Conversion of mammalian cell culture media waste to microbial fermentation feed efficiently supports production of recombinant protein by *Escherichia coli*

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Abbreviations: CHO, Chinese hamster ovary; LB, lysogeny broth; CDSM, chemically defined spent media;

Abstract

Deriving new value from waste streams through secondary processes is a central aim of the circular bioeconomy. In this study we investigate whether chemically defined spent media (CDSM) waste from cell culture bioprocess can be recycled and used as a feed in secondary microbial fermentation to produce new recombinant protein products. Our results show that CDSM supplemented with 2% glycerol supported a specific growth rate of *E. coli* cultures equivalent to that achieved using a nutritionally rich microbiological media (LB). The titre of recombinant protein produced following induction in a 4-hour expression screen was approximately equivalent in the CDSM fed cultures to that of baseline, and this was maintained in a 16-hr preparative fermentation. To understand the protein production achieved in CDSM fed culture we performed a quantitative analysis of proteome changes in the *E. coli* using mass spectrometry. This analysis revealed significant upregulation of protein synthesis machinery enzymes and significant downregulation of carbohydrate metabolism enzymes. We conclude that spent cell culture media, which represents 100s of millions of litres of waste generated by the bioprocessing industry annually, may be valorized as a feed resource for the production of recombinant proteins in secondary microbial fermentations.

Introduction

Diversion of waste streams generated by bio-industries to secondary processes to produce valuable products through microbial and chemical engineering has become a central pillar of the circular bioeconomy [1]. One example of a waste stream from bioindustry that has yet to be diverted to the creation of new valuable products is the cell culture media used in the bioprocessing of protein drug molecules. The commercial production of monoclonal antibodies using Chinese hamster ovary (CHO) cell bioprocess in 2019 alone resulted in approximately 30 metric tonnes of protein product [2]. The chemically defined cell culture media used to feed the mammalian cells is itself a sophisticated chemical formulation that also represents a significant waste product in downstream processing. Based on a product titre of 10 g/L of IgG in batch and fed batch systems, with the total yield of protein product produced in 2019 as a reference, we estimate that up to 300 million litres of cell culture waste is generated annually [2, 3]. Systematic approaches to valorize this waste as part of a commitment to a circular bioeconomy have not been investigated. We hypothesise that spent media from CHO cell culture has the potential to support *E. coli* fermentation and the production of recombinant protein titres when recycled from bioprocessing systems.

The re-use of spent media has been investigated in certain process systems, mostly through feeding spent media from the original culture as a supplement to fresh media in the same system [4-8]. These have reported some improvement in protein expression and growth rates. For example, IgG expression titre in mouse hybridoma cell culture was increased by as much as 50% when the cells were

grown in culture media with 33% spent media supplementation [6]. Conversely, feeding the cells with 100% spent media led to a significant decrease in growth and protein production by the mammalian cells. This decrease was attributed to the build-up of auto-inhibitory metabolites and lack of nutrients.

Genetic engineering of a wide array of bacteria has been a central pillar of the development of the circular bioeconomy, enabling new product development from diverse organic waste streams including food oils, agrochemical waste and used bioplastics [9-14]. We aimed to test our hypothesis using *Escherichia coli,* a robust and versatile bacteriological expression host that is widely used commercially to produce recombinant proteins. The production of recombinant human insulin in *E. coli* for example, is a major milestone in human drug production [15, 16]. *E. coli* has been shown to utilize breakdown metabolites such as lactate present in spent culture medias [17] and can grow successfully in spent media from the fermentation of other cell types [8].

Comparative analysis of culture growth rates of an E. coli BL21 strain harbouring a recombinant mCherry-EF2 expression construct in rich microbiological media (LB) and in chemically defined spent media (CDSM) that had previously been used to culture CHO cells, either with or without supplementation, confirmed CDSM as a viable feed for bacterial fermentation. Analysis of recombinant protein production by the cultures confirmed equivalent recombinant protein titres post-purification when compared to LB.

Results

Growth rate analysis of *E. coli* BL21 mCherry/EF2 in minimal media, baseline rich media and chemically defined spent media.

Growth rates of *E. coli* cultures grown in M9 minimal media with carbon source supplementation were measured to determine the optimal supplementation conditions that could then be applied to the CDSM fed cultures. Glycerol was selected as a suitable carbon supplementation as it is also a waste product from other processes. Gradients of glycerol additions were tested at concentrations of 1%-3% (figure 1A). 2% glycerol supplementation was shown to produce a specific growth rate of 0.673 generations per hour, as compared to the growth rates of 1% and 3% at 0.578 and 0.647. Volumes (v/v) over 3% greatly reduced the growth rate, while 2% glycerol addition to the reference LB media did not affect the growth rate seen in LB alone (data not shown).

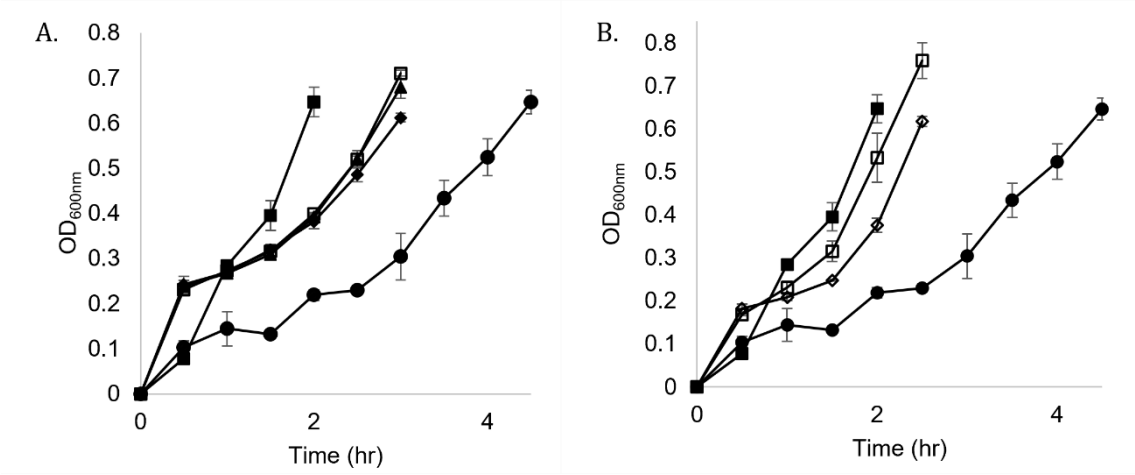

Figure 1. *E. coli* culture growth rates in bacteriological and cell culture media. (A.) Glycerol supplementation in M9 minimal media; ■ = baseline media, ● = minimal media, ◆ = minimal media + 1% glycerol, □= minimal media + 2% glycerol, ▲ = minimal media + 3% glycerol. **(B).** Unsupplemented and supplemented chemically defined spent media (CDSM). ■ = baseline media, ● = M9 media, ◇ = chemically defined spent media (CDSM) unsupplemented, □ = CDSM with 2% glycerol. All time points were completed in triplicate with standard deviation as error bars.

The chemically defined spent medium used was CHOgro® spent media harvested from CHO (Chinese Hamster Ovary) cell culture. The specific growth rate of the *E. coli* in the CDSM was 0.704 gen/hour, approximately 70% of the rate achieved in the baseline LB media. Supplementing CDSM with 2% glycerol led to a further increase in growth rates to ~94% of that of LB (figure 1B). This supplementation was chosen for all medias tested for protein expression analysis.

Protein expression analysis in chemically defined spent media fermentation.

Recombinant mCherry-EF2 expression was tested in cultures grown in CDSM supplemented with 2% glycerol and the baseline LB with 2% glycerol. A four-hour expression screen post-induction with IPTG showed that protein production in CDSM was equivalent to baseline LB, with an average yield of 100.58 mg/L compared to LB's 92.57 mg/L (figure 2A).

A.

Measurement	LB + 2% Glycerol	CDSM I + 2% Glycerol	CDSM II + 2% Glycerol
Specific growth rate (k)	1.07	0.94	0.92
R-squared coefficient	0.97	0.95	0.95
4-hour biomass (g) (±SD)*	0.25 (± 0.02)	0.43 (± 0.04)	**nd**
4-hour protein yield (mg/L) (±SD)*	92.57 (± 19.98)	100.58 (± 6.77)	**nd**
16-hour biomass (g) (±SD)*	0.46 (± 0.02)	0.47 (± 0.11)	0.56 (± 0.06)
16-hour protein yield (mg/L)	168.92	159.82	127.57

B.

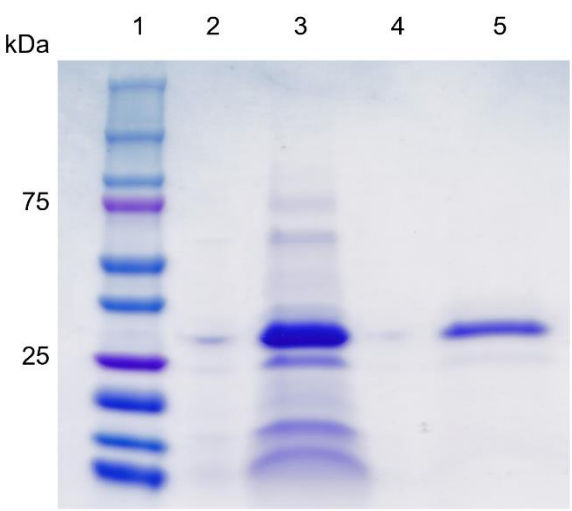

Figure 2 Protein expression and purification analysis. (A.) Table of growth characteristics, biomass, and protein yields. LB media; Lysogeny Broth baseline rich media. M9 media; minimal salts media. CDSM I; chemically defined spent media CHOgro®. CDSM II; chemically defined spent media Expi-CHO®. R^2 coefficient is the percentage of variability in the growth curve dataset that is accounted for by linear correlation between the OD600 (nm) and the time (hr). For the equation for the specific growth rate, see Methods. * n = 2 for all standard deviation calculations. **(B.)** SDS-PAGE analysis of purified protein versus input supernatant sample. Lane 1 = protein marker, lane 3 = post-boil supernatant sample from CDSM, lane 5 = purified monomeric fraction from size exclusion chromatography of CDSM.

We next tested a 16-hour expression post-induction with IPTG using CDSM, and included a second chemically defined spent medium, Expi-CHO® (termed CDSM II), to examine the robustness of our finding with widely used commercial medias. Protein yield from the CDSM I fed culture closely matched the yield of that from LB with a protein yield of 159.82 mg/L compared to 168.92 mg/L (figure 2A). The alternate spent media type tested, CDSM II, managed a successful yield of 127.57 mg/L. It should be noted that the CDSM II condition also lost some yield during

expression, seen by the presence of the recombinant protein in the extracellular media also. SDS-PAGE analysis confirmed that the monomeric peak taken from SEC corresponding to the mCherry-EF2 protein at 32 kDa .

Mass spectrometry analysis of E. coli cultures at the whole proteome level

We performed a proteomic analysis of the protein expression patterns in the bacterial cultures themselves using LC-MS/MS. The analysis of proteomic data files was carried out using MaxQuant. Using the protein expression pattern for *E. coli* grown in LB media as a baseline reference, a student's t-test with a false discovery rate of <0.05 identified 655 differentially expressed proteins in *E. coli* cultures grown in unsupplemented CDSM. In 2% glycerol supplemented CDSM conditions there were 167 proteins differentially expressed by comparison (Figure 3).

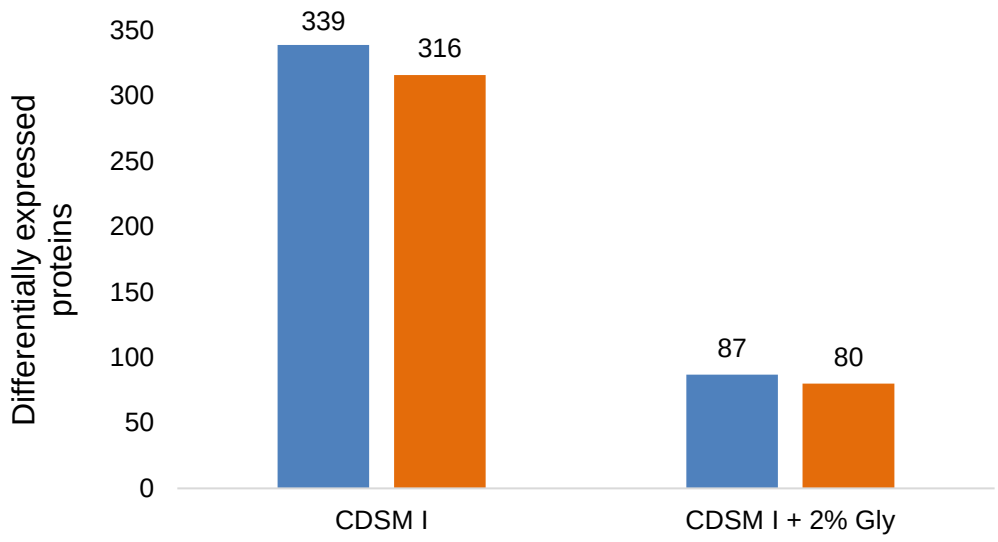

Figure 3. Number of statistically significant differentially expressed proteins compared to the baseline condition in LB media. Orange bars represent the number of downregulated proteins while blue represents all upregulated proteins compared to baseline LB media after a student's t-test with an FDR of < 0.05.

In CDSM I supplemented with 2% glycerol, 1,222 proteins were found to be dysregulated and of these, 167 proteins were statistically significant. From these

167 proteins, 87 proteins were identified as upregulated and 80 proteins as downregulated. A program that measures the quantitative differences in expression by difference in LFQ intensity was written using Python script and using a cut-off significance value of >0.5 or <-0.5 in intensity identified the most significantly changed expression levels, shown here for the first time as a pool table plot (figure 4). Proteins upregulated in the CDSM I + 2% glycerol condition were principally in the amino-acid and purine biosynthesis pathways, while proteins that were most significantly downregulated were in the carbohydrate metabolism pathway (figure 4).

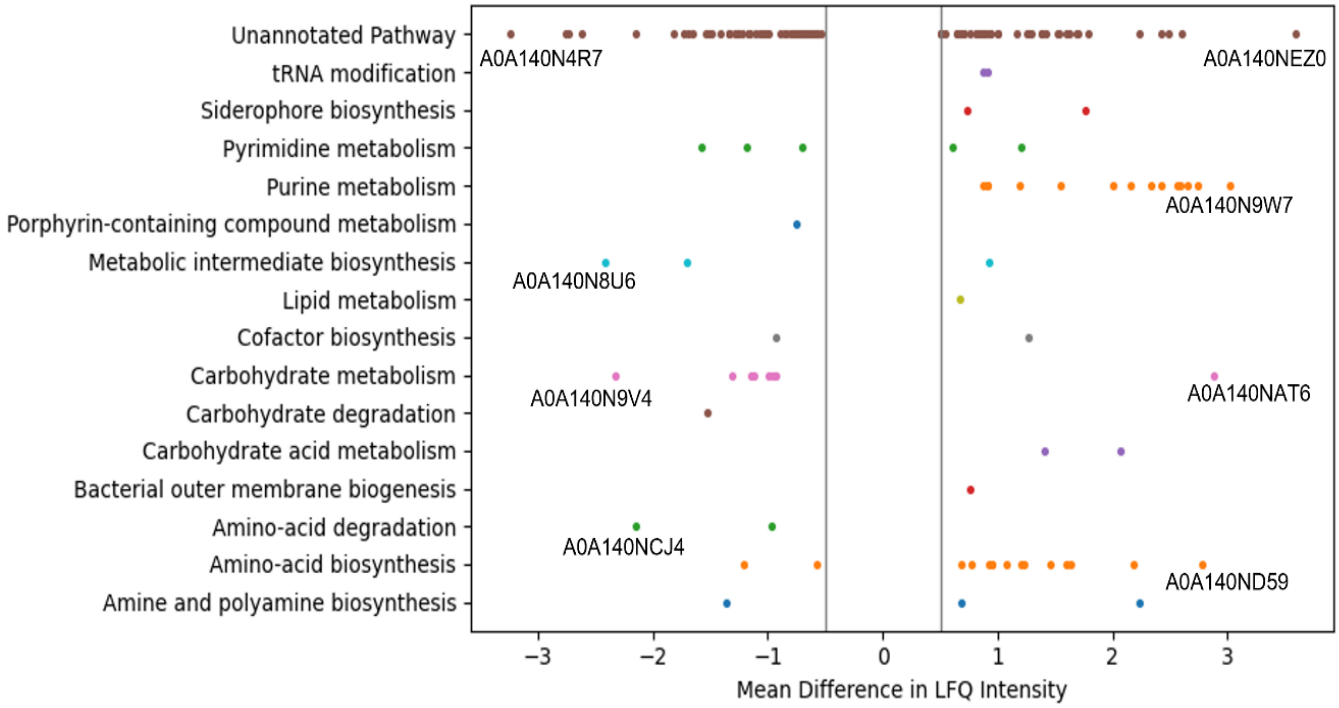

Figure 4. Pool-table plot of the proteomic analysis of the significantly dysregulated proteins from the sample condition of CHOgro® with 2% glycerol supplementation. This graph was constructed using the Matplotlib library in Python. Significant upregulation of expression is shown to the right of the central threshold divider (-0.5 to 0.5), with significant downregulation to the left. Significance in this case was defined as having a mean difference in LFQ intensity compared to the baseline media of more than 0.5 in either direction after a student's t-test and with an FDR of <0.05. The top three pathway proteins and the top one unannotated pathway protein are labelled directly below their representative point, for both up- and down-regulated.

Uniprot Entry	Protein Name	Gene	Pathway	Description	LFQ Difference
Up-regulated Proteins					
A0A140NEZ0	Periplasmic copper-binding protein	cusF	Unannotated	Homologue of Cation efflux system protein	3.59
A0A140N9W7	Amidophosphoribosyltransferase	purF	Purine metabolism	IMP biosynthesis via de novo pathway	3.02
A0A140NAT6	Phosphogluconate dehydratase	edd	Carbohydrate metabolism	Entner-Doudoroff pathway; catalyses glucose into pyruvate	2.89
A0A140ND59	Aspartate--ammonia ligase	asnA	Amino-acid biosynthesis	L-asparagine biosynthesis	2.79
Down-regulated Proteins					
A0A140N4R7	Protein YcfR	yhcN	Unannotated	Homologue of Peroxide/acid stress response protein YhcN	-3.24
A0A140N8U6	Phospho-2-dehydro-3-deoxyheptonate aldolase	aroF	Metabolic intermediate biosynthesis	Member of the chorismate biosynthesis pathway	-2.42
A0A140N9V4	Probable malate: quinone oxidoreductase	mqo	Carbohydrate metabolism	Tricarboxylic acid cycle; oxaloacetate from (S)-malate	-2.33
A0A140NCJ4	D-amino acid dehydrogenase	dadA	Amino-acid degradation	D-alanine degradation	-2.14

Table 1. Most significantly dysregulated *E. coli* proteins and the associated annotated functional pathway. Proteins highlighted by accession number in Figure 4 are described here with one example of an upregulated and downregulated protein lacking an annotated functional pathway.

Amino acid biosynthesis and purine metabolism functional pathways were up-regulated in all cultures grown in CDSM compared to the baseline. Carbohydrate metabolism by contrast was mainly downregulated. Within amino acid biosynthesis are some of the most statistically significantly upregulated enzymes, such as diaminopimelate decarboxylase and Aspartate-ammonia ligase, two enzymes that are upregulated with a mean difference of LFQ intensity of > 2, along with 10 other significantly upregulated enzymes in this pathway. Purine metabolism also features highly upregulated enzymes such as glutamine dependent amidophosphoribosyltransferase, with a difference in intensity of > 3 along with 12 other significantly upregulated enzymes.

Discussion

Can spent media from CHO cell culture be reused to feed *E. coli* fermentation?

The creation of chemically defined culture media has led to increasing recombinant protein titres and protein quality [18, 19]. These successful developments have resulted in this cell culture media becoming a significant waste stream with approximately 300 million litres sent for disposal annually [2].

Our data indicates that chemically defined spent media (CDSM) is a potentially valuable resource for producing new recombinant proteins when compared with microbiological media prepared with casein digests and yeast extract, such as the LB media studied here. In this study we investigated the expression of a recombinant fusion protein ligand (EF2) derived from mCherry and the calcium binding protein Calbindin D9k. This recombinant protein has been developed as a ligand for a highly specific and high affinity purification system [20-23]. The growth rate of the expression culture in the CDSM + 2% glycerol reached was similar to the LB at ~94% while the 4-hour protein yield was approximately equal, a striking and unanticipated finding (figure 2A). This finding was further verified in the 16-hour fermentation, a model of a preparative scale expression, whereby the CDSM cultures successfully supported a protein expression over this longer period with approximately the same yield (159.82 mg/L) as those cultures grown in the nutritionally rich LB media (168.92 mg/L) (figure 2A). This finding prompted us to investigate the proteome of the cultures to identify proteins responsible for metabolic changes that may contribute to this phenotype.

Proteomic analysis

Out of the 629 upregulated proteins identified in the optimised condition of CDSM + 2% Glycerol, the most statistically significantly upregulated proteins are enzymes involved in the amino acid biosynthesis pathway. For example, both Diaminopimelate decarboxylase and Aspartate-ammonia ligase are two highly upregulated proteins with LFQ differences of > 2 (Figure 4, table 1), involved in lysine biosynthesis and asparagine biosynthesis pathways that are dependent on glutamine uptake [24]. Glutamine (4 mM) is a supplement added to the chemically defined media prior to CHO cell culture. Amino acid accumulation such as increased L-asparagine is a known feature of the *E. coli* stress response, to make available the building blocks needed for synthesis of stress response proteins [25]. This upregulation may indicate the activation of a stress response in the cultures that is not activated in rich microbiological media but that contributes to recombinant protein expression. Other highly upregulated proteins (>2 fold) include glycerol metabolism enzymes such as Phosphogluconate dehydratase, purine metabolism enzymes such as glutamine dependent Amidophosphoribosyltransferase, and iron uptake proteins such as Enterobactin non-ribosomal peptide synthetase EntF, among others [26-28]. Interestingly the increased expression of the glycerol metabolism enzyme Phosphogluconate dehydratase and glutamine dependent Amidophosphoribosyltransferase correlates well with the supplementation with both glycerol and glutamine and confirms the sensitivity of this MS analysis.

Among the 595 downregulated proteins in the CDSM + glycerol condition are enzymes involved in the TCA cycle such as the probable malate:quinone oxidoreductase, some specific stress response proteins such as protein YcfR (an

acid stress response protein), and nucleotide synthesis/salvage proteins, such as cytidine deaminase. Many of these proteins depend on the presence of glucose in order to be active, leading to a possible reason for their downregulation in the CDSM + glycerol condition [29, 30]. Other downregulated proteins which are statistically significant include D-amino acid dehydrogenase, involved in amino-acid degradation, and generally present in high levels in LB rich broth due to extracellular D-amino acids which are not present in the CDSM [31, 32].

One of the main metabolic pathways that was upregulated in the CDSM media compared to LB was the amino-acid biosynthesis pathway. The baseline condition of LB contains tryptone, a source of nitrogen-containing peptides for *E. coli* growth, whereas the spent CHOgro® media must rely on the proteins released by the CHO cell culture conditions [33]. CHO cell growth in chemically defined media produces metabolites such as ammonium and lactate that can inhibit further growth [34]. These factors however can be used by *E. coli* to grow, utilising ammonium as its preferred nitrogen source and can break down lactate as a possible carbon source if needed [35]. The 102 proteins that are significantly dysregulated and are yet to be assigned a pathway on Uniprot are involved in a wide array of metabolic processes in the *E. coli* cell, such as the acid stress response protein seen to be the most downregulated in table 1. Further study into these individual proteins will help to understand the proteomic adaptions undertaken by the CDSM fed *E. coli*.

Proteomic analysis of the nutritional content of CDSM

CHO cells generally produce approximately 1,400 host cell proteins (HCPs) which are detectable in the clarified spent culture media, with ~80% of the top 1000 of

these HCPs in common across multiple cell lines [36, 37]. Mass spectrometry-based analysis has been widely employed to characterise HCP's across a number of studies [38-40].

Mass spectrometry analysis of the CDSM alone identified879 host cell proteins from CHO in the spent media after culturing (see Table S1). These proteins were identified from all cellular compartments suggesting they are debris from CHO cell lysis in addition to any active secretion by the growing cells. These host cell proteins represent a source of amino acid building blocks for the increased recombinant protein production capabilities of the *E. coli* cultures.

Conclusion

We have shown in this study that mammalian cell culture waste, the chemically defined synthetic media used to grow Chinese Hamster Ovary cells, is conditioned such that it provides a nutritious feed for the growth of *E. coli* cultures in secondary fermentation. The growth rate of the culture in this waste medium is similar to that of rich microbiological culture media and upon supplementation with another waste by-product, glycerol, the growth rate is enhanced. Importantly, the expression of a recombinant protein from an expression plasmid construct is seen to be equivalent in protein titre between 4 to 16 hours showing that this waste has a real value in a biotechnological context. This approach may be further developed based on a deeper understanding of the protein expression patterns analysed here, that show significant upregulation and downregulation of metabolic enzymes and pathways. This approach can begin a route for the capture of a bioprocessing waste stream for the circular bioeconomy.

Experimental Procedures

Mammalian Cell Culture

Chinese Hamster Ovary (CHO) cells were incubated in 20 ml of serum-free CHOgro® Expression media supplemented with 4 mM L-Glutamine in T75 adherent cell line flasks, at 37˚C with 5% CO_2 and 95% O_2. Cells were split at 70-80% confluency every 3-4 days. Spent media was harvested at each split and was clarified of cells and cellular debris by centrifugation at 300 x g for 4 minutes prior to storing at 4°C for up to 14 days.

Growth and Expression Cultures of *E. coli*

E. coli BL21 Gold was transformed with an mCherry-EF2 fusion protein expression construct with a T7 promoter expression system. A 10 ml starter culture of BL21 transformed *E. coli* was grown by incubating a single, isolated colony in Lysogeny Broth (LB) media, 2% glucose, and 100 µg/ml ampicillin. The culture was grown in a shaking incubator at 250 rpm, 37°C for 16 hours. Growth curves were taken from 50 ml cultures grown in triplicate in 250ml flasks by measuring OD_{600} every half an hour for growth curve plotting until the OD_{600} reached 0.6. The four-hour expression was carried out in duplicate 50 ml cultures with 2% glycerol and a 1 in 20 dilution of starter culture in the expression media in a shaking incubator at 250 rpm, 37°C.Expression of the fusion protein was induced by addition of 1 mM IPTG after OD_{600} reached 0.6. Cultures were then incubated on a shaking incubator at 250 rpm, 30°C for 4 hours or for 16 hours for the overnight expression experiment. Cultures were then spun at 4°C, 4000 x g for 20 minutes to harvest the pellets which were weighed prior to protein purification.

Calculations of Specific Growth Rate

$$k = \frac{log_{10}[X_t] - log_{10}[X_0]}{0.301 \times t}$$

Specific growth rate (k) was calculated by the above equation, where k is generations per hour and t is time in hours. Plots of growth curves of OD_{600} (nm) versus time (hrs) were generated to gather this data in Excel. X_t is one OD_{600} value at a later position, and X_0 is another OD_{600} value taken from an earlier position using a trendline.

Recombinant Protein Purification

Cell pellets were re-suspended using a buffer containing 10 mM Tris and 2 mM $CaCl_2$ pH 7.4 before lysing by sonication. The lysate was then boiled at 85 degrees Celsius and spun at 15,000 rcf for 30 minutes. Supernatant was harvested and referred to as the post-boil (PB) sample. 0.5 ml of this PB was run on a Superdex 200 10/300 size exclusion chromatography column, using Hepes Buffer Saline as a running buffer. Protein concentration was measured with a DeNovix DS-11 Spectrophotometer, using the UV-Vis application. Measurements were taken at 585 nm for mCherry yield, with an extinction coefficient calculated at 44,854.2 $M^{-1}cm^{-1}$ and a protein molecular weight of 30,667.4 g/mol.

Proteomic Analysis

4 ml of *E. coli* culture was harvested after reaching OD_{600} of 0.6, but before IPTG induction. These cultures were re-suspended in 8M urea. 5mM DTT was then added, and samples were incubated at room temperature for 10 minutes. After incubation, 10mM iodoacetamide was added, and samples were incubated in the dark for 10 minutes at room temperature. Samples were brought to neutral pH by addition of 150 µl of 200 mM NH_4HCO_3. Samples were then digested with trypsin at 37°C and 300 rpm on a thermomixer overnight. Samples were spun at 4000 x g

for 2 mins to prevent ZipTip® from getting blocked in the next steps. Digested peptides were filtered through ZipTip® columns and eluted using 70% acetonitrile in acidic water (0.1% formic acid). The elution was dried off by speed-vac at 45 °C. The dried peptides were then re-suspended in 30 µl Buffer A (5% acetonitrile and 0.1% TFA). Analysis of proteomic data files was carried out using MaxQuant [41] to assemble peptides using the *E. coli* BL21 proteome from Uniprot (UP000002032). The software Perseus [42] was used to analyse the resulting dataset for student's t-tests and heatmap generation. A Python programme was generated to give the remaining graphs, using the t-test results generated from Perseus and annotation information from Uniprot for *E. coli* strain BL21 (available on GitHub at https://github.com/Ciara-Lynch/Mass_Spec_Analysis.git).

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Conflict of interest

The authors declare no financial or commercial conflict of interest.

Author Contributions

CL performed the experiments, CL and DJO'C analysed the data, CL and DJOC wrote the paper. DJO'C designed the study.

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Supplementary Information

Protein ID	Protein names	Mean LFQ Intensity
G3HHR3_CRIGR	Vimentin	25.25
G3H0E4_CRIGR	Chondroitin sulfate proteoglycan 4	24.99
G3GVD0_CRIGR	ACTB (Actin, cytoplasmic 1)	24.92
G3GZG6_CRIGR	Beta-1 metal-binding globulin (Serotransferrin) (Siderophilin)	24.76
G3H4T5_CRIGR	Glypican-1 (Secreted glypican-1)	23.60
G3H584_CRIGR	Osteonectin (SPARC) (Secreted protein acidic and rich in cysteine)	23.45
G3I255_CRIGR	L-lactate dehydrogenase (EC 1.1.1.27)	23.35
G3H3Q1_CRIGR	Pyruvate kinase (EC 2.7.1.40)	23.18
G3IKI6_CRIGR	Keratin, type II cytoskeletal 1b	23.05
G3HKZ1_CRIGR	14-3-3 protein zeta/delta	23.04
G3IBN9_CRIGR	Keratin, type II cytoskeletal 71	23.03
G3GVL0_CRIGR	Ubiquitin	23.00
G3IDM2_CRIGR	Cofilin, non-muscle isoform (Cofilin-1)	22.80
G3IAQ0_CRIGR	2-phospho-D-glycerate hydro-lyase (EC 4.2.1.11)	22.62
G3I5N6_CRIGR	Insulin-like growth factor-binding protein 4	22.57
G3H2W6_CRIGR	Extracellular matrix protein 1	22.57
G3HNJ3_CRIGR	Clusterin	22.55
G3H3E4_CRIGR	Galectin-3-binding protein (Lectin galactoside-binding soluble 3-binding protein)	22.43
G3I664_CRIGR	Procollagen C-endopeptidase enhancer 1	22.13
G3H8F4_CRIGR	Alpha-dystroglycan (Beta-dystroglycan) (Dystroglycan) (Dystrophin-associated glycoprotein 1)	22.13
G3I3K5_CRIGR	ADGRG1 C-terminal fragment (ADGRG1 N-terminal fragment) (Adhesion G-protein coupled receptor G1) (G-protein coupled receptor 56) (GPR56 C-terminal fragment) (GPR56 N-terminal fragment) (GPR56 extracellular subunit) (GPR56 seven-transmembrane subunit) (GPR56 subunit alpha) (GPR56 subunit beta)	22.07
G3HH39_CRIGR	Elongation factor 1-alpha 1	22.05
G3IPU3_CRIGR	14-3-3 protein epsilon	22.03
G3HAI3_CRIGR	Follistatin-related protein 1	22.03
G3IH98_CRIGR	Keratin, type II cytoskeletal 8	22.01
G3H5Q0_CRIGR	Actin, alpha cardiac muscle 1	21.98
G3GUU5_CRIGR	Transketolase	21.97
G3IBH0_CRIGR	Metalloproteinase inhibitor 1 (Tissue inhibitor of metalloproteinases 1)	21.97
G3I1H5_CRIGR	Asparaginyl endopeptidase (EC 3.4.22.34) (Legumain) (Protease, cysteine 1)	21.96
G3GWQ1_CRIGR	Metavinculin (Vinculin)	21.92
G3GUM6_CRIGR	Glyceraldehyde-3-phosphate dehydrogenase	21.90
G3HSL4_CRIGR	Elongation factor 2	21.88
G3GU60_CRIGR	Phosphatidylethanolamine-binding protein 1	21.84
G3HC31_CRIGR	Protein S100 (S100 calcium-binding protein)	21.81
G3GYP9_CRIGR	Peroxiredoxin-1	21.79
BIP_CRIGR	Endoplasmic reticulum chaperone BiP (EC 3.6.4.10) (78 kDa glucose-regulated protein) (GRP-78) (Binding-immunoglobulin protein) (BiP) (Heat shock protein 70 family protein 5) (HSP70 family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)	21.76

G3GZ90_CRIGR	Calumenin	21.71
G3H5D5_CRIGR	Acyl-CoA-binding protein	21.71
G3IF52_CRIGR	Nucleobindin-2	21.67
G3HBG8_CRIGR	Calmodulin	21.64
G3INC5_CRIGR	Cathepsin L1	21.64
G3I1V3_CRIGR	Fibronectin	21.61
G3I8F9_CRIGR	Keratin, type I cytoskeletal 14	21.61
G3IPN2_CRIGR	Keratin, type I cytoskeletal 10 (Fragment)	21.59
G3HWE7_CRIGR	Dickkopf-related protein 3	21.55
G3H2I6_CRIGR	Neural cell adhesion molecule 1	21.51
G3HZX6_CRIGR	Nucleobindin-1	21.49
G3HJG6_CRIGR	Decorin (Bone proteoglycan II)	21.46
G3HPV6_CRIGR	Histone H4	21.40
G3GXB0_CRIGR	ARHGDIA (Rho GDP-dissociation inhibitor 1) (Rho GDP-dissociation inhibitor 1-like protein)	21.35
G3IBK8_CRIGR	V-type proton ATPase subunit S1	21.35
G3I4H6_CRIGR	Fructose-bisphosphate aldolase (EC 4.1.2.13)	21.35
G3IGL0_CRIGR	Helix-destabilizing protein (hnRNP core protein A1)	21.32
G3H0L9_CRIGR	Cathepsin B (EC 3.4.22.1) (Cathepsin B heavy chain) (Cathepsin B light chain)	21.28
G3H6V7_CRIGR	Lipoprotein lipase (LPL) (EC 3.1.1.34)	21.22
G3GUR1_CRIGR	Complement subcomponent C1r (EC 3.4.21.41)	21.21
G3H2J8_CRIGR	Heterogeneous nuclear ribonucleoproteins A2/B1	21.21
G3H1K9_CRIGR	Alpha-actinin cytoskeletal isoform (Alpha-actinin-1) (F-actin cross-linking protein) (Non-muscle alpha-actinin-1)	21.13
G3H0U6_CRIGR	Protein disulfide-isomerase (EC 5.3.4.1)	21.11
G3ILN5_CRIGR	Reticulocalbin-3	21.08
G3HLS2_CRIGR	14-3-3 protein beta/alpha	21.07
G3GZW8_CRIGR	Phosphoglycerate mutase 1	21.02
G3H0S7_CRIGR	Beta-2-microglobulin	20.96
G3H7Z2_CRIGR	Transgelin	20.94
G3H4Z8_CRIGR	HSPA2 (Heat shock-related 70 kDa protein 2)	20.90
G3IED5_CRIGR	Peptidyl-prolyl cis-trans isomerase A	20.89
G3H6Y6_CRIGR	NSFL1 cofactor p47 (p97 cofactor p47)	20.88
G3I4D4_CRIGR	Ribonuclease T2	20.86
G3H8V4_CRIGR	Phospholipid transfer protein	20.86
G3I412_CRIGR	45 kDa calcium-binding protein	20.85
G3IFV3_CRIGR	Exportin-1	20.81
G3I3Y6_CRIGR	GST class-pi (EC 2.5.1.18)	20.79
G3IEB7_CRIGR	Out at first protein homolog	20.79
G3IAS8_CRIGR	Heterogeneous nuclear ribonucleoprotein K (Queuosine salvage protein)	20.78
G3GWB3_CRIGR	Alpha-2-macroglobulin receptor-associated protein	20.75
G3HG95_CRIGR	Lamin-A/C	20.75
G3GUR0_CRIGR	Calcium-dependent serine proteinase	20.74
G3IDD4_CRIGR	Collagen-binding protein (Serpin H1)	20.69
G3IBG3_CRIGR	Ubiquitin-activating enzyme E1 (EC 6.2.1.45)	20.68
G3IEU2_CRIGR	Maillard deglycase (EC 3.5.1.124) (Parkinsonism-associated deglycase) (Protein DJ-1) (Protein/nucleic acid deglycase DJ-1)	20.67

G3HIM1_CRIGR	Basement membrane-specific heparan sulfate proteoglycan core protein	20.67
G3I2T9_CRIGR	3-phosphoinositide-dependent protein kinase 1	20.63
G3IBP3_CRIGR	Keratin, type II cytoskeletal 2 epidermal	20.60
G3HWJ3_CRIGR	Uncharacterized protein	20.59
G3H6S8_CRIGR	Inorganic diphosphatase (EC 3.6.1.1)	20.56
G3H7I6_CRIGR	Sulfhydryl oxidase (EC 1.8.3.2)	20.54
G3I8S7_CRIGR	Polyadenylate-binding protein (PABP)	20.53
G3HLK3_CRIGR	Granulins	20.51
G3I1Y9_CRIGR	Sulfated glycoprotein 1	20.50
G3HUU7_CRIGR	Calpactin I light chain (Calpactin-1 light chain) (Protein S100-A10) (S100 calcium-binding protein A10)	20.47
G3HTF8_CRIGR	Proto-oncogene C-crk	20.47
G3HTE5_CRIGR	Lysosomal alpha-glucosidase	20.46
G3I1P5_CRIGR	SH3 domain-binding glutamic acid-rich-like protein	20.45
G3HMV7_CRIGR	Alpha-L-fucosidase (EC 3.2.1.51)	20.44
G3HWE4_CRIGR	Nidogen-1	20.43
G3HYJ8_CRIGR	10 kDa heat shock protein, mitochondrial (Chaperonin 10)	20.41
G3IDN7_CRIGR	Protein FAM3C	20.39
G3GXD7_CRIGR	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (EC 1.1.1.100) (EC 1.3.1.39) (EC 2.3.1.38) (EC 2.3.1.39) (EC 2.3.1.41) (EC 2.3.1.85) (EC 3.1.2.14) (EC 4.2.1.59) (3-oxoacyl-[acyl-carrier-protein] reductase) (3-oxoacyl-[acyl-carrier-protein] synthase) (Acyl-[acyl-carrier-protein] hydrolase) (Enoyl-[acyl-carrier-protein] reductase) (Fatty acid synthase) ([Acyl-carrier-protein] S-acetyltransferase) ([Acyl-carrier-protein] S-malonyltransferase)	20.39
G3I278_CRIGR	Laminin subunit beta-1	20.37
G3I064_CRIGR	Neutral alpha-glucosidase AB	20.34
G3H832_CRIGR	Translationally-controlled tumor protein	20.34
G3H2Q4_CRIGR	Carbonic anhydrase (EC 4.2.1.1) (Fragment)	20.32
G3HDQ2_CRIGR	Malate dehydrogenase (EC 1.1.1.37)	20.31
G3HH30_CRIGR	Aldose reductase	20.29
G3H533_CRIGR	Peptidyl-prolyl cis-trans isomerase (PPIase) (EC 5.2.1.8)	20.29
G3GR73_CRIGR	Rab GDP dissociation inhibitor	20.28
G3GSG4_CRIGR	ATPase H(+)-transporting lysosomal accessory protein 2 (ATPase H(+)-transporting lysosomal-interacting protein 2) (Renin receptor) (Renin/prorenin receptor)	20.28
G3ILK7_CRIGR	Calsyntenin-1	20.25
G3IDC2_CRIGR	Heat shock cognate 71 kDa protein	20.24
G3IEY9_CRIGR	14-3-3 protein theta	20.18
G3GXS2_CRIGR	EMILIN-1	20.18
G3HBI1_CRIGR	Peroxidase (EC 1.11.1.7)	20.15
G3HJG5_CRIGR	Lumican	20.13
G3HEJ4_CRIGR	Neogenin	20.11
G3I1V4_CRIGR	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase (EC 2.1.2.3) (EC 3.5.4.10) (AICAR transformylase) (AICAR transformylase/inosine monophosphate cyclohydrolase) (Bifunctional purine biosynthesis protein ATIC) (IMP synthase) (Inosinicase) (Phosphoribosylaminoimidazolecarboxamide formyltransferase)	20.09
G3HBD3_CRIGR	Nucleoside diphosphate kinase (EC 2.7.4.6)	20.08
G3I948_CRIGR	Eukaryotic translation initiation factor 5A (eIF-5A)	20.08
G3HRQ4_CRIGR	Myosin light polypeptide 6	20.07
G3HD97_CRIGR	Thioredoxin domain-containing protein 5	20.06

G3H8Y5_CRIGR	Collagen alpha-1(VI) chain	20.05
G3GR90_CRIGR	Isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2)	20.05
G3HC47_CRIGR	Glucosylceramidase (EC 3.2.1.45)	20.04
G3GR64_CRIGR	Inter-alpha-trypsin inhibitor heavy chain H5	20.01
G3HGW6_CRIGR	Laminin subunit alpha-5	20.00
G3IE21_CRIGR	Aldose reductase-related protein 2	20.00
G3H4S3_CRIGR	Heat shock 70 kDa protein 13	20.00
G3HTZ1_CRIGR	Myelin peripheral protein (Myelin protein P0) (Myelin protein zero)	19.98
G3HGM6_CRIGR	AGA (N(4)-(Beta-N-acetylglucosaminyl)-L-asparaginase)	19.94
G3HIL0_CRIGR	Triosephosphate isomerase (EC 5.3.1.1)	19.94
G3HC01_CRIGR	Tropomyosin alpha-3 chain	19.94
G3I6T1_CRIGR	Phospholipase B-like (EC 3.1.1.-)	19.93
G3I2H0_CRIGR	Dipeptidyl peptidase 3 (EC 3.4.14.4) (Dipeptidyl aminopeptidase III) (Dipeptidyl peptidase III)	19.93
G3H1S2_CRIGR	UDP-glucose:glycoprotein glucosyltransferase 1	19.89
G3H3E6_CRIGR	Metalloproteinase inhibitor 2 (Tissue inhibitor of metalloproteinases 2)	19.87
G3GXZ0_CRIGR	Protein-glutamine gamma-glutamyltransferase 2	19.87
G3GYP7_CRIGR	AKR1A1 (Alcohol dehydrogenase [NADP+])	19.84
Q9EPP7_CRIGR	Cathepsin X (EC 3.4.18.1)	19.84
G3GZZ0_CRIGR	Aspartate aminotransferase (EC 2.6.1.1)	19.84
G3HK90_CRIGR	14-3-3 protein eta	19.82
G3IGW0_CRIGR	CTLA2B (Protein CTLA-2-beta)	19.82
G3HQD5_CRIGR	Peptidyl-glycine alpha-amidating monooxygenase B	19.81
G3IMH4_CRIGR	Sphingomyelin phosphodiesterase (EC 3.1.4.12)	19.81
G3GXA9_CRIGR	Protein disulfide-isomerase	19.80
G3I3G8_CRIGR	Transaldolase (EC 2.2.1.2)	19.79
G3IEF1_CRIGR	Ferritin	19.78
G3H8V1_CRIGR	Matrix metalloproteinase-9	19.76
G3H5W5_CRIGR	LIM and SH3 domain protein 1	19.74
G3HZ42_CRIGR	CCT-beta (T-complex protein 1 subunit beta)	19.72
G3HSM3_CRIGR	Thimet oligopeptidase	19.72
G3IE06_CRIGR	Transmembrane protein 132A	19.69
G3HZ28_CRIGR	Twisted gastrulation protein-like 1	19.69
G3GWX6_CRIGR	Leukocyte elastase inhibitor A (SERPINB1A)	19.67
G3I3F3_CRIGR	Ribonuclease inhibitor (Ribonuclease/angiogenin inhibitor 1)	19.66
G3H7B3_CRIGR	Galectin	19.65
G3I936_CRIGR	Epididymal secretory protein E1 (NPC intracellular cholesterol transporter 2)	19.65
G3HGP4_CRIGR	ACAT2 (Acetyl-CoA acetyltransferase, cytosolic)	19.65
G3IM20_CRIGR	Collagen alpha-1(III) chain	19.64
G3HCW9_CRIGR	PRDX2 (Peroxiredoxin-2)	19.63
G3HEQ3_CRIGR	Ran-specific GTPase-activating protein	19.63
G3HAP7_CRIGR	Glutathione synthetase (GSH-S) (EC 6.3.2.3)	19.62
G3HRN0_CRIGR	ATP synthase subunit beta (EC 7.1.2.2)	19.62
G3H2E2_CRIGR	HNRNPAB (Heterogeneous nuclear ribonucleoprotein A/B)	19.59
G3H412_CRIGR	Proliferating cell nuclear antigen	19.58
G3IKX2_CRIGR	Pigment epithelium-derived factor	19.58
G3GX17_CRIGR	Polypeptide N-acetylgalactosaminyltransferase (EC 2.4.1.-) (Protein-UDP	19.57

	acetylgalactosaminyltransferase)	
G3H284_CRIGR	Endoplasmic reticulum resident protein 29	19.55
G3H2P3_CRIGR	Beta-galactosidase (EC 3.2.1.23) (Fragment)	19.53
G3HFY9_CRIGR	Ubiquitin-conjugating enzyme E2 L3	19.53
G3H1U2_CRIGR	Heterogeneous nuclear ribonucleoprotein A3	19.52
G3HWJ2_CRIGR	Plectin-1	19.52
G3HEN3_CRIGR	Protein HIRA	19.51
G3I9X8_CRIGR	Spectrin alpha chain, brain	19.49
G3IL84_CRIGR	Oligoribonuclease, mitochondrial	19.48
G3HZE3_CRIGR	Exo-alpha-sialidase (EC 3.2.1.18)	19.47
G3IIE7_CRIGR	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	19.47
G3IHY5_CRIGR	6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	19.47
G3HG25_CRIGR	Laminin subunit gamma-1	19.46
G3ILF1_CRIGR	Glutathione S-transferase (EC 2.5.1.18)	19.46
G3H177_CRIGR	LMAN2 (Vesicular integral-membrane protein VIP36) (Vesicular integral-membrane protein VIP36-like protein)	19.46
G3HB04_CRIGR	Protein disulfide-isomerase A6	19.45
G3HDE5_CRIGR	Proteasome activator complex subunit 1	19.43
G3GTB7_CRIGR	Heterogeneous nuclear ribonucleoprotein Q	19.42
G3I973_CRIGR	Hypoxia up-regulated protein 1	19.42
G3HMY0_CRIGR	3-hydroxy-3-methylglutaryl coenzyme A synthase (HMG-CoA synthase) (EC 2.3.3.10)	19.40
G3HG83_CRIGR	T-complex protein 1 subunit gamma	19.37
G3HY03_CRIGR	D-dopachrome decarboxylase (DDT)	19.35
G3GVX2_CRIGR	Actin-depolymerizing factor (Destrin)	19.35
G3HAN8_CRIGR	Adenosylhomocysteinase (EC 3.3.1.1)	19.33
G3GUX9_CRIGR	Metalloendopeptidase (EC 3.4.24.-)	19.32
G3HQX0_CRIGR	40S ribosomal protein SA	19.30
G3HXN7_CRIGR	Beta-hexosaminidase (EC 3.2.1.52)	19.30
G3HC25_CRIGR	Protein S100-A13 (S100A13)	19.30
G3H3E3_CRIGR	CANT1 (Soluble calcium-activated nucleotidase 1)	19.30
G3IEE6_CRIGR	Spermidine synthase	19.29
G3HL18_CRIGR	Anionic trypsin-2	19.28
G3IKH3_CRIGR	Collagen alpha-2(V) chain	19.27
G3IKQ6_CRIGR	CSTB (Cystatin-B)	19.27
G3HUC4_CRIGR	Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1	19.27
G3H2T7_CRIGR	Histone H3	19.27
G3I1R2_CRIGR	Inosine phosphorylase (EC 2.4.2.1) (Inosine-guanosine phosphorylase) (Fragment)	19.26
G3HXL1_CRIGR	PCBP1 (Poly(RC)-binding protein 1)	19.26
G3I5R2_CRIGR	40S ribosomal protein S28	19.26
G3I4W7_CRIGR	Cathepsin D (EC 3.4.23.5)	19.25
G3HWC3_CRIGR	EZR (Ezrin)	19.24
G3HRK9_CRIGR	Matrix metalloproteinase-19	19.23
G3IBK2_CRIGR	Filamin-A	19.20
G3H7K5_CRIGR	CCT5 (T-complex protein 1 subunit epsilon)	19.19
G3HRP2_CRIGR	CNPY2 (Protein canopy-like 2)	19.16
G3I873_CRIGR	Ubiquitinyl hydrolase 1 (EC 3.4.19.12)	19.15
G3HC39_CRIGR	Farnesyl pyrophosphate synthetase	19.14

G3HS88_CRIGR	Ubiquitin-conjugating enzyme E2 N (Fragment)	19.13
G3I3H2_CRIGR	60S acidic ribosomal protein P2 (60S acidic ribosomal protein P2-like protein) (RPLP2)	19.13
G3H170_CRIGR	Drebrin	19.13
G3I737_CRIGR	40S ribosomal protein S12	19.11
G3HEY8_CRIGR	Nucleotide exchange factor SIL1	19.09
G3I952_CRIGR	EF-hand domain-containing protein D2	19.09
G3HHM2_CRIGR	Histone H3.1t	19.08
G3I5Z5_CRIGR	15-oxoprostaglandin 13-reductase (EC 1.3.1.48) (EC 1.3.1.74) (NADP-dependent leukotriene B4 12-hydroxydehydrogenase) (Prostaglandin reductase 1)	19.08
G3IBL4_CRIGR	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)	19.07
G3I6J4_CRIGR	ADP-ribosylation factor 3	19.06
G3IAW1_CRIGR	Golgi membrane protein 1	19.05
G3H604_CRIGR	Alpha-galactosidase (EC 3.2.1.-)	19.05
G3HCX3_CRIGR	Deoxyribonuclease II (EC 3.1.22.1)	19.05
G3HL13_CRIGR	60 kDa chaperonin (EC 5.6.1.7) (60 kDa heat shock protein, mitochondrial) (Chaperonin 60) (Heat shock protein 60)	19.04
G3GZA9_CRIGR	Reticulocalbin-1 (Fragment)	19.04
G3HTF0_CRIGR	N-sulphoglucosamine sulphohydrolase (SGSH)	19.03
G3HBI9_CRIGR	Leukotriene A-4 hydrolase	19.01
G3H5V0_CRIGR	Importin subunit beta-1	19.01
G3H6K1_CRIGR	Heterogeneous nuclear ribonucleoprotein G	19.00
G3I692_CRIGR	CNDP2 (Cytosolic non-specific dipeptidase)	19.00
G3I3V6_CRIGR	Discoidin, CUB and LCCL domain-containing protein 2	18.97
G3HDE3_CRIGR	Proteasome activator complex subunit 2	18.96
LDLR_CRIGR	Low-density lipoprotein receptor (LDL receptor)	18.95
G3HJ89_CRIGR	Clathrin heavy chain	18.95
G3GUI3_CRIGR	Peptidylprolyl isomerase (EC 5.2.1.8)	18.95
G3HK00_CRIGR	Guanine nucleotide-binding protein subunit beta-2-like 1	18.94
G3HKQ7_CRIGR	Microtubule-associated protein	18.94
G3HUI4_CRIGR	Lysosomal Pro-X carboxypeptidase (PRCP)	18.94
G3HNK4_CRIGR	Dihydropyrimidinase-related protein 2	18.92
G3H3B2_CRIGR	Cysteine-rich protein 2	18.90
G3HGY8_CRIGR	Elongation factor 1-alpha	18.89
G3HLD0_CRIGR	Lactoylglutathione lyase	18.88
G3I7J6_CRIGR	Non-POU domain-containing octamer-binding protein	18.88
G3GZB2_CRIGR	Acid ceramidase	18.88
G3I877_CRIGR	Stress-induced-phosphoprotein 1	18.87
G3H9Z4_CRIGR	Serine-threonine kinase receptor-associated protein	18.87
G3GZL3_CRIGR	RING-type E3 ubiquitin transferase (EC 2.3.2.27)	18.87
G3HPZ5_CRIGR	Macrophage-capping protein	18.86
G3H319_CRIGR	Tubulin-specific chaperone A	18.84
G3GRM2_CRIGR	Disintegrin and metalloproteinase domain-containing protein 10 (EC 3.4.24.81) (Kuzbanian protein homolog) (Mammalian disintegrin-metalloprotease)	18.84
G3H9U3_CRIGR	Splicing factor, proline-and glutamine-rich	18.83
G3GUP7_CRIGR	Ubiquitin carboxyl-terminal hydrolase (EC 3.4.19.12)	18.82
G3GYY2_CRIGR	Caprin-1	18.81
G3HN14_CRIGR	GPI ethanolamine phosphate transferase 3	18.81

G3I5Q9_CRIGR	Ras-related protein Rab-11B	18.80
G3HAQ2_CRIGR	Eukaryotic translation initiation factor 6 (eIF-6)	18.80
G3HX84_CRIGR	Actin-depolymerizing factor (Brevin) (Gelsolin)	18.77
G3H8K2_CRIGR	alpha-1,2-Mannosidase (EC 3.2.1.-)	18.76
G3IEG2_CRIGR	Serpin B6	18.75
G3HWU6_CRIGR	Ubiquilin-2	18.75
G3HXU0_CRIGR	Tubulin--tyrosine ligase-like protein 12	18.73
G3HY08_CRIGR	MIF (Macrophage migration inhibitory factor)	18.73
G3HW66_CRIGR	Multiple inositol polyphosphate phosphatase 1	18.73
G3HKP7_CRIGR	Protein shisa-5	18.73
G3GT05_CRIGR	T-complex protein 1 subunit theta	18.72
G3I073_CRIGR	Elongation factor 1-gamma	18.72
G3GS73_CRIGR	Heterogeneous nuclear ribonucleoprotein A3-like 1	18.72
G3H577_CRIGR	Ganglioside GM2 activator	18.70
G3HFP8_CRIGR	KDEL motif-containing protein 2	18.69
G3HN88_CRIGR	Adenylyl cyclase-associated protein	18.68
G3HRG8_CRIGR	Endoplasmic reticulum resident protein ERp44 (Fragment)	18.68
G3GY95_CRIGR	Eukaryotic translation initiation factor 5A-1	18.67
G3GYZ1_CRIGR	CD44 antigen (Extracellular matrix receptor III) (GP90 lymphocyte homing/adhesion receptor) (HUTCH-I) (Hermes antigen) (Hyaluronate receptor) (Phagocytic glycoprotein 1) (Phagocytic glycoprotein I)	18.67
G3GTX5_CRIGR	Amyloid-like protein 2	18.65
G3HJJ1_CRIGR	Ribose-5-phosphate isomerase (EC 5.3.1.6)	18.65
G3H1B3_CRIGR	Lamin-L(I)	18.63
G3HS71_CRIGR	Vasorin	18.63
G3H4D3_CRIGR	6-phosphogluconolactonase (6PGL) (EC 3.1.1.31)	18.62
G3I4N3_CRIGR	Lysine--tRNA ligase (EC 6.1.1.6) (Lysyl-tRNA synthetase)	18.61
G3HP71_CRIGR	Heterogeneous nuclear ribonucleoprotein H (Fragment)	18.61
G3HFI4_CRIGR	Protein FAM49A	18.60
G3HMG4_CRIGR	ABPP (Amyloid precursor protein) (Amyloid-beta A4 protein) (Amyloid-beta precursor protein) (Amyloid-beta protein 40) (Amyloid-beta protein 42) (Beta-APP40) (Beta-APP42) (Gamma-CTF(57)) (Gamma-CTF(59)) (Gamma-secretase C-terminal fragment 57) (Gamma-secretase C-terminal fragment 59) (Soluble APP-beta)	18.59
G3HM03_CRIGR	Synaptic vesicle membrane protein VAT-1-like	18.58
G3HKD6_CRIGR	Histone-binding protein RBBP7	18.56
G3H928_CRIGR	Nucleoside-diphosphate kinase (EC 2.7.4.6)	18.55
G3IN86_CRIGR	DPP7 (Dipeptidyl-peptidase 2)	18.54
G3IB32_CRIGR	Twinfilin-1	18.52
G3HRX0_CRIGR	Sorcin (Fragment)	18.52
G3IKQ5_CRIGR	Pyridoxal kinase (EC 2.7.1.35) (Pyridoxine kinase)	18.52
G3HUM5_CRIGR	Glucose-6-phosphate isomerase (EC 5.3.1.9)	18.52
G3I2B6_CRIGR	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform (Fragment)	18.52
G3IH84_CRIGR	ARSA (Arylsulfatase A)	18.51
G3I782_CRIGR	Heterogeneous nuclear ribonucleoprotein D0	18.51
G3HFJ1_CRIGR	m7GpppX diphosphatase (EC 3.6.1.59)	18.51
G3IJV7_CRIGR	Cytosolic acyl coenzyme A thioester hydrolase	18.50

G3HU51_CRIGR	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)	18.50
G3HQ98_CRIGR	Neuroserpin	18.49
G3HQM6_CRIGR	Endoplasmin	18.47
G3I2F5_CRIGR	Barrier-to-autointegration factor	18.47
G3I6H3_CRIGR	Splicing factor 1	18.46
G3HW48_CRIGR	DCTN2 (Dynactin subunit 2) (Dynactin subunit 2-like isoform 1)	18.45
G3I0I7_CRIGR	S-methyl-5'-thioadenosine phosphorylase (EC 2.4.2.28) (5'-methylthioadenosine phosphorylase) (MTA phosphorylase) (MTAP) (MTAPase)	18.44
G3HTG9_CRIGR	Glyoxalase domain-containing protein 4	18.44
G3HP89_CRIGR	GTP-binding nuclear protein Ran	18.44
G3HGP6_CRIGR	CCT-alpha (T-complex protein 1 subunit alpha)	18.44
G3H6Z4_CRIGR	Alpha-1,4 glucan phosphorylase (EC 2.4.1.1)	18.43
G3HID1_CRIGR	RAB7A (Ras-related protein Rab-7a)	18.43
G3HA23_CRIGR	Malate dehydrogenase (EC 1.1.1.37) (Fragment)	18.43
G3ICH9_CRIGR	Ataxin-10	18.42
G3H4A9_CRIGR	Mpv17-like protein 2	18.42
G3H697_CRIGR	Glucosidase 2 subunit beta (Glucosidase II subunit beta)	18.41
G3IKH9_CRIGR	Phosphohydroxythreonine aminotransferase (EC 2.6.1.52)	18.40
G3IHT7_CRIGR	Semaphorin-4B	18.36
G3H1W4_CRIGR	Tubulointerstitial nephritis antigen-like	18.33
G3H2K2_CRIGR	Cytochrome c, somatic	18.32
G3I2M1_CRIGR	T-complex protein 1 subunit zeta	18.32
G3H1D5_CRIGR	Carboxypeptidase (EC 3.4.16.-)	18.32
G3HCH0_CRIGR	MYDGF (UPF0556 protein C19orf10-like)	18.31
G3HLR7_CRIGR	Adenosine aminohydrolase (EC 3.5.4.4) (Adenosine deaminase)	18.30
G3HRK0_CRIGR	PA2G4 (Proliferation-associated protein 2G4)	18.30
G3HP75_CRIGR	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	18.29
G3H4I2_CRIGR	Tropomyosin alpha-1 chain-like protein (Tropomyosin beta chain)	18.29
G3IKI7_CRIGR	Keratin, type II cytoskeletal 2 oral	18.29
G3I7D7_CRIGR	RNA-binding protein FUS	18.28
G3IF62_CRIGR	Ras GTPase-activating-like protein IQGAP1	18.28
G3GWE9_CRIGR	Solute carrier family 2, facilitated glucose transporter member 9	18.28
G3HBX0_CRIGR	N-acetylglucosamine-1-phosphotransferase subunit gamma	18.28
G3HW12_CRIGR	Tyrosine-protein kinase (EC 2.7.10.2)	18.27
G3I2H6_CRIGR	Beta-1,4-glucuronyltransferase 1 (I-beta-1,3-N-acetylglucosaminyltransferase) (N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase) (Poly-N-acetyllactosamine extension enzyme) (UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1)	18.27
G3HDL6_CRIGR	Elongation factor 1-beta	18.27
G3IHC7_CRIGR	PRMT1 (Protein arginine N-methyltransferase 1)	18.26
G3IH36_CRIGR	Small ubiquitin-related modifier (SUMO)	18.25
G3H6E1_CRIGR	Eukaryotic translation initiation factor 3 subunit G (eIF3g) (Eukaryotic translation initiation factor 3 RNA-binding subunit) (eIF-3 RNA-binding subunit) (Eukaryotic translation initiation factor 3 subunit 4) (eIF-3-delta) (eIF3 p42) (eIF3 p44)	18.25
G3HH02_CRIGR	Uncharacterized protein C20orf135-like	18.25
G3I0M2_CRIGR	Platelet-activating factor acetylhydrolase IB subunit gamma	18.25
G3GUV4_CRIGR	Stromelysin-2	18.24

G3IBF4_CRIGR	Serine protease HTRA1	18.21
G3IFK8_CRIGR	MAM domain-containing protein 2	18.21
G3HS35_CRIGR	Beta-type platelet-derived growth factor receptor	18.19
G3ICC2_CRIGR	BAG family molecular chaperone regulator 3	18.19
G3GTX3_CRIGR	Suppressor of tumorigenicity 14 protein homolog (EC 3.4.21.109) (Serine protease 14)	18.18
G3H2Z7_CRIGR	26S proteasome non-ATPase regulatory subunit 4	18.16
G3I2M2_CRIGR	O-phosphoserine phosphohydrolase (EC 3.1.3.3) (Phosphoserine phosphatase)	18.13
G3GZD2_CRIGR	Phosphoglucomutase-1	18.13
G3HP03_CRIGR	RNA-binding protein EWS	18.11
G3IBY4_CRIGR	Plastin-3	18.10
G3HU28_CRIGR	F-actin-capping protein subunit beta	18.09
G3HW06_CRIGR	Adenylosuccinate lyase (ASL) (EC 4.3.2.2) (Adenylosuccinase)	18.08
G3H750_CRIGR	Calpain inhibitor (Calpastatin)	18.06
G3HQH7_CRIGR	Olfactomedin-like protein 3	18.06
G3I1J6_CRIGR	[Protein ADP-ribosylarginine] hydrolase	18.05
G3I8D0_CRIGR	Suppressor of G2 allele of SKP1-like	18.05
G3GYY6_CRIGR	Catalase (EC 1.11.1.6)	18.04
G3IIB1_CRIGR	Sialate O-acetylesterase	18.04
G3HUQ9_CRIGR	Dentin matrix protein 4	18.03
G3IDE4_CRIGR	Tripeptidyl-peptidase 1	18.03
G3HSM4_CRIGR	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	18.02
G3H9C9_CRIGR	Elongin-C	18.01
G3HR08_CRIGR	Cytosol aminopeptidase	18.01
G3H0T9_CRIGR	Huntingtin-interacting protein K	18.00
G3IID2_CRIGR	Complement C1q tumor necrosis factor-related protein 5	17.99
G3IBF7_CRIGR	E2 ubiquitin-conjugating enzyme (EC 2.3.2.23)	17.99
G3HDD4_CRIGR	NEDD8 (Neddylin) (Ubiquitin-like protein Nedd8)	17.98
G3H4Z5_CRIGR	C-1-tetrahydrofolate synthase, cytoplasmic (EC 1.5.1.5) (EC 3.5.4.9) (EC 6.3.4.3) (Formyltetrahydrofolate synthetase) (Methenyltetrahydrofolate cyclohydrolase) (Methylenetetrahydrofolate dehydrogenase)	17.97
G3IPD7_CRIGR	14-3-3 protein gamma	17.97
G3HV50_CRIGR	Prefoldin subunit 5	17.97
G3H6M5_CRIGR	Fumarate hydratase, mitochondrial (EC 4.2.1.2)	17.97
G3GZZ7_CRIGR	DNA-directed RNA polymerase subunit beta (EC 2.7.7.6)	17.95
G3HJA4_CRIGR	26S proteasome non-ATPase regulatory subunit 8	17.94
G3H2C9_CRIGR	S-phase kinase-associated protein 1	17.93
G3H2U4_CRIGR	BolA-like protein 1	17.93
G3IH63_CRIGR	Myosin-9	17.92
G3HE67_CRIGR	CREG1 (Protein CREG1)	17.92
G3HFM4_CRIGR	Filamin-B	17.89
G3HCK9_CRIGR	Far upstream element-binding protein 2	17.89
G3HR96_CRIGR	Bleomycin hydrolase (EC 3.4.22.40)	17.89
G3IE25_CRIGR	Clathrin light chain	17.88
G3HC84_CRIGR	Heat shock protein HSP 90-beta	17.86
G3HYB7_CRIGR	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta)	17.85
G3HQK5_CRIGR	UDP-N-acetylhexosamine pyrophosphorylase	17.84
G3HG78_CRIGR	Apolipoprotein A-I-binding protein	17.84

G3GVB5_CRIGR	Ras-related C3 botulinum toxin substrate 1	17.83
G3INL9_CRIGR	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2, 3-sialyltransferase	17.81
G3HXY1_CRIGR	PDZ and LIM domain protein 1	17.81
G3IFE7_CRIGR	Phosphoglucomutase-2	17.76
G3HMM0_CRIGR	Protein-tyrosine-phosphatase (EC 3.1.3.48)	17.76
G3HMU4_CRIGR	Chloride intracellular channel protein	17.76
G3HAJ9_CRIGR	Coiled-coil domain-containing protein 58	17.74
G3I437_CRIGR	Agrin	17.72
G3GTE4_CRIGR	Adapter protein GRB2 (Growth factor receptor-bound protein 2) (SH2/SH3 adapter GRB2)	17.68
G3GSH5_CRIGR	RNA helicase (EC 3.6.4.13)	17.68
G3ICM8_CRIGR	Hemoglobin subunit epsilon-Y2	17.67
G3I620_CRIGR	Aspartyl aminopeptidase (EC 3.4.11.21)	17.67
G3HE84_CRIGR	APC-binding protein EB1 (End-binding protein 1) (Microtubule-associated protein RP/EB family member 1)	17.66
G3HH37_CRIGR	CD109 antigen	17.65
G3HKV9_CRIGR	Group XV phospholipase A2 (PLA2G15)	17.64
G3HF46_CRIGR	Polypyrimidine tract-binding protein 1	17.64
G3GV64_CRIGR	Mammalian ependymin-related protein 1	17.64
G3I7A8_CRIGR	Proteasome subunit alpha type-5 (EC 3.4.25.1) (Fragment)	17.63
G3II02_CRIGR	Serine/threonine-protein phosphatase 2A activator (EC 5.2.1.8) (Phosphotyrosyl phosphatase activator) (Fragment)	17.62
G3I3W4_CRIGR	S-formylglutathione hydrolase (EC 3.1.2.12)	17.62
G3IKS9_CRIGR	Glutaredoxin-3	17.62
G3HKX2_CRIGR	NUTF2 (Nuclear transport factor 2)	17.62
G3IBV7_CRIGR	Cytochrome b5	17.62
G3IBF1_CRIGR	Nucleophosmin	17.61
G3HU10_CRIGR	Prefoldin subunit 2	17.61
G3H256_CRIGR	26S proteasome non-ATPase regulatory subunit 9 (26S proteasome regulatory subunit p27)	17.61
G3H8W5_CRIGR	6-phosphofructokinase (EC 2.7.1.11) (Phosphohexokinase)	17.61
G3GS70_CRIGR	Importin-5	17.58
G3HES3_CRIGR	Chromosome segregation 1-like protein (Exportin-2) (Importin-alpha re-exporter)	17.57
G3HCL3_CRIGR	TNFSF9 (Tumor necrosis factor ligand superfamily member 9)	17.57
G3I9P1_CRIGR	LDLR chaperone MESD (LRP chaperone MESD) (Mesoderm development candidate 2) (Mesoderm development protein)	17.56
G3H3S4_CRIGR	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	17.56
G3HLV6_CRIGR	ATP citrate synthase (EC 2.3.3.8)	17.56
G3H0D2_CRIGR	Reticulocalbin-2	17.55
G3GXB1_CRIGR	THO complex subunit 4	17.55
G3GRX4_CRIGR	Coactosin-like protein	17.53
G3GRT0_CRIGR	Adenine phosphoribosyltransferase (EC 2.4.2.7)	17.52
G3H576_CRIGR	Annexin	17.50
G3GVF0_CRIGR	Beta-1,3-N-acetylglucosaminyltransferase (EC 2.4.1.222) (O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase)	17.49
G3GX59_CRIGR	Putative sodium-coupled neutral amino acid transporter 10	17.48
G3HBH4_CRIGR	Low molecular weight cytosolic acid phosphatase (EC 3.1.3.2) (EC 3.1.3.48) (Low molecular weight phosphotyrosine protein phosphatase)	17.46

G3H7Y4_CRIGR	15 kDa phosphoprotein enriched in astrocytes (Astrocytic phosphoprotein PEA-15)	17.44
G3IF80_CRIGR	Nucleolin	17.44
G3H485_CRIGR	Coatomer subunit epsilon	17.44
G3HQ69_CRIGR	Src substrate cortactin	17.44
G3IG19_CRIGR	HD domain-containing protein 3	17.43
G3IGZ8_CRIGR	Torsin-1B	17.43
G3H8C9_CRIGR	Semaphorin-3B	17.42
G3HLW5_CRIGR	RAB5C (Ras-related protein Rab-5C)	17.41
G3HNY4_CRIGR	Phosphoglycerate kinase (EC 2.7.2.3)	17.39
G3IG23_CRIGR	Alanine--tRNA ligase (EC 6.1.1.7)	17.39
G3HJB1_CRIGR	Alpha-actinin-4	17.38
G3GWQ3_CRIGR	Adenosine kinase (EC 2.7.1.20)	17.37
G3HB42_CRIGR	Heme-binding protein 1	17.37
G3I9A3_CRIGR	Neudesin	17.37
G3I2F2_CRIGR	Splicing factor 3B subunit 2	17.36
G3HRP3_CRIGR	Citrate synthase	17.34
G3HL16_CRIGR	Splicing factor 3B subunit 1 (Splicing factor 3B subunit 1-like protein)	17.32
G3GX96_CRIGR	Actin-related protein 2/3 complex subunit 4	17.32
G3I2K8_CRIGR	RRM2 (Ribonucleoside-diphosphate reductase subunit M2)	17.32
G3HND9_CRIGR	Putative RNA-binding protein 3	17.31
G3GTH2_CRIGR	Na(+)/H(+) exchange regulatory cofactor NHE-RF	17.31
G3HIS0_CRIGR	26S proteasome non-ATPase regulatory subunit 6 (26S proteasome regulatory subunit RPN7)	17.31
G3HN89_CRIGR	Palmitoyl-protein hydrolase 1 (EC 3.1.2.22) (Palmitoyl-protein thioesterase 1)	17.29
G3HZC7_CRIGR	Lysosomal thioesterase PPT2	17.28
G3HRR5_CRIGR	ELAV-like protein	17.27
G3HTF5_CRIGR	Phosphatidylinositol transfer protein alpha isoform	17.27
G3HQL6_CRIGR	Thioredoxin reductase 1, cytoplasmic	17.26
G3GTC9_CRIGR	Phosphoacetylglucosamine mutase (PAGM) (EC 5.4.2.3) (Acetylglucosamine phosphomutase) (N-acetylglucosamine-phosphate mutase)	17.25
G3HQ86_CRIGR	BH3-interacting domain death agonist	17.24
G3IEX0_CRIGR	Procollagen-proline 3-dioxygenase (EC 1.14.11.7)	17.22
G3H1P3_CRIGR	Enhancer of rudimentary homolog	17.22
G3GVX1_CRIGR	Ribosome-binding protein 1	17.21
G3H2G5_CRIGR	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	17.21
G3HYJ9_CRIGR	Moesin	17.21
G3GRK8_CRIGR	HECT-type E3 ubiquitin transferase (EC 2.3.2.26)	17.20
G3I027_CRIGR	Heat shock protein 75 kDa, mitochondrial	17.19
G3IDU7_CRIGR	Beta-glucuronidase (EC 3.2.1.31)	17.17
G3I8H3_CRIGR	Putative myosin light chain kinase 3 (Vacuolar protein sorting-associated protein 35)	17.17
G3HGW7_CRIGR	40S ribosomal protein S21	17.17
G3H3D3_CRIGR	Branched-chain-amino-acid aminotransferase, cytosolic	17.17
G3HCX8_CRIGR	Calreticulin	17.17
G3GU76_CRIGR	60S acidic ribosomal protein P0	17.16
Q9JJN7_CRIGR	CBR3 (Carbonyl reductase) (EC 1.1.1.184) (Carbonyl reductase 3) (Carbonyl reductase [NADPH] 3)	17.16
G3ICL7_CRIGR	K(+) channel subunit beta-1 (Kv-beta-1) (Voltage-gated potassium channel subunit beta-	17.15

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G3I783_CRIGR	Heterogeneous nuclear ribonucleoprotein D-like	17.15
G3HWJ5_CRIGR	60 kDa poly(U)-binding-splicing factor (Poly(U)-binding-splicing factor PUF60)	17.14
G3H2N6_CRIGR	Programmed cell death 6-interacting protein	17.14
G3IFY1_CRIGR	Thymidylate synthase (EC 2.1.1.45)	17.12
G3H343_CRIGR	Sulfatase-modifying factor 1	17.12
G3HN76_CRIGR	Polyadenylate-binding protein 4	17.11
G3GVT2_CRIGR	Far upstream element-binding protein 1	17.11
G3I5H3_CRIGR	Elongation factor 1-delta	17.10
G3I837_CRIGR	Mannose-6-phosphate isomerase (EC 5.3.1.8)	17.09
G3H2C4_CRIGR	Heat shock 70 kDa protein 4 (Fragment)	17.09
G3GTC7_CRIGR	NADP-dependent malic enzyme (Fragment)	17.08
G3ILS7_CRIGR	26S proteasome non-ATPase regulatory subunit 5	17.07
G3I886_CRIGR	Multifunctional methyltransferase subunit TRM112-like protein (tRNA methyltransferase 112 homolog)	17.07
G3HC59_CRIGR	Disintegrin and metalloproteinase domain-containing protein 15	17.06
G3HR88_CRIGR	Integral membrane protein 2	17.06
G3ICD3_CRIGR	Lactadherin	17.06
G3H8D0_CRIGR	Guanine nucleotide-binding protein G(I), alpha-2 subunit	17.06
G3HX58_CRIGR	Leucine-rich repeat transmembrane protein FLRT3	17.06
G3HRF8_CRIGR	Activated leukocyte cell adhesion molecule (CD166 antigen)	17.05
G3IDS2_CRIGR	F-actin-capping protein subunit alpha	17.04
G3H133_CRIGR	Component 3 of promoter of RISC (Translin)	17.04
G3HYT5_CRIGR	2'-deoxynucleoside 5'-phosphate N-hydrolase 1 (EC 3.2.2.-) (c-Myc-responsive protein RCL)	17.03
G3H1Z4_CRIGR	DnaJ-like subfamily C member 8	17.03
G3GY52_CRIGR	Formylglycinamide ribonucleotide amidotransferase (EC 6.3.5.3) (Formylglycinamide ribotide amidotransferase)	17.02
G3HVZ2_CRIGR	Protocadherin Fat 1	17.02
G3IA94_CRIGR	MYL12B (Myosin regulatory light chain 12B)	17.01
G3HM98_CRIGR	Drebrin-like protein	17.01
G3II69_CRIGR	DNA damage-binding protein 1 (Damage-specific DNA-binding protein 1)	16.99
G3IL75_CRIGR	Collagen alpha-1(V) chain	16.99
G3I6W5_CRIGR	Prefoldin subunit 6	16.98
G3H7F9_CRIGR	Sialic acid synthase	16.97
G3HLX3_CRIGR	Alpha-N-acetylglucosaminidase	16.96
G3H609_CRIGR	Glutathione-disulfide reductase (EC 1.8.1.7)	16.95
G3HF18_CRIGR	Tudor domain-containing protein 12	16.94
G3I4I9_CRIGR	Major vault protein	16.94
G3HA24_CRIGR	Heat shock protein beta-1 (Fragment)	16.93
G3INU6_CRIGR	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	16.93
G3HJS0_CRIGR	Spectrin beta chain, brain 1	16.93
G3HU02_CRIGR	Olfactomedin-like protein 2B	16.91
G3H571_CRIGR	Histidine triad nucleotide-binding protein 1	16.91
G3HGQ1_CRIGR	Cation-independent mannose-6-phosphate receptor	16.90
G3H298_CRIGR	Serine/threonine-protein phosphatase (EC 3.1.3.16)	16.90
G3H8F9_CRIGR	Transforming protein RhoA	16.90

G3HUK8_CRIGR	NIF3-like protein 1	16.90
G3GZ85_CRIGR	Staphylococcal nuclease domain-containing protein (EC 3.1.31.1)	16.89
G3IMP5_CRIGR	N-myc downstream-regulated gene 1 protein (Protein NDRG1)	16.89
G3HBR8_CRIGR	Hemoglobin subunit alpha	16.88
G3HIT7_CRIGR	Microtubule-associated protein 1B	16.88
G3H945_CRIGR	Eukaryotic translation initiation factor 3 subunit I (eIF3i) (Eukaryotic translation initiation factor 3 subunit 2) (eIF-3-beta) (eIF3 p36)	16.88
G3GR63_CRIGR	Inter-alpha-trypsin inhibitor heavy chain H2	16.87
G3H354_CRIGR	Heat shock protein HSP 90-alpha	16.87
G3GRH9_CRIGR	Tropomodulin-3	16.87
G3I2E9_CRIGR	Ras-related protein Rab-1B	16.87
G3H3W4_CRIGR	Insulin-degrading enzyme	16.87
G3H585_CRIGR	ATOX1 (Copper transport protein ATOX1)	16.87
G3I519_CRIGR	LXN (Latexin)	16.86
G3HJB6_CRIGR	Ras and Rab interactor-like protein	16.86
G3GVP7_CRIGR	ADP-sugar pyrophosphatase	16.85
G3HLZ2_CRIGR	Proteasome activator complex subunit 3	16.85
G3IHJ6_CRIGR	Gc-globulin (Group-specific component) (Vitamin D-binding protein)	16.85
G3I9F1_CRIGR	Ras GTPase-activating protein-binding protein 2	16.85
G3GYJ1_CRIGR	Rho GTPase-activating protein 1	16.84
G3HJB0_CRIGR	Alpha-actinin-4 (Fragment)	16.84
G3HBY2_CRIGR	HN1L (Hematological and neurological expressed 1-like protein)	16.83
G3HCL2_CRIGR	Tubulin beta chain	16.83
G3IFA9_CRIGR	Transcription elongation factor B polypeptide 2	16.81
G3HV39_CRIGR	Poly(RC)-binding protein 2	16.80
G3H748_CRIGR	Aminopeptidase (EC 3.4.11.-)	16.80
G3H3X1_CRIGR	Apoptosis-inducing factor 1 (EC 1.-.-.-) (Apoptosis-inducing factor 1, mitochondrial)	16.78
G3IJB9_CRIGR	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	16.78
G3IAG0_CRIGR	Xaa-Pro aminopeptidase 1	16.77
G3HQN3_CRIGR	H-2 class I histocompatibility antigen, D-D alpha chain	16.77
G3HN65_CRIGR	Ras suppressor protein 1	16.76
G3H9W6_CRIGR	Trafficking protein particle complex subunit	16.76
G3GX92_CRIGR	CAMK1 (Calcium/calmodulin-dependent protein kinase type 1)	16.75
Q9ERF7_CRIGR	Intercellular adhesion molecule 1 (Intracellular adhesion molecule 1)	16.75
G3HH63_CRIGR	Phospholipase A-2-activating protein	16.74
G3HFZ9_CRIGR	CRKL (Crk-like protein)	16.73
G3IMD1_CRIGR	S-(hydroxymethyl)glutathione dehydrogenase (EC 1.1.1.284)	16.73
G3I1R6_CRIGR	RNase 1 (EC 4.6.1.18) (RNase A) (Ribonuclease pancreatic)	16.72
G3IIH3_CRIGR	Eukaryotic translation initiation factor 4E	16.71
IMDH2_CRIGR	Inosine-5'-monophosphate dehydrogenase 2 (IMP dehydrogenase 2) (IMPD 2) (IMPDH 2) (EC 1.1.1.205) (IMPDH-II)	16.71
G3HDR3_CRIGR	T-complex protein 1 subunit delta	16.69
G3H8Y4_CRIGR	Collagen alpha-2(VI) chain	16.69
G3GRS9_CRIGR	Chondroitinsulfatase (EC 3.1.6.4) (Galactose-6-sulfate sulfatase) (N-acetylgalactosamine-6-sulfatase) (N-acetylgalactosamine-6-sulfate sulfatase)	16.68
G3H204_CRIGR	Syntaxin-12	16.68
G3HY23_CRIGR	Small nuclear ribonucleoprotein Sm D3	16.67

G3H1N2_CRIGR	Cytochrome c oxidase assembly protein COX16 homolog, mitochondrial	16.66
G3I436_CRIGR	Ubiquitin cross-reactive protein (Ubiquitin-like protein ISG15-like protein)	16.65
G3H9Y7_CRIGR	NudC domain-containing protein 2	16.65
G3HN02_CRIGR	Talin-1	16.64
G3HR95_CRIGR	Carboxypeptidase D (EC 3.4.17.22) (Metallocarboxypeptidase D)	16.64
G3H8A8_CRIGR	Mesencephalic astrocyte-derived neurotrophic factor	16.63
G3H892_CRIGR	N-acyl-L-amino-acid amidohydrolase (EC 3.5.1.14)	16.63
G3IJ02_CRIGR	Leucine-rich repeat flightless-interacting protein 1	16.62
G3I5W2_CRIGR	TAR DNA-binding protein 43	16.62
G3GZR1_CRIGR	Aspartate--tRNA ligase, cytoplasmic (EC 6.1.1.12) (Aspartyl-tRNA synthetase)	16.62
G3IFQ8_CRIGR	15 kDa selenoprotein	16.61
G3HIX6_CRIGR	T1-TrpRS (EC 6.1.1.2) (T2-TrpRS) (Tryptophan--tRNA ligase, cytoplasmic) (Tryptophanyl-tRNA synthetase)	16.61
G3GWT7_CRIGR	Guanine nucleotide-binding protein G(S) subunit alpha isoforms XLas	16.61
G3HJ24_CRIGR	Procollagen-proline 4-dioxygenase (EC 1.14.11.2)	16.61
G3H5N5_CRIGR	UDP-glucuronate decarboxylase 1 (EC 4.1.1.35) (UDP-glucuronic acid decarboxylase 1)	16.60
G3HE03_CRIGR	FHL3 (Four and a half LIM domains protein 3)	16.60
G3HDQ1_CRIGR	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	16.59
G3I2G7_CRIGR	EGF-containing fibulin-like extracellular matrix protein 2	16.59
G3I9W7_CRIGR	Ras-related protein Rab-6A (Fragment)	16.58
G3IMV1_CRIGR	40S ribosomal protein S6	16.56
G3GT56_CRIGR	Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (Glycinamide ribonucleotide synthetase) (GARS) (Phosphoribosylglycinamide synthetase); Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) (AIR synthase) (AIRS) (Phosphoribosyl-aminoimidazole synthetase); Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) (5'-phosphoribosylglycinamide transformylase) (GAR transformylase) (GART)]	16.55
G3GVR5_CRIGR	Cerebral dopamine neurotrophic factor	16.55
G3H6C5_CRIGR	Hsp90 chaperone protein kinase-targeting subunit (Hsp90 co-chaperone Cdc37) (p50Cdc37)	16.55
G3H4V1_CRIGR	Septin-2	16.54
G3HBR6_CRIGR	Phosphoglycolate phosphatase	16.53
G3I1X8_CRIGR	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	16.53
G3I5H1_CRIGR	Glutathione transferase (EC 2.5.1.18)	16.52
G3I581_CRIGR	Prefoldin subunit 1	16.52
G3IC91_CRIGR	von Willebrand factor A domain-containing protein 5A	16.50
G3GSK4_CRIGR	Non-specific serine/threonine protein kinase (EC 2.7.11.1)	16.50
G3HGW5_CRIGR	ADRM1 (Proteasomal ubiquitin receptor ADRM1)	16.49
G3IIA1_CRIGR	Methylosome protein 50 (Fragment)	16.48
G3HYP6_CRIGR	Nuclear distribution protein C homolog (Nuclear migration protein nudC)	16.48
G3I740_CRIGR	Pantetheinase	16.48
G3IHB4_CRIGR	Endothelial differentiation-related factor 1	16.47
G3I2N4_CRIGR	Lamina-associated polypeptide 2, isoforms alpha/zeta	16.47
G3HF76_CRIGR	DAZ-associated protein 1	16.47
OFUT1_CRIGR	GDP-fucose protein O-fucosyltransferase 1 (EC 2.4.1.221) (Peptide-O-fucosyltransferase 1) (O-FucT-1)	16.46
G3ID62_CRIGR	EXTL2 (Exostosin-like 2)	16.46
G3HEJ5_CRIGR	ADP-dependent glucokinase	16.46

G3I7Q5_CRIGR	Zinc finger protein ZPR1	16.46
G3GZY4_CRIGR	Lysyl oxidase homolog (EC 1.4.3.13)	16.45
G3HUI7_CRIGR	Protein ERGIC-53	16.44
G3H3I2_CRIGR	Importin-9	16.44
G3H092_CRIGR	Coiled-coil domain-containing protein 80	16.43
G3GVA0_CRIGR	Golgin subfamily A member 4	16.43
G3HCL6_CRIGR	C3-beta-c (C3a anaphylatoxin) (Complement C3) (Complement C3 alpha chain) (Complement C3 beta chain) (Complement C3b alpha' chain) (Complement C3c alpha' chain fragment 1) (Complement C3c alpha' chain fragment 2) (Complement C3d fragment) (Complement C3dg fragment) (Complement C3f fragment) (Complement C3g fragment)	16.42
G3HSZ6_CRIGR	Aldose 1-epimerase (EC 5.1.3.3)	16.42
G3HN31_CRIGR	Semaphorin-3E	16.40
G3H2G1_CRIGR	Layilin	16.40
G3GRT8_CRIGR	Diphosphomevalonate decarboxylase (EC 4.1.1.33)	16.39
G3HSA7_CRIGR	Thioredoxin domain-containing protein 17	16.38
G3HAP1_CRIGR	Microtubule-associated proteins 1A/1B light chain 3A	16.37
G3HWE9_CRIGR	Tubulin alpha chain	16.37
G3HW36_CRIGR	Serine hydroxymethyltransferase (EC 2.1.2.1)	16.37
G3H8G0_CRIGR	Glutathione peroxidase	16.37
G3HBZ8_CRIGR	Ubiquitin-associated protein 2-like	16.36
G3H3H9_CRIGR	Aminopeptidase B	16.36
G3H7M3_CRIGR	Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	16.36
G3H894_CRIGR	ABHD14B (Abhydrolase domain-containing protein 14B)	16.36
G3IAI6_CRIGR	Heme oxygenase (EC 1.14.14.18)	16.34
G3H2S5_CRIGR	RNA-binding protein 8A	16.33
G3GV81_CRIGR	Glycerol-3-phosphate dehydrogenase [NAD(+)] (EC 1.1.1.8)	16.33
G3HV83_CRIGR	Prefoldin subunit 3	16.33
G3H5G6_CRIGR	Thioredoxin-like protein 1	16.32
G3HQY6_CRIGR	Lipase	16.31
G3HWP9_CRIGR	Heterogeneous nuclear ribonucleoprotein C-like 1-like isoform 5 (Heterogeneous nuclear ribonucleoproteins C1/C2)	16.31
G3GUB4_CRIGR	Histone acetyltransferase type B catalytic subunit	16.30
G3HMA7_CRIGR	Synaptobrevin-like YKT6	16.29
G3I958_CRIGR	Protein DDI1-like 2	16.29
G3HI29_CRIGR	Ceroid-lipofuscinosis neuronal protein 5	16.27
G3IPK2_CRIGR	Protein FAM49B	16.26
G3II12_CRIGR	Calcium-binding protein 39	16.26
G3HZG6_CRIGR	BCL2-associated athanogene 6 (HLA-B-associated transcript 3) (Large proline-rich protein BAG6)	16.25
G3GWF3_CRIGR	Beta-1,3-glucosyltransferase	16.24
G3I8P7_CRIGR	N-acetylglucosamine-6-sulfatase (EC 3.1.6.14) (Glucosamine-6-sulfatase)	16.23
G3HDQ9_CRIGR	Hexosyltransferase (EC 2.4.1.-)	16.21
G3GYC6_CRIGR	Profilin-1	16.20
G3GZG1_CRIGR	Toll-like receptor 9 (Fragment)	16.20
G3GT45_CRIGR	Interferon-alpha/beta receptor beta chain	16.20
G3H3G9_CRIGR	Septin-9	16.19

G3H3I9_CRIGR	Cysteine and glycine-rich protein 1	16.18
G3H1I6_CRIGR	U6 snRNA-associated Sm-like protein LSm1	16.16
G3HFY6_CRIGR	Stromal cell-derived factor 2-like protein 1	16.15
G3HYG7_CRIGR	DnaJ-like subfamily B member 11	16.13
G3H843_CRIGR	TSC22 domain family protein 1	16.13
G3IMZ0_CRIGR	Very low-density lipoprotein receptor	16.13
G3H8M2_CRIGR	Protein quaking (Fragment)	16.13
G3HLU1_CRIGR	Ubiquitin-conjugating enzyme E2 C	16.12
G3H953_CRIGR	KH domain-containing, RNA-binding, signal transduction-associated protein 1	16.09
G3HWY2_CRIGR	Exostosin-2	16.08
G3HEB6_CRIGR	TGF-beta receptor type III	16.08
G3I220_CRIGR	Cytoskeleton-associated protein 4	16.08
G3H7M8_CRIGR	Heterogeneous nuclear ribonucleoprotein U	16.07
G3GWR8_CRIGR	Proteasome endopeptidase complex (EC 3.4.25.1) (Fragment)	16.07
G3HWJ6_CRIGR	Poly(U)-binding-splicing factor PUF60	16.05
G3I7E2_CRIGR	Non-specific protein-tyrosine kinase (EC 2.7.10.2)	16.05
G3H2U6_CRIGR	Splicing factor 3B subunit 4 (Splicing factor 3B subunit 4-like protein)	16.05
G3GRG8_CRIGR	Ras GTPase-activating protein-binding protein 1	16.05
G3HLT3_CRIGR	Syndecan	16.04
G3H4X1_CRIGR	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	16.03
G3IHR6_CRIGR	Macrophage colony-stimulating factor 1 (CSF-1) (MCSF)	16.02
G3H2P1_CRIGR	NF-kappa-B inhibitor-like protein 2 (Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 2)	16.01
G3HPT8_CRIGR	Suprabasin	16.01
G3I683_CRIGR	Plasminogen activator inhibitor 1 RNA-binding protein	15.98
G3HB86_CRIGR	Chemerin (Retinoic acid receptor responder protein 2)	15.96
G3GUK0_CRIGR	Putative fructose-2,6-bisphosphatase TIGAR	15.96
G3I7E1_CRIGR	Contactin-1	15.96
G3INX6_CRIGR	Spliceosome RNA helicase BAT1	15.95
G3HPR6_CRIGR	Tubulin-folding cofactor B	15.95
Q2MH30_CRIGR	Dihydrofolate reductase (EC 1.5.1.3)	15.95
G3H1W2_CRIGR	PEF1 (Peflin)	15.94
G3I784_CRIGR	Enolase-phosphatase E1 (EC 3.1.3.77) (2,3-diketo-5-methylthio-1-phosphopentane phosphatase) (MASA homolog)	15.94
G3HP80_CRIGR	SEC22B (Vesicle-trafficking protein SEC22b)	15.93
G3HPE9_CRIGR	Echinoderm microtubule-associated protein-like 2	15.93
G3I7D8_CRIGR	Apoptosis-associated speck-like protein containing a CARD	15.91
G3HRT6_CRIGR	Solute carrier family 12 member 1	15.91
G3H1H6_CRIGR	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	15.90
G3GWF4_CRIGR	Heat shock protein 105 kDa (Fragment)	15.90
G3GVQ8_CRIGR	Selenide, water dikinase (EC 2.7.9.3)	15.90
G3H853_CRIGR	cAMP-dependent protein kinase type I-alpha regulatory subunit	15.90
G3IPB7_CRIGR	Golgi SNAP receptor complex member 2	15.90
G3HIM4_CRIGR	Cell division control protein 42 homolog (EC 3.6.5.2)	15.89
G3HAR2_CRIGR	CPNE1 (Copine-1)	15.88
G3GXT2_CRIGR	Aspartate carbamoyltransferase (EC 2.1.3.2) (EC 3.5.2.3) (EC 6.3.5.5) (CAD protein) (Dihydroorotase) (Glutamine-dependent carbamoyl-phosphate synthase)	15.87

G3HY75_CRIGR	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B	15.87
G3I4E6_CRIGR	Inositol-1-monophosphatase (EC 3.1.3.25)	15.86
G3HW57_CRIGR	Cell division protein kinase 4	15.85
G3HMV3_CRIGR	Acyl-protein thioesterase 2	15.83
G3IEK1_CRIGR	Arp2/3 complex 34 kDa subunit	15.83
G3IFX0_CRIGR	Programmed cell death protein 6	15.83
G3IH47_CRIGR	Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit delta	15.82
G3GVM9_CRIGR	Calcium-regulated heat stable protein 1	15.81
G3HNG2_CRIGR	Acyl-coenzyme A thioesterase 2, mitochondrial	15.80
G3ID68_CRIGR	Selenoprotein P	15.80
G3HNP6_CRIGR	26S proteasome AAA-ATPase subunit RPT3 (26S proteasome regulatory subunit 6B) (Proteasome 26S subunit ATPase 4) (Fragment)	15.79
G3H5Z0_CRIGR	Sushi repeat-containing protein SRPX2	15.78
G3GXW5_CRIGR	N-myc downstream-regulated gene 3 protein (Protein NDRG3)	15.78
G3I6V9_CRIGR	Protein CutA	15.77
G3HGI4_CRIGR	Hypoxanthine-guanine phosphoribosyltransferase	15.77
G3I8H9_CRIGR	Cysteine and histidine-rich domain-containing protein 1	15.77
G3H4W0_CRIGR	dTMP kinase (EC 2.7.4.9)	15.76
G3I142_CRIGR	Splicing factor 3 subunit 1 (Splicing factor 3A subunit 1 isoform 1)	15.76
G3H1G7_CRIGR	Pyridoxal phosphate homeostasis protein (PLP homeostasis protein) (Proline synthase co-transcribed bacterial homolog protein)	15.75
G3HK39_CRIGR	Carboxypeptidase Q (Plasma glutamate carboxypeptidase)	15.75
G3GTS6_CRIGR	26S proteasome non-ATPase regulatory subunit 11	15.74
G3HVP7_CRIGR	NHL repeat-containing protein 3 (NHLRC3)	15.74
G3HXR8_CRIGR	Phosphatidylinositol-binding clathrin assembly protein	15.74
G3HSM8_CRIGR	Lamin-B2	15.74
G3GX55_CRIGR	Brain-specific angiogenesis inhibitor 1-associated protein 2	15.73
G3HMN4_CRIGR	Omega-amidase NIT2	15.72
G3I0S4_CRIGR	Protocadherin-7	15.72
G3HC56_CRIGR	EFNA1 (Ephrin-A1)	15.71
G3H5Z5_CRIGR	Cleavage stimulation factor 64 kDa subunit	15.71
G3H638_CRIGR	AHSA1 (Activator of 90 kDa heat shock protein ATPase-like 1)	15.71
G3I4B9_CRIGR	Mps one binder kinase activator-like 1A	15.71
G3I638_CRIGR	Eukaryotic translation initiation factor 3 subunit F (eIF3f) (Eukaryotic translation initiation factor 3 subunit 5) (eIF-3-epsilon) (eIF3 p47)	15.71
G3GRE1_CRIGR	Prolyl-tRNA synthetase (EC 6.1.1.15) (Fragment)	15.70
G3HMI5_CRIGR	Di-N-acetylchitobiase	15.69
G3HU24_CRIGR	Aflatoxin B1 aldehyde reductase member 2 (EC 1.1.1.n11)	15.69
G3H9Z5_CRIGR	Epidermal growth factor receptor kinase substrate 8	15.68
G3I4G0_CRIGR	EH domain-containing protein 3	15.68
G3HE59_CRIGR	TIP41-like protein	15.66
G3I3Z1_CRIGR	AH receptor-interacting protein (Aryl-hydrocarbon receptor-interacting protein)	15.65
G3HEE8_CRIGR	Alpha-L-iduronidase	15.65
G3I5V6_CRIGR	Mitotic checkpoint protein BUB3	15.65
G3H7L5_CRIGR	Protein-tyrosine-phosphatase (EC 3.1.3.48) (Fragment)	15.63
G3I6B8_CRIGR	Coatomer subunit zeta	15.62
G3HCI6_CRIGR	Receptor-type tyrosine-protein phosphatase S	15.62

G3HTU8_CRIGR	Galactokinase	15.60
G3I3A8_CRIGR	Nuclear mitotic apparatus protein 1	15.60
G3H6F2_CRIGR	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	15.59
G3IQ91_CRIGR	Vesicle-fusing ATPase (EC 3.6.4.6)	15.59
G3HAE2_CRIGR	ATP synthase subunit alpha, mitochondrial	15.58
G3I366_CRIGR	Post-proline cleaving enzyme (EC 3.4.21.26) (Prolyl endopeptidase)	15.58
G3I2Q7_CRIGR	Transcription intermediary factor 1-beta	15.57
G3HNV5_CRIGR	U6 snRNA-associated Sm-like protein LSm8	15.57
G3HQ75_CRIGR	Murinoglobulin-1	15.56
G3H0B5_CRIGR	Isocitrate dehydrogenase [NAD] subunit, mitochondrial	15.55
G3ILI6_CRIGR	26S proteasome non-ATPase regulatory subunit 3	15.55
G3HV18_CRIGR	60S ribosomal protein L12	15.55
G3GTN1_CRIGR	Protein mago nashi-like	15.54
G3HJM2_CRIGR	Glycine--tRNA ligase	15.53
G3GWM7_CRIGR	Calcineurin-like phosphoesterase domain-containing protein 1 (EC 3.1.3.16) (Serine/threonine-protein phosphatase CPPED1)	15.53
G3IL43_CRIGR	Glucosamine-6-phosphate isomerase (EC 3.5.99.6) (Glucosamine-6-phosphate deaminase)	15.53
G3GZE6_CRIGR	Actin-related protein 3	15.52
G3GUA5_CRIGR	Golgi reassembly-stacking protein 2	15.50
G3HNR0_CRIGR	Flavin reductase	15.50
G3I5L5_CRIGR	Retinal dehydrogenase 1	15.48
G3HNJ6_CRIGR	60S ribosomal protein L5	15.48
G3I505_CRIGR	Eukaryotic translation initiation factor 3 subunit L (eIF3l) (Eukaryotic translation initiation factor 3 subunit 6-interacting protein) (Eukaryotic translation initiation factor 3 subunit E-interacting protein)	15.48
G3HCS4_CRIGR	26S proteasome non-ATPase regulatory subunit 12	15.47
G3HFG7_CRIGR	Putative hydroxypyruvate isomerase	15.47
G3GSM5_CRIGR	Transferrin receptor protein 1	15.46
G3I7X7_CRIGR	Carboxylic ester hydrolase (EC 3.1.1.-)	15.46
G3GYK8_CRIGR	26S protease regulatory subunit 6A	15.45
G3HQ88_CRIGR	Bcl-2-like protein 13	15.41
G3GUQ4_CRIGR	Protein C10	15.41
G3HLW9_CRIGR	Signal transducer and activator of transcription	15.40
G3HQ97_CRIGR	Golgi integral membrane protein 4	15.38
G3H5W0_CRIGR	Proteasome subunit beta (EC 3.4.25.1)	15.37
G3HZV0_CRIGR	Ribosomal protein	15.37
G3H6T8_CRIGR	Vacuolar protein sorting-associated protein 26A	15.34
G3HFP1_CRIGR	Radixin	15.33
Q9Z2J2_CRIGR	DNA-(apurinic or apyrimidinic site) endonuclease (EC 3.1.-.-)	15.32
G3GZ09_CRIGR	PSMG4 (Proteasome assembly chaperone 4)	15.32
G3I3H9_CRIGR	Chitinase domain-containing protein 1	15.31
G3I5S7_CRIGR	Coatomer subunit delta	15.30
G3H453_CRIGR	Small nuclear ribonucleoprotein-associated protein	15.30
G3HYU7_CRIGR	Exportin-5	15.29
G3I1P0_CRIGR	Isochorismatase domain-containing protein 1	15.29
G3HU11_CRIGR	Nitrilase-like 1 (Putative nitrilase-like protein) (EC 3.5.-.-)	15.29

G3HR10_CRIGR	Dihydropteridine reductase (Dihydropteridine reductase-like protein) (EC 1.5.1.34)	15.28
G3GXB5_CRIGR	Ethanolamine-phosphate cytidylyltransferase	15.28
G3H4V0_CRIGR	Vigilin	15.26
G3I595_CRIGR	Histidine--tRNA ligase (EC 6.1.1.21)	15.25
G3ILX2_CRIGR	26S proteasome non-ATPase regulatory subunit 13 (26S proteasome regulatory subunit RPN9) (26S proteasome regulatory subunit S11) (26S proteasome regulatory subunit p40.5)	15.24
G3I303_CRIGR	DNA-directed RNA polymerases I, II, and III subunit RPABC3	15.23
G3I0Z2_CRIGR	Alpha-soluble NSF attachment protein	15.20
G3HRD3_CRIGR	Protein arginine N-methyltransferase 5 (EC 2.1.1.-)	15.20
G3H5A7_CRIGR	Tight junction protein ZO-1	15.20
G3HUE5_CRIGR	PBDC1 (UPF0368 protein Cxorf26-like)	15.20
G3I863_CRIGR	Receptor protein-tyrosine kinase (EC 2.7.10.1)	15.19
G3I7M1_CRIGR	Ataxin-2-like protein	15.19
G3I2L9_CRIGR	Sulfatase-modifying factor 2	15.19
G3H168_CRIGR	PDZ and LIM domain protein 7	15.19
G3HX83_CRIGR	Ras-related protein Rab-14	15.18
G3I308_CRIGR	26S proteasome non-ATPase regulatory subunit 2	15.18
G3IKQ9_CRIGR	Osteopontin	15.17
G3I3J1_CRIGR	Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4) (Glutamine-dependent asparagine synthetase)	15.17
G3I3Z5_CRIGR	Coronin	15.17
G3II47_CRIGR	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.-)	15.16
G3IHB0_CRIGR	14 kDa phosphohistidine phosphatase (EC 3.9.1.3) (Phosphohistidine phosphatase 1) (Protein histidine phosphatase)	15.13
G3H938_CRIGR	Protein archease	15.10
G3HRX5_CRIGR	Protein DBF4-like A	15.09
G3GUS2_CRIGR	ADP-ribosylation factor 4	15.09
G3HC77_CRIGR	Cell division cycle 5-related protein	15.09
G3HEH6_CRIGR	UBL7 (Ubiquitin-like protein 7)	15.08
G3HD67_CRIGR	Ribose-phosphate diphosphokinase (EC 2.7.6.1)	15.08
G3HF56_CRIGR	Calponin	15.08
G3H416_CRIGR	Major prion protein	15.07
G3HCW3_CRIGR	ATPase ASNA1 (EC 3.6.-.-) (Arsenical pump-driving ATPase) (Arsenite-stimulated ATPase)	15.07
G3HIB0_CRIGR	Cyclin-dependent kinases regulatory subunit	15.05
G3I2K6_CRIGR	HPCAL1 (Hippocalcin-like protein 1)	15.04
G3HDG6_CRIGR	Paraspeckle component 1	15.02
G3H7U0_CRIGR	3-hydroxyacyl-CoA dehydrogenase type-2 (3-hydroxyacyl-CoA dehydrogenase type-2-like protein) (EC 1.1.1.35)	15.02
G3HMP0_CRIGR	Protein TFG	15.01
G3H0F1_CRIGR	Alpha-mannosidase (EC 3.2.1.24)	15.00
G3GX75_CRIGR	Hepatocyte growth factor-regulated tyrosine kinase substrate	14.99
G3II57_CRIGR	Leucine carboxyl methyltransferase 1 (EC 2.1.1.233)	14.98
G3GWP2_CRIGR	Alpha-(1,3)-fucosyltransferase (EC 2.4.1.-)	14.97
G3IEG3_CRIGR	Ribosyldihydronicotinamide dehydrogenase [quinone]	14.95
G3GWC4_CRIGR	GrpE protein homolog	14.94
G3H194_CRIGR	Clathrin light chain (Fragment)	14.94

G3HRM8_CRIGR	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	14.93
G3HAA1_CRIGR	Heterogeneous nuclear ribonucleoprotein H3	14.92
G3HIK1_CRIGR	Nuclear pore complex protein Nup93	14.92
G3HLX0_CRIGR	Polymerase I and transcript release factor	14.92
G3II56_CRIGR	Actin-related protein 2	14.92
G3H4X0_CRIGR	LanC-like protein 1 (Fragment)	14.92
G3GZQ9_CRIGR	DNA helicase (EC 3.6.4.12)	14.91
G3IEX5_CRIGR	PPCS (Phosphopantothenate--cysteine ligase)	14.89
G3GW47_CRIGR	Arginine--tRNA ligase, cytoplasmic (EC 6.1.1.19) (Arginyl-tRNA synthetase)	14.88
G3IMT0_CRIGR	Thioredoxin, mitochondrial	14.88
G3GU92_CRIGR	Lupus La protein-like	14.87
G3HHY9_CRIGR	V-type proton ATPase subunit G	14.87
G3HR63_CRIGR	Protein canopy-like 3	14.87
G3HCF8_CRIGR	Endophilin-A2	14.87
G3HFN7_CRIGR	Pyridoxal-dependent decarboxylase domain-containing protein 1 (EC 4.1.1.-)	14.86
G3IL63_CRIGR	Caspase-7	14.86
G3HC68_CRIGR	SHC-transforming protein 1 (Src homology 2 domain-containing-transforming protein C1)	14.85
SYSC_CRIGR	Serine--tRNA ligase, cytoplasmic (EC 6.1.1.11) (Seryl-tRNA synthetase) (SerRS) (Seryl-tRNA(Ser/Sec) synthetase)	14.84
G3HCI0_CRIGR	Perilipin	14.81
G3H497_CRIGR	Inositol-3-phosphate synthase 1 (EC 5.5.1.4)	14.78
G3GXC5_CRIGR	Tether containing UBX domain for GLUT4	14.77
G3H902_CRIGR	Prostaglandin F2 receptor negative regulator	14.73
G3ICB9_CRIGR	Nucleolysin TIAR	14.73
G3I7L6_CRIGR	Desmocollin-1	14.73
G3ICW1_CRIGR	Osteoclast-stimulating factor 1 (Osteoclast-stimulating factor 1-like protein)	14.73
G3IKW4_CRIGR	GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase (EC 1.1.1.271)	14.70
G3IEA9_CRIGR	Far upstream element-binding protein 3	14.70
G3I887_CRIGR	Peroxiredoxin-5 (EC 1.11.1.24)	14.69
G3HRI3_CRIGR	Mitochondrial import inner membrane translocase subunit Tim10 (TIMM10)	14.69
G3HR69_CRIGR	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit	14.66
G3IB69_CRIGR	Laminin subunit beta-2	14.66
G3GUG5_CRIGR	NHL repeat-containing protein 1	14.65
G3I2J3_CRIGR	Chromobox protein-like 6 (Fragment)	14.62
G3H4J6_CRIGR	Sec1 family domain-containing protein 1	14.61
G3IAS6_CRIGR	Ubiquilin-1	14.61
G3HCU8_CRIGR	26S protease regulatory subunit 8	14.60
G3HMA9_CRIGR	NudC domain-containing protein 3	14.60
G3HN66_CRIGR	Ras-related GTP-binding protein	14.59
G3HBG5_CRIGR	26S protease regulatory subunit 4	14.58
G3GZB1_CRIGR	Eukaryotic translation initiation factor 3 subunit M (eIF3m)	14.56
G3HFY1_CRIGR	Protein phosphatase 1F	14.55
G3HZ34_CRIGR	Ras-related protein Rab-31	14.51
G3IIV2_CRIGR	ADP-ribosylation factor-binding protein GGA2	14.50
G3GU78_CRIGR	Paxillin	14.50
G3H7Y1_CRIGR	Peroxin-19 (Peroxisomal biogenesis factor 19) (Peroxisomal farnesylated protein)	14.49

G3HFL2_CRIGR	Endoplasmic reticulum lectin 1	14.48
G3I8G0_CRIGR	Keratin, type I cytoskeletal 17	14.42
G3HDI8_CRIGR	HCLS1-binding protein 3	14.41
G3HAV4_CRIGR	Vacuolar protein sorting-associated protein VTA1-like	14.41
G3I1W1_CRIGR	Synapse-associated protein 1	14.41
G3GVN0_CRIGR	Phosphomannomutase (EC 5.4.2.8)	14.39
G3HH94_CRIGR	Vascular endothelial growth factor D	14.39
G3IBN8_CRIGR	Keratin, type II cytoskeletal 6A	14.37
G3H229_CRIGR	Glutamine amidotransferase (EC 6.3.5.2)	14.36
G3HRJ2_CRIGR	182 kDa tankyrase-1-binding protein	14.31
G3HDM0_CRIGR	Neuropilin	14.28
G3IA32_CRIGR	COP9 signalosome complex subunit 4	14.27
G3HGY3_CRIGR	ADP-ribosylation factor GTPase-activating protein 1	14.26
G3GS62_CRIGR	NEDD8-activating enzyme E1 catalytic subunit (NEDD8-activating enzyme E1C) (Ubiquitin-activating enzyme E1C) (Ubiquitin-like modifier-activating enzyme 3)	14.20
G3IAE3_CRIGR	RNA transcription, translation and transport factor protein	14.20
G3I4H1_CRIGR	Mitogen-activated protein kinase (EC 2.7.11.24)	14.16
G3GX12_CRIGR	Tetratricopeptide repeat protein 13 (Fragment)	14.16
G3HEP7_CRIGR	Catechol O-methyltransferase (EC 2.1.1.6)	14.13
G3HCT4_CRIGR	DEAD box protein 5 (EC 3.6.4.13) (Probable ATP-dependent RNA helicase DDX5)	14.03
G3GWD3_CRIGR	Alpha-mannosidase (EC 3.2.1.-)	14.02
G3H8Q6_CRIGR	Importin subunit alpha	14.01
G3HQ99_CRIGR	Programmed cell death protein 10	14.00
G3I390_CRIGR	Actin-related protein 2/3 complex subunit	13.95
G3HEZ0_CRIGR	75 kDa glucose-regulated protein (Heat shock 70 kDa protein 9) (Stress-70 protein, mitochondrial)	13.90
G3GRA4_CRIGR	Protein enabled-like	13.73
G3I6H5_CRIGR	Fermitin family-like 2	13.17
G3IFK1_CRIGR	Flap endonuclease 1 (FEN-1) (EC 3.1.-.-) (Flap structure-specific endonuclease 1)	13.06

Table S1: Table of CHO host cell proteins detected by LC-MS/MS in a spent CHOgro® media sample. Completed in triplicate with mean LFQ values displayed in third column above.