7.9
#VALUE!
2.1
4.6
2.4
#VALUE!
2.4
1.0
#VALUE!
#VALUE!
1.5
5.4
#VALUE!
2.3
#VALUE!
#VALUE!
#VALUE!
2.2
4.5
1.4
#VALUE!
#VALUE!
1.3
#VALUE!
#VALUE!
1.9
#VALUE!
#VALUE!
9.1
#VALUE!
#VALUE!
3.2
#VALUE!
#VALUE!
#VALUE!
#VALUE!
1.4
2.1
#VALUE!
1.1
1.2
#VALUE!
#VALUE!
#VALUE!
1.1

1.3
#VALUE!
1.4
2.4
1.2
0.8
2.2
1.3
10.4
1.5
#VALUE!
#VALUE!
#VALUE!
1.2
1.7
#VALUE!
3.6
#VALUE!
1.2
#VALUE!
#VALUE!
1.4
1.1
1.7
#VALUE!
#VALUE!
1.1
#VALUE!
#VALUE!
#VALUE!
#VALUE!
3.2
4.3
#VALUE!
#VALUE!
#VALUE!
3.3
#VALUE!
#VALUE!
#VALUE!
2.2
#VALUE!
#VALUE!
11.9
#VALUE!
#VALUE!
3.0
#VALUE!
1.6
#VALUE!

2.0
#VALUE!
2.3
1.5
1.1
#VALUE!
#VALUE!
#VALUE!
#VALUE!
2.5
#VALUE!
1.5
1.5
1.4
#VALUE!
#VALUE!
#VALUE!
#VALUE!
#VALUE!

Cluster	Gene ID	Gene Type	Gene Start	Gene Stop	Direction
CGC01	NP_387896.1	TC	23146	23769	-
CGC01	NP_387897.1	CAZyme	23868	25151	-
CGC02	NP_388035.1	TC	157421	158479	+
CGC02	NP_388036.1	-	158515	159072	-
CGC02	NP_388037.1	-	159182	159778	+
CGC02	NP_388038.1	CAZyme	159779	160543	-
CGC02	NP_388039.1	TC	177083	178519	+
CGC02	NP_388040.2	TC	178665	179585	+
CGC02	NP_388041.2	-	179595	180347	-
CGC02	NP_388042.2	TC	180344	181354	-
CGC02	NP_388043.1	TC	181347	182351	-
CGC02	NP_388044.1	TC	182370	183323	-
CGC02	NP_388045.1	TF	183414	185003	-
CGC02	NP_388046.1	-	185194	186438	-
CGC02	NP_388047.1	CAZyme	186452	188380	-
CGC03	NP_388174.1	TC	314025	314798	+
CGC03	NP_388175.1	-	314883	316496	+
CGC03	NP_388176.1	-	316512	317603	+
CGC03	NP_388177.1	TC	317725	318927	+
CGC03	NP_388178.1	TC	319180	320352	-
CGC03	NP_388179.1	-	320421	320723	-
CGC03	NP_388180.2	TC	321013	322269	+
CGC03	NP_388181.1	TC	322271	323119	+
CGC03	NP_388182.1	TC	323119	324000	+
CGC03	NP_388183.2	-	324038	325189	-
CGC03	NP_388184.2	TC	325339	326772	+
CGC03	NP_388185.2	-	326888	327469	+
CGC03	NP_388186.2	CAZyme	327618	329597	+
CGC03	NP_388187.2	-	329774	330739	+
CGC03	NP_388188.2	TC	330771	332396	+
CGC03	NP_388189.2	TC	332441	333979	-
CGC04	NP_388307.1	TC	476558	478741	+
CGC04	NP_388308.1	CAZyme	478944	480032	+
CGC04	NP_388309.1	-	480013	480864	+
CGC04	NP_388310.1	-	480875	482584	+
CGC04	NP_388311.1	TC	482577	483839	+
CGC04	NP_388312.1	-	483845	485956	+
CGC04	NP_388313.1	TC	486432	488255	+
CGC05	NP_388442.1	TC	604736	606379	-
CGC05	NP_388443.1	TC	606699	608075	-
CGC05	NP_388444.1	-	608246	608764	-
CGC05	NP_388445.1	-	608933	609391	+
CGC05	NP_388446.1	TC	609388	612045	+
CGC05	NP_388447.1	-	612191	612820	-
CGC05	NP_388448.1	-	612836	613330	-
CGC05	NP_388449.1	TC	613641	614849	+
CGC05	NP_388450.2	-	614885	615622	-
CGC05	NP_388451.1	-	615871	616545	+
CGC05	NP_388452.2	CAZyme	616672	617934	+

CGC05	NP_388453.2	CAZyme	618095	619282	+
CGC06	NP_388575.1	TC	758093	758722	+
CGC06	NP_388576.1	TC	758719	760452	+
CGC06	NP_388577.1	TF	760452	761558	+
CGC06	NP_388578.2	-	761662	762945	+
CGC06	NP_388579.1	TC	762942	763871	+
CGC06	NP_388580.1	TC	763875	764765	+
CGC06	NP_388581.1	CAZyme	764781	765815	+
CGC06	NP_388582.1	-	765838	768123	+
CGC06	NP_388583.1	CAZyme	768137	768835	+
CGC06	NP_388584.1	-	768828	769490	+
CGC06	NP_388585.1	TC	769487	770113	+
CGC06	NP_388586.1	CAZyme	770234	772096	+
CGC06	NP_388587.1	CAZyme	772142	773980	+
CGC06	NP_388588.1	CAZyme	774138	774791	+
CGC06	NP_388589.1	CAZyme	774799	776790	+
CGC06	NP_388590.2	CAZyme	776834	779407	+
CGC06	NP_388591.1	TC	779529	781037	+
CGC06	NP_388592.1	TC	781092	782048	+
CGC06	NP_388593.1	TC	782062	782949	+
CGC06	NP_388594.1	CAZyme	782958	784298	+
CGC07	NP_388610.1	CAZyme	800232	801143	+
CGC07	NP_388611.1	CAZyme	801172	802350	+
CGC07	NP_388612.1	CAZyme	802351	803286	+
CGC07	NP_388613.1	TC	803317	804546	-
CGC07	NP_388614.1	-	804657	805364	-
CGC07	NP_388615.1	TC	805456	806841	-
CGC07	NP_388616.1	-	807091	808548	+
CGC07	NP_388617.1	-	808562	809422	+
CGC07	NP_388618.1	TC	809557	811446	+
CGC07	NP_388619.1	-	811569	812015	+
CGC07	NP_388620.1	TF	812140	812562	+
CGC07	NP_388621.1	TC	812628	813818	+
CGC07	NP_388622.1	-	814109	814264	+
CGC07	NP_388623.2	TC	814384	815940	-
CGC07	NP_388624.1	TC	816113	817243	+
CGC08	NP_388630.1	TC	822903	823703	-
CGC08	NP_388631.1	TC	823716	824717	-
CGC08	NP_388632.1	TC	824714	825715	-
CGC08	NP_388633.1	TC	825787	826734	-
CGC08	NP_388634.1	-	826843	827211	-
CGC08	NP_388636.1	-	827455	827802	+
CGC08	NP_388637.1	CAZyme	827993	829255	+
CGC08	NP_388638.1	TC	829382	830818	+
CGC09	NP_388671.1	TC	862836	863663	+
CGC09	NP_388672.1	TC	863862	865037	-
CGC09	NP_388673.1	TC	865205	866260	+
CGC09	NP_388674.1	-	866331	867125	+
CGC09	NP_388675.1	TC	867164	868006	-
CGC09	NP_388677.2	-	868007	869128	-

CGC09	NP_388678.1	-	869273	869458	+
CGC09	NP_388679.1	CAZyme	869559	870350	+
CGC09	NP_388680.2	-	870388	871248	-
CGC09	NP_388681.1	TC	871347	872306	-
CGC10	NP_388699.1	CAZyme	890022	891371	+
CGC10	NP_388700.1	-	891436	892200	+
CGC10	NP_388701.1	TC	892215	893798	+
CGC10	NP_388702.1	TC	893904	895625	+
CGC10	NP_388703.1	TC	895619	897433	+
CGC11	NP_388834.1	TC	1030265	1031260	+
CGC11	NP_388835.1	-	1031395	1031994	+
CGC11	NP_388836.1	TC	1032063	1033397	-
CGC11	NP_388837.1	-	1033458	1033889	-
CGC11	NP_388838.1	-	1034046	1035227	+
CGC11	NP_388840.1	TC	1035554	1036939	+
CGC11	NP_388841.1	-	1036953	1037309	-
CGC11	NP_388842.1	TC	1037306	1037701	-
CGC11	NP_388843.1	-	1037688	1038419	-
CGC11	NP_388844.1	-	1038653	1038760	+
CGC11	NP_388845.1	TC	1038909	1040024	+
CGC11	NP_388846.1	-	1040094	1040837	+
CGC11	NP_388847.1	CAZyme	1040861	1041709	-
CGC11	NP_388848.1	-	1041994	1042842	+
CGC11	NP_388849.1	TC	1042885	1044246	-
CGC11	NP_388850.2	-	1044373	1044873	-
CGC11	NP_388851.1	-	1045037	1045198	+
CGC11	NP_388852.1	TC	1045318	1047075	+
CGC11	NP_388853.1	TC	1047072	1049093	+
CGC12	NP_388882.2	TC	1074646	1075164	-
CGC12	NP_388883.1	-	1075289	1076368	-
CGC12	NP_388884.1	-	1076515	1076952	-
CGC12	NP_388885.1	TC	1077440	1078183	+
CGC12	NP_388886.1	TC	1078176	1079402	+
CGC12	NP_388887.1	TC	1079422	1080132	+
CGC12	NP_388888.2	-	1080150	1081340	-
CGC12	NP_388889.1	TC	1081413	1082804	-
CGC12	NP_388890.1	-	1082870	1083184	-
CGC12	NP_388891.1	-	1083229	1083729	-
CGC12	NP_388892.2	CAZyme	1083851	1085995	+
CGC13	NP_389104.1	CAZyme	1292557	1293735	+
CGC13	YP_003097710.1	-	1293776	1293964	-
CGC13	NP_389105.1	-	1294138	1294950	+
CGC13	NP_389106.1	TC	1294996	1295748	-
CGC13	NP_389107.1	TC	1295748	1296500	-
CGC14	NP_389163.1	TC	1347013	1347276	+
CGC14	NP_389164.1	CAZyme	1347289	1348182	+
CGC14	YP_009513952.1	-	1348219	1348356	-
CGC14	NP_389165.1	-	1348442	1348612	-
CGC14	NP_389166.1	TC	1348612	1349358	-
CGC14	NP_389167.2	TC	1349468	1350469	-

CGC14	NP_389168.1	-	1350482	1351099	-
CGC14	NP_389169.1	TC	1351375	1352691	-
CGC14	NP_389170.1	-	1353080	1354030	+
CGC14	YP_009513953.1	-	1354131	1354277	+
CGC14	NP_389171.2	TC	1354285	1356435	+
CGC14	NP_389172.2	TC	1356447	1357418	+
CGC14	NP_389173.2	TC	1357936	1359285	-
CGC14	NP_389174.1	-	1359454	1360272	+
CGC14	NP_389175.2	TC	1360401	1361225	+
CGC14	NP_389176.1	TC	1361242	1362168	+
CGC14	NP_389177.1	TC	1362174	1363136	+
CGC14	NP_389178.1	TC	1363141	1364148	+
CGC14	NP_389179.2	TC	1364151	1365800	+
CGC15	NP_389402.2	TC	1587926	1588900	+
CGC15	NP_389403.1	-	1588901	1590256	+
CGC15	NP_389404.1	TC	1590317	1591417	+
CGC15	NP_389405.2	CAZyme	1591540	1592631	+
CGC16	NP_389639.2	TC	1887352	1888743	+
CGC16	NP_389640.2	CAZyme	1888774	1890375	+
CGC17	NP_389694.1	TC	1938925	1940322	+
CGC17	NP_389695.2	CAZyme	1940625	1942124	+
CGC17	NP_389696.1	-	1942192	1942455	+
CGC17	NP_389697.1	CAZyme	1942714	1943982	-
CGC17	NP_389698.1	CAZyme	1944113	1945654	-
CGC18	NP_389742.2	TC	2029429	2031114	-
CGC18	NP_389743.2	-	2031439	2032890	+
CGC18	NP_389744.1	CAZyme	2032927	2033625	-
CGC18	NP_389745.1	TC	2033895	2034572	-
CGC18	NP_389746.1	CAZyme	2034745	2035782	+
CGC19	NP_389802.1	CAZyme	2092899	2093762	-
CGC19	NP_389803.1	TC	2094010	2095785	-
CGC20	NP_389823.1	TC	2115425	2116669	-
CGC20	NP_389824.2	CAZyme	2117051	2118268	-
CGC20	NP_389825.3	-	2118504	2119127	-
CGC20	NP_389826.1	TC	2119393	2120751	+
CGC21	NP_390025.1	TC	2264680	2264892	+
CGC21	NP_390026.1	TC	2264903	2265169	+
CGC21	NP_390027.1	-	2265225	2265671	-
CGC21	NP_390028.1	CAZyme	2265668	2266936	-
CGC21	NP_390029.1	-	2266936	2267349	-
CGC21	NP_390030.1	TC	2267346	2269463	-
CGC22	NP_390467.1	CAZyme	2664573	2665391	-
CGC22	NP_390468.1	TC	2665436	2665858	-
CGC23	NP_390560.1	TC	2741357	2742112	-
CGC23	NP_390561.1	-	2742244	2742774	-
CGC23	NP_390562.2	TC	2742909	2743889	+
CGC23	NP_390563.1	TC	2744163	2745479	-
CGC23	NP_390564.1	TF	2745594	2746463	-
CGC23	NP_390565.2	-	2746608	2747711	+
CGC23	NP_390566.1	CAZyme	2747984	2748817	-

CGC24	NP_390581.1	CAZyme	2758043	2760076	-
CGC24	YP_009513989.1	-	2759985	2760152	-
CGC24	NP_390582.1	TC	2760233	2761060	-
CGC24	NP_390583.1	TC	2761081	2761890	-
CGC24	NP_390584.1	TC	2761907	2762395	-
CGC24	NP_390585.1	TC	2762395	2762835	-
CGC24	NP_390586.2	TF	2763025	2765832	-
CGC24	YP_009513990.1	-	2766379	2766519	+
CGC24	NP_390587.2	TC	2766558	2767946	+
CGC24	NP_390588.1	TC	2768042	2768674	-
CGC25	NP_390659.2	TC	2841611	2843065	+
CGC25	NP_390660.1	-	2843106	2843828	-
CGC25	NP_390661.2	-	2843931	2844527	-
CGC25	NP_390662.1	CAZyme	2844675	2845838	-
CGC25	NP_390663.1	-	2845955	2847061	-
CGC25	NP_390664.1	-	2847048	2847917	-
CGC25	NP_390665.1	TC	2847871	2849466	-
CGC26	NP_390749.2	TC	2936382	2938178	-
CGC26	NP_390750.2	CAZyme	2938330	2939832	-
CGC26	NP_390751.2	TC	2939851	2940696	-
CGC26	NP_390752.1	TC	2940697	2941638	-
CGC26	NP_390753.2	TC	2941674	2942975	-
CGC27	NP_390890.3	CAZyme	3081131	3082252	-
CGC27	NP_390892.2	TC	3082260	3083225	-
CGC27	NP_390893.1	-	3083441	3085759	+
CGC27	NP_390894.3	TC	3085800	3087296	-
CGC27	NP_390895.1	TC	3087321	3088181	-
CGC28	NP_390906.1	TC	3099123	3100034	+
CGC28	NP_390907.1	TC	3100031	3100861	+
CGC28	NP_390908.1	CAZyme	3100881	3102179	+
CGC29	NP_390966.1	CAZyme	3157961	3159184	+
CGC29	NP_390967.1	-	3159258	3159689	-
CGC29	NP_390968.1	-	3159691	3160746	-
CGC29	NP_390969.1	CAZyme	3160761	3161894	-
CGC29	NP_390970.1	-	3162084	3163157	+
CGC29	NP_390971.1	TC	3163237	3163704	+
CGC29	NP_390972.1	CAZyme	3163735	3166131	-
CGC29	NP_390973.1	CAZyme	3166118	3167572	-
CGC29	NP_390974.1	-	3167569	3168600	-
CGC29	NP_390975.1	-	3168624	3169766	-
CGC29	NP_390976.1	CAZyme	3169763	3171646	-
CGC29	NP_390977.1	TC	3179306	3179884	+
CGC30	NP_391026.2	TC	3232640	3233818	+
CGC30	NP_391027.2	CAZyme	3233911	3235785	+
CGC31	NP_391281.1	TC	3489910	3491253	-
CGC31	NP_391282.1	CAZyme	3491655	3492689	-
CGC32	NP_391288.1	TC	3497614	3498351	-
CGC32	NP_391289.1	TC	3498352	3499257	-
CGC32	NP_391290.1	TF	3499541	3500350	+
CGC32	NP_391291.1	-	3500386	3501597	+

CGC32	NP_391292.2	CAZyme	3501651	3502940	-
CGC32	NP_391293.1	CAZyme	3503020	3505083	-
CGC32	NP_391294.1	TC	3505102	3505953	-
CGC32	NP_391295.1	TC	3505957	3507213	-
CGC32	NP_391296.1	TC	3507253	3508518	-
CGC32	NP_391297.1	TF	3508659	3509651	-
CGC32	NP_391298.2	TF	3509831	3510490	-
CGC32	NP_391299.1	TC	3510780	3512471	+
CGC33	NP_391305.1	TC	3516880	3517488	-
CGC33	YP_003097789.1	-	3517485	3519002	-
CGC33	NP_391308.1	TC	3518999	3520033	-
CGC33	NP_391309.1	-	3520030	3521106	-
CGC33	NP_391310.1	CAZyme	3521111	3522145	-
CGC33	NP_391311.1	TC	3522170	3523273	-
CGC33	NP_391312.1	TC	3523270	3524424	-
CGC33	NP_391313.2	CAZyme	3524417	3525253	-
CGC33	NP_391314.1	CAZyme	3525250	3526395	-
CGC33	NP_391315.1	TC	3526407	3528203	-
CGC33	NP_391316.1	TC	3528462	3529145	-
CGC33	NP_391317.1	TC	3529151	3529855	-
CGC34	NP_391325.1	CAZyme	3536012	3537433	+
CGC34	NP_391326.1	CAZyme	3537507	3539057	+
CGC34	NP_391327.1	TC	3539165	3540727	+
CGC34	NP_391328.2	TF	3540717	3541406	+
CGC34	NP_391329.1	TC	3541488	3541823	+
CGC34	NP_391330.1	TC	3541823	3542143	+
CGC35	NP_391336.1	TC	3547550	3549235	-
CGC35	NP_391337.1	CAZyme	3549228	3551501	-
CGC35	NP_391338.1	-	3551479	3552363	-
CGC35	NP_391339.1	TC	3552369	3553205	-
CGC35	NP_391340.1	TC	3553206	3554513	-
CGC35	NP_391341.1	TC	3554553	3555806	-
CGC35	NP_391342.1	CAZyme	3555902	3557671	-
CGC36	NP_391433.1	TC	3648654	3649730	-
CGC36	NP_391434.1	CAZyme	3649875	3651068	-
CGC36	NP_391435.1	CAZyme	3651097	3651855	-
CGC37	NP_391439.1	CAZyme	3655586	3656755	-
CGC37	NP_391440.1	TC	3656752	3658203	-
CGC38	NP_391451.1	TC	3673564	3675147	-
CGC38	NP_391452.1	TC	3675167	3675994	-
CGC38	NP_391453.1	CAZyme	3676159	3678399	-
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CGC38	NP_391455.1	-	3680581	3680970	-
CGC38	NP_391456.1	CAZyme	3681370	3682140	+
CGC38	NP_391457.1	-	3682173	3683318	+
CGC38	NP_391458.1	-	3683438	3684766	+
CGC38	NP_391459.1	TC	3684826	3687468	-
CGC38	NP_391460.1	-	3687597	3688547	-
CGC38	NP_391461.2	TC	3688812	3690263	+
CGC38	NP_391462.2	TC	3690269	3691375	+

CGC38	NP_391463.1	-	3691372	3692496	+
CGC38	NP_391464.2	TC	3692533	3693906	-
CGC39	NP_391526.1	TC	3749487	3750677	+
CGC39	NP_391527.1	CAZyme	3750768	3752174	-
CGC39	NP_391528.1	TC	3752280	3753752	-
CGC39	NP_391529.1	TC	3753933	3755291	-
CGC40	NP_391631.2	CAZyme	3849818	3851893	+
CGC40	NP_391632.1	-	3852186	3852704	-
CGC40	NP_391633.1	TC	3852718	3853377	-
CGC41	NP_391670.1	CAZyme	3892351	3893121	-
CGC41	NP_391671.1	-	3893441	3893986	+
CGC41	NP_391672.2	-	3894030	3894401	-
CGC41	NP_391673.2	TC	3894463	3895785	-
CGC42	NP_391683.2	CAZyme	3902210	3903649	-
CGC42	NP_391684.3	TF	3903646	3905031	-
CGC42	NP_391685.1	TC	3905333	3906103	+
CGC43	NP_391718.1	TC	3938307	3939641	-
CGC43	NP_391719.1	TC	3939869	3941806	+
CGC43	NP_391720.1	TF	3942234	3943613	+
CGC43	NP_391721.1	TF	3943667	3944509	+
CGC43	NP_391722.1	CAZyme	3944560	3945420	-
CGC44	NP_391735.1	CAZyme	3958516	3959844	-
CGC44	NP_391736.1	TC	3959841	3960173	-
CGC44	NP_391737.1	TC	3960192	3961550	-
CGC44	NP_391738.1	TC	3961566	3961874	-
CGC45	NP_391750.1	TC	3971060	3972433	+
CGC45	NP_391751.1	-	3972448	3973278	-
CGC45	NP_391752.1	TC	3973364	3975091	-
CGC45	NP_391753.1	TC	3975088	3976791	-
CGC45	NP_391754.1	TC	3976791	3977807	-
CGC45	NP_391755.1	TC	3977791	3979197	-
CGC45	NP_391756.1	TC	3979753	3981105	+
CGC45	NP_391757.1	-	3981227	3982915	+
CGC45	NP_391758.1	-	3982973	3983173	+
CGC45	NP_391759.1	CAZyme	3983187	3984026	-
CGC45	NP_391760.1	TC	3984133	3985230	-
CGC45	NP_391761.1	-	3985351	3986244	-
CGC45	NP_391762.1	-	3986428	3987885	+
CGC45	NP_391763.1	TC	3987927	3988763	-
CGC46	NP_391785.2	TC	4010404	4011684	+
CGC46	NP_391786.1	CAZyme	4011842	4012570	-
CGC46	NP_391787.2	TF	4012866	4013699	-
CGC46	NP_391788.1	-	4013795	4014475	-
CGC46	NP_391789.1	TC	4014682	4015968	+
CGC46	NP_391790.2	TC	4015987	4017426	-
CGC46	NP_391791.2	CAZyme	4017508	4018656	-
CGC47	NP_391802.2	CAZyme	4023544	4030548	-
CGC47	NP_391803.1	-	4030710	4031645	-
CGC47	NP_391804.1	-	4031797	4032243	-
CGC47	NP_391805.2	TC	4032346	4033755	-

Database

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