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Proteome response of *Phaeodactylum tricornutum*, during lipid accumulation induced by nitrogen depletion



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ABSTRACT

Nitrogen stress is a common strategy employed to stimulate lipid accumulation in microalgae, a biofuel feedstock of topical interest. Although widely investigated, the underlying mechanism of this strategy is still poorly understood. We examined the proteome response of lipid accumulation in the model diatom, *Phaeodactylum tricomutum* (CCAP 1055/1), at an earlier stage of exposure to selective nitrogen exclusion than previously investigated, and at a time point when changes would reflect lipid accumulation more than carbohydrate accumulation. In total 1043 proteins were confidently identified (≥ 2 unique peptides) with 645 significant (p < 0.05) changes observed, in the LC-MS/MS based iTRAQ investigation. Analysis of significant changes in KEGG pathways and individual proteins showed that under nitrogen starvation *P. tricornutum* reorganizes its proteome in favour of nitrogen scavenging and reduced lipid degradation whilst rearranging the central energy metabolism that deprioritizes photosynthetic pathways. By doing this, this species appears to increase nitrogen availability inside the cell and limit its use to the pathways where it is needed most. Compared to previously published proteomic analysis of nitrogen starvation in *Chlamydomonas reinhardtii*, central energy metabolism and photosynthesis appear to be affected more in the diatom, whilst the green algae appears to invest its energy in reorganizing respiration and the cellular organization pathways.

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1. Introduction

In the last few decades there has been a growing interest in developing microalgae as the third generation biofuel feedstock [1–3]. However, in order to develop economically viable processes for biofuel production using microalgae, a greater understanding of microalgal metabolism and its organization in effecting the accumulation of biofuel precursors (lipids and carbohydrates) is necessary. One of the most widely employed strategies that triggers the storage of energy reserves in microalgae is nitrogen limitation or depletion in the growth medium, which has been described for several species [4]. Recent studies have attempted to further understand this stress at the '-omic' level, primarily using the model algal species *Chlamydomonas reinhardtii* [5–9]. However, given the diverse lineage of organisms classified under 'microalgae' [10,11], such investigations are required in other lineages to develop a broader understanding of biofuel precursor synthesis and accumulation.

Diatoms play a significant role in the global carbon cycle, accounting for ~20% of total photosynthesis [12], and are of ecological significance.

In addition, diatoms are also very interesting for conducting studies in algal physiology and applied phycology. Specifically, the marine diatom Phaeodactylum tricornutum has been used for aquaculture [13] and as a model for cell morphological investigations [14]. The marine nature of this organism is also of interest as a biofuel crop, as it allows for surmounting the water resource limitations associated with fresh water cultivations [15]. In this sense, *P. tricornutum* has been recommended as a favorable species for biodiesel production, with high lipid content (up to 61%) and lipid productivity (up to 26.75 mg $L^{-1} d^{-1}$) being reported [16], as well as having suitable lipid profiles for the derivation of biodiesel with desirable octane rating, iodine number and cloud point. The fact that its genome is sequenced [17], with descriptive information available in UniProt and KEGG, makes this species an excellent model organism for studying diatom based biofuel production [18]. As with many other microalgal species, P. tricornutum has been shown to increase lipid content in response to nitrogen stress [4]. Therefore, it is an excellent candidate to investigate the metabolic effect of the nitrogen trigger in diatoms, allowing its comparison with previous investigations from other taxonomic groups, such as Chlorophyta, and enabling a broader understanding of lipid accumulation in microalgae under this condition.

The effect of nitrogen stress has been examined previously at the molecular level in *P. tricornutum*, but this has been predominantly at the transcriptomic level using microarrays [19] and RNAseq [20–22].

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In these investigations, changes in the proteome has been inferred from transcript expression profiles. Such approaches only provide assessment of the transcriptional control, disregarding the fact that both translational and degradation controls also affect the amount of protein present inside the cell [23]. This is of particular relevance in a nitrogen stress environment where protein degradation, as a way of nitrogen recovery, may play a significant role in fulfilling cellular nitrogen demands [6]. Hence, transcriptomic studies themselves cannot be relied upon to represent the true protein cellular levels [24–26]. These should either be supported with targeted protein analysis, such as western blots or multiple reaction monitoring, or a global proteomic investigation.

Whilst several proteomic investigations have been published in the Chlorophyta [9,27–34], there is limited information in other phyla. Within diatoms, Thalassiosira pseudonana [26,35-41] and P. tricornutum [22,37,42–45] have been the species most investigated. Some of these studies have referred to nitrogen stress in some form [22,38,39,42,44, 45]. Among these studies, the recent investigation by Ge et al. [42] reported proteomic changes using isobaric tags for relative and absolute quantitation (iTRAQ). iTRAQ utilizes amine linking isobaric tags to allow quantitative comparison of numerous proteins in an unbiased way and has become a popular tool for proteomics, being a major improvement compared to 2D SDS PAGE gel methodology [46-48]. Proteins detected in the work by Ge et al. [42] showed an increase in the carbohydrate metabolic processes (glycolysis and tricarboxylic acid cycle) and branched-chain amino acid catabolism, and a decrease in enzymes involved in cellular amino acid biosynthesis and photosynthesis. However, the proteomic analysis was done when P. tricornutum growth was well advanced and lipid accumulation was triggered by the natural depletion of nitrogen in the medium after 60 h of growth. In that kind of setting, the physiological state of P. tricornutum would be the result of the simultaneous change of other components in the medium in addition to the nitrogen concentration, and therefore, the observed proteomic changes could not be solely attributed to the nitrogen limitation. In the present analysis we aimed to study the effect of nitrogen starvation as the sole trigger of lipid accumulation in P. tricornutum by controlled removal of this key element from the culture medium, and by observing the changes relatively earlier than other investigations so far. The dynamics of P. tricornutum proteome reorganization were analysed using the iTRAO methodology at 24 h after nitrogen removal, when lipid production in the nitrogen starved culture, compared to the nitrogen replete control conditions, was noticed to be at its highest, and when lipid accumulation appeared to take precedence over carbohydrate accumulation. The choice of the time point to analyse was based on the criteria to observe changes early enough under nitrogen depletion, but sufficiently delayed so as to differentiate the changes attributable to carbohydrate accumulation. We believe this aspect has not been addressed in previous investigations on the subject and would offer a more informed access to the relevant metabolic changes. Through the use of this mass spectrometry based proteomic quantification method and the unique design mentioned above, we aimed to increase current understanding of the relationship between nitrogen stress and lipid accumulation within microalgae. The results are also compared with previous analysis in C. reinhardtii [6], to gain insights into metabolic differences and similarities between different taxonomic affiliations. The ultimate goal is to acquire a better knowledge of the universality of the molecular mechanisms underlying the induction of lipid accumulation in microalgae that will lead to improved strategies for biofuel production from microalgae.

2. Materials and methods

2.1. Organism of study and medium

P. tricornutum (CCAP 1055/1) was obtained from the Culture Collection of Algae and Protozoa (CCAP, Oban, U.K.). F/2 + Si medium was prepared as described by CCAP diluting in seawater made with 33.6 g

Ultramarine synthetic salts (Waterlife Research Industries Ltd. Middlesex, U.K.) per liter. Cultures were grown in either F/2 + Si medium (Nitrogen replete treatment) or F/2 + Si medium omitting sodium nitrate (Nitrogen deplete treatment).

2.2. Experimental approach

P. tricornutum was cultured in 250 mL bubble columns (40 mm diameter) sparged with air at 2.4 L min⁻¹. Filtered (0.22 μ m) air was first passed through sterile water for humidification, before being introduced by silicone tubing to the bottom of the column providing both mixing and gas transfer. The top of the bubble column was sealed using a foam bung. The columns were placed in a water bath maintained at 25 °C and under 24 h continuous lighting with two side facing halogen lamps (230 V 11 W bulbs (OSRAM, Munich, Germany)). The lamps were placed horizontally across a series of columns. This arrangement resulted in an average light intensity of 200 μ E m⁻² s⁻¹ for each column that varied by \pm 50 μ E m⁻² s⁻¹ along the length of the column, as measured using a Quantum Scalar Laboratory Radiometer (Biospherical Instruments, San Diego, CA, USA) in a water filled column. All columns in the experimental set-up received similar light exposure along the lines indicated above, such that the average for each column fell within sufficient to saturating light intensity for P. tricornutum [22, 49]).

Given that a considerable culture volume was required for proteomics, two batch cultures were carried out for each condition in triplicate. The first batch was used to generate sufficient biomass for profiling chlorophyll a, carbohydrate and (neutral) lipid profiles (collectively referred to as biochemical analyses, hereafter), and the second batch was used to generate the biomass for proteomics. The biochemical analyses were also carried out on a single time point from the second batch to ensure comparability of the batches. For both batches, the cultures were grown in nitrogen replete medium for 48 h reaching an optical density $(OD_{750nm}) > 0.4$. Culture from four columns was then pooled and the combined optical density used to calculate the culture volume required for giving an OD_{750nm} of 0.2 upon re-suspension to 250 mL. The calculated culture volume was then harvested from the pooled culture by centrifugation at 3000 g for 5 min and resuspended in F/2 + Si medium with or without nitrate to generate the nitrogen replete and deplete treatments, respectively. These treatments were then sampled at 0, 6, 12, 18, 24, 36, 48, and 72 h, post resuspension, in the first batch to generate the biochemical profiles. Similarly sampling was done at 24 h for proteomic analysis and 72 h for biochemical analyses, with the second batch.

2.3. Biochemical analysis

For the first three time points the sample volume was 20 mL, whilst it was 15 mL for the subsequent five time points, for each biological replicate, for each treatment. Culture samples were pelleted in a preweighed 1.5 mL eppendorf tube by centrifugation at 3000 *g* for 5 min. Pellets were frozen before freeze drying for >12 h in a Modulyo freeze drier (Edwards, Crawley, U.K.). Dried samples were weighed to determine the dry cell weight (DCW) and stored at -20 °C. Chlorophyll a, carbohydrate and lipid analysis were conducted in the stored samples using modified versions of the Wellburn [50], Anthrone [51] and Nile red [52] methods respectively, as described in Longworth et al. [6]. In the same manner, chlorophyll *a*, carbohydrate and lipid analysis were conducted on the single time point sample collected from the second batch. There were thus four replicate data sets that were combined for the data analysis.

2.4. Microscopy

Samples for microscopy were taken from the proteomic experimental set (second batch) at 24 h post resuspension in each treatment condition by centrifugation of 1 mL sample at 3000 g for 5 min. After removing 950 μ L, the pellet was resuspended in the remaining 50 μ L and 10 μ L was then placed on a glass slide with a cover slip on top. Visualization was done on an Olympus BX51 microscope (Olympus, Southend-on-Sea, U.K.) and images captured by using ProgRes CapturePro 2.6 (PandA, Berkshire, U.K.).

2.5. Proteomic sampling and processing

At 24 h after starting the treatments, two 50 mL aliquots were taken in each biological replicate and centrifuged at 3000 g for 10 min at 4 °C, then resuspended in 1 mL 500 mM triethylammonium bicarbonate buffer (TEAB) (pH 8.5) and transferred to protein low bind tubes. Samples were then stored at -20 °C till all harvests were completed. Protein extraction was achieved by liquid nitrogen grinding. Stored cell samples were resuspended with 500 µL 500 mM TEAB (pH 8.5). Samples were immersed in a cooled sonication water bath for 5 min and subsequently ground using a mortar and pestle cooled by liquid nitrogen. Samples were then collected into a fresh protein low bind tube (Eppendorf, U.K.) and then immersed in a cooled sonication water bath for a further 5 min and sonicated for two cycles with a Micro tip Branson sonifier (Enerson, Danbury, CT, USA). Subsequently, samples were centrifuged at 18,000 g for 30 min at 4 °C to separate the soluble and insoluble fractions. After quantifying using RCDC (BioRad, U.S.A), 100 µg of protein was acetone-precipitated before being resuspended in 30 µL 500 mM TEAB (pH 8.5) with 0.1% sodium dodecyl sulphate. Proteomic samples were then reduced, alkylated, digested and labelled with the 8-plex iTRAQ reagents (AB Sciex, Framingham, MA, USA), as described in the manufacturer's protocol. To assess the proteomic changes occurring within P. tricornutum under nitrogen stress an 8-plex iTRAQ experiment was designed. iTRAQ labels 114, 113 and 119 were used for nitrogen replete biological triplicate cultures and 116, 117 and 118 for nitrogen depleted biological triplicate ones. Note that labels 115 and 121 were intended for analysing the samples from a silicon stress experiment. However, silicon was not effectively depleted and thus these proteomic results were incorporated into the nitrogen replete ones.

2.6. Off line HPLC fractionation and clean-up

High-resolution hydrophilic interaction chromatography (HILIC) was carried out using an Agilent 100-series HPLC (Agilent, Wokingham, UK). One iTRAO labelled sample was resuspended in 100 µL buffer A (10 mM ammonium formate, 90% ACN, pH 3 (adjusted with formic acid (FA)). The resuspended sample was loaded onto PolyHydroxyethyl A column, 5 µm particle size, 20 cm length, 2.1 mm diameter, 200 Å pore size (PolyLC, Columbia, MD, USA). With a flow of 0.5 mL min⁻¹ buffer A was exchanged with buffer B (10 mM ammonium formate, 10% ACN, pH 4 (adjusted with (FA)) to form a linear gradient as follows: 0% B (0-5 min), 0-15% B (5-7 min), 15% B (7-10 min), 15-60% B (10-50 min), 60-100% B (50-55 min), 100% B (55-65 min), 0% B (65-75 min). Fractions were collected every minute from 18 min through to 41 min followed by three, 3 min fractions to 50 min. The fractions were vacuum centrifuged, before being cleaned up using C18 UltraMicroSpin Columns (Nest, Southborough, MA, USA) according to the manufacturer's guidelines.

2.7. LC-MS/MS

RPLC-MS was conducted using an Ultimate 3000 HPLC (Dionex, Sunnyvale, CA, USA) coupled to a QStar XL Hybrid ESI Quadrupole time-of-flight tandem mass spectrometer (Applied Biosystems (now ABSciex), Framingham, MA, USA). Samples were resuspended in 20 μ L buffer A (3% ACN, 0.1% FA) before loading 9 μ L onto a Acclaim PepMap 100 C18 column, 3 μ m particle size, 15 cm length, 75 μ m diameter, 100 Å pore size (Dionex, Sunnyvale, CA, USA). With a flow of 300 μ min⁻¹, buffer A was exchanged with buffer B (97% ACN, 0.1% FA) to form a linear

gradient as follows: 3% B (0–5 min), 3–35% B (5–95 min), 35–90% B (95–97 min), 90% B (97–102 min), 3% B (102–130 min). The mass detector range was set to 350–1800 m/z and operated in the positive ion mode saving data in centroid mode. Peptides with +2, +3, and +4 were selected for fragmentation. The remaining sample was subsequently injected in the same manner to acquire two RPLC-MS runs for each submitted fraction.

2.8. Data analysis

Proteomic identifications were conducted using Mascot, Ommsa, X!Tandem, Phenyx, Peaks and ProteinPilot for searching against the Uniprot reference proteome for Phaeodactylum tricornutum (Uniprot id 10,465). Each search was conducted with a decoy database formed using reversed sequences (Mascot, Ommsa, X!Tandem and ProteinPilot) or randomized sequence (Phenyx and Peaks). Searches were restricted to a peptide false discovery rate (FDR) of 3% prior to decoy hits being removed and peptide spectral matches from the six search engines being merged using an R based script that was also used to remove those showing disagreement in terms of peptide assignment or protein identification between the search engines. Where protein groups were clustered, such as with Mascot, the most common identification between the search engines was selected. Separately, for quantification, the reporter ion intensities for each peptide spectral match (PSM) were extracted and matched to the merged results. Thus only reporter ion intensities from PSM's matched by the above merging contributed to the protein reporter ion intensities, each PSM match having equal weighting whether identified by single or multiple search engines. Variance stabilization normalization, isotopic correction and median correction were performed on the label intensities before averaging by protein and performing a *t*-test between replicate conditions to determine significance and fold change. (Supporting Information Fig. S1).

KEGG analysis was derived using the KEGG "Search&Color Pathway" tool [53]. Proteins with a significant (*p*-value <0.05) positive fold change were labelled with "blue" whilst proteins with a significant (*p*-value <0.05) negative fold "red".

Gene ontology (GO) annotations were identified using the functional annotation tool DAVID [54,55]. The GO terms were then grouped into biological concepts as shown in Supporting Information Table S1. To determine the relative change, the number of proteins identified as increasing within a class was divided by the number of proteins identified as decreasing with the change being log transformed (base 10). This provides an observation of the relative change observed in each species balanced on 0 for each grouping of GO terms.

3. Results and discussion

3.1. Biochemical characterization under nitrogen stress

The assessment of *P. tricornutum* biochemical changes under the exclusive influence of nitrogen deprivation is shown in Fig. 1. Here, the ratio of the relative biomass normalized response of the variables under nitrogen depletion with respect to the control (nitrogen replete scenario) can be studied. As can be seen from the plot, both carbohydrates and lipids are produced at higher levels under nitrogen depleted conditions compared to the replete scenario, in the initial stages of the exposure. The carbohydrate levels peak initially (at 12 h post incubation) reaching a maximum of 3 fold increase under nitrogen depleted condition. Neutral lipid levels are significantly higher in relative terms at all times, and peak latter than carbohydrates, at 24 h. This initial increase in carbohydrates followed by increase in lipids is as was observed in *C. reinhardtii* under nitrogen stress [6]. As can be seen from the upper panel of the figure, the ratio of Chlorophyll A response decreased rapidly over the first 24 h. This was confirmed by the visible decrease in



Fig. 1. Ratio of biomass normalized biochemical responses under nitrogen deplete (N-) compared to nitrogen replete (N+) condition; lipids by Nile red fluorescence (lower panel), carbohydrates (lower panel); and chlorophyll A (upper panel). The lipid response in N- condition (upper panel) is the Nile-red fluorescence response that is normalized to the maximum observed for the condition. Error bars refer to standard error about the mean of the four biological replicates. The block arrow at 24 h, in the upper panel, indicates the sampling point for proteomics.

chloroplast content in the nitrogen depleted treatment as observed under the microscope (Fig. 2).

Considering the results observed in Fig. 1 and in order to investigate changes in the proteome associated with the lipid accumulation, a sampling point of 24 h post resuspension in nitrogen free medium was chosen for conducting the proteomics analysis. The chosen time point is one where the lipids were being accumulated at a rate higher than in the control condition, but one where the relative carbohydrate accumulations were minimal, suggesting a switch in resources from carbohydrate accumulation to lipid accumulation. A snapshot of metabolism at this time point can be considered to reflect changes that are more relevant to lipid accumulation than those attributable to carbohydrate accumulation.

3.2. Biochemical analysis of proteomic culture setting

To ensure culture comparability to the biochemical profile data set, samples for biochemical and microscopy analysis were also taken

Nitrogen Replete Nitrogen Deplete



Fig. 2. Microscope images at 100× magnification of *P. tricornutum* 24 h after transfer to test conditions.

along with those for proteomic analysis at 24 h post resuspension. A *t*-test showed a statistically significant (*p*-value <0.05) increase in carbohydrates and lipids when cultures were under nitrogen stress for 24 h. Conversely, pigmentation showed a significant reduction in the nitrogen depleted treatment (Supporting Information Fig. S2). Concurrent with proteomics and biochemical analysis, 1 mL of culture was also prepared for microscopy (Fig. 2). The nitrogen stressed cells were observed to have reduced pigmentation, which is in accordance with the observations made for the Chlorophyll *a* and Carotenoids concentration (Supporting Information Fig. S2).

3.3. Overview of proteomic data

Within the proteome dataset, 23,544 spectra were matched to peptide and protein without disagreement among the six search engines, each of which were limited to a false discovery rate of 3% at the peptide level. The derived PSM list represented 7777 unique sequences matched to 1761 proteins of which 1043 had two or more unique peptides (Supporting Information Table S2). To assess sample arrangement, hierarchal clustering and principal component analysis (Supporting Information Fig. S3) was performed on the merged PSM list. From this analysis, it can be seen that the nitrogen stress replicates cluster apart from the replete cultures and is responsible for >80% of the variation between the samples. The list of PSM(s) was then processed to provide the degree and significance of the change between the two treatments (Supporting Information Table S3). Between the nitrogen replete and deplete conditions, 645 significant changes (Fig. 3) were observed $(p \le 0.05)$, which corresponds to 62% of the confidently identified proteins. Though double that observed by Ge et al. (29% [42]) this high level of statistically significant change is comparable with other studies of nitrogen stress in algae (53% [6] and 33% [9] for C. reinhardtii, 57% [27] for Chlorella vulgaris). For biological description two sets of statistically significant proteins were used. The 645 changes identified as showing a significant difference ($p \le 0.05$) were used for pathway and gene ontology analysis, which requires deduction of hypotheses based on protein clusters rather than individual observations. A more stringent significance level ($p \le 0.01$) comprising of 498 differences was used for direct hypothesis derivation in Table 1.

3.4. Resourcing of internal nitrogen, scavenging and the reduction of lipid degradation

Significant changes (p < 0.05) between nitrogen replete and deplete conditions were used to colour KEGG maps. The overall map of the metabolism is shown in Fig. 4 (specific pathway maps grouped by concept are shown in Supplementary Information Figs. S5–10). Given limited annotation of KEGG available for *P. tricornutum*, the most significant changes were further investigated individually. Within the dataset, the



Fig. 3. Volcano plot of proteins identified showing fold change and statistical significance of change. Significant changes to a *p*-value <0.05 are indicated by red *. The *p*-value cut-off of 0.01 and 0.1 are indicated by a dotted and solid line respectively.

Table 1

Table of all significant (p < 0.01) changes observed omitting "Predicted Proteins". Each protein is reported with its Uniprot ID, Descriptive name, Number of unique peptides and fold change observed under nitrogen stress. Positive fold changes are shown in bold.

Uniprot ID	Protein name	# Peptides	Fold Change
	Hydrophilic amino acid synthesis		
B7GEJ6	Acetylornithine aminotransferase	7	1.28
B7G5H9	Aspartokinase	2	-1.50
B7GBH2	Delta l-pyrroline-5-carboxylate synthetase	12	-1.35
B7G3A2	Diaminopimelate decarboxylase	6	1.31
	Hydrophobic amino acid synthesis		
B7FUP6	2-Isopropylmalate synthase	6	-1.55
B/FRJ9	3-Deoxy-/-phosphoheptulonate synthase	15	- 1.69
B/F114 P7C2T0	Adenosylnomocysteinasee	18	-2.36
B76215 B7FS76	Charlismate synthese	2	1.27
B7C117		2	-1.27
brain	Other amino acid synthesis	0	1.22
B7FT50	Asparagine synthetasee	4	1.53
B7G5Z8	Glycine decarboxylase p-protein	16	- 1.63
B7FZB0	Synthase of glutamate synthase	18	1.33
	Photosynthesis		
A0T0C9	Apocytochrome f	17	- 1.91
A0T0D1	ATP synthase epsilon chain, chloroplastic	7	-1.84
A0T0F1	ATP synthase subunit alpha, chloroplastic	40	-2.18
A0T0E9	ATP synthase subunit b, chloroplastic	5	-2.89
A0T0E8	ATP synthase subunit b', chloroplastic	2	-2.80
A0T0D2	ATP synthase subunit beta, chloroplastic	49	-2.37
AUTOPO	ATP synthase subunit delta, chloroplastic	3	- 2.26
AUTUA3 DZECNIZ	Cytochronie b559 subunit alpha (PSII reaction center subunit V)	0	-2./3
D/F3N/ P7C2I6	Della-allillolevullille actu dellydi alase	0	- 1.27
0/1003	Fucovanthin chlorophyll a/c protein, deviant	5	-1.71
AOTOR5	Magnesium-chelatase subunit I	16	-2.42
B7FZ96	Oxygen-evolving enhancer protein 1	14	- 1.35
A0T0B9	Photosystem I ferredoxin-binding protein	28	-1.48
A0T0M1	Photosystem I protein F	9	-1.54
A0T0M6	Photosystem I reaction center subunit XI	4	-1.78
A0T096	Photosystem II CP43 chlorophyll apoprotein	15	-2.49
A0T0B2	Photosystem II CP47 chlorophyll apoprotein	17	-3.15
A0T097	Photosystem II D2 protein	3	-2.69
A0T0H5	Photosystem II reaction center psb28 protein	9	1.78
A0T0G9	Photosystem Q(B) protein	3	- 1.85
B/FZL9	Phytoene dehydrogenase	2	- 1.67
B/FKW2 B7EOE0	Protein fucovantnin chlorophyl a/c	24	- 1.53
D/FQEU P7EOE1	Protein fucovanthin chlorophyl a/c	4	- 1.40
B7FR60	Protein fucovanthin chlorophyl a/c	4	1.05
B7FRW4	Protein fucoxanthin chlorophyl a/c	3	-149
B7FV42	Protein fucosanthin chlorophyl a/c	4	-1.77
B7G6Y1	Protein fucoxanthin chlorophyl a/c	3	-1.85
B7G955	Protein fucoxanthin chlorophyl a/c	3	-1.72
B7GCV9	Protein fucoxanthin chlorophyl a/c	3	3.13
B5Y3F4	Protoporphyrin IX magnesium chelatase, subunit H	6	-2.14
B7GDU9	Protoporphyrinogen oxidase	2	- 1.65
B7FUT6	Uroporphyrinogen decarboxylase	10	-2.19
B7FUR6	Violaxanthin deepoxidase	4	1.56
0071/52	Carbon fixation	20	2.22
Q91K52	Ribulose displiospliate carboxylase large chain Dibulose 1.5 himbosplate carboxylase (ourgenace small subunit	38	-2.33
AUTUEZ	Kibulose-1.5-bispilospilate carboxyiase/0xygeilase siilali subuliit	5	- 1.92
B7FXB6	6-Phosphogluconate dehydrogenase, decarboxylating	6	1.66
B5Y3C9	Cytochrome b6-f complex iron-sulfur subunit	11	-172
O8GTB5	Cytochrome c6 (Precursor cytochrome c6)	4	1.79
B5Y578	Cytochrome c6, cytochrome <i>c</i> 553	10	1.43
B7FRC1	Cytosolic aldolase	8	1.90
Q9M7R3	Cytosolic glyceraldehyde-3-phosphate dehydrogenase	18	1.89
Q84XB5	Fructose-1.6-bisphosphate aldolase	16	1.42
B7GDK9	Glucose-6-phosphate isomerase	7	1.50
B7G6T5	Glutamine-fructose-6-phosphate transaminase	4	1.61
B7G518	Isocitrate lyase	3	-1.90
B7FYD8	Kinase adenylate kinase	3	-1.53
B/GUK/	Ligase succinate-coa ligase	3	1.58
B/G9G3 D7EVTO	Lipoannue denydrogenase Malata supthase	15	1.19
B7CCC9	ivialate Syllulidse PEP pyrophosphate dependent phosphofructokingse	0 11	- 1.41 1.58
B7GEI2	Phosphoglycerate mutase	1 I 2	1.30
B7G492	Phosphorannose mutase	5	1.66
		-	

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 Table 1 (continued)

BYGR/E Parcence of APR-APR-APR genums submit 11 1-1.58 BYGR/E Presence of APR-APR-APR genums submit 11 1-1.58 BYGR/E Presence of APR-APR-APR genums submit 11 1-1.58 BYGR/E Presence of APR-APR APR genums submit 11 1-1.58 BYGR/E Presence of APR-APR APR genums submit 11 1-1.58 BYGR/E Presence of APR-APR APR genums submit 12 1.46 CUTXWS Pyroact binas 5 1.37 DYSWS Pyroact binas 13 1.36 BYGR/E Socialate derived/opersus for average 16 1.42 DYSWS Pyroact binas 10 1.14 DYSGR Socialate derived/opersus for average 10 1.14 DYSGR Associalate derived/opersus for average 10 1.14 <t< th=""><th>Uniprot ID</th><th>Protein name</th><th># Peptides</th><th>Fold Change</th></t<>	Uniprot ID	Protein name	# Peptides	Fold Change
BirCoMM Percentrol of Arbase Arbase gamma submit 11 -1.58 BTZR1 Percentrol of dipdyngames groups et algoba and fera submits 24 L52 TOPSC Province in biological dipdyngames groups et algoba and fera submits 24 L52 TOPSC Province in biological dipdyngames groups et algoba and fera submits 24 L52 OUTSWN Pyrovate instance and requested in submits 5 L52 OUTSWN Pyrovate instance and requested in submits 5 L52 OUTSWN Pyrovate instance and requested in submits 5 L52 DTGAGA Transferabase 10 L53 DTGAGA Transferabase 10 L54 DTGAGA Transferabase 10 L54 DTGAGA Transferabase in protein 11 L54 DTGAGA Transferabase in protein 12 L66 DTGAGA Transferabase 12 L65 DTGAGA Anagot [angle charine protein 12 L65 DTGAGA Anagot [angle charine protein 12 L65 <td>B7GEF2</td> <td>Plastidic enolase</td> <td>17</td> <td>1.20</td>	B7GEF2	Plastidic enolase	17	1.20
BTR21 Precision of delphologenase private achopyenase E1, siphs and beta subunits 24 1.62 BTSX3 Practice problem by private achopyenase E1, siphs and beta subunits 3 1.34 DTGN3 Private kinase 3 1.34 DTGN3 Succinite delphotopyenase Environ 36 1.34 DTGN3 Succinite delphotopyenase Environ 36 1.34 DTGN3 Tradice/Date Environ 6 1.42 DTGN3 Tradice/Date Environ 1 1 DTGN3 Tradice/Date Environ 1 1 DTGN3 Tradice/Date Environ 1 1 1 DTGN3 Succinity AC/C cantrine protein Jathafant 1 1 1 DTGN3 Succinity AC/C cantrine protein Jathafant 2 1 1 DTGN3 Succinity AC/C cantrine protein Jathafant 2 1 1	B7G0M9	Precursor of ATPase ATPase gamma subunit	11	-1.58
FISO3 Particle phonolement provide categorianse 5 1.54 BYR267 Pyroteck brack 0 1.40 COPNO Pyroteck brack 0 1.40 COPNO Pyroteck brack 0 1.37 BYR567 Sciencial effyringersace in any parties 0 1.34 BYR567 Sciencial effyringersace in any parties 10 1.36 BYR567 Tricosphorphate ionerace 0 1.32 BYR567 Tricosphorphate ionerace 0 1.42 BYR567 Tricosphorphate ionerace 0 1.42 BYR567 Tricosphorphate ionerace 0 1.51 BYR567 Tricosphorphate ionerace 2 1.36 BYR567 Tricosphorphate ionerace 2 1.36 BYR568 Ac/ (arter porcin) 2 1.38 BYR568 Ac/ (arter porcin) 2 1.38 BYR568 Ac/ (arter porcin) 2 1.38 BYR568 Ac/ (arter porcin) 1.38 BYR568 Ac/ (arter	B7FZE1	Precursor of dehydrogenase pyruvate dehydrogenase E1, alpha and beta subunits	24	1.62
BYRAGY Provale lanae 9 1-40 CCRNNN Provale lanae 3 1-125 CCRNNN Provale lanae 5 134 BYRAM Succinat delynogenes iron sullar procein 5 259 BYRAM Succinat delynogenes iron sullar procein 5 259 BYRAM Succinat delynogenes iron sullar procein 6 1.02 BYRAM Trainskoholk 6 1.02 BYRAM Trainskoholk 6 1.02 BYRAM Successf-lage-lage-trainsprocein 6 1.02 BYRAM Successf-lage-lage-trainsprocein 11 1.11 BYRAM Successf-lage-lage-trainsprocein 11 1.12 BYRAM And desynthesis 2 1.58 BYRAM And and angle-scale procein 1 1.02 BYRAM Angl and rage-scale procein 1 1.02 BYRAM Angl angl scale procein 1 1.02 BYRAM Angl angl scale procein 1 1.02 BYRAM	F1SXA3	Putative phosphoenolpyruvate carboxykinase	5	1.54
CGT300 Pyrotek base 3 -1.25 CGT300 Pyrotek base 5 1.34 DENSIN Surinar edpologenzes transming motin 5 2.39 DENSIN Surinar edpologenzes transming motin 5 2.39 DENSIN Surinar edpologenzes transming motin 5 2.39 DENCAL Transkrohze 5 -1.37 DENCE Transkrohze 5 -1.32 DENCE Transkrohze 6 1.42 DENCE Transkrohze 6 1.42 DENCE Transkrohze 1 1.42 DENS Transkrohze 1 1.42 DENS Transkrohze<	B7FZG7	Pyruvate kinase	6	1.40
Q2TXNN Protocie Name 7 1.37 Q2TXNN Protocie Name 10 1.36 DFCA04 Succinate delydrogenate ion suffer protein 5 2.59 DFTULIO Transketolase 10 1.38 DFTUT Transketolase 10 1.38 DFTUT Transketolase 1 1.42 DFTUT Transketolase 1 1.42 DFTUT Transketolase 1 1.71 DFTUT Transketolase 2 1.73 DFTUT Transketolase 2 1.73 DFTUT Mutchomital giveraldedyname 2 1.73 DFTUT Mutchomital giveraldedyname 2 1.73 DFTUT Mutchomital giveraldedyname 2 1.73 DFTUT<	Q2TSW8	Pyruvate kinase	3	-1.25
QUISN Private brace 5 1.44 QUISN Socialize dividentiance brogenetia 5 1.45 DFR100 Transference 6 1.25 DFR100 Transference 6 1.42 DFR100 Transference 7 1.46 DFR100 Transference 1 1.51 DFR100 Transference 2 1.53 DFR100 Bray of a carbo protein particle dividragenase 2 1.53 DFR100 Bray of a carbo protein particle dividragenase 2 -1.53 DFR007 Transference 2 -1.53 DFR007 Dray of An apy Cox purplex dividragenase 2 -2.01 DFR007 Dray of An apy Cox purplex dividragenase 2 -2.01 DFR007 Dray of An apy Cox purplex	Q2TSW9	Pyruvate kinase	7	1.37
BatisaniDisDisDisBatisaniDisDisDisBatisaniTransferbiageDisDisBTGSDTransferbiageDisDisBTGSDTransferbiageDisDisBTGSDTransferbiageDisDisBTGSDTransferbiageDisDisBTGSDTransferbiageDisDisBTGSDDissophiatis isomeraseIIBTGSDDissophiatis isomeraseIIBTGSD <td>Q2TSX0</td> <td>Pyruvate kinase</td> <td>5</td> <td>1.34</td>	Q2TSX0	Pyruvate kinase	5	1.34
BOTHONAnithal interiorS2.107BYROSTransferenciase101.58BYROSTransferenciase61.42BYROSTransferenciase41.66BYROSTransferenciase101.31BYROSByrosterias101.31BYROSAccilenciase21.63BYROSAccilenciase21.63BYROSAccilenciase21.63BYROSAccilenciase21.63BYROSAccilenciase21.63BYROSAccilenciase21.63BYROSAccilenciase21.63BYROSInterferenciase21.63BYROSInterferenciase2-1.73BYROSInterferenciase2-2.03BYROSInterferenciase2-1.23BYROSSoft Chartane1.43BYROSNucleonia Identification2-1.43BYROSSoft Chartane1.23BYROSSoft Chartane2-1.23BYROSSoft Chartane2-1.43BYROSSoft Chartane2-1.43BYROSSoft Chartane2-1.43BYROSSoft Chartane2-1.43BYROSSoft Chartane2-1.43BYROSSoft Chartane2-1.43BYROSSoft Chartane2-1.43BYROSNucleoxid eiphosphate innee 3-1.43BYROS<	B5Y5N6	Succinate dehydrogenase flavoprotein	19	1.66
IntroductionIndex of the sectorInteractionInteractionBYR107Tronsephosphate isomerase61.42BYR107Tronsephosphate isomerase61.42BYR107Tronsephosphate isomerase11.71BYR1073 sonaryl (ap) (arring profin11.71BYR1073 sonaryl (ap) (arring profin21.86BYR1073 sonaryl (ap) (arring profin21.86BYR1073 sonaryl (ap) (arring profin21.86BYR107Arring profin21.81BYR107Arring profin21.81BYR108Aryl (arring profin21.81BYR109Deg (arring arring profin21.81BYR109Deg (arring arring	B/GA40 P7EUU0	Succinate denydrogenase from sunur protein Trapekotolaco	26	2.59
IPTPTP Tissephosphate isomerase 6 1.42 FCGSC1 Tissephosphate isomerase 4 1.46 FCGR1 3-coaxe/1-lay/-arrite-protein 1 1.71 FCGR0 3-coaxe/1-lay/-arrite-protein 1 1.71 FCGR0 3-coaxe/1-lay/-arrite-protein 1 1.71 FCGR0 3-coaxe/1-lay/-arrite-protein 1 1.71 FCGR0 A-coaxe/1-lay/-arrite-protein 2 1.73 FCGR0 Malon/1-CA/CP cranacylase 2 1.73 FCGR0 Malon/1-CA/CP cranacylase 2 -1.73 FCGR0 Long chain cy/-C-arrite-rotein 7 -1.31 FCGR0 Long chain cy/-C-arrite-rotein 7 -1.31 FCGR0 Long chain cy/-C-arrite-rotein 7 -1.24 FCGR0 Long chain cy/-C-arrite-rotein 7 <td>B7C5R3</td> <td>Transketolase</td> <td>10</td> <td>1.57</td>	B7C5R3	Transketolase	10	1.57
B7C3C1 Trisophosphate isomeraze 4 1.46 BTG IBR 3-coaxe/1-key/-critrie protein 11 1.71 BTG IBR 3-coaxe/1-key/-critrie protein 10 1.51 BTG IBR 3-coaxe/1-key/-critrie protein 10 1.51 BTG IBR 3-k-hydroxyac/key/-arrier protein 2 1.50 BTG IBR 3-k-hydroxyac/key/-arrier protein 2 1.53 BTG IBR 3-k-hydroxyac/key/-arrier protein 2 1.53 BTG IBR 3-k-hydroxyac/key/-arrier protein 2 1.53 BTG IBR 3-k-hydroxyac/key/-arrier protein 2 -1.23 BTG IBR 3-k-hydroxyac/key/-arrier protein 2 -1.23 BTG IBR 3-k-hydroxyac/key/-arrier protein 2 -1.23 BTG IBR N-kacoside diphosphate Kinase 3 -1.23 -1.23 BTG IBR N-kacoside diphosphate Kinase 3 -1.24 -1.24 BTG IBR N-kacoside diphosphate Kinase 3 -1.23 -1.24 BTG IBR N-kacoside diphosphate Kinase 3 -1.24 -1.24 <	B7FT67	Triosephosphate isomerase	6	1.50
Forty and biosynthesis second (-) lexy-carity protein () with a (-) 11 1.71 BTCCN0 3-conde (-) lexy-carity-protein () with a (-) 1.81 1.81 CTC118 R-by downed (-) lexy-carity-protein () with a (-) 1.81 1.81 CTC118 R-by downed (-) 2 1.81 CTC110 A (-) carrier protein () with a (-) 2 1.81 CTC110 A (-) carrier protein () with a (-) 2 1.81 CTC110 A (-) carrier protein () with a (-) 2 1.81 CTC110 A (-) carrier protein () with a (-) 2 -1.73 CTC110 A (-) carrier protein () with a (-) -1.23 -2.03 CTC110 A (-) carrier protein () with a (-) -1.23 -2.03 CTC110 Nond (-) carrier protein () with a (-) -1.24 -1.24 CTC110 Nond (-) carrier protein () with a (-) -1.24 -1.24 CTC110 Nond (-) carrier protein () with a (-) -1.24 -1.24 CTC110 Nond (-) carrier protein () with a (-) -1.24 -1.24 CTC110 No	B7G3C1	Triosephosphate isomerase	4	1.46
BTC188 3. oxacyl-(ay'-ariter protein) synthac 10 1.51 BTC718 3R-bytoxyacyl-gyt-ariter protein) synthac 2 1.60 BTC718 3R-bytoxyacyl-gyt-ariter protein 2 1.60 BTC718 Ark bytoxyacyl-gyt-ariter protein 2 1.61 BTC718 Ark bytoxyacyl-gyt-ariter protein 2 1.61 BTC718 Mathemyl-GAA CF manarylaci 2 1.61 BTC718 Mathemyl-GAA CF manarylaci 2 1.61 BTC718 Mathemyl-GAA CF dy synthesize 2 1.61 BT7526 Long chan acyl-GA synthesize 2 -1.51 BT7555 Inosine-S -monophase A delydrogenace 2 -1.23 BT7555 Inosine-S -monophase A delydrogenace 2 -1.44 ATTR8 Nucceoide diphosphate Kinas 1 6 1.23 BT7555 Inosine-S -monophase M delydrogenace 2 -1.44 ATTR8 Nucceoide diphosphate Kinas 2 -1.45 BT7550 Nucceoide diphosphate Kinas 2 -1.55 BT7819 365 riboonnal protein		Fatty acid biosynthesis		
BTCOM3-oxozó/l-jcy/-raire/potein) synthase101.51BTCAHSRayl carrier potein21.96BTRSNAyl carrier potein32.00BTRSNAyl carrier potein32.00DTRSNMinchandial giveraidehyte's phosphare dehydrogenase21.85BTSNSStacany AP destrusos2-1.73BTSNSStacany AP destrusos2-2.03BTSNSStacany AP destrusos2-2.03BTSNSStacany AP destrusos2-2.03BTSNSStarn dua ayl-con synthetase2-1.24BTSNSStarn dua ayl-con synthetase2-1.24BTSNSStarn dua ayl-con synthetase2-1.24BTTSNSNucleoside diphosphate kinase 161.25BTTSNSNucleoside diphosphate kinase 3-1.24BTTSNSNucleoside diphosphate kinase 1-1.44BTTSNSNucleoside diphosphate kinase 1-1.45BTTSNSNucleoside diphosphate kinase 1-1.45BTTSNSNucleoside diphosphate kinase 1-1.45BTTSNSNucleoside diphosphate kinase 1-1.46BTTSNSNucleoside diphosphate kinase 1-1.46BTTSNSStarlbanna prote	B7G1R8	3-oxoacyl-[acyl-carrier protein	11	1.71
FICDRB38-hydroxac/1-apd carrier protein41.41AGTORSAcyl carrier protein21.56BTRAXOMalagi/CoALAP transcriate21.31BTRAXOMainchontrial gyrenale/byte-3-photphate dehydrogenase21.31BTRAXOMainchontrial gyrenale/byte-3-photphate dehydrogenase21.31BTRAXOLong chain acyl-CoX professor7-1.78BTRAXOLong chain acyl-CoX professor7-1.31BTRAXOLong chain acyl-CoX professor7-1.31BTRAXOLong chain acyl-CoX professor7-1.32BTRAXOMacdocide biopathesis7-1.32BTRAXOMacdocide biopathesis7-1.43BTRAXOMacdocide biopathesis7-1.44BTRAXOMacdocide biopathesis1.5-1.45BTRAXOMacdocide biopathesis1.5-1.45BTRAXOSto fibosomal protein S13, chioroplastic2-1.45BTRAXOSto fibosomal protein S14, chioroplastic3-1.45BTRAXOSto fibosomal protein S14, chioroplas	B7GCM0	3-oxoacyl-[acyl-carrier-protein] synthase	10	1.51
ATTORSAdj Cartier protein2156BTRXMAdj Cartier protein32.00BTRXMMalonyl-CoA.PT transcrylase21.53CTSX2Mitconfold ally celladovel delydrogenase21.87BTRXMDiscryl CoA.Protectarane7-1.31BTRXMLang chain acj-CoA.Protectarae2-2.33BTRXMLang chain acj-CoA.Protectarae2-1.28BTRXMLang chain acj-CoA.Protectarae2-1.28BTRXMNetocic diposphate delydrogenase2-1.24Netocic diposphate delydrogenase2-1.24BTRMMNetocis diposphate delydrogenase2-1.24BTRMMNetocis diposphate kinase 11.25Transchoor1.251.24BTRMMNetocis diposphate kinase 1Transchoor1.251.24BTRMMNetocis diposphate kinase 1Transchoor1.251.24BTRMMNetocis diposphate kinase 1Transchoor1.251.24BTRMMNetocis diposphate kinase 1ADTRMS305 ribosomal protein 51, chloroplastic2-1.37ADTRMS305 ribosomal protein 51, chloroplastic2-1.37ADTRMS305 ribosomal protein 51, chloroplastic3-1.48CSD704305 ribosomal protein 51, chloroplastic3-1.46ADTRMS305 ribosomal protein 561.5- <tr< td=""><td>B7G7H8</td><td>3R-hydroxyacyl-[acyl carrier protein] dehydrase</td><td>4</td><td>1.41</td></tr<>	B7G7H8	3R-hydroxyacyl-[acyl carrier protein] dehydrase	4	1.41
BFR8b Adj carrier protein 3 2.00 DFC3D4 Minochondri al gorcaldetyde-3-phosphate detydrogenase 2 1.33 DFC3D4 Minochondri al gorcaldetyde-3-phosphate detydrogenase 2 1.38 DFW8D Long than Ag/-CA synthesia 2 -1.38 DFW7D5 Long than Ag/-CA synthesia 2 -2.03 DFW7D5 Stort of Advergenate 2 -2.03 DFW7D5 Nucleoride biosynthesis - -1.38 DFW7D5 Nucleoride biosynthesis - -1.44 DFW7D5 Nucleoride biosynthesis - -1.45 DFW7D5 Nucleoride biosynthesis -	A0T0F8	Acyl carrier protein	2	1.96
BTCDPAMaknyi-CoxArt transarylase21.41CUTNX2Minchondni al giveral delydrogenase21.33EV909Steuroyi-Art de staturase7-1.73BV509Luty chain acyt-Cox synthesize7-1.31BV709Luty chain acyt-Cox synthesize7-1.31BV709Luty chain acyt-Cox synthesize7-1.32BV709Purciscian 2-4 dennyt-Cox reductase2-1.32BV705Brott chain acyt-cox synthesize7-1.32BV7055Brott chain acyt-cox synthesize2-1.44BV7067Purciscian 2-4 dennyt-Cox reductase61.25BV7078Brott chain acyt-cox synthesize2-1.42BV7080Nucleoside diphosphate linase 161.25BV7081Brotsmoomal protein 514 chioroplastic2-1.62CUTN191Brotsmoomal protein 514 chioroplastic2-1.62CUTN191Brotsmoomal protein 5152-1.62CUTN191Brotsmoomal protein 514 chioroplastic2-1.51AUTOEDBrotsmoomal protein 52, chioroplastic3-1.63CUTN191Brotsmoomal protein 53, chioroplastic3-1.64CUTN191Brotsmoomal protein 54, chioroplastic3-1.64CUTN191Brotsmoomal protein 52, chioroplastic7-1.66CUTN191Brotsmoomal protein 54, chioroplastic7-1.66CUTN191Brotsmoomal protein 55-1.66-1.42CUTN191Brotsmoomal protein 55-1.66-1	B7FRX6	Acyl carrier protein	3	2.00
Q2TSX2 Mitochandral glyceraldehyde-3-phosphate dehydrogenase 2 1.38 ESYB25 Stacayl-ART desaturase 2 1.38 ESYB25 Long chain ayl-CoA synthetase 2 -1.38 ESYB25 Long chain ayl-CoA synthetase 2 -1.38 ESYB25 Long chain ayl-CoA synthetase 2 -1.38 ESYB25 Long chain ayl-CoA synthetase 2 -1.34 ESYB25 Long chain ayl-CoA synthetase 2 -1.44 ESYB25 Long chain ayl-CoA synthetase 2 -1.45 ESYB25 Long chain ayl-CoA synthetase 2 -1.45 ESYB26 Nuclosside diphosphate kinase 1 6 1.25 Translation 2 -1.45 1.55 Translation 2 -1.45 1.55 CD7040 30 fibosonal protein S14, chioroplastic 3 -1.56 AUT051 30 fibosonal protein S15, chioroplastic 3 -1.66 AUT052 30 fibosonal protein S12, chioroplastic 3 -1.43 DIFFM1 40 fibosonal	B7G3D4	Malonyl-CoA:ACP transacylase	2	1.41
F6Y083 Staramy-ACP desturase 2 1.48 Fry ADP Long chait asyl-Cox synthetase 2 -1.33 BYTAX0 Long chait asyl-Cox synthetase 7 -1.31 BYTAY7 Peroxisonial 2.4 denonyl-Cox incluctase 2 -2.03 BYTAY5 Short Chait asyl-con synthetase 2 -1.28 BYTAY5 Inclusion-5'-manaphanphate delydrogenase 2 -1.44 BYTAY5 Inclusion-5'-manaphanphate delydrogenase 2 -1.45 BYTAY5 Inclusion-5'-manaphanphate delydrogenase 2 -2.04 BYTAY5 Inclusion-5'-manaphanphate delydrogenase 2 -2.04 BYTAY5 Inclusion-1 protein S13, chloroplastic 2 -2.04 BYTAY5 Starbannal protein S14, chloroplastic 3 -1.57 BYTAY5 Starbannal protein S14, chloroplastic 3 -1.51 AUTOS 30's fibosonal protein S14, chloroplastic 3 -1.51 AUTOS 30's fibosonal protein S14, chloroplastic 3 -1.52 AUTOS 30's fibosonal protein S14 7	Q2TSX2	Mitochondrial glyceraldehyde-3-phosphate dehydrogenase	2	1.53
Fatty acid catabolism Path acid catabolism Path acid catabolism B7RAX6 Long chain acid-cos synthetase 7 -1.38 B7N977 Peroxisom 24-4 denoty-Colar reductase 2 -2.03 BYS185 Short chain acid-cos synthetase 3 -1.28 BYS185 Nucleotide biosynthese 6 -1.44 BYR180 Nucleotide biosynthese biase 1 6 -1.45 BYR180 Nucleotide biosynthese biase 1 6 -1.45 BYR180 Nucleotide biosynthese biase 1 6 -1.45 BYR180 306 ribosomal protein S13 (chioroplastic 2 -1.45 AUTORS 305 ribosomal protein S15 3 -1.12 AUTORS 305 ribosomal protein S2, chioroplastic 2 -1.37 AUTORS 305 ribosomal protein S2, chioroplastic 3 -1.13 AUTORS 305 ribosomal protein S2, chioroplastic 2 -2.26 DIFFN1 305 ribosomal protein S12 3 -1.45 AUTORS 305 ribosomal protein S12 -1.86 AUTORS	E6Y9B3	Stearoyl-ACP desaturase	2	1.48
BSYADPLong chain asyl-coa synthetase2-1.38BTRXOSLong chain asyl-coa synthetase7-1.31BTRXOSShort chain asyl-coarsigner A delydrogenase7-1.28PTTPSNuclear S- nonpublicis2-1.28PTTPSNuclear S- nonpublicis2-1.44PTTPSNuclear S- nonpublicis2-1.45PTTPSNucleoside chiphosphate kinase 161.55PTTPSNucleoside chiphosphate kinase 3-1.45AUTOBS30S ribosomal protein S13, chioroplastic2-2.04BTRS30S ribosomal protein S14, chioroplastic2-1.45CUSDT0430S ribosomal protein S15, chioroplastic3-1.51AUTOBS30S ribosomal protein S15, chioroplastic3-1.51AUTODS30S ribosomal protein S15, chioroplastic3-1.53AUTODS30S ribosomal protein S5, chioroplastic3-1.53AUTODS30S ribosomal protein S5, chioroplastic3-1.63AUTOS30S ribosomal protein S2, chioroplastic3-1.63AUTOS30S ribosomal protein S27-2.84PTTPND40S ribosomal protein S27-1.66AUTOS30S ribosomal protein S215-2.28PTTPND40S ribosomal protein S315-2.28PTTPND40S ribosomal protein S315-2.28PTTPND40S ribosomal protein S33-1.66AUTOS50S ribosomal protein S42-1.87PTTPND40S		Fatty acid catabolism		
BFTXX7 Perconsional 2-4-dinopleCons clustese 7 -1-31 BTXV77 Perconsional 2-4-dinopleCons clustese 2 -2.03 BSYRS Short chan acy-conzyme A dehydrogenase 2 -1.28 BYTES Incorine-5-monophosphate dehydrogenase 2 -1.44 BYTES Incorine-5-monophosphate dehydrogenase 6 1.55 BYTES Incorine-5-monophosphate dehydrogenase 2 -2.04 BYTES Translation 3 -1.45 AGTOBS 305 ribosomal protein S13, chirorplastic 2 -2.04 GST704 305 ribosomal protein S14, chirorplastic 3 -1.15 GST0704 305 ribosomal protein S2, chirorplastic 3 -1.63 AGTOBS 305 ribosomal protein S2, chirorplastic 3 -1.63 AGTOS 305 ribosomal protein S2, chirorplastic 3 -1.63 AGTOS 305 ribosomal protein S2, chirorplastic 3 -1.63 AGTOS 305 ribosomal protein S2, chirorplastic 3 -1.64 AGTOS 305 ribosomal protein S2 -1.64	B5Y4D9	Long chain acyl-CoA synthetase	2	-1.78
B/HW// Peroxisemal 2.4 -denonyl-CoA returkse 2 -1.23 BSFRES Short Chain Acyl-corexpine A dehydrogenase 2 -1.44 BSFRES Inosine-5-monophosphate dehydrogenase 2 -1.44 BSFRES Nucleoside diphosphate kinase 1 6 1.25 BSFRES Nucleoside diphosphate kinase 3 - - 1.45 AVTORS 305 ribosomal protein S14, chioroplastic 2 - 1.45 AVTORS 305 ribosomal protein S16, chioroplastic 2 - 1.51 AVTORS 305 ribosomal protein S16, chioroplastic 3 - 1.43 AVTORS 305 ribosomal protein S2, chioroplastic 3 - 1.43 AVTORS 305 ribosomal protein S2, chioroplastic 3 - 1.43 AVTORS 305 ribosomal protein S2, chioroplastic 3 - 1.43 AVTORS 305 ribosomal protein S2, chioroplastic 3 - 1.43 AVTORS 305 ribosomal protein S4 - - 1.56 BYTFMA1 405 ribosomal protei	B7FXX6	Long chain acyl-coa synthetase	7	- 1.31
BSTRO Short Chan Agy-Contryme / a drivingenase 5 - 1.28 B7FPS3 Inosine -5 - monophosphate delyrogenase 2 - 1.44 B7FPS3 Nucleoside diphosphate kinase 3 6 1.25 B7FR80 Nucleoside diphosphate kinase 3 6 1.25 A0708 305 ribosonal protein S13, chioroplastic 2 - 2.04 B7FR93 Maciecosite diphosphate kinase 3 3 - 1.82 G7008 305 ribosonal protein S14, chioroplastic 2 - 1.57 A0708 305 ribosonal protein S1, chioroplastic 3 - 1.48 G70704 305 ribosonal protein S1, chioroplastic 3 - 1.68 A07055 305 ribosonal protein S1, chioroplastic 3 - 1.63 A0705 305 ribosonal protein S1, chioroplastic 3 - 1.64 A0705 305 ribosonal protein S1 - - 1.65 J777N1 406 ribosonal protein S2 - - J777N2 406 ribosonal protein S2 - - J777N3 406 ribosonal protein 112, chioroplastic 7 - <td>B7FW77</td> <td>Peroxisomal 2.4-dienoyl-CoA reductase</td> <td>2</td> <td>- 2.03</td>	B7FW77	Peroxisomal 2.4-dienoyl-CoA reductase	2	- 2.03
Nucleance obsymbilities - 1.44 B7TPS5 Incidence obsymbilities - 1.44 B7TPS6 Nucleosite diphosphate kinase 1 6 1.25 ATOBS Translation - 1.45 ATOBS 30 inbound protein \$13. chloroplastic 2 - 1.45 ATOBS 30 inbound protein \$14. chloroplastic 3 - 1.82 COSD704 30 inbound protein \$16. chloroplastic 3 - 1.71 ATOBS 30 inbound protein \$16. chloroplastic 3 - 1.66 ATOBS 30 inbound protein \$2. chloroplastic 3 - 1.61 ATOBS 30 inbound protein \$3. chloroplastic 3 - 1.61 ATOBS 30 inbound protein \$3. chloroplastic 3 - 1.63 ATOBS 30 inbound protein \$3. chloroplastic 3 - 1.66 ATTPRA 40 inbound protein \$3. Chloroplastic 3 - 1.66 B7TPRA 40 inbound protein \$2. chloroplastic 7 - 1.66 ATTPRA 40 inbound protein \$6 - 1.87 - 1.87 ATTPRA 40 inbound protein \$6 - 1.42	B5Y5R5	Short chain acyl-coenzyme A dehydrogenase	5	- 1.28
D/Tr33 III03IIIC>3.101001010pliate kinase 1 6 1.23 B7TR80 Nucleoside diphosphate kinase 3 6 1.55 Transition 7 7 1.53 A0T03 305 ribosonal protein 514, chloroplastic 2 -2.04 B7TR91 305 ribosonal protein 514, chloroplastic 3 -1.57 A0T035 305 ribosonal protein 516, chloroplastic 3 -1.61 A0T055 305 ribosonal protein 52, chloroplastic 3 -1.61 A0T055 305 ribosonal protein 52, chloroplastic 3 -1.61 A0T055 305 ribosonal protein 52, chloroplastic 3 -1.63 A0T055 305 ribosonal protein 52, chloroplastic 3 -1.65 A0T055 305 ribosonal protein 52, chloroplastic 3 -1.65 A0T050 305 ribosonal protein 52, chloroplastic 3 -1.65 A0T051 405 ribosonal protein 53 -1.65 -1.66 A0T052 305 ribosonal protein 53 -1.66 -1.66 A0T051 55 ribosonal protein 111 -1.65 -1.67	DZEDEE	Nucleotide Diosynthesis	2	1 44
brtes Nuclessite injuspinate Kinsse 1 0 1.23 BTR80 Nuclessite injuspinate Kinsse 1 6 15 AUT0JS 305 ribosonal protein S13, chloroplastic 2 -1.45 AUT0JS 305 ribosonal protein S13, chloroplastic 2 -1.45 AUT0JS 305 ribosonal protein S16 3 -1.82 Q5D704 305 ribosonal protein S16, chloroplastic 3 -1.71 AUT055 305 ribosonal protein S2, chloroplastic 3 -1.63 AUT052 305 ribosonal protein S3, chloroplastic 3 -1.63 AUT052 305 ribosonal protein S3, chloroplastic 3 -1.63 AUT054 305 ribosonal protein S3, chloroplastic 3 -1.65 B7FHA1 405 ribosonal protein S3, chloroplastic 3 -1.65 B7FHA1 405 ribosonal protein S4 -1.64 -1.65 B7FHA1 405 ribosonal protein S4 -1.64 -1.65 B7FHA1 405 ribosonal protein S4 -2.28 -1.65 B07CC1 505 ribosonal protein S4 -2.17 -1.65	B/FP33 D7EDE9	Inosine-5'-monophosphale denydrogenase	2	- 1.44 1.25
Drikot Transition 1.33 A0T018 305 ribosomal protein S13, chloroplastic 5 -1.45 A0T018 305 ribosomal protein S14, chloroplastic 2 -2.04 B7T491 305 ribosomal protein S16, chloroplastic 2 -1.57 A0T018 305 ribosomal protein S16, chloroplastic 3 -1.71 A0T015 305 ribosomal protein S3, chloroplastic 4 -1.66 A0T015 305 ribosomal protein S3, chloroplastic 3 -1.51 A0T015 305 ribosomal protein S3, chloroplastic 3 -1.51 A0T015 305 ribosomal protein S16, chloroplastic 3 -1.66 A0T014 405 ribosomal protein S12 7 -1.66 B7FPM3 405 ribosomal protein S12 7 -1.66 B7FPM3 405 ribosomal protein S6 15 -2.28 B7FP80 405 ribosomal protein S13 -1.56 -1.45 A0T012 505 ribosomal protein S14 -1.66 -1.45 A0T014 505 ribosomal protein S14 -1.67 -1.68 A0T015 <td>D/FFE0 D7ED00</td> <td>Nucleoside diphosphate kinase 1</td> <td>6</td> <td>1.20</td>	D/FFE0 D7ED00	Nucleoside diphosphate kinase 1	6	1.20
ATTOB 305 ribosonal protein S14, chloroplastic 5 -1.45 MTTUB3 305 ribosonal protein S14, chloroplastic 2 -2.04 BTTUB1 305 ribosonal protein S16, chloroplastic 3 -1.82 GDTO4 305 ribosonal protein S2, chloroplastic 3 -1.87 AUTUB5 306 ribosonal protein S2, chloroplastic 4 -1.66 AUTUB5 306 ribosonal protein S2, chloroplastic 3 -1.41 AUTUB5 306 ribosonal protein S2, chloroplastic 3 -1.43 AUTUB5 306 ribosonal protein S2, chloroplastic 3 -1.45 AUTUS2 306 ribosonal protein S2, chloroplastic 3 -1.45 AUTUS4 406 ribosonal protein S4 7 -1.66 BTFNA1 406 ribosonal protein S4 7 -1.66 AUTUC1 506 ribosonal protein S4 3 -1.45 AUTUC2 506 ribosonal protein S4 -1.45 -1.45 AUTUC3 506 ribosonal protein S14, chloroplastic 3 -1.45 AUTUS4 506 ribosonal protein S14, chloroplastic 2	DTIKOU	Translation	0	1.55
ATTORB3 305 ribosomal protein S14, chloroplastic 2 -2.04 BTRU91 305 ribosomal protein S16, chloroplastic 2 -1.57 AOTDE0 306 ribosomal protein S1, chloroplastic 3 -1.71 AOTDE0 306 ribosomal protein S2, chloroplastic 4 -1.66 AOTDE3 306 ribosomal protein S2, chloroplastic 9 -1.51 AOTDE3 306 ribosomal protein S7, chloroplastic 3 -1.43 AOTDE2 305 ribosomal protein S7, chloroplastic 3 -1.66 BTFPN1 405 ribosomal protein S12 7 -1.66 BTFPN3 405 ribosomal protein S12 7 -1.66 BTFPN3 405 ribosomal protein S12 7 -1.66 AOTOC2 505 ribosomal protein S13 3 -1.56 AOTOC2 505 ribosomal protein S14 7 -1.66 AOTOC3 505 ribosomal protein S13 7 -1.66 AOTOC4 505 ribosomal protein S14 7 -1.67 AOTOC5 505 ribosomal protein S14 7 -1.68 AO	A0T018	30S ribosomal protein S13 chloroplastic	5	-145
B7191 305 rbssomal protein 515 3 -1.82 GSD704 305 rbssomal protein 516, chloroplastic 3 -1.57 A07050 305 rbssomal protein 52, chloroplastic 3 -1.71 A07055 305 rbssomal protein 52, chloroplastic 9 -1.51 A07055 305 rbssomal protein 57, chloroplastic 3 -1.43 A07052 305 rbssomal protein 57, chloroplastic 2 -2.56 B77PA1 405 rbssomal protein 58, chloroplastic 3 -1.66 B77PA1 405 rbssomal protein 53 3 -1.56 B77PA1 405 rbssomal protein 58 3 -1.66 B77PA1 405 rbssomal protein 58 3 -1.66 A070C1 505 rbssomal protein 11.1, chloroplastic 7 -1.66 A070C2 505 rbssomal protein 11.2, chloroplastic 3 -1.42 A070F0 505 rbssomal protein 11.2, chloroplastic 2 -1.87 A070F0 505 rbssomal protein 11.6, chloroplastic 2 -1.66 A070F0 505 rbssomal protein 11.6, chloroplastic 2 <td< td=""><td>A0T0B3</td><td>30S ribosomal protein S14, chloroplastic</td><td>2</td><td>-2.04</td></td<>	A0T0B3	30S ribosomal protein S14, chloroplastic	2	-2.04
CSD704305 ribsonal protein 52, chloroplastic2-1.57AOT05305 ribsonal protein 53, chloroplastic4-1.66AOT05305 ribsonal protein 53, chloroplastic3-1.43AOT05305 ribsonal protein 57, chloroplastic2-2.56BYTRA1405 ribsonal protein 53, chloroplastic2-2.56BYTRA1405 ribsonal protein 53, chloroplastic7-1.66BYTRA1405 ribsonal protein 538-1.87BYTRA1405 ribsonal protein 533-1.56BYTRA1405 ribsonal protein 5615-2.28BYTRA0405 ribsonal protein 577-1.66AOT05C505 ribsonal protein 11, chloroplastic7-1.66AOT05C505 ribsonal protein 11, chloroplastic6-1.45AOT05C505 ribsonal protein 11, chloroplastic2-1.87AOT06505 ribsonal protein 11, chloroplastic2-1.81AOT05C505 ribsonal protein 11, chloroplastic2-1.81AOT06505 ribsonal protein 11, chloroplastic2-1.81AOT06505 ribsonal protein 11, chloroplastic2-1.81AOT06505 ribsonal protein 12, chloroplastic2-1.81AOT06505 ribsonal protein 12, chloroplastic2-1.81AOT063505 ribsonal protein 12, chloroplastic2-1.81AOT064605 ribsonal protein 15, chloroplastic2-1.60AOT063505 ribsonal protein 15, chloroplastic3-1.26BYT03 </td <td>B7FU91</td> <td>30S ribosomal protein S15</td> <td>3</td> <td>-1.82</td>	B7FU91	30S ribosomal protein S15	3	-1.82
ATTORED 305 rhbosomal protein S2, chloroplastic 3 -1.71 ATTOR 305 rhbosomal protein S3, chloroplastic 9 -1.51 ATTORS 305 rhbosomal protein S3, chloroplastic 3 -1.43 ATTORS 305 rhbosomal protein S3, chloroplastic 3 -2.56 B7TPA1 405 rhbosomal protein S12 7 -1.66 B7TPA3 405 rhbosomal protein S3 8 -1.87 B5Y4X4 405 rhbosomal protein S6 15 -2.28 B7TPA3 405 rhbosomal protein S1 7 -1.66 A0TOCC 505 rhbosomal protein S1 7 -1.67 A0TOCC 505 rhbosomal protein L12, chloroplastic 7 -1.68 A0TOCC 505 rhbosomal protein L12, chloroplastic 3 -1.51 A0TOCC 505 rhbosomal protein L12, chloroplastic 2 -1.81 A0TOCC 505 rhbosomal protein L12, chloroplastic 2 -1.36 A0TOC1 505 rhbosomal protein L2, chloroplastic 2 -1.30 A0TOC3 505 rhbosomal protein L2, chloroplastic 2 -1.3	Q5D704	30S ribosomal protein S16, chloroplastic	2	-1.57
A0T015 305 rbsomal protein 53, chloroplastic 9 -1.51 A0T015 305 rbsomal protein 57, chloroplastic 3 -1.43 A0T015 305 rbsomal protein 57, chloroplastic 2 -2.56 B7FPA1 405 rbsomal protein 53, chloroplastic 7 -1.66 B7FPA1 405 rbsomal protein 53 8 -1.87 B7FPA1 405 rbsomal protein 53 3 -1.56 B7FPA1 405 rbsomal protein 51 -2.28 B7FPS0 405 rbsomal protein 11, chloroplastic 7 -1.66 A0T0C1 505 rbsomal protein 11, chloroplastic 7 -1.69 A0T0C2 505 rbsomal protein 11, chloroplastic 3 -1.17 A0T015 505 rbsomal protein 11, chloroplastic 3 -1.18 A0T016 505 rbsomal protein 11, chloroplastic 3 -1.17 A0T015 505 rbsomal protein 11, chloroplastic 2 -1.87 A0T016 505 rbsomal protein 112, chloroplastic 2 -1.60 A0T014 505 rbsomal protein 113 -1.25 -1.25	A0T0E0	30S ribosomal protein S2, chloroplastic	3	-1.71
A01015 305 ribosomal protein S5, chloroplastic 9 -1.51 A0100K2 305 ribosomal protein S9, chloroplastic 2 -2.56 B77PA1 405 ribosomal protein S12 7 -1.66 B77PA1 405 ribosomal protein S3 8 -1.87 B55YAK4 405 ribosomal protein S4 5 -2.28 B77PA1 405 ribosomal protein S5 -1.56 -2.28 B77PA3 405 ribosomal protein 11, chloroplastic 7 -1.66 A0T0C1 505 ribosomal protein 11, chloroplastic 7 -1.67 A0T0C2 505 ribosomal protein 114, chloroplastic 7 -1.87 A0T0C4 505 ribosomal protein 114, chloroplastic 2 -1.81 A0T016 505 ribosomal protein 12, chloroplastic 2 -1.81 A0T011 505 ribosomal protein 12, chloroplastic 2 -1.36 A0T014 505 ribosomal protein 12, chloroplastic 2 -1.36 A0T013 505 ribosomal protein 12, chloroplastic 2 -1.36 A0T014 505 ribosomal protein 12, chloroplastic 2 <td>A0T0I5</td> <td>30S ribosomal protein S3, chloroplastic</td> <td>4</td> <td>-1.66</td>	A0T0I5	30S ribosomal protein S3, chloroplastic	4	-1.66
ATORS305 ribosomal protein S7, chioroplastic3-1.43ATORX305 ribosomal protein S12-2.56B7FPA1405 ribosomal protein S127-1.66B7FPM3405 ribosomal protein S38-1.87B5Y484405 ribosomal protein S43-1.55ATORC505 ribosomal protein S63-1.56ATORC505 ribosomal protein 1.1, chioroplastic7-1.66ATORC505 ribosomal protein 1.1, chioroplastic17-1.69ATORC505 ribosomal protein 1.1, chioroplastic2-1.87ATORC505 ribosomal protein 1.14, chioroplastic2-1.81ATORC505 ribosomal protein 1.14, chioroplastic2-1.81ATORC505 ribosomal protein 1.14, chioroplastic2-1.81ATORC505 ribosomal protein 1.14, chioroplastic2-1.81ATORC505 ribosomal protein 1.2, chioroplastic2-1.36ATORC3505 ribosomal protein 1.2, chioroplastic2-1.36ATORC3505 ribosomal protein 1.2, chioroplastic2-1.37ATORC3605 ribosomal protein 1.3, chioroplastic2-1.37ATORC3605 ribosomal protein 1.3-1.42-1.32ATORC4605 ribosomal protein 1.3-1.43-1.32ATORC5605 ribosomal protein 1.3-1.36-1.42ATORC4605 ribosomal protein 1.36-1.42-1.32ATORC5605 ribosomal protein 1.36-1.43-1.52B7RU5605 ribosomal protein	A0T0J5	30S ribosomal protein S5, chloroplastic	9	-1.51
A0T00K2 305 ribosomal protein S9, chloroplastic 2 -2.56 B7FPA1 405 ribosomal protein S3a 8 -1.87 B5Y4X4 405 ribosomal protein S6 15 -2.28 B5Y4X4 405 ribosomal protein S6 3 -1.56 A0T0C1 505 ribosomal protein L1, chloroplastic 6 -1.45 A0T0C2 505 ribosomal protein L1, chloroplastic 7 -1.69 A0T0C0 505 ribosomal protein L12, chloroplastic 3 -1.42 A0T004 505 ribosomal protein L14, chloroplastic 3 -1.42 A0T019 505 ribosomal protein L16, chloroplastic 2 -1.81 A0T011 505 ribosomal protein L16, chloroplastic 2 -1.81 A0T014 505 ribosomal protein L2, chloroplastic 2 -1.81 A0T014 505 ribosomal protein L2, chloroplastic 2 -1.81 A0T013 505 ribosomal protein L18, chloroplastic 2 -1.81 A0T014 505 ribosomal protein L18, chloroplastic 2 -1.81 A0T013 505 ribosomal protein L18, chloroplastic 2 -1.81 A0T014 505 ribosomal prot	A0T0K5	30S ribosomal protein S7, chloroplastic	3	-1.43
B7PPA1 405 ribosonal protein S12 7 -1.66 B7PPA3 405 ribosonal protein S6 15 -2.28 B7PF80 405 ribosonal protein S8 3 -1.66 A0T0C1 505 ribosonal protein L1, chloroplastic 7 -1.66 A0T0C2 505 ribosonal protein L1, chloroplastic 6 -1.45 A0T0C1 505 ribosonal protein L13, chloroplastic 7 -1.69 A0T0C1 505 ribosonal protein L14, chloroplastic 3 -1.42 A0T0C1 505 ribosonal protein L14, chloroplastic 3 -1.42 A0T0C1 505 ribosonal protein L14, chloroplastic 2 -1.81 A0T0C3 505 ribosonal protein L14, chloroplastic 2 -1.60 A0T0C4 505 ribosonal protein L12, chloroplastic 2 -1.36 A0T0C3 505 ribosonal protein L21, chloroplastic 2 -1.36 A0T014 505 ribosonal protein L3, chloroplastic 2 -1.37 A0T033 505 ribosonal protein L3, chloroplastic 2 -1.36 A0T045 605 ribosonal protein L3 60 -1.62 B7C045 605 ribosonal protein L36	A0T0K2	30S ribosomal protein S9, chloroplastic	2	-2.56
B7PPM3405 ribosomal protein S365-1.87B5Y4X4405 ribosomal protein S615-2.28B7PR0405 ribosomal protein S63-1.66A0T0C1505 ribosomal protein 11, chloroplastic7-1.66A0T0C2505 ribosomal protein 11, chloroplastic6-1.45A0T0C1505 ribosomal protein 11, chloroplastic7-1.69A0T0C1505 ribosomal protein 1132-1.87A0T019505 ribosomal protein 114, chloroplastic3-1.42A0T016505 ribosomal protein 119, chloroplastic2-1.81A0T017505 ribosomal protein 119, chloroplastic2-1.60A0T018505 ribosomal protein 12, chloroplastic2-1.60A0T014505 ribosomal protein 12, chloroplastic2-1.61A0T014505 ribosomal protein 12, chloroplastic2-1.61A0T014505 ribosomal protein 12, chloroplastic2-1.61A0T018505 ribosomal protein 13, chloroplastic2-1.61A0T014505 ribosomal protein 137-1.34B7C0R5605 ribosomal protein 14810-1.77B7F113605 ribosomal protein 1489-1.62B7C0R6Glutamyl-tran synthase6-1.62B7C0R7Elukarjoti Cator Tu10-1.62B7C0R8Eukaryotic translation initiation factor 3 subunit A9-1.62B7C0R6Glutamyl-tran synthase6-1.62B7C0R7Ribosomal protein 1156	B7FPA1	40S ribosomal protein S12	7	-1.66
B5Y4X4405 ribosomal protein S615-2.28B7FP80405 ribosomal protein L1, chloroplastic7-1.56A0T0C1505 ribosomal protein L1, chloroplastic6-1.45A0T0C2505 ribosomal protein L12, chloroplastic17-1.69A0T0K1505 ribosomal protein L12, chloroplastic3-1.42A0T016505 ribosomal protein L14, chloroplastic3-1.42A0T016505 ribosomal protein L16, chloroplastic2-1.81A0T016505 ribosomal protein L12, chloroplastic2-1.81A0T016505 ribosomal protein L2, chloroplastic2-1.36A0T014505 ribosomal protein L2, chloroplastic2-1.36A0T014505 ribosomal protein L2, chloroplastic2-1.36A0T014505 ribosomal protein L2, chloroplastic2-1.36A0T014505 ribosomal protein L2, chloroplastic2-1.34A0T013505 ribosomal protein L3, chloroplastic2-1.34A0T014505 ribosomal protein L37-1.24A0T013505 ribosomal protein L37-1.34B7CB3605 ribosomal protein L39-2.08B7FUV3605 ribosomal protein L37-1.48E9PA17Elongation factor Ts.10-1.62B7CG16Glutamyl-tran synthase4-1.52B7SU3Ribosomal protein L197-1.49Protein processing7-1.48B7CG16Glutamyl-tran synthase11-1.33	B7FPM3	40S ribosomal protein S3a	8	-1.87
B/H80 40s mbosomal protein L1, chloroplastic 7 -1.56 AOTOC1 50s ribosomal protein L1, chloroplastic 6 -1.45 AOTOC2 50s ribosomal protein L1, chloroplastic 6 -1.45 AOTOC4 50s ribosomal protein L12, chloroplastic 7 -1.69 AOTOK1 50s ribosomal protein L14, chloroplastic 3 -1.42 AOTOG1 50s ribosomal protein L16, chloroplastic 3 -1.42 AOTOC7 50s ribosomal protein L12, chloroplastic 2 -1.81 AOTO14 50s ribosomal protein L2, chloroplastic 2 -1.60 AOTO45 50s ribosomal protein L2, chloroplastic 2 -1.36 AOTO44 50s ribosomal protein L2, chloroplastic 2 -1.36 AOTO45 50s ribosomal protein L3, chloroplastic 2 -1.36 AOTO44 50s ribosomal protein L3, chloroplastic 2 -1.37 AOTO45 60s ribosomal protein L3 10 -1.77 B7GO85 60s ribosomal protein L36 9 -2.08 B7FUV3 60s ribosomal protein L36 9 -1.30 B7GC16 Glutamyl-tran synthase<	B5Y4X4	40S ribosomal protein S6	15	-2.28
A010C1 505 mbosomal protein 11, chloroplastic 6 -1.45 A070C2 505 mbosomal protein 112, chloroplastic 17 -1.69 A070C1 505 mbosomal protein 113, chloroplastic 2 -1.87 A070C2 505 mbosomal protein 114, chloroplastic 3 -1.42 A07016 505 mbosomal protein 116, chloroplastic 4 -2.17 A070C7 505 mbosomal protein 12, chloroplastic 6 -2.03 A07011 505 mbosomal protein 12, chloroplastic 6 -2.03 A07023 505 mbosomal protein 12, chloroplastic 2 -1.80 A07044 505 mbosomal protein 12, chloroplastic 2 -1.30 A07053 505 mbosomal protein 12, chloroplastic 2 -1.31 A07064 505 mbosomal protein 13, chloroplastic 2 -1.31 B7C085 605 mbosomal protein 13 10 -1.77 B7C085 605 mbosomal protein 16 7 -1.48 B7C075 605 mbosomal protein 16 9 -1.30 B7C076 Gluamyl-rtna synthase 9 -1.36 B7C078 Eukaryotic translation inititof factor 3 subunit A <td>B7FP80</td> <td>40S ribosomal protein S8</td> <td>3</td> <td>-1.56</td>	B7FP80	40S ribosomal protein S8	3	-1.56
AUTOC2 SDS TROSOMAL protein L11, chloroplastic 6 -1.45 AOTOC0 SDS ribosomal protein L12, chloroplastic 17 -1.69 AOTOK1 SDS ribosomal protein L13, chloroplastic 2 -1.87 AOTOC1 SDS ribosomal protein L16, chloroplastic 3 -1.42 AOTOC7 SDS ribosomal protein L19, chloroplastic 2 -1.81 AOTOC3 SDS ribosomal protein L21, chloroplastic 2 -1.60 AOTOG3 SDS ribosomal protein L21, chloroplastic 2 -1.36 AOTOG4 SDS ribosomal protein L21, chloroplastic 2 -1.31 AOTOG3 SDS ribosomal protein L3, chloroplastic 2 -1.32 AOTOJ3 SOS ribosomal protein L3, chloroplastic 2 -1.31 AOTOJ3 SOS ribosomal protein L3 0 -1.77 B7GQ5 GOS ribosomal protein L36 9 -2.08 B7FUY3 GOS ribosomal protein L36 9 -1.62 B7GQ7 Elongation factor Ts, mitochondrial 6 -1.36 B7GC16 Glutamyl-tran synthase 4	AUTOCI	505 ribosomal protein L1, chloroplastic	/	- 1.66
A0TOK1 505 Thosomal protein L12, chloroplastic 17 -1.69 A0TOK1 505 ribosomal protein L13 2 -1.87 A0TOK1 505 ribosomal protein L14, chloroplastic 3 -1.42 A0TOK1 505 ribosomal protein L19, chloroplastic 4 -2.17 A0TOK7 505 ribosomal protein L2, chloroplastic 2 -1.81 A0TOK3 505 ribosomal protein L2, chloroplastic 2 -1.36 A0TOK3 505 ribosomal protein L2, chloroplastic 2 -1.36 A0TOK4 505 ribosomal protein L3, chloroplastic 2 -1.36 A0TOK8 505 ribosomal protein L3, chloroplastic 2 -1.31 A0TOK3 505 ribosomal protein L3, chloroplastic 2 -1.34 B7GQC2 605 ribosomal protein L13 7 -1.34 B7GQR5 605 ribosomal protein L6 7 -1.48 E9PAI7 Elongation factor Ts, mitochondrial 7 -1.48 E9PAI7 Elongation factor Ts, subunit A 9 -1.52 B7CG05 605 ribosomal protein L19 7 -1.49 Protein processing 7 -1.49	AUTUC2	505 ribosomal protein L11, chloroplastic	5	- 1.45
AOTON Sol hussimal protein 113 2 -1.87 AOTON 505 ribosomal protein 114, chloroplastic 3 -1.42 AOTON 505 ribosomal protein 114, chloroplastic 4 -2.17 AOTON 505 ribosomal protein 12, chloroplastic 2 -1.81 AOTON 505 ribosomal protein 12, chloroplastic 2 -1.60 AOTON 505 ribosomal protein 12, chloroplastic 2 -1.36 AOTON 505 ribosomal protein 12, chloroplastic 2 -1.92 AOTON 505 ribosomal protein 12, chloroplastic 2 -1.91 AOTON 505 ribosomal protein 13, chloroplastic 2 -1.91 AOTON 505 ribosomal protein 13, chloroplastic 2 -1.91 B7GOR5 605 ribosomal protein 136 10 -1.77 B7FT13 605 ribosomal protein 136 9 -2.08 B7GOR5 605 ribosomal protein 16 -1.36 -1.36 B7GC11 Elongation factor Tu 10 -1.62 B7GC18 Eukaryotic translation initiation factor 3 subunit A 9 -	A010C0 A0T0K1	505 ribosomal protein L12, chioropiastic	17	- 1.09
ArtolicSol hosomal protein L16, chloroplasticJ1.42AOTOIC505 ribosomal protein L19, chloroplastic2-1.81AOTOIT505 ribosomal protein L2, chloroplastic6-2.03AOTOIA505 ribosomal protein L2, chloroplastic2-1.60AOTOIA505 ribosomal protein L2, chloroplastic2-1.36AOTOIA505 ribosomal protein L2, chloroplastic2-1.91AOTOIA505 ribosomal protein L3, chloroplastic2-1.91AOTOIA505 ribosomal protein L3, chloroplastic2-1.91B7CGQC2605 ribosomal protein L310-1.77B7CQR5605 ribosomal protein L369-2.08B7FUV3605 ribosomal protein L369-2.08B7FUV3605 ribosomal protein L369-1.48E9PAI/TElongation factor Ts, mitochondrial6-1.36B7CGT6Glutamyl-trna synthase4-1.52B7CGT6Glutamyl-trna synthase6-1.62B7CAA5Ribosomal protein L197-1.49Protein processing-1.45-1.45B7CS14Importin subunit alpha10-1.62B7CG15Glucacharpterian, chloroplastic3-1.45B7CS14Importin subunit alpha101.54B7CS15Peptidyl-prolyl cis-trans isomerase91.61B7CF13Peptidyl-prolyl cis-trans isomerase171.63B7FU3Peptidyl-prolyl cis-trans isomerase41.59	ΑΟΤΟΙΟ	505 ribosomal protein L15	2	-1.47
AOTOC50S ribosomal protein L19, chloroplastic2-1.81AOTOC150S ribosomal protein L2, chloroplastic6-2.03AOTOG350S ribosomal protein L2, chloroplastic2-1.60AOTO450S ribosomal protein L2, chloroplastic2-1.36AOTO450S ribosomal protein L2, chloroplastic2-1.37AOTO450S ribosomal protein L3, chloroplastic2-1.91B7C9C260S ribosomal protein L137-1.34B7C9C560S ribosomal protein L18a10-1.77B7FL1360S ribosomal protein L67-1.48B9RV7Elongation factor Ts, mitochondrial6-1.36B7C075GU sribosomal protein L67-1.48B7C078Eukaryotic translation initiation factor 3 subunit A9-1.30B7C076Gu tamyl-tran synthase4-1.52B5Y502Ribosomal protein L197-1.49Protein processing	A0T015	505 ribosomal protein L16, chloroplastic	4	-217
AOTOI150S ribosomal protein 12, chloroplastic6-2.03AOTTOC350S ribosomal protein 121, chloroplastic2-1.60AOTTOI450S ribosomal protein 12, chloroplastic2-1.36AOTTOI850S ribosomal protein 13, chloroplastic4-1.92AOTTOI350S ribosomal protein 13, chloroplastic2-1.31B7C9G260S ribosomal protein 137-1.34B7C0R560S ribosomal protein 1369-2.08B7FUV360S ribosomal protein 167-1.48B7FLV360S ribosomal protein 167-1.48B7CAT1Elongation factor Ts, mitochondrial6-1.36B7CAT1Elongation factor Ts, mitochondrial6-1.30B7CCT6Gutanyl-transynthase4-1.52B7SD2Ribosomal protein 1156-1.62B7CCT6Gutanyl-transynthase4-1.52B7CDT6Glubasomal protein 119-1.33-1.49Protein processing7-1.49AOTOH660 kDa chaperonin, chloroplastic11-1.33B7CB7ER luminal binding protein33-1.45B7CS14Importin subunit alpha1001.54B7CG13Peptidyl-prolyl cis-trans isomerase3-1.26B7C914Peptidyl-prolyl cis-trans isomerase3-1.26B7C915Peptidyl-prolyl cis-trans isomerase171.63	A0T0C7	505 ribosomal protein L19, chloroplastic	2	-1.81
A0T0C350S ribosomal protein L2, chloroplastic2-1.60A0T01450S ribosomal protein L2, chloroplastic2-1.36A0T01850S ribosomal protein L3, chloroplastic4-1.92A0T01350S ribosomal protein L3, chloroplastic2-1.91B7C9C260S ribosomal protein L137-1.34B7C0K560S ribosomal protein L130-1.77B7C0K560S ribosomal protein L137-1.48B7TL360S ribosomal protein L369-2.08B7FLV360S ribosomal protein L67-1.48E9PA17Elongation factor Ts, mitochondrial6-1.36B7CC16Glutamyl-trna synthase4-1.52B7C502Ribosomal protein L197-1.49Protein processing7-1.49Protein processing11-1.33B7CB7ER luminal binding protein33-1.45B7C514Importin subunit alpha101.54B7C528Oligosaccharyl transferase3-1.26B7C544Importin subunit alpha101.54B7C545Peptidyl-prolyl cis-trans isomerase91.61B7C546Peptidyl-prolyl cis-trans isomerase91.61B7FC13Peptidyl-prolyl cis-trans isomerase41.59	A0T0I1	50S ribosomal protein L2. chloroplastic	6	-2.03
A0T01450S ribosomal protein L22, chloroplastic2-1.36A0T014850S ribosomal protein L3, chloroplastic4-1.92A0T01350S ribosomal protein L6, chloroplastic2-1.91B7G9G260S ribosomal protein L137-1.34B7C0R560S ribosomal protein L18a10-1.77B7FT1360S ribosomal protein L369-2.08B7FUV360S ribosomal protein L67-1.48B7C0R560S ribosomal protein L66-1.36B7FL1360S ribosomal protein L67-1.48B7G0T4Elongation factor Ts, mitochondrial6-1.36B7C0T8Eukaryotic translation initiation factor 3 subunit A9-1.62B7C0T8Eukaryotic translation initiation factor 3 subunit A9-1.62B7C0T8Eukaryotic translation initiation factor 3 subunit A9-1.30B7CCT6Glutamyl-trna synthase4-1.52B7CAA5Ribosomal protein L197-1.49Protein processing7-1.49Protein processing11-1.33B7C514Importin subunit alpha101.54B7C624B7C624Ingortin subunit alpha101.54B7C514Importin subunit alpha101.54B7C625Oligosaccharyl transferase3-1.26B7C913Peptidyl-prolyl cis-trans isomerase91.61B7FD3Peptidyl-prolyl cis-trans isomerase41.59	A0T0G3	50S ribosomal protein L21, chloroplastic	2	-1.60
A0T0H8 50S ribosomal protein L3, chloroplastic 4 -1.92 A0T0J3 50S ribosomal protein L6, chloroplastic 2 -1.91 B7G0G2 60S ribosomal protein L13 7 -1.34 B7C0R5 60S ribosomal protein L18 10 -1.77 B7FTL3 60S ribosomal protein L36 9 -2.08 B7FUV3 60S ribosomal protein L6 7 -1.48 E9PA/7 Elongation factor Ts, mitochondrial 6 -1.52 B7CC0T6 Glutamyl-tran synthase 9 -1.30 B7CCT6 Glutamyl-tran synthase 9 -1.32 B7CC4A5 Ribosomal protein L19 7 -1.49 Protein processing 7 -1.49 B7FUB7 ER luminal binding protein 10 -1.52 B7GC16 Glutamyl-tran synthase 7 -1.49 Protein processing 7 -1.49 -1.49 B7GC16 Glutamyl-tran synthase 7 -1.49 B7GC16 Glutamyl-tran synthase 7 -1.49 B7GC16 Glutamyl-tran synthase 10 1.54	A0T0I4	50S ribosomal protein L22, chloroplastic	2	-1.36
A0T0]3 50S ribosomal protein L6, chloroplastic 2 -1.91 B7C0GC2 60S ribosomal protein L13 7 -1.34 B7G0R5 60S ribosomal protein L18a 10 -1.77 B7FLT3 60S ribosomal protein L36 9 -2.08 B7FLV3 60S ribosomal protein L6 7 -1.48 E9PA17 Elongation factor Ts, mitochondrial 6 -1.36 B7CG11 Elongation factor Tu 10 -1.62 B7CG76 Glutamyl-trna synthase 4 -1.52 B5Y502 Ribosomal protein L15 6 -1.62 B7CG76 Glutamyl-trna synthase 7 -1.49 Protein processing 7 -1.49 -1.49 Protein processing 7 -1.33 -1.49 B7CG14 Importin subunit alpha 10 1.54 B7CG54 Dilgosacharyl transferase 33 -1.45 B7G514 Importin subunit alpha 10 1.54 B7CE38 Oligosacharyl tris-trans isomerase 9 1.61 B7FQT3 Peptidyl-prolyl cis-trans isomerase 17 1.63<	A0T0H8	50S ribosomal protein L3, chloroplastic	4	-1.92
B7G9C260S ribosmal protein L137-1.34B7C0R560S ribosmal protein L18a10-1.77B7FTL360S ribosmal protein L369-2.08B7FUV360S ribosmal protein L67-1.48E9PAI7Elongation factor Ts, mitochondrial6-1.36B7CA11Elongation factor Tu10-1.62B7C0T8Eukaryotic translation initiation factor 3 subunit A9-1.30B7CCT6Glutamyl-trna synthase4-1.52B7GAA5Ribosmal protein L156-1.62B7CAT6Glutamyl-trna synthase7-1.49Protein processing7-1.49Protein processing7-1.45B7C514Importin subunit alpha101.54B7C538Oligosaccharyl transferase3-1.26B7C73Peptidyl-prolyl <i>cis</i> -trans isomerase91.63B7FSV6Peptidyl-prolyl <i>cis</i> -trans isomerase171.63	A0T0J3	50S ribosomal protein L6, chloroplastic	2	- 1.91
B7G0R560S ribosomal protein L18a10-1.77B7FTL360S ribosomal protein L369-2.08B7FUV360S ribosomal protein L67-1.48E9PAI7Elongation factor Ts, mitochondrial6-1.36B7GA11Elongation factor Tu10-1.62B7C0T8Eukaryotic translation initiation factor 3 subunit A9-1.30B7GCT6Glutamyl-trna synthase4-1.52B7S502Ribosomal protein L156-1.62B7CAA5Ribosomal protein L197-1.49Protein processing7-1.49B7FUB7ER luminal binding protein11-1.33B7G514Importin subunit alpha101.54B7G538Oligosaccharyl transferase3-1.26B5Y4H4Peptidyl-prolyl cis-trans isomerase91.61B7FVS6Peptidyl-prolyl cis-trans isomerase41.59	B7G9G2	60S ribosomal protein L13	7	-1.34
B7FTL3 60S ribosomal protein L36 9 -2.08 B7FUV3 60S ribosomal protein L6 7 -1.48 E9PAI7 Elongation factor Ts, mitochondrial 6 -1.36 B7GA1 Elongation factor Tu 10 -1.62 B7COT8 Eukaryotic translation initiation factor 3 subunit A 9 -1.30 B7GCT6 Glutamyl-trna synthase 4 -1.52 B5YS02 Ribosomal protein L15 6 -1.62 B7GAA5 Ribosomal protein L19 7 -1.49 Protein processing 7 -1.49 A0T0H6 60 kDa chaperonin, chloroplastic 11 -1.33 B7FCB3 ER luminal binding protein 33 -1.45 B7GC54 Importin subunit alpha 10 1.54 B7CE38 Oligosaccharyl transferase 3 -1.26 B37H44 Peptidyl-prolyl <i>cis</i> -trans isomerase 9 1.61 B37EV56 Peptidyl-prolyl <i>cis</i> -trans isomerase 4 1.59	B7G0R5	60S ribosomal protein L18a	10	-1.77
B7FUV360S ribosomal protein L67-1.48E9PAI7Elongation factor Ts, mitochondrial6-1.36B7CA11Elongation factor Tu10-1.62B7CA13Eukaryotic translation initiation factor 3 subunit A9-1.30B7CCT6Glutamyl-trna synthase4-1.52B5Y502Ribosomal protein L156-1.62B7CAA5Ribosomal protein L197-1.49Protein processing7-1.49A0T0H660 kDa chaperonin, chloroplastic11-1.33B7FUB7ER luminal binding protein33-1.45B7C514Importin subunit alpha101.54B7CE38Oligosaccharyl transferase3-1.26B7FU73Peptidyl-prolyl <i>cis</i> -trans isomerase91.61B7FSV6Peptidyl-prolyl <i>cis</i> -trans isomerase41.59	B7FTL3	60S ribosomal protein L36	9	-2.08
E9PAI7Elongation factor Ts, mitochondrial6-1.36B7CA11Elongation factor Tu10-1.62B7CA11Elongation factor Tu9-1.30B7COT8Eukaryotic translation initiation factor 3 subunit A9-1.30B7CCT6Glutamyl-trna synthase4-1.52B5YS02Ribosomal protein L156-1.62B7CAA5Ribosomal protein L197-1.49Protein processing11-1.33B7FUB7ER luminal binding protein33-1.45B7C514Importin subunit alpha101.54B7CE38Oligosaccharyl transferase3-1.26B7FU73Peptidyl-prolyl <i>cis</i> -trans isomerase91.61B7FSV6Peptidyl-prolyl <i>cis</i> -trans isomerase171.63B7FSV6Peptidyl-prolyl <i>cis</i> -trans isomerase41.59	B7FUV3	60S ribosomal protein L6	7	-1.48
B7GA11Elongation factor Tu10-1.62B7GOT8Eukaryotic translation initiation factor 3 subunit A9-1.30B7GCT6Glutamyl-trna synthase4-1.52B5Y502Ribosomal protein L156-1.62B7GAA5Ribosomal protein L197-1.49Protein processing11-1.33B7FUB7ER luminal binding protein33-1.45B7G514Importin subunit alpha101.54B7GE38Oligosaccharyl transferase3-1.26B7FU73Peptidyl-prolyl <i>cis</i> -trans isomerase91.61B7FSV6Peptidyl-prolyl <i>cis</i> -trans isomerase171.63	E9PAI7	Elongation factor Ts, mitochondrial	6	-1.36
B7G018Eukayotic translation initiation factor 3 subunit A9-1.30B7GCT6Glutamyl-trna synthase4-1.52B5Y502Ribosomal protein L156-1.62B7GA45Ribosomal protein L197-1.49Protein processing11-1.33B7FUB7ER luminal binding protein33-1.45B7G514Importin subunit alpha101.54B7GE38Oligosaccharyl transferase3-1.26B7FU37Peptidyl-prolyl <i>cis</i> -trans isomerase91.61B7FV67Peptidyl-prolyl <i>cis</i> -trans isomerase171.63B7FSV6Peptidyl-prolyl <i>cis</i> -trans isomerase41.59	B7GA11	Elongation factor Tu	10	-1.62
BYGC16Glutallyl-trila Synthase4-1.52BSY502Ribosomal protein L156-1.62B7GAA5Ribosomal protein L197-1.49Protein processing11-1.33B7FUB7ER luminal binding protein33-1.45B7G514Importin subunit alpha101.54B7GE38Oligosaccharyl transferase3-1.26B7FU73Peptidyl-prolyl cis-trans isomerase91.61B7FV67Peptidyl-prolyl cis-trans isomerase171.63B7FSV6Peptidyl-prolyl cis-trans isomerase41.59	B/G018	Eukaryotic translation initiation factor 3 subunit A	9	- I.30
B3502Ribosonial protein L156- 1.62B7GA45Ribosonal protein L197- 1.49Protein processing11- 1.33B7FUB7ER luminal binding protein33- 1.45B7G514Importin subunit alpha101.54B7G538Oligosacharyl transferase3- 1.26B374H4Peptidyl-prolyl cis-trans isomerase91.61B7FV67Peptidyl-prolyl cis-trans isomerase171.63B7FV6Peptidyl-prolyl cis-trans isomerase41.59	B/GCI6	Giutamyi-trna syntnase	4	- 1.52
AOTOH660 kDa chaperonin, chloroplastic11-1.33B7FUB7ER luminal binding protein33-1.45B7G514Importin subunit alpha101.54B7G538Oligosaccharyl transferase3-1.26B5Y4H4Peptidyl-prolyl <i>cis</i> -trans isomerase91.61B7FQT3Peptidyl-prolyl <i>cis</i> -trans isomerase171.63B7FSV6Peptidyl-prolyl <i>cis</i> -trans isomerase41.59	BOYOUZ BZCAAE	Ribosonial protein L10	5	- 1.62
A0T0H660 kDa chaperonin, choroplastic11-1.33B7FUB7ER luminal binding protein33-1.45B7C514Importin subunit alpha101.54B7C58Oligosaccharyl transferase3-1.26B5Y4H4Peptidyl-prolyl <i>cis</i> -trans isomerase91.61B7FQT3Peptidyl-prolyl <i>cis</i> -trans isomerase171.63B7FSV6Peptidyl-prolyl <i>cis</i> -trans isomerase41.59	D/GAAD	NUUSUIIdi PIOLEII LIS	/	- 1.49
RotorioDo the imperior11- 1.33B7FUB7ER luminal binding protein33- 1.45B7G514Importin subunit alpha101.54B7G28Oligosaccharyl transferase3- 1.26B5Y4H4Peptidyl-prolyl <i>cis</i> -trans isomerase91.61B7FQT3Peptidyl-prolyl <i>cis</i> -trans isomerase171.63B7FSV6Peptidyl-prolyl <i>cis</i> -trans isomerase41.59	AOTOHS	60 kDa chaperonin chloronlastic	11	_1 32
B7C514Importin subunit photon101.54B7C538Oligosaccharyl transferase3-1.26B5Y4H4Peptidyl-prolyl <i>cis</i> -trans isomerase91.61B7FQT3Peptidyl-prolyl <i>cis</i> -trans isomerase171.63B7FSV6Peptidyl-prolyl <i>cis</i> -trans isomerase41.59	R7FUR7	FR luminal hinding protein	33	-1.55 -1.45
B7CE38Oligosaccharyl transferase1071.04B7CE38Oligosaccharyl transferase3-1.26B5Y4H4Peptidyl-prolyl <i>cis</i> -trans isomerase91.61B7FQT3Peptidyl-prolyl <i>cis</i> -trans isomerase171.63B7FSV6Peptidyl-prolyl <i>cis</i> -trans isomerase41.59	B7G5I4	Importin subunit alpha	10	1.4
B5Y4H4Peptidyl-prolyl <i>cis</i> -trans isomerase91.61B7FQT3Peptidyl-prolyl <i>cis</i> -trans isomerase171.63B7FSV6Peptidyl-prolyl <i>cis</i> -trans isomerase41.59	B7GE38	Oligosaccharvl transferase	3	-1.26
B7FQT3Peptidyl-prolyl <i>cis</i> -trans isomerase171.63B7FSV6Peptidyl-prolyl <i>cis</i> -trans isomerase41.59	B5Y4H4	Peptidyl-prolyl <i>cis</i> -trans isomerase	9	1.61
B7FSV6 Peptidyl-prolyl <i>cis</i> -trans isomerase 4 1.59	B7FQT3	Peptidyl-prolyl <i>cis</i> -trans isomerase	17	1.63
	B7FSV6	Peptidyl-prolyl cis-trans isomerase	4	1.59

Table 1 (continued)

Uniprot ID	Protein name	# Peptides	Fold Change
B7FPA6	Peptidyl-prolyl cis-trans isomerase	2	1.88
B7FZL3	Peptidyl-prolyl <i>cis</i> -trans isomerase	7	1.50
B7G5I3	Peptidyl-prolyl <i>cis</i> -trans isomerase	2	1.55
B7GB02	T-complex protein 1 subunit delta	3	-1.28
	Proteolysis		
B7FU90	Proteasome subunit alpha type	2	-1.29
B7G2F7	Regulatory proteasome non-atpase subunit 1	2	- 1.39
B7FY02	Ubiquitin extension protein 3	18	1.51
	Nitrogen Metabolism		
B7G8X8	Aliphatic amidase	2	2.24
B7GEG8	CPS III, carbamoyl-phosphate synthase mitochondrial	39	-2.57
B7FYS6	Formidase	5	2.27
B7G997	Nitrate reductase	22	-2.33
B7FZW5	Urea transporter	3	2.38
	Cytoskeleton/cellular transport		
B7G5C0	Actin/actin like protein	9	1.70
B7G878	Actin/actin like protein	23	1.42
B7FY56	Coronin	5	1.31
B7FTS7	Det3-like protein	7	1.54
B7FUJ2	Gelosin/severin like protein	6	2.42
	Histone		
B7FR39	Histone H3	8	1.29
B7FX68	Histone H4	12	-2.13
B7FX66	Histone linker H1	6	1.51
B7FTP2	N-terminal histone linker H1	5	1.66
P7C204	Antioxidant	-	2.11
B/G384	Ascorbate peroxidase	5	2.11
B/GDIO R7CDIO	Gludedoxiii	2	1.90
B7GDIZ B7C110	GIYUXdidse	2	1.00
B7G1J9 P7C016	L-ascolidate peroxidase	8	1.30
B7G0L0 B7FD57	Thioredoxin	4	2.22
B7C0C9	Thioredoxin	5	2.00
B7G0P5	Thioredoxin	3	1 31
B7G7L6	Thioredoxin h	3	2 44
DIGIES	Heat shock protein	3	2.11
041074	BiP	6	-1.84
A0T0H7	Chaperone protein dnaK	33	-1.40
B7FXO8	Heat shock protein Hsp20	2	1.97
B7GEF7	Heat shock protein Hsp90	11	-1.42
B7GCE9	Protein heat shock protein	10	-1.42
	Miscellaneous		
B7G5Y2	14–3-3-like protein	11	1.64
B7FV10	1-Hydroxy-2-methyl-2-	7	-1.70
B7S4B2	Alcohol dehydrogenase	2	3.30
A0T0F2	ATP-dependent zinc metalloprotease FtsH	11	- 1.75
B7FQH4	Calcyclin-binding protein	2	1.56
B7FNY6	Early light induced protein	3	- 1.95
B7FU89	Farnesyltranstransferase	5	-2.13
B7GB73	FeS assembly protein suf	5	- 1.36
B7FUG8	Glycolate oxidase	10	-1.50
B7FWY2	Hydroxymethylbilane synthase	22	-1.84
B7FYL2	Iron starvation induced protein	6	- 3.90
A0T0E5	Iron-sulfur cluster formation ABC transporter ATP-binding subunit	5	- 1.36
B7G6D3	Metacaspase	5	1.69
B7S4C8	Methionine aminopeptidase	2	- 1.39
Q8LKV0	Microsomal cytochrome b5	3	- 1.81
B7FQ72	Mitochondria-targeted chaperonin	58	-1.30
B/FU88	P2B, P type A1Pase	3	-1.28
B515C8	Snort-chain alcohol denydrogenase with NAD or NADP as acceptor	/	1.65
B51356	I FANSAIGOIASE	5	1.96
D/GEF3	mansiocator of the inner chloropiast envelope memorane 110 K	13	- 1.63

abundance of 498 confidently identified proteins (≥ 2 unique peptides) was significantly (p < 0.01) altered. These were matched to protein names using UniProt. Discounting those described as 'Predicted Protein' or 'Predicted protein (Fragment)' 193 identifications with descriptive names were grouped using the protein name and information provided on the UniProt entry page (Table 1). Both KEGG and individual analysis showed significant trends in the reorganization of *P. tricornutum* proteome under nitrogen stress, mostly towards maximizing the use of the remaining nitrogen. Among others, those pathways involved in increasing the availability of the intracellular nitrogen and minimising its loss were favoured.

Amino acid synthesis was reorganized between the different families, as is suggested by the decrease in the synthesis of the families of the aromatic-like, aspartate-like and pyruvate-like amino acids (Supporting Information Fig. S6 and Table 1). There was, however, observation of an increase in serine tRNA, suggesting that whilst decreased in general, proteins associated with some amino acid synthesis may have increased. In contrast to previous reports that suggest a general decrease of amino acid synthesis in *P. tricornutum* [45], grouping the amino acid production based on their type (e.g. aromatic and hydrophobicity) did not reveal any meaningful trend. The ample coverage of the decrease of ribosomal proteins (Supporting Information Fig. S5 and



Fig. 4. Metabolic pathway diagram from KEGG. showing proteins with significant (p-value < 0.05) increase or decrease in abundance in blue and red respectively.

Table 1) confirmed the reduction of protein synthesis associated with nitrogen stress that has been reported previously [34,56]. This would be linked to the cellular need to economize the use of the available nitrogen. Given the nature of the stress condition, it was also expected that nitrogen scavenging would be strongly promoted within the cell as a way of supplying nitrogen demands. In this sense, focusing on the nitrogen metabolism pathway, proteins with greater abundance in the nitrogen depleted treatment included aliphatic amidase and formidase, both of which are known to free ammonia from other macromolecular compounds (Table 1) [57]. Conversely, nitrate reductase, responsible for converting the available nitrate in the medium to nitrite in the initial step of nitrate assimilation, was decreased, contrasting with recent studies in *P. tricornutum* [22], likely due to the fact that in these studies the effect of nitrogen limitation rather than nitrogen starvation was addressed. Similar down-regulation has been reported for the diatom T. pseudonana under nitrogen starvation and iron stress [38,58] that also coincided with an increase of the enzyme urease in the former, matching the increased abundance of the urea transporter found in this study. The possession of a complete urea cycle by the diatoms has been suggested to be a way of increasing the efficiency of nitrogen reassimilation from catabolic processes [22,59]. An increased abundance of the proteins involved has been reported to be linked to the increase in the glycolytic pathway of P. tricornutum facing nitrogen deprivation [60]. In conclusion, this increase in nitrogen scavenging when seen with the reduction in the nitrogen assimilation enzyme suggests a more active rather than a passive response to the nitrogen stress focused on intracellular nitrogen recycling.

The possession of this active nitrogen scavenging strategy might also be demonstrated by the increases in proteasome proteins and the changes of endocytosis and phagosome. KEGG analysis showed an increase in 'Endocytosis' and 'Phagosome' activity under nitrogen stress (Supporting Information Fig. S10). Such increases in phagosomal activity have previously been reported for other algae under nitrogen stress, for example in Bihan et al.'s proteomic study on *Ostreococcus tauri* [61], This would suggest a scavenging response of microalgae under nitrogen deprivation. In this sense, when facing reduced nitrogen availability, *P. tricornutum* cells might enhance the intake and processing of extracellular debris and perhaps attempts to consume other organisms such as bacteria to obtain additional nitrogen supplies. Thus, nitrogen stress could be suggested to induce phagotrophy [62,63], In addition to external nitrogen retrieval, many of the proteins associated with endocytosis and phagocytosis have been reported to be similarly involved in autophagy [64,65]. Transcriptional evidence of a link between nitrogen stress and autophagy induction has been previously shown in the chlorophyta *Neochloris* [66].

Pathways associated with fatty acid metabolism were also significantly changed under nitrogen stress, coinciding with the previously described enhancement in the lipid content (Supporting Information Fig. S9 and Table 1). Increases in KEGG pathways included 'biosynthesis of unsaturated fatty acids', 'fatty acid biosynthesis' and "short chain fatty acids"; and a relative decrease was observed in 'fatty acid elongation' and 'fatty acid metabolism'. Coinciding with previous reports [34,42], individual protein changes also displayed an active dynamism of the proteome involved in this metabolic pathway, implying an increased abundance of enzymes key to lipid biosynthesis, such as acyl-carrier proteins and malonyl-CoA:ACP transacyclase. Additionally, a decrease in fatty acid catabolism related proteins was found, suggesting that a down-regulation in the degradation of fatty acids might be a key metabolic route for explaining lipid accumulation under nitrogen stress conditions. These results have been shown previously [6,66,67] and are supported by recent reports of the preservation of existing triacylglyderides after nitrogen stress situations [68]. Similar dynamism of the proteins related to the fatty acid synthesis and degradation has been reported previously for Chlorophyta [6,28,66]. These results contradict those shown by the transcriptomic study conducted in P. tricornutum by Valenzuela et al. [21], highlighting the inappropriateness

of using transcriptomic data to infer proteomic changes, as has been previously reported [24–26]. The discord between these findings might suggest a translational control for proteins associated with fatty acid biosynthesis and degradation that would not be necessarily reflected at the transcriptomic level.

3.5. Preference of the central energy metabolism over photosynthetic pathways

The photosynthetic pathway was significantly down-regulated under nitrogen stress in *P. tricornutum*, as observed by a decrease in the relative abundance of the most important enzyme in the carbon fixation pathway (RuBISCO), and the general decreased abundance of key proteins of photosynthesis such as the light harvesting proteins and the photosynthetic electron transport system (e.g., fucoxanthin chlorophyll *a*/c, ATP synthase, PSI, PSII and cytochrome c, Table 1). This observation matches a similar trend detected by the KEGG analysis (Supporting information S8) and the decrease in pigment content described previously (Fig. 1). Further, it is in agreement with previous studies both in *P*. tricornutum and other algae, supporting ample evidence on the close linkage between carbon and nitrogen metabolism [6,9,38,45]. Such degradation of the photosynthetic pathway would be due to the fact that photosynthetic proteins (including pigments such as chlorophyll a) have a high content of nitrogen, and therefore, under conditions of nitrogen scarcity, cells tend to actively down-regulate their synthesis in order to preserve the little nitrogen that is left and to divert it to the synthesis of those proteins that are essential for cell maintenance [6,56].

The reorganization of the proteome under nitrogen starvation would also have an impact on the central energy metabolism. Acetyl CoA plays an important role in the carbon partitioning for oil accumulation within the cell, and therefore, metabolic pathways would be redirected to increase of the availability of this metabolite in the cell. In addition, fatty acid synthesis requires high levels of ATP and NADPH that would be generated through a switch from a gluconeogenic to a glycolytic metabolism. In this sense, in our study an increased abundance of those proteins involved in the Kreb's cycle, the glycolysis and the oxidative pentose phosphate pathways were observed. Conversely, those enzymes regulating the glycolytic and the gluconeogenic pathways reported decreased abundance(Table 1 and Supporting information S7), confirming previous reports for diatoms and cyanobacteria under nitrogen stress [20,22,38,42,45,69].

Finally, nine proteins with antioxidant properties were increased under nitrogen stress, suggesting a change in the concentration of reactive oxygen species (ROS) within the cellular environment (Table 1). An increase in ROS has been reported to be a major source of cellular damage under abiotic and biotic stresses in plants [70]. Specifically, ROS increases under nitrogen starvation conditions are closely linked with the malfunctioning of the photosynthetic pathway. Nitrogen uptake and metabolism require reducing equivalent power and ATP that under nitrogen deprived conditions tend to accumulate, causing metabolic imbalance and leading to the generation of oxidative stress. Nitrogen is also required for the synthesis of photosynthetic proteins, especially light harvesting proteins, and, as has been explained before, its lack tends to slow-down the electron flow through the photosynthetic apparatus, in turn causing the production of more ROS. Therefore, it can be hypothesized that the observed increase in antioxidant proteins is a mechanism used by P. tricornutum to limit this oxidative stress damage, as has been reported for algae facing other or similar stressful conditions [38,45,71]. Another indication of the stress to which P. tricornutum was subjected to under nitrogen starvation is the increased abundance of the heat-shock protein HSP20. Heat shock protein expression has been reported to be triggered in microalgae growing under stressful conditions [71], including nitrogen stresses [45]. However, it is also interesting that, while HSP20 was increased, other heat shock proteins, which have also been described to be present in stress responses, showed an opposite pattern, suggesting their possible differential role in the cell.

3.6. Comparison of the response of P. tricornutum and C. reinhardtii

To investigate differences in the proteome response under nitrogen stress between very different microalgae taxonomic affiliations such as *Bacillariophyceae* and *Chlorophyceae*, the results obtained in this study for *P. tricornutum* and the published earlier work of ours for *C. reinhardtii* [6] were compared. Although there were differences in terms of sampling time points and culture conditions between the studies, both were conducted under active increase of cellular lipid content and thus this comparison is of interest. As far as we know this is the first study aiming at such comparison under situations of nitrogen starvation. Observing the changes in the GO groupings did not show any strong unidirectional change between the two species, however observation of the relative changes in proteins captured showed some differences (Fig. 5).

The direction of the protein abundance change in the number of proteins was the same for both species with two exceptions, those proteins that are involved in energy metabolism and protein degradation. Both showed increases in *C. reinhardtii* and decreases in *P. tricornutum*. *P. tricornutum* also demonstrated more consistent protein abundance changes involved in photosynthesis, pigment metabolism, carbohydrates metabolism, central energy metabolism and glycolysis than *C. reinhardtii*; suggesting that the reorganization of the proteome in this species towards these metabolic pathways was more important.

Of special note is the markedly larger number of proteins involved in the photosynthetic pathway that were reduced in abundance in P. tricornutum. This might be due to the differences in the photosynthetic machinery between both species in terms of energy dissipation pathways and photosynthetic components of the electron transport system. Accessory pigments are very important in diatoms for dissipating excess energy due to the photosynthetic activity and, given their high nitrogen content, tend to be scavenged very early in the onset of nitrogen starvation [56]. The larger number of proteins with increased abundance in central energy metabolism, mainly the GO terms acetyl-CoA and acyl-CoA metabolic processes (Supporting Information Table S1), and glycolysis in P. tricornutum also suggest the relevance of these pathways in the cellular response to nitrogen starvation. These are likely involved in increasing the availability of the acetyl-CoA, chemical energy and reductant power required for lipid biosynthesis (see more details above). The relative higher increase of glycolysis and carbohydrate catabolism also might indicate that *P. tricornutum* tends to mobilize carbon stores rather than increase them under nitrogen scarcity, as has been previously reported [38].

Conversely, C. reinhardtii had more proteins regulated that relate to cellular homeostasis, respiration, phosphorous metabolism, DNA metabolism and cell organization compared to P. tricornutum; of practical note are the relatively large number of proteins involved in respiration and cellular organization. In our previous work [6] C. reinhardtii was grown in the presence of organic carbon and the observed higher number of respiratory proteins could be explained by the diversion of the metabolism towards heterotrophy as a consequence of the compromise of the photosynthetic pathway in conditions of nitrogen scarcity. This switch from photoheterotrophic to heterotrophic metabolism has been described before for this species under conditions of Iron deprivation [72]. The respiratory pathway would be used for generating chemical energy and reductant power needed for lipid biosynthesis. Induction of gametogenesis in C. reinhardtii under nitrogen stress has been reported [73], and the active increased abundance of cellular organization proteins (mainly cytoskeletal proteins - personal comment by the authors) observed here might play an important role in such physiological response.

Finally, *C. reinhardtii* seemed to be more susceptible than *P. tricornutum* to the oxidative stress caused by nitrogen starvation, as suggested by the observed relatively higher number of oxidative stress proteins. Oxidative stress increase in microalgae under nitrogen starvation conditions has been described widely in the past [38,45,70,71], and has



Fig. 5. Comparison of proteomic response in *P. tricornutum* and *C. reinhardtii*. The relative change within each GO grouping between the number of proteins assigned with increased and decreased abundances are shown.

been related to the damage of the photosynthetic electron system proteins due to the nitrogen scarcity. However, the results of our comparison would suggest that there would be differences in both species in the way they counteract the oxidative stress damage, with a higher protein response in *C. reinhardtii* that might be associated to a different source of oxidative stress. While *P. tricornutum* remained photoautotrophic when growing under nitrogen starvation and therefore mostly the oxidative stress was caused by an inefficient functioning of the photosynthetic pathway and the xanthophyll cycle, *C. reinhardtii* growth conditions were mixotrophic (acetate as a source of organic Carbon) and in conditions of Nitrogen starvation would switch towards a heterotrophic growth and the oxidative stress associated to the increase in respiration would be added to that caused by the damaged photosynthetic pathway.

It must be noted that the above comparison is not comprehensive, taking into consideration all the relevant physiological and biological differences between the organisms and cultivation conditions. Nevertheless, it provides vital clues that will enable us to explore and develop a better understanding of microalgal metabolism needed for developing viable strategies for bioenergy generation.

4. Conclusions

In the present study, the biochemical and proteomic changes associated with nitrogen starvation as a trigger for enhancing lipid production was addressed in *P. tricornutum* and compared with those previously described for *C. reinhardtii*. From biochemical analysis, it can be concluded that nitrogen stress increases energy storage molecules in *P. tricornutum*. This increase would be coupled with a decrease in photosynthetic pigments. We examined the proteome at an earlier stage of exposure to exclusive nitrogen starvation than has been reported, but at a time point when changes attributable to lipid accumulation can be captured in preference to those due to carbohydrate accumulation. Through the use of an iTRAQ methodology, 1043 proteins were confidently identified, of which 645 were shown to be significantly altered abundance under nitrogen stress. This represents a 17-fold increase with respect to the number of proteins detected in previous nitrogen stress assessments of *P. tricornutum*, and as such provides greater understanding of the effects of nitrogen stress in this model diatom species.

The extent to which the proteome changes in response to nitrogen stress has been demonstrated to be >60%, with over 60% of the confidently identified proteins being significantly changed (p-value <0.05) in abundance. Several patterns of response have been identified within the proteome highlighting increased scavenging of nitrogen and the reduction of lipid degradation, as well as stimulation of central energy metabolism in preference to photosynthetic pathways.

The GO comparison of *P. tricornutum* and *C. reinhardtii* conducted here highlights important differences in the degree of protein investment among the different metabolic pathways. In this sense, under nitrogen starvation, whilst *P. tricornutum* might reorganize its proteome by largely decreasing the number of photosynthetic proteins and increasing the ones involved in central energy metabolism, *C. reinhardtii* appears to invest in cellular reorganization, respiration and oxidative stress response.

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Conflict of interest

The authors declare no competing financial interest.

Author contributions

JL contributed to the conception, design, data acquisition and drafting of the article, DW contributed in the data acquisition and drafting of the article, MHO contributed to the design, and drafting of the article with critical insights and input, PCW contributed to the design, conception and drafting of the article, and SV contributed to the conception, design, supervision and drafting of the article. All authors give their final approval of the submitted manuscript.

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