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Flow cytometry-based study of model marine microalgal consortia revealed an ecological advantage of siderophore utilization by the dinoflagellate *Amphidinium carterae*



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ABSTRACT

Investigations of phytoplankton responses to iron stress in seawater are complicated by the fact that iron concentrations do not necessarily reflect bioavailability. Most studies to date have been based on single species or field samples and are problematic to interpret. Here, we report results from an experimental cocultivation model system that enabled us to evaluate interspecific competition as a function of iron content and form, and to study the effect of nutritional conditions on the proteomic profiles of individual species. Our study revealed that the dinoflagellate *Amphidinium carterae* was able to utilize iron from a hydroxamate siderophore, a strategy that could provide an ecological advantage in environments where siderophores present an important source of iron. Additionally, proteomic analysis allowed us to identify a potential candidate protein involved in iron acquisition from hydroxamate siderophores, a strategy that is largely unknown in eukaryotic phytoplankton.

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1. Introduction

The importance of iron for marine phytoplankton, a key nutrient controlling phytoplankton production in high nutrient/low chlorophyll ocean regions, has been known for three decades [1]. Consequently, phytoplankton employ a great diversity of strategies to overcome iron limitation, including reducing cell size and iron

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requirements [2], efficiently acquiring iron with iron uptake rates reaching the universal upper limit [3], utilizing xenosiderophores [4], and possessing iron storage mechanisms [5]. Considering the variability in chemical and biogeochemical aspects of iron, such as its concentration, form, distribution or seasonal variations in availability, it is extremely difficult to predict how phytoplankton communities will respond to changing iron conditions. Nevertheless, it is extremely important to understand the consequences of iron stress on phytoplankton considering the alterations in iron bioavailability and distribution that we expect due to global climate changes [6].

Cocultivation experiments represent powerful tools to study interspecific interactions, particularly for characterization of symbiosis and parasitism (e.g., [7,8]). The potential of cocultivation is now enhanced by a growing number of available microbial genomes and/or transcriptomes, as well as by the technical improvement and increased accessibility of omics techniques, particularly proteomics. In marine phytoplankton research, studies are mostly based on lab-scale experiments focused on single species or on investigations of complex field samples that are difficult to interpret. Nevertheless, lab-scale coculture studies of marine phytoplankton have revealed important findings, such as

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Abbreviations: AtpE, ATP synthase; AUC, area under curve; BCS, bathocuproinedisulfonic acid disodium salt; CREG1, cellular repressor of E1A stimulated genes 1; DFOB, desferrioxamine B; EDTA, ethylenediaminetetraacetic acid; ENT, enterobactin; FACS, fluorescence-activated cell sorting; FBAI, fructose-bisphosphate aldolase I; FBAII, fructose-bisphosphate aldolase II; FBP1, putative ferrichrome-binding protein; FOB, ferrioxamine B; ISIP, iron starvation induced protein; LHCX, light-harvesting complex subunits; LL, long-term iron limitation; LR, iron enrichment; NBD, nitrobenz-2-oxa-1,3-diazole; NPQ, nonphotochemical quenching; PAGE, polyacrylamide gel electrophoresis; PetA, cytochrome b6/f; PSI, photosystem I; PSII, photosystem II; PsaC, photosystem I reaction center subunit II; PsaE, photosystem I reaction center subunit IX; PsbC, photosystem II CP43 reaction center protein; PsV, cytochrome *c*-550; RR, long-term iron sufficiency; (s)PLS-DA, (sparse) partial least squares discriminant analysis; SOD1, superoxide dismutase [Cu-Zn].

mutualistic algal-bacterial interactions involving vitamin B12 [9,10] or iron [11].

Comparative studies of iron metabolism in different species are complicated by the virtual impossibility of achieving the same iron conditions in different cultures, particularly in time-course experiments, while the analysis of complex natural samples is biased by heterogeneity even in the dominant species. The aim of our study was to establish cocultivation experiments where each species in the community would be distinguishable by flow cytometry and present in quantities enabling homogenous detection of proteins, within a reasonable timeframe to observe the effect of nutritional changes. Such a system would provide equal iron conditions for each member of the consortia in time and allow us to study dynamic changes in the growth and proteomes of individual species.

2. Materials and methods

2.1. Cell culture

Amphidinium carterae (CCMP1314), Bigelowiella natans (CCMP2755), Eutreptiella gymnastica (K-0333), Emiliania huxleyi (CCMP371), Heterocapsa triquetra (CCMP449), Phaeodactylum tricornutum (CCMP2561), Tetraselmis sp. (CCMP961), Thalassiosira oceanica (CCMP1005) and Thalassiosira pseudonana (CCMP1335) were grown at 18 °C under a 12 h/12 h light (50 μ mol m⁻² s⁻¹) /dark regime in filtered modified f (Mf) medium, as described previously [12]. The composition of the Mf medium was as follows: 40 g/l sea salts; 75 mg/l NaNO₃; 2.66 mg/l NH₄NO₃; 22.8 mg/l Na₂-SiO₃·5H₂O; 15 mg/l NaH₂PO₄; 1 ml of trace metal stock (200 mg/l MnCl₂·4H₂O; 40 mg/l ZnSO₄·7H₂O; 20 mg/l Na₂MoO₄·2H₂O; 14 mg/ 1 CoCl₂·6H₂O; 10 mg/l Na₃VO₄·nH₂O; 10 mg/l NiCl₂; 10 mg/ml H₂SeO₃) and 1 ml of vitamin stock (20 mg/l thiamine-HCl, 1 mg/ ml biotin, 1 mg/ml B12). The medium was buffered with 1 g/l HEPES (pH 7.5). Iron-rich conditions were achieved by the addition of 0.1 µM ferric citrate (1:20). To establish copper-deficient conditions, 10 µM BCS (bathocuproinedisulfonic acid disodium salt) was added to the growth medium. All chemicals, including growth medium reagents, were purchased from Sigma-Aldrich (USA).

2.2. Flow cytometry

Before each cocultivation experiment, starting cultures of Amphidinium carterae, Bigelowiella natans, Eutreptiella gymnastica, Emiliania huxleyi, Heterocapsa triquetra, Phaeodactylum tricornutum, Tetraselmis sp., Thalassiosira oceanica and Thalassiosira pseudonana were maintained under iron-rich (Mf medium with the addition of 0.1 µM ferric citrate) or iron-limited (Mf medium without iron addition) conditions for seven days. Cell counts for each species were determined on a Guava easyCyte 8HT flow cytometer (Luminex Corporation, USA). To study the effect of copper availability, T. oceanica and T. pseudonana cultures were additionally maintained under copper-deficient (Mf medium with the addition of 10 μ M BCS) or copper-sufficient (without BCS addition) conditions. Starting cultures for the five consortia species (Fig. 1) contained 2.6×10^4 A. carterae and Tetraselmis sp. cells and 5.2×10^4 B. natans, *E. huxlevi* and *T. oceanica* cells. Cultures were combined and grown for seven days under appropriate iron conditions in three biological replicates. On the seventh day, consortia were analyzed using a BD LSRFortessaTM SORP flow cytometer (BD Biosciences, USA) with a 488 nm laser (100 mW) for excitation and PerCP-Cy5.5 (BP710/50) and FITC (BP530/30) emission filters corresponding to red and green fluorescence parameters. Starting cultures for dual Thalasiosira cocultivation (Fig. 2) contained 7.5 \times 10⁴ T. oceanica and T. pseudonana cells. Cultures were combined, grown for seven days

under appropriate iron and copper conditions in three biological replicates and analyzed using a Guava easyCyte 8HT flow cytometer with a 488 nm laser (150 mW) for excitation and Red-B (BP695/50) and Green-B (BP525/30) emission filters corresponding to red and green fluorescence parameters. Starting cultures in the consortia to study the effect of ferrioxamine B contained $5.2 \times 10^4 \text{B}.$ natans cells, 2.6 \times 10^4 A. carterae cells and 2.6 \times 10^4 cells of either Tetraselmis sp. or E. gymnastica. Cultures were combined, allowed to grow for seven days under iron-limited (without iron addition) or iron-rich (addition of 0.1 μ M ferric citrate (1:20) or 0.1 µM ferrioxamine B (1:1.1)) conditions and measured using a Guava easyCyte 8HT flow cytometer with a 488 nm laser (150 mW) for excitation and Red-B (BP695/50) and Green-B (BP525/30) emission filters corresponding to red and green fluorescence parameters. All data were analyzed using FlowJo v10 software (BD Biosciences).

2.3. Proteomic analysis

Label-free whole-cell comparative proteomic analysis of *Amphidinium carterae*, *Bigelowiella natans*, *Heterocapsa triquetra* and *Phaeodactylum tricornutum* mixed cultures was performed in independent biological triplicates. Iron-rich (maintained in Mf medium with 0.1 μ M ferric citrate) and iron-limited (Mf medium without iron addition) starting cultures containing 6×10^4 *A. carterae* cells, $1.25 \times 10^5 B$. *natans* cells, $1.25 \times 10^5 P$. *tricornutum* cells and $2 \times 10^4 H$. *triquetra* cells were combined and allowed to grow for one day under appropriate iron conditions. At the beginning of the experiment, 0.1 μ M ferric citrate was added to achieve iron enrichment in iron-limited cultures. At given timepoints (1, 6 and 24 h), cells were counted using flow cytometry and centrifuged (1000g; 5 min; 4 °C), and the dry pellet was subjected to proteomic analysis according to [13]. Detailed characteristics of the proteomic analysis are summarized in Table S2.

2.4. Statistical analysis

Single-OMIC analyses do not provide a deep understanding of biological systems. Thus, two-step normalization was employed to overcome hidden variation due to different cell numbers and variable expression levels. First, size-factor vector normalization was used, where the normalizing factor was estimated from cell counts using flow cytometry. Next, quantile normalization was used on cell count-normalized data, which is a technique for making two (or more) distributions identical in statistical properties. We used the *preprocessCore* package in R software [14]. This method uses the concept of a quantile-quantile plot in ndimensions and is amenable for normalizations of multi-OMICS data. To detect the changes in variation due to two-step normalization, we used (s)PLS-DA: (sparse) partial least squares discriminant analysis in the R package *mixOmics* [15] and the area under the curve (AUC) for the extraction of sensitivity values, specificity of discriminations and corresponding p values.

2.5. Iron uptake

The incorporation of iron into protein complexes was analyzed by blue native PAGE as described in [16]. Prior to iron uptake experiments, cultures were grown in iron-deficient Mf medium (without added Fe) for 7 days. Then, $0.1 \,\mu M^{55}$ Fe (29,600 MBq mg⁻¹) was added in the form of ferric citrate (1:20), ferric EDTA (1:10), ferrioxamine B (FOB; 1:1.1) or enterobactin (FeENT; 1:1.1) to the cell cultures and incubated for 24 h. Stock solutions of ⁵⁵Felabeled siderophores (FOB, FeENT) were prepared according to [4]. The cells were harvested by centrifugation and washed three times with ice-cold cultivation medium. Subsequently, the cells

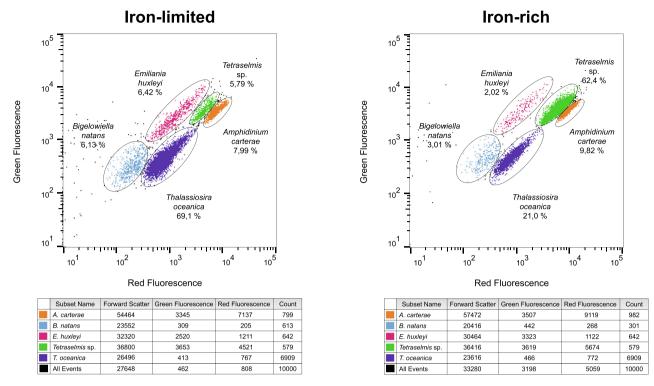


Fig. 1. Effect of iron availability on representative microalgal consortia. Flow cytograms of microalgal consortia containing five microalgal species (*B. natans, E. huxleyi, Tetraselmis* sp., *A. carterae* and *T. oceanica*) grown for one week under iron-limited or iron-rich conditions. Tables under flow cytograms contain median values for Forward Scatter, Green Fluorescence and Red Fluorescence parameters together with cell counts for each species. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

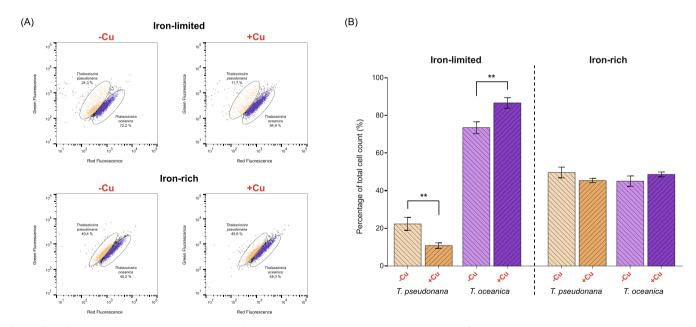


Fig. 2. Effect of iron and copper availability on coastal and oceanic *Thalassiosira*. (A) Flow cytograms with gates of two cocultivated species (*T. pseudonana* and *T. oceanica*) grown for one week under iron-limited or iron-rich conditions and copper-deprived (-Cu) or copper-sufficient (+Cu) conditions. (B) Percentage of total cell count for *T. oceanica* and *T. pseudonana* under iron-limited or iron-rich conditions and copper deprived (-Cu) or copper sufficient (+Cu) conditions, measured in three replicates (mean ± SD, ** p less than 0.01).

were disrupted by sonication in the presence of 1% digitonin, and protein complexes were separated by blue native PAGE using the Novex Native PAGE Bis–Tris Gel 4–16% system (Invitrogen) according to the manufacturer's protocol. The gels were vacuum-dried and autoradiographed for 5 days using a BAS-IP TR 2025 E tritium storage phosphor screen (GE Life Sciences) and visualized using a Typhoon FLA 7000 (GE Life Sciences).

2.6. Siderophore utilization

FOB coupled to a fluorescent moiety, nitrobenz-2-oxa-1,3diazole (FOB-NBD), was previously synthesized as described by [17]. *A. carterae, B. natans, Tetraselmis* sp. and *E. gymnastica* were grown in iron-deficient Mf medium (without iron addition) in independent biological triplicates for seven days. FOB-NBD $(1~\mu M)$ was added to the cell cultures and incubated for 1, 3 and 6 h in the dark at 18 °C. Cultures were measured using a Guava easy-Cyte 8HT flow cytometer with a 488 nm laser (150 mW) for excitation and Yellow-B (BP583/26) emission filter to detect DFOB-NBD accumulated within cells. Data were analyzed using FlowJo v10 software.

3. Results

We were able to set up a series of experiments with different combinations of species distinguishable by flow cytometry, allowing us to study the effect of iron on the fitness of each member of the consortia. Species were chosen based on their ability to grow at the same temperature and light intensity at relatively similar rates. differences in iron requirements (low-iron-adapted E. huxlevi and T. oceanica vs. species with higher iron demand), distinguishability by flow cytometry and the availability of axenic strains. For all species, genomic and/or transcriptomic data are available, allowing interpretation of results at molecular level, particularly in proteomic analysis. The discriminability of chosen species in each experiment was ensured by setting the flow cytometric parameters for monoxenic cultures, in most cases red and green fluorescence corresponding to autofluorescence of their chlorophyll, phycoerythrin and carotenoid pigments. Importantly, the cell populations were analyzed under changing iron availability. As shown in Fig. S1, the cell population parameters changed significantly for Amphidinium carterae, Eutreptiella gymnastica, Phaeodactylum tricornutum, Tetraselmis sp., Thalassiosira oceanica and Thalassiosira pseudonana.

Fig. 1 illustrates a cocultivation system containing five species: the chlorarachniophyte *Bigelowiella natans*, the coccolithophore *Emiliania huxleyi*, the flagellated chlorophyte *Tetraselmis* sp., the dinoflagellate *Amphidinium carterae* and the diatom *Thalassiosira oceanica*. Species are clearly distinguishable under both iron-rich and iron-limiting conditions using red and green fluorescence, and as expected, low iron availability provided a competitive advantage for *E. huxleyi* and *T. oceanica*, species adapted to iron-limited ocean regions. Iron limitation resulted in a more than 3-fold increase in the community proportion of both microalgae after one week.

An exemplary experiment demonstrating adaptation to metal availability is depicted in Fig. 2. In this dual culture, two *Thalassiosira* species were cocultivated. While *T. oceanica* is an openocean, low-iron-adapted diatom employing copper-containing plastocyanin for electron transport from the cytochrome $b_{G}f$ complex to PSI [18], *T. pseudonana* is a coastal strain with high iron demand and plastocyanin has been replaced by cytochrome c6 [19]. Consistent with these differences, cultivation under iron-limited conditions supported the growth of *T. oceanica*, while copper deprivation favored *T. pseudonana* when iron was limiting.

In an attempt to observe complex cellular responses to changing iron availability at the molecular level, we employed labelfree comparative proteomics to analyze algal consortia of four selected species. Iron-limited cocultures were supplemented with iron (LR) and compared at different time points over a 24-hour time course with cells maintained under conditions of iron limitation (LL). After 24 h, proteomic profiles were also compared with cells maintained under conditions of long-term iron sufficiency (RR). Flow cytograms of the consortia at 24 h and 6 days after iron enrichment are depicted in Fig. S2. Proteins detected from all studied organisms are shown in Table S1. We detected 6100 unique proteins throughout all species and conditions: 3717 proteins from *A. carterae*, 972 proteins from *P. tricornutum*, 737 proteins from *H. triquetra* and 735 proteins from *B. natans*. We used sparse partial least squares discriminant analysis (sPLS-DA) and the area under the curve (AUC) [15] to determine whether specific conditions of our experiment yielded significant changes in the proteomic profiles. Graphical results of sPLS discriminations (Fig. 3) demonstrate that the predictive performance for all comparisons was improved after cell count normalization. While long-term iron-rich cells (RR24 in Fig. 3) revealed perfect discrimination on all sPLS-DA panels regardless of the type of normalization (Comp. 2: AUC = 1, p = 0.006), iron-limited cells 24 h after enrichment (LR24 in Fig. 3) showed better predictive performances after cell count and quantile normalization (two-step normalization). The suitability of the two-step normalization is demonstrated in Fig. 3C, G, K, where iron-limited *A. carterae* cells were well separated 6 h after iron supplementation.

Upon iron enrichment, we were able to observe the downregulation of the homologs of proteins named the iron-starvationinduced proteins (or ISIPs) and upregulation of the lightharvesting complex subunits and fructose bisphosphate aldolase class II, in all analyzed species. For simplicity, we demonstrate an iron-induced response by analysis of preselected proteins whose abundance was expected to be affected by iron status (Table 1) in the proteomic data obtained for P. tricornutum and A. carterae, the two species with the best proteomic coverage. Within 1 h after iron enrichment, only 9 out of 102 preselected proteins detected in these two species had changed more than 2-fold (8 in P. tricornutum and 1 in A. carterae). Within 6 h after iron addition, the number of affected proteins increased to 23 (13 in P. tricornutum and 10 in A. carterae). After 24 h, 47 proteins had changed more than 2-fold (23 in P. tricornutum and 24 in A. carterae), similar to the difference observed between long-term iron-rich and iron-limited conditions. In general, the fastest induced proteins (which changed more than 2-fold within 6 h after iron enrichment) were the subunits of photosystem I (PSI): PsaC, PsaD, PsaE and PsaL; photosystem II (PSII): PsbV; cytochrome b6/f - PetA and ATP synthase - AtpE; the enzyme magnesium chelatase, which is involved in chlorophyll synthesis; and the iron-containing enzyme fructose bisphosphate aldolase class II (FBAII), which is replaced by metal-free FBAI [20]. Iron starvation-induced proteins and the *P. tricornutum* cellular repressor of E1A stimulated genes 1 (CREG1) were downregulated more than 2-fold 6 h after iron enrichment. These proteins are known to be major markers of iron limitation [12,21]. Proteins that changed more than 2-fold only 24 h after iron enrichment included other ISIPs, flavodoxins (downregulated) and ascorbate peroxidase, PsbC, SOD1 (upregulated). An interesting difference between A. carterae and P. tricornutum in the response to iron starvation was the regulation of light-harvesting complex subunits (LHCX). While one of the 3 detected LHC subunits (LHCX2) of P. tricornutum was upregulated under iron-limited conditions, which was also reported by [22], all 12 detected homologs of A. carterae LHCX were downregulated or unchanged, including the probable homolog of LHCX2 (CAMPEP_0176611302). LHCX2 is believed to be a regulator of nonphotochemical quenching (NPQ), the capacity of which is increased under iron-limited conditions [22]. The different responses of NPQ regulation to iron could reflect the different general light response flexibilities of both species. In their natural environment, bloom-forming dinoflagellates live in a stable stratified layer at the subsurface, usually below approximately 10 m depth, where illumination can sometimes be reduced to 1% [23]. As a result, A. carterae is genotypically adapted to low quantum flux densities and lacks an effective mechanism for de-excitation when excess light is absorbed [24]. On the other hand, planktonic diatoms, inhabiting turbulent surface waters, acclimatize to fluctuating light conditions better than dinoflagellates [23]. Diatoms are well known for their general light-response flexibility and potential for tuning their photosynthetic efficiency by NPQ under prolonged and potentially unfavorable conditions (reviewed in [25]).

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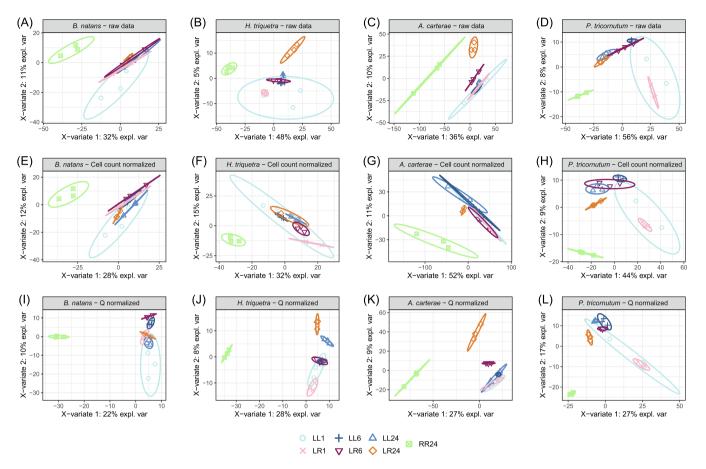


Fig. 3. Divergent patterns of protein abundances in raw and normalized datasets. Sparse PLS discriminant analysis revealed that raw data (A, B, C, D), cell count-normalized data (E, F, G, H) and quantile-normalized data after cell count normalization (I, J, K, L) had different predictive performances. We observed clear discriminations after cell count normalizations, which further improved most of these discriminations (e.g., A, E, I). LL: long-term iron limitation, RR: long-term iron sufficiency, LR: iron enrichment. The number denotes time (hours) after beginning an experiment (after iron enrichment of LR cells).

Interestingly, while changes in the expression of the proteins most significantly affected by iron resupply were generally similar or more pronounced in cells maintained continuously under iron-rich conditions, the levels of ISIPs (and Creg1 in *P. tricornutum*) were lower in resupplied cells than in those cultivated under conditions of long-term iron sufficiency. We believe that cells grown under long-term iron-sufficient conditions maintain a stable level of basal expression of these strong iron stress markers, while it is possible that sudden iron enrichment led to their overrepression. This can be explained by the continuous utilization of iron sparing pathways in long-term iron-deprived cells.

An important observation was made when the siderophore ferrioxamine B (FOB) was used as an iron source in cultures containing B. natans and A. carterae with Tetraselmis sp. (Fig. 4A), or the euglenid E. gymnastica (Fig. 4B). In contrast to other members of the consortia, the growth of A. carterae was stimulated by the addition of iron in the form of FOB. This observation indicates the presence of machinery responsible for siderophore acquisition. We thus decided to investigate the ability to acquire iron from siderophores in A. carterae as well as in other species whose growth in these cocultures was suppressed when iron was supplied as FOB. We exposed A. carterae, B. natans, Tetraselmis sp. and E. gymnastica monocultures to ⁵⁵Fe chelated by citrate (a relatively weak iron chelator), EDTA (a strong chelator) or two siderophores (hydroxamate-type FOB and catecholate-type enterobactin). The incorporation of iron from those sources into cellular proteins was visualized after separation on blue native electrophoresis gels.

The results are presented in Figs. 5A and S3, where it is evident that only A. carterae was able to effectively utilize iron from FOB, consistent with our flow cytometry results. None of the species tested in our study showed efficient incorporation of iron into cellular proteins when iron was chelated by enterobactin, including A. carterae, indicating that this dinoflagellate preferably acquires hydroxamate-type siderophores. Experiments with the fluorescent conjugate of desferrioxamine B complexed with iron (FOB-NBD) further demonstrated the capacity for siderophore iron utilization by Amphidinium. The fluorescence of this siderophore conjugate is quenched by iron; therefore, the release of iron from siderophores can be monitored by flow cytometry. Fig. 5B, C presents an effective acquisition of iron from FOB by A. carterae traced in time, which contrasts with the absence of iron release from the siderophore by the rest of the members of the algal consortia (Fig. S4). These observations are additionally supported by our complex proteomic analysis, where we identified among A. carterae proteins downregulated by iron resupply, a potential siderophore binding protein that showed a 2.5-fold decrease 24 h after iron enrichment (CAMPEP_0176544322, Table S1). It is a homolog of the P. tricornutum FBP1 protein that was recently shown to participate in iron acquisition from hydroxamate siderophores [26]. Homologs of FBP1 protein, identified in different marine microalgae, were shown to share a common ancestor with hydroxamate siderophore lipoprotein receptors found in gram-positive bacteria. The protein from A. carterae appears to be among the closely related homologs to the actinobacterial iron siderophore ABC transporter solute binding proteins [26].

Table 1

Effect of iron availability on the abundance of selected *A. carterae* and *P. tricornutum* proteins. Data represent fold change in protein abundance in iron-limited (LL) cells 24 h after iron supply (LR) and differences between iron-limited cells and cells grown under long-term iron-rich conditions (RR). *A. carterae* (highlighted in green) and *P. tricornutum* (highlighted in red) cells were cocultivated in a consortium that included *B. natans* and *H. triquetra*. An asterisk (*) in the protein name denotes fold change higher than 2-fold as early as 6 h after iron enrichment.

Accoduse peroxidias*AcCAMPEP_017652279646Accoduse peroxidias*PiCAMPEP_01766140641.7AppEAcCAMPEP_01766140641.7AppEAcCAMPEP_01765500461.6AppEPiSplArTD01ATPE_PHATC1.3AppEAcCAMPEP_01765500461.8AppEAcCAMPEP_0176551136-2.1CRECLAcCAMPEP_01765323321.2CRECLAcCAMPEP_01765323321.2Pa classilAcCAMPEP_01765323321.2Pa classilAcCAMPEP_01765323321.2Pa classilAcCAMPEP_01765323321.2Pa classilAcCAMPEP_0176532332-1.2Pa classilAcCAMPEP_0176610881.3Pa classilAcCAMPEP_0176610881.4Pa classilAcCAMPEP_017661222-1.2Pa classilAcCAMPEP_0176613724-1.2Pa classilAcCAMPEP_0176610881.4Pa classilAcCAMPEP_0176610881.4Pa classilAcCAMPEP_017667541.4Fa classilAcCAMPEP_017667541.4Fa classilAcCAMPEP_017667541.4Cat_2AcCAMPEP_017667541.4Cat_2AcCAMPEP_017667541.4Gat_2AcCAMPEP_017667541.4Gat_2AcCAMPEP_0176675401.3FavodoxinAcCAMPEP_0176675401.3Gat_2<	24 h LL-RR	24 h LL-LR	Protein ID	Organism	Protein name
Ascordare peroxidase"Pirtl975-91187-5401_PHATC1.1Atple"AcCAMPPE_01766146541.7AtpGAcCAMPPE_017656146541.8AtpGAcCAMPPE_017656149681.8AtpGAcCAMPPE_01765619681.8AtpGAcCAMPPE_01765200661.8CBCG1PiPIPSTEP_11ATC-2.3CBCG1PiPIPSTEP_11767223731.2CBCG1AcCAMPPE_01765223851.2Pa class1AcCAMPPE_0176522385-1.2Pa class1AcCAMPPE_0176522365-1.2Pa class1AcCAMPPE_0176523737-1.3Pa class1AcCAMPPE_0176523736-1.3Pa class1AcCAMPPE_017652378-1.3Pa class1AcCAMPPE_017652378-1.3Pa class1AcCAMPPE_017653174-6.3Pa class1AcCAMPPE_0176523788-1.4Pa class1PiPIPSTC0617675605311.4Pa class1PiPIPSTC061767505341.4Pa class1PiPIPSTC061767505341.4Pa class1PiPIPSTC061767505341.1Fa class1PiPIPSTC0617767605341.1Fa class1PiPIPSTC061776705341.1Fa class1PiPIPSTC061775605341.1Gr.2AcCAMPPE_017653140C1.1Gr.2AcCAMPPE_017653140C1.1Gr.2AcCAMPPE_017653140C1.1Gr.	4,0	4,6	CAMPEP_0176532796	Ac	Ascorbate peroxidase*
ApEPISplATDD1/ATE_PHATC1.3ApGCAcCAMPE_017550461.5ApGGAcCAMPE_017550461.8CREC1AcCAMPE_017551126-2.1CREC1RCUBTOS017651128-2.1CREC1PICUBTOS017681128-1.2Fba classIAcCAMPE_0176512321.2Fba classIAcCAMPE_017651232-1.2Fba classIAcCAMPE_017661228-1.2Fba classIAcCAMPE_017661422-1.2Fba classIIAcCAMPE_017661422-1.2Fba classIIAcCAMPE_017661422-1.2Fba classIIRHIFTGS08175308_PHATC-1.4Fba classIIPIHIFTGS08175308_PHATC-1.4Fba classIIPIHIFTGS08175308_PHATC-1.5Fba classIIPIHIFTGS08175308_PHATC-1.5FlavdoXinAcCAMPE_01766135738-1.5FlavdoXinAcCAMPE_01766135738-1.5FlavdoXinAcCAMPE_0176670554-1.1Ga 2AcCAMPE_0176670554-1.1Ga 2AcCAMPE_0176670554-1.1Ga 2AcCAMPE_0176670554-1.1Ga 2AcCAMPE_0176670554-1.1Ga 2AcCAMPE_0176670554-1.1Ga 2AcCAMPE_0176670554-1.1Ga 2AcCAMPE_0176670574-1.1Ga 2AcCAMPE_0176670574-1.1Ga 2RHIFTG7	6,5	1,1	tr B7S491 B7S491_PHATC	Pt	-
ArbG Ac CAMPPP_D17555046 1.6 ArbG Pt splATDGE51126 -2.1 CREG1 Ac CAMPPP_D17551126 -2.1 CREG1 Ac CAMPPP_D175512332 1.2 CREG1 Ac CAMPPP_D176523323 1.2 Fba class1 Ac CAMPPP_D176512332 -1.2 Fba class1 Ac CAMPPP_D17661422 -1.2 Fba class1 Ac CAMPPP_D17651128 -1.4 Fba class1 Ac CAMPPP_D17651748 -1.4 Fba class1 Pt H187C60797642 -1.4 Fba class1 Pt H187C607976642 -1.5 Fba class1 Pt H187C607976642 -1.6 Fba class1 Pt H187C60797660 -1.6 Fba class1 Pt H187C60797664 1.4 <td>5,2</td> <td>1,7</td> <td>CAMPEP_0176614664</td> <td>Ac</td> <td>AtpE*</td>	5,2	1,7	CAMPEP_0176614664	Ac	AtpE*
AbjCAcCAMPPP 01766419681.8AbjCPHspl/ATDE81/HTP2_PHATC1.8CREC1*PHHP37C08197683.2PMATC-2.1Fac classlAcCAMPPP.01765312301.2Fac classlAcCAMPPP.01765232331.2Fac classlAcCAMPPP.017652239-1.2Fac classlAcCAMPPP.0176614222-1.2Fac classlAcCAMPPP.0176614222-1.2Fac classlAcCAMPPP.0176614223-1.3Fac classlAcCAMPPP.01766131794-1.3Fac classlPhH197C48127687.PHATC4.6Fac classlPhH197C48127663.PHATC4.6Fac classlPhH197C48127663.PHATC4.6Fac classlPhH197C48127663.PHATC4.6Fac classlPhH197C48127663.PHATC-1.5Fac classlPhH197C48127663.PHATC-1.6Fac classlPhH197C48127663.PHATC-1.6Fac classlPhH197C4812763.PHATC-1.6Fac classlPhH197C4812763.PHATC-1.7Fac classlPhH197C4812763.PHATC-1.7Fac classlPhH197C4812763.PHATC-1.7Fac classlPhH197C4812763.PHATC-1.7Fac classlPhH197C4812763.PHATC-1.7Fac classlPhH197C4812763.PHATC-1.7Fac classlPhH197C4812763.PHATC-1.7Fac classlPhH197C4812763.PHATC-1.7	1,7	1,3	sp A0T0D1 ATPE_PHATC	Pt	AtpE
AnjcPIsplATOTESHATE2_PHATCL8CREG1AcCAMPEP_DTOSS1426-2.1CREG1*PtHTGTOSS187083_PHATC-23.5Fba class1AcCAMPEP_DTOSS23321.2Pac lass1AcCAMPEP_DTOSS23321.2Fba class1AcCAMPEP_DTOSS2332-1.2Fba class1AcCAMPEP_DTOSS1126-5.3Fba class1AcCAMPEP_DTOSS1794-1.3Fba class1AcCAMPEP_DTOSS1794-1.3Fba class1AcCAMPEP_DTOSS1794-1.4Fba class1*AcCAMPEP_DTOSS1794-1.4Fba class1*AcCAMPEP_DTOSS25_PHATC4.4Fba class1*PtHTGTOGRIPTOSCE_PHATC-1.5Fba class1*AcCAMPEP_DTOSS754-1.5Fba class1*AcCAMPEP_DTOSS754-1.5Fba class1*AcCAMPEP_DTOSS754-1.4Fba class1*AcCAMPEP_DTOSS754-1.5Fba class1*AcCAMPEP_DTOSS754-1.4Fba class1*AcCAMPEP_DTOSS754-1.4Fba class1*AcCAMPEP_DTOSS754-1.4Fba class1*AcCAMPEP_DTOSS754-1.4Fba class1*AcCAMPEP_DTOSS754-1.4Fba class1*AcCAMPEP_DTOSS754-1.4Fba class1*AcCAMPEP_DTOSS754-1.2Fba class1*AcCAMPEP_DTOSS754-1.4Fba class1*AcCAMPEP_DTOSS754-1.1Fba class1*Ac <td< td=""><td>1,1</td><td>1,6</td><td>CAMPEP_0176550046</td><td>Ac</td><td>AtpG</td></td<>	1,1	1,6	CAMPEP_0176550046	Ac	AtpG
CREC1AcCAMPEP_DITESTI26-2.1FBa classiAcCAMPEP_DITEST3321.2FBa classiAcCAMPEP_DITEST33321.2FBa classiAcCAMPEP_DITEST3321.2FBa classiAcCAMPEP_DITEST332-1.2FBa classiAcCAMPEP_DITEST378-1.2FBa classiAcCAMPEP_DITEST378-1.3FBa classiAcCAMPEP_DITEST378-1.3FBa classiAcCAMPEP_DITEST378-1.3FBa classiPtttpTSTNBJFTARS_PIATC4.6FBa classiPtttpTSTNBJFTARS_PIATC-6.3FBa classiPtttpTSTNBJFTARS_PIATC-6.3FBa classiPtttpTSTNBJFTARS_PIATC-6.3FBa classiPtttpTSTNBJFTARS_PIATC-6.3FBa classiPtttpTSTNBJFTARS_PIATC-6.3FBa classiPtttpTSTNBJFTARS_PIATC-6.3FBa classiPtttpTSTNBJFTARS_PIATC-6.3FBa classiPtttpTSTNBJFTARS_PIATC-6.3FBa classiPtttpTSTNBJFTARS_PIATC-1.1FBa classiPtttpTSTNBJFTARS_PIATC-1.4FBa classiPtttpTSTNBJFTARS_PIATC-1.3FBa classiPtttpTSTNBJFTARS_PIATC-1.4FBa classiPtttpTSTSTBFTARS_PIATC-1.1FBa classiPtttpTSTSTBFTARS_PIATC-1.1FBa classiPtttpTSTSTBFTARS_PIATC-1.1FBa classiPtttpTSTSTBFTARS_PIAT	1,4	1,8	CAMPEP_0176641968	Ac	AtpG
CREC1*PtPtPt3/C083/B7C082_PHATC-22.5Pba class1AcCAMPEP_0176522321.2Pba class1PtPt3/DESP/B7C67_PHATC-5.3Pba class1AcCAMPEP_017651282-1.2Pba class1AcCAMPEP_0176513811.4Pba class1AcCAMPEP_0176513811.4Pba class1AcCAMPEP_0176513811.4Pba class1PtHjB7C4R2]B7C4R2_PHATC-1.7Pba class1PtHjB7C4R2]B7C4R2_PHATC4.6Pba class1PtHjB7C4R2]B7C4R2_PHATC-1.5Pba class1PtHjB7C4R2]B7C4R3_PHATC-1.5Pba class1PtHjB7C4R2]B7C4R3_PHATC-1.6Pba class1PtHjB7C4R2]B7C4R3_PHATC-1.6Pba class1PtHjB7C4R2]B7C4R3_PHATC-1.6Pba class1PtHjB7C502]B7C502_PHATC-1.6FavodoxinPtHjB7C502]B7C502_PHATC-1.1Gr.2AcCAMPEP_017667754-1.1Gr.2AcCAMPEP_017667574-1.1Gr.2AcCAMPEP_017667584-1.2Gr.2PtHjB7C502]B7C502_PHATC-1.7Gr.2PtHjB7C502]B7C602_PHATC-1.1Gr.2PtHjB7C502]B7C602_PHATC-1.6Gr.2PtHjB7C502]B7C602_PHATC-1.6Gr.2PtHjB7C502]B7C602_PHATC-1.6Gr.2PtHjB7C502]B7C602_PHATC-1.6Gr.2PtHjB7C602]B7C602_PHATC-1.6<	1,1	1,8	sp A0T0E8 ATPF2_PHATC	Pt	AtpG
Pha class!AcCAMPEP_01765232321.2Pha class!PtCAMPEP_017661288-1.2Pha class!PtHI%7C657187C66.2PHATC-5.3Pha class!AcCAMPEP_017661422-1.2Pha class!AcCAMPEP_0176513784-1.3Pha class!AcCAMPEP_0176513784-1.3Pha class!PtHI%7C671871678-1.4Pha class!PtHI%7C671871678-1.7Pha class!PtHI%7C671871678-1.7Pha class!PtHI%7C671871678-1.4Pha class!PtHI%7C671871678-1.4Pha class!PtHI%7C671871678-1.5Pha class!PtHI%7C671975473-1.4Pha class!PtHI%7C67197547-1.4Pha class!PtHI%7C67197541.4Pha class!PtHI%7C6719754-1.4Pha class!PtHI%7C67197541.4Pha class!PtHI%7C6719754-1.4Pha class!	-4,3	-2,1	CAMPEP_0176541126	Ac	CREG1
Fib.AcCAMPEP.0176622298-1.2Fib.aclassIAcCAMPEP.017661688.1.9Fib.aclassIIAcCAMPEP.017661688.1.9Fib.aclassIIAcCAMPEP.0176517941.2Fib.aclassIIAcCAMPEP.0176517941.3Fib.aclassIIPtttjB7C4R2JB7C4R2_PLATC.4.6Fib.aclassIIPtttjB7C4R2JB7C4R2_PLATC.4.6Fib.aclassIIPtttjB7C4R2JB7C4R2_PLATC.4.6Fib.aclassIIPtttjB7C4R2JB7C4R2_PLATC1.5FlavodoxinAcCAMPEP_01766173531.5FlavodoxinAcCAMPEP_01766173541.1Gaz.2AcCAMPEP_01766173541.1Gaz.2AcCAMPEP_01766173541.1Gaz.2AcCAMPEP_01766173541.1Gaz.2AcCAMPEP_01766173541.2Gaz.2AcCAMPEP_01766173541.1Gaz.2AcCAMPEP_01766173621.1Gaz.2PtttjB7C43JB7C43_PLATC.NAGaz.2PtttjB7C43JB7C43_PLATC1.3Gaz.2PtttjB7C43JB7C43_PLATC1.3Gaz.2PtttjB7C43JB7C43_PLATC1.3Gaz.2PtttjB7C43JB7C43_PLATC1.3Gaz.2PtttjB7C43JB7C43_PLATC1.3Gaz.2PtttjB7C43JB7C43_PLATC1.4Gaz.2PtttjB7C43JB7C43_PLATC1.4Gaz.2PtttjB7C43JB7C43_PLATC1.4Gaz.2 </td <td>-2,0</td> <td></td> <td>tr B7G9B3 B7G9B3_PHATC</td> <td></td> <td>CREG1*</td>	-2,0		tr B7G9B3 B7G9B3_PHATC		CREG1*
Pha classiPtPtPt/B7C1657/BF4ATC-5.3Pha classilAcCAMPEP.0176614222-1.2Pha classilAcCAMPEP.0176513734-1.3Pha classilAcCAMPEP.01765337374-1.3Pha classilPtPt/B7C30831831.4Pha classilPtPt/B7C3081753788-1.5Pha classilPtPt/B7C30817620-1.5Pha classilPtPt/B7C30817620-1.5Pha classilAcCAMPEP.0176517328-1.5PhavdoxinAcCAMPEP.0176517324-1.5RivodoxinAcCAMPEP.0176617524-1.6Car_2AcCAMPEP.01766175441.4Gar_2AcCAMPEP.01766175461.1Car_2AcCAMPEP.01766175461.1Gar_2AcCAMPEP.01766175461.1Gar_2AcCAMPEP.01766176361.1Gar_2AcCAMPEP.01766176361.1Gar_2PtH1B770238174732.PHATC1.1Gar_2PtH1B770238174732.PHATC-1.3SiBP2AcCAMPEP.017651824-7.8SiBP2AcCAMPEP.01765182-7.8SiBP2AcCAMPEP.01765182-7.8SiBP2AcCAMPEP.01765182-7.8SiBP2AcCAMPEP.01765182-7.8SiBP2AcCAMPEP.01765184-4.1SiBP2AcCAMPEP.0176519182-7.8SiBP2PtH1B774187741.PHATC-6.4SiBP3 </td <td>-1,1</td> <td></td> <td></td> <td>Ac</td> <td>Fba classI</td>	-1,1			Ac	Fba classI
Fba classilAcCAMPEP. 01766108881.9Fba classilAcCAMPEP. 0176610888-1.2Fba classil'AcCAMPEP. 01766331794-1.3Fba classil'PttriB70481870483.PtATC-1.7Fba classil'PttriB70581875318.PtATC4.6Fba classil'PttriB705809.PtATC1.4Fba classil'PttriB705809.PtATC1.4Fba classil'PttriB705809.PtATC1.4Fba classil'PttriB705809.PtATC-1.5FlavdoxinAcCAMPEP.017657538-1.5FlavdoxinAcCAMPEP.01766705541.4Gc 2AcCAMPEP.01766705541.1Gc 2AcCAMPEP.0176637541.1Gc 2AcCAMPEP.0176637541.1Gc 2AcCAMPEP.0176637541.1Gc 2AcCAMPEP.0176637541.1Gc 2PttriB705031B7026.0 PHATC1.1Gc 2PttriB705031B7026.0 PHATC1.1Gc 2PttriB705031B7021.PHATC-1.2Gc 2PttriB705031B7021.PHATC-2.1Gc 2PttriB705031B7021.PHATC-4.6SiB27'AcCAMPEP.017661382-7.8SiB22'AcCAMPEP.0176613402-3.6SiB22'AcCAMPEP.0176613402-3.6SiB22'PttriB705011402-4.6SiB22'AcCAMPEP.0176613402-4.1SiB22'AcCAMPEP.0176613402-4.6 <td>-2,0</td> <td></td> <td>_</td> <td></td> <td></td>	-2,0		_		
Fba classilAcCAMPEP. 017651742-1.2Fba classil*AcCAMPEP. 017653734-1.3Fba classil*AcCAMPEP. 0176537341.4Fba classil*PtH187C34817C48.3PHATC-1.7Fba classil*PtH187C3058175398.PHATC4.6Fba classil*PtH187C3058175398.PHATC1.4Fba classil*AcCAMPEP. 0176511622-1.5FlavadoxinAcCAMPEP. 0176511622-1.5FlavadoxinAcCAMPEP. 0176511622-1.1Car.2AcCAMPEP. 0176517541.4Car.2AcCAMPEP. 01765122-1.2Car.2AcCAMPEP. 0176612241.0Car.2AcCAMPEP. 017661224601.0Car.2AcCAMPEP. 017661224601.0Car.2AcCAMPEP. 0176612324601.0Car.2PtH187C302187232.PHATC-1.1Car.2PtH187C302187232.PHATC-1.1Car.2PtH187C30218723.PHATC-1.3Car.2PtH187C30218724.PHATC-3.2Car.2PtH187C30218724.PHATC-4.6SIB12*AcCAMPEP.0176513402-4.6SIB12*AcCAMPEP.0176513402-3.2SIB12*AcCAMPEP.0176513402-1.3SIB12*AcCAMPEP.0176513402-1.3SIB12*AcCAMPEP.0176513402-1.3SIB12*AcCAMPEP.0176513402-1.3 <trr>SIB12*AcCAMPEP.0176511892</trr>	-4,3				
Fib classifAcCAMPEP.0176331794-1.3Fib classifPtCAMPEP.017663317841.4Fib classifPtHTB7C4R3187C4R3.PHATC-1.7Fib classifPtHTB7C3R318725N8.PHATC4.66Fib classifPtHTB7C3R21872508.PHATC1.4Fib classifPtHTB7C3R218725N2.PHATC1.4Fib classifPtHTB7C3R218725N2.PHATC-1.5Fib classifPtHTB7C3R218725N2.PHATC-6.3Gr.2AcCAMPEP.0176673541.4Gr.2AcCAMPEP.017667354-1.1Gr.2AcCAMPEP.017663754-1.2Gr.2AcCAMPEP.017663754-1.2Gr.2AcCAMPEP.0176637840-1.2Gr.2AcCAMPEP.0176637840-1.2Gr.2PtHTB7C9C31877C3.PHATC-1.1Gr.2PtHTB7C9C31877C3.PHATC-1.3Gr.2PtHTB7C9C31877C3.PHATC-1.3Gr.2PtHTB7C9C31877C3.PHATC-3.3Gr.2PtHTB7C9C31877C3.PHATC-3.3Gr.2PtHTB7C9C31877C3.PHATC-3.3SIP2'AcCAMPEP.0176593704-5.2SIP2'AcCAMPEP.0176593704-5.2SIP2'AcCAMPEP.0176591402-7.8SIP2'AcCAMPEP.01765914704-1.3SIP2'AcCAMPEP.01765914704-5.5SIP2'AcCAMPEP.01765914704-5.5SIP2'AcCAMPEP.01765914704-1.3 </td <td>2,8</td> <td></td> <td></td> <td></td> <td></td>	2,8				
Pha classII* Ac CAMPEP_017663818 1.4 Pha classII* Pt HPR753N8JPATC -1.7 Pha classII* Pt HPR753N8JPS3N8_PHATC 4.6 Pha classII* Pt HPR753N8JPS3N8_PHATC 1.4 Plavedoxin Ac CAMPEP_0176557388 -1.5 Plavedoxin Pt HPR7CM3JPS7AN_PHATC -6.3 Gsr_2 Ac CAMPEP_017662754 1.4 Gsr_3 Ac CAMPEP_0176623561 -1.1 Gsr_2 Ac CAMPEP_0176623561 -1.2 Gsr_3 Ac CAMPEP_0176635261 -1.2 Gsr_4 Ac CAMPEP_0176635261 -1.1 Gsr_2 Pt HB70503167030_21740C -1.7 Gsr_2 Pt HB70503167030_21741C -1.3 SB12* Ac CAMPEP_017659304 -5.2 SB12* Ac CAMPEP_017559304 -5.2 SB12* Pt HB7050316703_217412 -1.3 SB12* Ac CAMPEP_017559304	-1,1				
Fba classil Pt tr B7C4R3]B7C4R3_PHATC -1,7 Fba classil Pt tr B7C3C9]B7C4R3_PHATC 4.6 Fba classil Pt tr B7C3C9]B7C360_PHATC 1.4 Fba classil Ac CAMPEP_017657388 -1.5 Flavodoxin Ac CAMPEP_017661522 -1.5 Flavodoxin Ac CAMPEP_0176670554 1.4 Gst_2 Ac CAMPEP_0176670554 1.4 Gst_2 Ac CAMPEP_0176625400 1.0 Gst_2 Ac CAMPEP_0176625400 1.1 Gst_2 Ac CAMPEP_0176625400 1.1 Gst_2 Pt tt B7C326]B7C32.BP1ATC 1.1 Gst_2 Pt tt B7C326]B7C32.BP1ATC 1.1 Gst_2 Pt tt B7C326]B7C30.DP1ATC -2.1 Gst_2 Pt tt B7C3B7D703.BP1ATC -3.3 SIP2 Ac CAMPEP_017651940 -5.2 SIP2 Pt tt B7C4B1B7C4BP7L4PHATC -6.4 SIP2 Pt tt B7C4B1B7C4BP7L4	-1,1				
Fba classII* Pt trip753N8JPYATC 4.6 Fba classII Pt trip753N8JPYATC 1.4 Flavodoxin Ac CAMPEP_0176517388 -1.5 Flavodoxin Pt trip57C603p75602,PHATC -6.3 Flavodoxin Pt trip57C603p76402,PHATC -6.3 Gx 2 Ac CAMPEP_017662754 -1.1 Gx 2 Ac CAMPEP_0176625460 1.0 Gx 2 Ac CAMPEP_0176625640 -1.2 Gx 2 Ac CAMPEP_0176625640 -1.1 Gx 2 Ac CAMPEP_0176625640 -1.1 Gx 2 Pt trip72623617236_0_FATC -1.7 Gx 2 Pt trip72623617236_0_FATC -1.7 Gx 2 Pt trip72632617236_0_FHATC NA Gx 2 Pt trip72632617236_0_FHATC -1.3 SiP2 Pt trip72632617236_0_FHATC -1.3 SiP2 Pt trip726317623_0_FHATC -1.3 SiP2 Ac CAMPEP_0176513402	1,5				
Fba Pt IPTCSOSIPTCGCS_PHATC 1.4 Flavodoxin Ac CAMPEP_0176511522 -1.5 Flavodoxin Ac CAMPEP_0176511522 -1.5 Flavodoxin Pt triB7CCM3B7CGM3PHATC -6.3 Gsr.2 Ac CAMPEP_0176670554 1.4 Gsr.2 Ac CAMPEP_017667054 -1.1 Gsr.2 Ac CAMPEP_0176625460 1.0 Gsr.2 Ac CAMPEP_0176625460 1.1 Gsr.2 Pt ttB762G3B76263_PHATC -1.7 Gsr.2 Pt ttB762G3B762G3_PHATC -1.1 Gsr.2 Pt ttB762G3B762G3_PHATC -1.1 Gsr.2 Pt ttB762G3B762G3_PHATC -1.3 SIP27 Ac CAMPEP_017651402 -4.6 SIP27 Ac CAMPEP_017651402 -4.6 SIP28 Pt ttB7741877712_PHATC -6.4 SIP27 Pt ttB774187712_PHATC -6.4 SIP28 Pt ttB774187712_PHATC -6.4	1,0				
Flavodoxin Ac CAMPEP. 017657388 -1.5 Plavodoxin Pt tr B7CCM3]B7CCM3_PHATC -6.3 Gsr.2 Ac CAMPEP. 0176670554 1.4 Gsr.2 Ac CAMPEP. 0176670554 -1.1 Gsr.2 Ac CAMPEP. 0176652460 1.0 Gsr.2 Ac CAMPEP. 017663524 -1.2 Gsr.2 Ac CAMPEP. 017663524 -1.7 Gsr.2 Pt tt B7G32]B7C326_PHATC 1.1 Gsr.2 Pt tt B7G32]B7C326_PHATC -1.7 Gsr.2 Pt tt B7G32]B7C326_PHATC -1.3 Gsr.2 Pt tt B7C32]B7C3C3_PHATC -3.3 SIP2* Ac CAMPEP.0176513402 -7.8 ISIP2* Ac CAMPEP.0176513402 -7.8 ISIP2* Ac CAMPEP.0176513402 -1.3 ISIP2* Ac CAMPEP.0176513402 -1.3 ISIP2* Pt tt B7C4 B77L2 PHATC -6.4 ISIP2* Ac CAMPEP.0176513402 -1.	4,4				
FlavedoxinAcCAMPEP.0176611622-1.5Gar.2AcCAMPEP.01766705541.4Gsr.2AcCAMPEP.01766705541.4Gsr.2AcCAMPEP.017662754-1.1Gsr.2AcCAMPEP.01766254601.0Gsr.2AcCAMPEP.01766254601.1Gsr.2AcCAMPEP.017662362-1.2Gsr.2PtH187623187623.26.PHATC-1.7Gsr.2PtH187623187623.PHATCNAGsr.2PtH18762911876901LPHATC-2.1Gsr.2PtH187762911876901LPHATC-1.6Gsr.2PtH187762911876901LPHATC-1.6Gsr.2PtH187762911876901LPHATC-1.6SIP2*AcCAMPEP.0176513402-4.6SIP2*AcCAMPEP.0176513402-7.8SIP2*AcCAMPEP.0176533694-5.2SIP2*AcCAMPEP.0176533694-1.6SIP2*AcCAMPEP.0176533694-4.1SIP2*AcCAMPEP.0176533694-4.1SIP2*AcCAMPEP.017651402-1.6SIP2*AcCAMPEP.0176518901.3SIP3AcCAMPEP.0176518901.3SIP3*AcCAMPEP.0176518901.3SIP3*AcCAMPEP.0176518901.3SIP3*AcCAMPEP.0176518901.3SIP3*AcCAMPEP.0176518901.3SIP3*AcCAMPEP.0176518901.5LhcxAcCAMPEP.01766107923.	4,3				
Flavodoxin Pt tr B7CCM3 B7CCM3_PHATC -6.3 Gsr.2 Ac CAMPEP.0176670554 1.4 Gsr.2 Ac CAMPEP.017662754 -1.1 Gsr.2 Ac CAMPEP.0176635824 -1.2 Gsr.2 Ac CAMPEP.0176635824 -1.7 Gsr.2 Ac CAMPEP.01766325.PHATC 1.1 Gsr.2 Pt tr B705261B705.32.PHATC 1.1 Gsr.2 Pt tr B75261B705.32.PHATC -2.1 Gsr.2 Pt tr B75761B765.3402 -4.6 Gsr.2 Pt tr B75761B765.3402 -4.6 SIP2* Ac CAMPEP.0176513402 -5.2 ISIP2* Ac CAMPEP.0176513402 -5.4 ISIP2* Ac CAMPEP.0176513402 -7.8 ISIP2 Pt tr B77414PFTV12.PHATC -1.6 ISIP2 Ac CAMPEP.0176513602 -1.3 ISIP2 Pt tr B77414PFTV12.PHATC -6.5 ISIP2 Rt tr B77414PFTV12.PHATC -1.6	-4,3				
Gr.2 Ac CAMPEP.017662754 1.4 Gsr.2 Ac CAMPEP.017662754 -1.1 Gsr.2 Ac CAMPEP.0176625460 1.0 Gsr.2 Ac CAMPEP.0176625461 1.1 Gsr.2 Ac CAMPEP.0176642616 1.1 Gsr.2 Pt ttlB7C3261B7C305_PHATC -1.7 Gsr.2 Pt ttlB7C301B7C305_PHATC -1.1 Gsr.2 Pt ttlB7C301B7C305_PHATC -7.8 Gsr.2 Pt ttlB7C301B7C30_PHATC -1.3 Gsr.2 Pt ttlB7C301B7FV3_PHATC -3.3 ISIP2* Ac CAMPEP.0176613402 -4.6 SIP2* Ac CAMPEP.0176613402 -7.8 ISIP2 Pt ttlB7TVL3PHATC -1.6 ISIP2 Pt ttlB7TVL3PHATC -1.6 ISIP2 Pt ttlB7TVL3PHATC -1.6 ISIP2 Pt ttlB7TVL3PHATC -1.6 ISIP2 Pt ttlB7TVL3PHATC -1.1 IS	-3,9		_		
Gsr.2 Ac CAMPEP.0176627544 -1.1 Gsr.2 Ac CAMPEP.0176625460 1.0 Gsr.2 Ac CAMPEP.0176625824 -1.2 Gsr.2 Ac CAMPEP.0176625824 -1.2 Gsr.2 Ac CAMPEP.0176625824 -1.2 Gsr.2 Pt ttlB70236187352.PHATC -1.7 Gsr.2 Pt ttlB75236187253.PHATC NA Gsr.2 Pt ttlB7723187723.PHATC NA Gsr.2 Pt ttlB7723187723.PHATC -1.3 Gsr.2 Pt ttlB7723187723.PHATC -1.3 SIP2 Pt ttlB774187741.PHATC -1.6 SIP2 Ac CAMPEP.017661392 -7.8 SIP2 Pt ttlB774187741.PHATC -1.6 SIP2A Pt ttlB774187741.PHATC -1.6 SIP2B' Pt ttlB705811B7081.PHATC -6.4 SIP2B' Pt ttlB70581B7081.PHATC -1.6 SIP2B' Pt ttlB70581B7081.PHATC -1.6 SIP2A Pt ttlB70581B7081.PHATC -1.6 <t< td=""><td>-2,9</td><td></td><td> –</td><td></td><td></td></t<>	-2,9		–		
Gr.2 Ac CAMPEP_0176635460 1.0 Gsr.2 Ac CAMPEP_0176635824 -1,2 Gsr.2 Ac CAMPEP_0176642616 1,1 Gsr.2 Pt ttpS7G32B73C3_PHATC -1,7 Gsr.2 Pt ttpS7G32B73C3_PHATC 1,1 Gsr.2 Pt ttpS7G3B73C3_PHATC -2,1 Gsr.2 Pt ttpS7G3B73C3_PHATC -2,1 Gsr.2 Pt ttpS7G3D1B73C3_PHATC -1,3 Gsr.2 Pt ttpS7G3D1PFX3_PHATC -1,6 SIP2* Ac CAMPEP_0176519302 -7,8 SISP2* Ac CAMPEP_0176519302 -5,2 ISIP2* Ac CAMPEP_0176533694 -4,1 ISIP2* Pt ttpS7G4B187FV12_PHATC -6,6 ISIP2* Pt ttpS7G4B187FV14_PHATC -6,5 ISIP3 Ac CAMPEP_0176611690 1,3 ISIP3 Ac CAMPEP_0176611690 1,3 ISIP3 Ac CAMPEP_017651761 1,1 <t< td=""><td>1,3</td><td></td><td></td><td></td><td></td></t<>	1,3				
Gr.2AcCAMPEP_0176635824-1.2Gsr.2AcCAMPEP_01766426161.1Gsr.2PtUIB7G326187G326_PHATC-1.7Gsr.2PtUIB7G326187G326_PHATC1.1Gsr.2PtUIB7C326187G326_PHATC1.1Gsr.2PtUIB7EC30187EG3_PHATC-2.1Gsr.2PtUIB7EC30187EG3_PHATC-1.3Gsr.2PtUIB7EC30187EG3_PHATC-1.3SIP2AcCAMPEP_0176513402-4.6SIP2*AcCAMPEP_0176513402-5.2SIP2*AcCAMPEP_0176513402-6.4SIP2*AcCAMPEP_0176513402-6.4SIP2*PtUIB7FVL487FVL4_PHATC-1.6SIP2*PtUIB7FVL487FVL4_PHATC-6.5SIP2PtUIB7FVL487FVL2_PHATC-6.5SIP2PtUIB7FVL387FVL3_PHATC-6.5SIP2PtUIB7C48187FVL3_PHATC-6.5SIP2PtUIB7C48187FVL3_PHATC-6.5SIP3*AcCAMPEP_0176533694-4.1SIP3*PtUIB7C481887C48_PHATC-6.5RbcLAcCAMPEP_01765376161.1LbcxAcCAMPEP_01765376161.1LbcxAcCAMPEP_01765321221.5LbcxAcCAMPEP_01765321221.5LbcxAcCAMPEP_0176532701.5LbcxAcCAMPEP_0176532701.5LbcxAcCAMPEP_0176532701.5LbcxAcCAMPEP_017653776 <td>-1,6</td> <td></td> <td></td> <td></td> <td></td>	-1,6				
Gr.2 Ac CAMPEP_0176642616 1.1 Gsr.2 Pt trlB7G326]B7G326_PHATC -1.7 Gsr.2 Pt trlB7G326]B7G9G3_PHATC 1.1 Gsr.2 Pt trlB7G26]B7G9G3_PHATC NA Gsr.2 Pt trlB7C9G3]B7C9G3_PHATC -2.1 Gsr.2 Pt trlB7C9G1]B7C9G1_PHATC -3.3 SIP2* Ac CAMPEP_0176513402 -4.6 SIP2* Ac CAMPEP_0176513402 -5.2 ISIP2* Ac CAMPEP_0176513402 -7.8 ISIP2* Ac CAMPEP_0176518402 -6.4 ISIP2* Ac CAMPEP_0176511892 -7.8 ISIP2 Pt trlB7C9B1 B7G9B1_PHATC -6.5 ISIP3 Ac CAMPEP_0176511892 -4.1 ISIP3 Ac CAMPEP_0176511890 1.3 ISIP3 Ac CAMPEP_017651056 1.1 IsiP3 Ac CAMPEP_017651056 1.1 IsiP3 Ac CAMPEP_017651076 2.2	-2,3				
Gr.2 Pt tr B7G326 B7G362,PHATC -1,7 Gsr.2 Pt tr B7G9G3 B7G9G3,PHATC 1,1 Gsr.2 Pt tr B7C9G3 B7C3C3,PHATC NA Gsr.2 Pt tr B7C9G1 B7C3G3,PHATC -2,1 Gsr.2 Pt tr B7C9G1 B7C9G1,PHATC -1,3 ISIP2* Ac CAMPEP_0176513402 -4,6 ISIP2* Ac CAMPEP_0176513402 -4,6 ISIP2* Ac CAMPEP_0176513402 -7,8 ISIP2 Pt tr B7V14 B7V14_PHATC -6,4 ISIP2 Pt tr B7V14 B7V12_PHATC -6,4 ISIP3 Ac CAMPEP_0176513802 -7,8 ISIP3 Ac CAMPEP_0176513804 -4,1 ISIP3 Ac CAMPEP_0176513604 -4,1 ISIP3 Ac CAMPEP_017651090 1,3 RbcL Ac CAMPEP_017651090 1,3 RbcL Ac CAMPEP_0176512150 1,5 Lbcx Ac CAMPEP_0176512122 1,5 Lbcx Ac CAMPEP_0176532122 1,5 <t< td=""><td>-1,4</td><td></td><td></td><td></td><td></td></t<>	-1,4				
Gsr_2 Pt tr[B7GG2]B7GG3_PHATC 1,1 Gsr_2 Pt tr[B7FZC3]B7EZG3_PHATC NA Gsr_2 Pt tr[B7FQ2]B7C90]_PHATC -2,1 Gsr_2 Pt tr[B7FVM3]B7HATC -1.3 $SIP2^*$ Ac CAMPEP_0176513402 -46 $SIP2^*$ Ac CAMPEP_01765199704 -5,2 $SIP2^*$ Ac CAMPEP_01765199704 -5,2 $SIP2^*$ Ac CAMPEP_0176519872 -7,8 $SIP2^*$ Ac CAMPEP_0176518402 -6,4 $SIP2^*$ Ac CAMPEP_0176531894 -4,1 $SIP2^*$ Pt tr[B7C94]B7C96B]PTATC -1,3 $SIP2^*$ Pt tr[B7C4H8]B7C4H8_PHATC -6,5 $SIP3^*$ Pt tr[B7C4H8]B7C4H8_PHATC -1,1 $ISP3^*$ Pt tr[B7C53]B69 -4,1 $SIP3^*$ Pt tr[B7C4H8]B7C4H8_PHATC -1,1 $Ibcx$ Ac CAMPEP_017661090 1,3 $Ibcx$ Ac CAMPEP_0176517516 1,1 $Ibcx$ Ac CAMPEP_017661092	-1,8		CAMPEP_0176642616		Gsr_2
Gsr.2Pttt $ PTZC3 PTZC3 PTATCNAGsr.2Pttt PTZC3 PTZC3 PTATC-2.1Gsr.2Pttt PTC3 PTC3]PTVM3 PTVM3 PTATC-1.3ISIP2AcCAMPEP_0176513402-4.6ISIP2*AcCAMPEP_0176513402-7.8ISIP2AcCAMPEP_0176611892-7.8ISIP2Pttt PTC14 PTATC-6.4ISIP2Pttt PTC14 PTATC14 PTATC-6.4ISIP2Pttt PTC4H8 PTC14 PTATC-6.5ISIP2Pttt PTC3P14 PTATC14 PTATC-6.5ISIP2Pttt PTC4H8 PTC14 PTATC-1.1ISIP3AcCAMPEP_01766115901.3RbcLAcCAMPEP_01766116901.3RbcLAcCAMPEP_01766107923.0LhcxAcCAMPEP_01766107923.0LhcxAcCAMPEP_01766109662.2LhcxAcCAMPEP_0176631462.2LhcxAcCAMPEP_0176631462.2LhcxAcCAMPEP_0176631462.4LhcxAcCAMPEP_0176631462.4LhcxAcCAMPEP_0176631461.5LhcxAcCAMPEP_0176631761.4LhcxAcCAMPEP_0176631761.4LhcxAcCAMPEP_0176632701.5LhcxAcCAMPEP_01766387381.5LhcxAcCAMPEP_01766381462.4LhcxAcCAMPEP_01766382701.5LhcxAcCAMPEP_01766383$	-1,2				Gsr_2
Gsr.2 Pt triB7GQ1_PHATC -2.1 Gsr.2 Pt triB7FVM3_PHATC -1.3 ISIP2* Ac CAMPEP_0176513402 -4.6 ISIP2* Ac CAMPEP_0176513402 -5.2 ISIP2* Ac CAMPEP_0176513402 -7.8 ISIP2 Ac CAMPEP_0176511892 -7.8 ISIP2 Pt triB7FV14/B7FV12_PHATC -6.4 ISIP2 Pt triB7FV16/GB11892 -4.1 ISIP2 Pt triB7FV16/GB1187C4H_PHATC -6.5 ISIP3 Ac CAMPEP_0176513694 -4.1 ISIP3 Ac CAMPEP_017661792 3.0 ISIP3* Pt triB7C4H3/B74H3_PHATC -6.5 RbcL Ac CAMPEP_017661792 3.0 Lhcx Ac CAMPEP_017661792 1.5 Lhcx A	1,2		tr B7G9G3 B7G9G3_PHATC		Gsr_2
Gsr.2 Pt tr[B7FVM3]B7FVM3_PHATC -1.3 ISIP2* Ac CAMPEP_0176513402 -4.6 ISIP2* Ac CAMPEP_0176513402 -5.2 ISIP2* Ac CAMPEP_0176611892 -7.8 ISIP2 Pt tr[B7FY14]B7FY14_PHATC -1.6 ISIP2 Pt tr[B7G91]B7C9B1_PHATC -6.4 ISIP2b* Pt tr[B7G91]B7C9B1_PHATC -6.5 ISIP3 Ac CAMPEP_0176613694 -4.1 ISIP3* Pt tr[B7G41B3P7G418_PHATC -6.5 RbcL Ac CAMPEP_0176613690 1.3 RbcL Ac CAMPEP_0176610590 3.0 Lbcx Ac CAMPEP_0176610792 3.0 Lbcx Ac CAMPEP_0176513402 1.5 Lbcx Ac CAMPEP_0176513402 1.5 Lbcx Ac CAMPEP_0176610792 3.0 Lbcx Ac CAMPEP_0176513102 1.5 Lbcx Ac CAMPEP_017651370 1.5 Lbcx Ac CAMPEP_017661370 1.5 Lbcx <td>1,3</td> <td></td> <td>tr B7FZC3 B7FZC3_PHATC</td> <td></td> <td>Gsr_2</td>	1,3		tr B7FZC3 B7FZC3_PHATC		Gsr_2
ISIP2*AcCÅMPEP_0176513402-4.6ISIP2*AcCAMPEP_0176611892-5.2ISIP2*AcCAMPEP_0176611892-7.8ISIP2Pttr[B7FYL4]B7FYL4]B7FYL4_PHATC-1.6ISIP2b*Pttr[B7G9B]B7G9B]_PHATC-6.4ISIP2b*Pttr[B7G9B]B7G9B]_PHATC-6.5ISIP2b*Pttr[B7G9B]B7G9B]_PHATC-6.5ISIP3AcCAMPEP_0176616901.3RbcLAcCAMPEP_0176616901.3RbcLAcCAMPEP_01766107923.0LhcxAcCAMPEP_01766107923.0LhcxAcCAMPEP_01766107921.1LhcxAcCAMPEP_01766109662.2LhcxAcCAMPEP_01766318162.2LhcxAcCAMPEP_01766318462.2LhcxAcCAMPEP_01766318162.4LhcxAcCAMPEP_01766318462.2LhcxAcCAMPEP_0176631701.5LhcxAcCAMPEP_0176631761.4LhcxAcCAMPEP_0176532001.4LhcxAcCAMPEP_0176638701.5LhcxAcCAMPEP_0176638781.5LhcxAcCAMPEP_0176638781.5LhcxAcCAMPEP_0176638781.5LhcxAcCAMPEP_0176638781.5LhcxAcCAMPEP_01766387881.5LhcxAcCAMPEP_0176638781.5LhcxAcCAMPEP_01766387381.5Lhcx<	1,5		tr B7G9Q1 B7G9Q1_PHATC		
ISIP2*AcCAMPEP_0176599704-5.2ISIP2*AcCAMPEP_0176611892-7.8ISIP2Pttr B7FYL4 B7FYL4_PLATC-1.6ISIP2.Pttr B7FYL4 B7FYL2,PHATC-6.4ISIP2.b*Pttr B7G9B1_PHATC-6.5ISIP3AcCAMPEP_0176533694-4.1ISIP3AcCAMPEP_01765116901.3RbcLAcCAMPEP_01766116901.3RbcLAcCAMPEP_01766107923.0LhcxAcCAMPEP_01766107923.0LhcxAcCAMPEP_01766107923.0LhcxAcCAMPEP_01766109662.2LhcxAcCAMPEP_0176575161.1LhcxAcCAMPEP_01765321221.5LhcxAcCAMPEP_01765321221.5LhcxAcCAMPEP_01765320001.4LhcxAcCAMPEP_01765367761.4LhcxAcCAMPEP_01765387761.4LhcxAcCAMPEP_0176385381.5LhcxAcCAMPEP_0176385381.5LhcxAcCAMPEP_0176385381.5LhcxAcCAMPEP_0176385381.5LhcxAcCAMPEP_0176385381.5LhcxAcCAMPEP_0176385381.5LhcxAcCAMPEP_0176385381.5LhcxAcCAMPEP_0176519762.3LhcxAcCAMPEP_0176519762.3LhcxPttt B7FK0 B7FK0_PHATC1.6LhcxPt <t< td=""><td>-1,1</td><td></td><td>tr B7FVM3 B7FVM3_PHATC</td><td>Pt</td><td></td></t<>	-1,1		tr B7FVM3 B7FVM3_PHATC	Pt	
ISIP2*AcCAMPEP_0176611892-7.8ISIP2Pttr B7Y14,2PHATC-1.6ISIP2Pttr B7Y14,2PHATC-6.4ISIP2Pttr B7S91187C9B1,PHATC-13.8ISIP3AcCAMPEP_0176533694-4,1ISIP3*Pttr B7C4H8,B7C4H8,PHATC-6.5RbcLAcCAMPEP_01766116901,3RbcLAcCAMPEP_01765175161,1LhcxAcCAMPEP_01765575161,1LhcxAcCAMPEP_01765575161,1LhcxAcCAMPEP_01765321221,5LhcxAcCAMPEP_017661381462,2LhcxAcCAMPEP_01765321221,5LhcxAcCAMPEP_01765321221,5LhcxAcCAMPEP_01765321221,5LhcxAcCAMPEP_01765321221,5LhcxAcCAMPEP_01765321221,5LhcxAcCAMPEP_01765321221,5LhcxAcCAMPEP_01765321221,5LhcxAcCAMPEP_0176532701,4LhcxAcCAMPEP_01766382701,4LhcxAcCAMPEP_01766385381,5LhcxAcCAMPEP_01766385381,5LhcxAcCAMPEP_01766385381,5LhcxAcCAMPEP_01766385381,5LhcxAcCAMPEP_01766385381,5LhcxAcCAMPEP_01765759762,3Magnesium chelatase*//Pttr B7FR0J8FR60_PHATC-5,5	-1,7	-4,6	CAMPEP_0176513402	Ac	ISIP2*
ISIP2 Pt tr B7FYL4 B7FYL4_PHATC -1.6 ISIP2a Pt tr B7G9B1 B7YL2_PHATC -6.4 ISIP2b* Pt tr B7G9B1 B7GSB1_PHATC -13.8 ISIP3* Ac CAMPEP_0176533694 -4.1 ISIP3* Pt tr B7G9B1 B7G418_PHATC -6.5 RbcL Ac CAMPEP_0176611690 1.3 RbcL Ac CAMPEP_0176610792 3.0 Lhcx Ac CAMPEP_0176610792 3.0 Lhcx Ac CAMPEP_0176637516 1.1 Lhcx Ac CAMPEP_0176633146 2.2 Lhcx Ac CAMPEP_0176532122 1.5 Lhcx Ac CAMPEP_0176532122 1.5 Lhcx Ac CAMPEP_017653276 1.4 Lhcx Ac CAMPEP_0176638270 1.5 Lhcx Ac CAMPEP_0176638270 1.5 Lhcx Ac CAMPEP_0176638278 1.5 Lhcx Ac CAMPEP_0176638278 1.5	-2,8	-5,2	CAMPEP_0176599704	Ac	ISIP2*
ISIP2a Pt tr B7FYL2 B7FYL2_PHATC -6,4 ISIP2b* Pt tr B7G9B1 B7G9B1_PHATC -13,8 ISIP3 Ac CAMPEP_0176533694 -4,1 ISIP3* Pt tr B7G4H8 B7G4H8_PHATC -6,5 RbcL Ac CAMPEP_0176611690 1,3 RbcL Ac CAMPEP_0176610792 3,0 Lhcx Ac CAMPEP_0176610966 2,2 Lhcx Ac CAMPEP_0176631466 2,2 Lhcx Ac CAMPEP_0176632122 1,5 Lhcx Ac CAMPEP_01766331466 2,2 Lhcx Ac CAMPEP_0176632122 1,5 Lhcx Ac CAMPEP_0176632000 1,4 Lhcx Ac CAMPEP_0176638270 1,5 Lhcx Ac CAMPEP_0176638270 1,5 Lhcx Ac CAMPEP_017661897 1,6 Lhcx Ac CAMPEP_0176638270 1,5 Lhcx Ac CAMPEP_0176618023 1,5 Lhcx </td <td>-1,4</td> <td>-7,8</td> <td>CAMPEP_0176611892</td> <td>Ac</td> <td>ISIP2*</td>	-1,4	-7,8	CAMPEP_0176611892	Ac	ISIP2*
ISIP2b* Pt tr[B7G9B1[B7G9B1_PHATC -13,8 ISIP3 Ac CAMPEP_0176533694 -4,1 ISIP3* Pt tr[B7G4H8]B7G4H8_PHATC -6,5 RbcL Ac CAMPEP_0176611690 1,3 RbcL Pt splQ9TK52[RBL_PHATC -1,1 Lhcx Ac CAMPEP_0176610792 3,0 Lhcx Ac CAMPEP_0176610796 2,2 Lhcx Ac CAMPEP_0176610796 2,2 Lhcx Ac CAMPEP_0176633146 2,2 Lhcx Ac CAMPEP_0176532122 1,5 Lhcx Ac CAMPEP_0176532000 1,4 Lhcx Ac CAMPEP_0176532000 1,4 Lhcx Ac CAMPEP_0176633270 1,5 Lhcx Ac CAMPEP_0176633270 1,5 Lhcx Ac CAMPEP_0176633538 1,5 Lhcx Ac CAMPEP_0176638270 1,1 Lhcx Ac CAMPEP_01766385383 1,5 Lhcx	-2,2	-1,6	tr B7FYL4 B7FYL4_PHATC	Pt	ISIP2
ISIP3 Ac CÅMPEP_0176533694 -4,1 ISIP3* Pt tt B7C4H8 B7C4H8_PHATC -6.5 RbcL Ac CAMPEP_0176611690 1,3 RbcL Pt splQ9TK52[RBL_PHATC -1.1 Lhcx Ac CAMPEP_0176610792 3,0 Lhcx Ac CAMPEP_0176610666 2,2 Lhcx Ac CAMPEP_0176638146 2,2 Lhcx Ac CAMPEP_0176532122 1,5 Lhcx Ac CAMPEP_0176532000 1,4 Lhcx Ac CAMPEP_0176610776 2,4 Lhcx Ac CAMPEP_017663270 1,5 Lhcx Ac CAMPEP_017663870 1,4 Lhcx Ac CAMPEP_017663870 1,5 Lhcx Ac CAMPEP_017663870 1,5 Lhcx Ac CAMPEP_0176638538 1,5 Lhcx Ac CAMPEP_0176638538 1,5 Lhcx Ac CAMPEP_0176638538 1,5 Lhcx Ac<	-2,4	-6,4	tr B7FYL2 B7FYL2_PHATC	Pt	ISIP2a
ISIP3* Pt tr[B7G4H8]B7G4H8_PHATC -6,5 RbcL Ac CAMPEP_0176611690 1,3 RbcL Pt sp[Q9TK52]R8L_PHATC -1,1 Lhcx Ac CAMPEP_0176610792 3,0 Lhcx Ac CAMPEP_0176610792 3,0 Lhcx Ac CAMPEP_0176610966 2,2 Lhcx Ac CAMPEP_0176638146 2,2 Lhcx Ac CAMPEP_0176632122 1,5 Lhcx Ac CAMPEP_0176532122 1,5 Lhcx Ac CAMPEP_0176638270 1,5 Lhcx P	-4,5	-13,8	tr B7G9B1 B7G9B1_PHATC	Pt	ISIP2b*
RbcL Ac CAMPEP_0176611690 1,3 RbcL Pt splQ9TK52IRBL_PHATC -1,1 Lhcx Ac CAMPEP_0176610792 3,0 Lhcx Ac CAMPEP_0176510792 3,0 Lhcx Ac CAMPEP_0176510792 3,0 Lhcx Ac CAMPEP_0176510792 3,0 Lhcx Ac CAMPEP_01765010760 2,2 Lhcx Ac CAMPEP_017652122 1,5 Lhcx Ac CAMPEP_017651200 1,4 Lhcx Ac CAMPEP_0176532000 1,4 Lhcx Ac CAMPEP_0176532000 1,4 Lhcx Ac CAMPEP_017653276 1,5 Lhcx Ac CAMPEP_0176638576 1,4 Lhcx Ac CAMPEP_0176638576 1,4 Lhcx Ac CAMPEP_0176638538 1,5 Lhcx Ac CAMPEP_0176638538 1,5 Lhcx Pt tr B7FK0 B7FVP_DPHATC -1,6 Lhcx [*] Pt<	-2,6	-4,1	CAMPEP_0176533694	Ac	ISIP3
RbcL Pt splQ9TK52 RBL_PHATC -1,1 Lhcx Ac CAMPEP_0176610792 3,0 Lhcx Ac CAMPEP_0176557516 1,1 Lhcx Ac CAMPEP_0176539146 2,2 Lhcx Ac CAMPEP_0176638146 2,2 Lhcx Ac CAMPEP_0176532122 1,5 Lhcx Ac CAMPEP_0176532122 1,5 Lhcx Ac CAMPEP_0176532000 1,4 Lhcx Ac CAMPEP_0176536776 1,4 Lhcx Ac CAMPEP_0176638270 1,5 Lhcx Ac CAMPEP_0176638270 1,5 Lhcx Ac CAMPEP_0176638378 1,5 Lhcx Ac CAMPEP_0176638538 1,5 Lhcx Ac CAMPEP_0176638538 1,5 Lhcx Pt tr B7FVI0]B7FVI0_PHATC -1,1 Lhcx Pt tr B7F0B]B7FV5_P_PHATC -5,5 Magnesium chelatase* Ac CAMPEP_0176575976 2,3 Mag	-4,8	-6,5	tr B7G4H8 B7G4H8_PHATC	Pt	ISIP3*
LhcxAcCAMPEP_01766107923,0LhcxAcCAMPEP_01765175161,1LhcxAcCAMPEP_01766109662,2LhcxAcCAMPEP_01766381462,2LhcxAcCAMPEP_01765321221,5LhcxAcCAMPEP_01765211501,5LhcxAcCAMPEP_01765320001,4LhcxAcCAMPEP_01765320001,4LhcxAcCAMPEP_01765367761,4LhcxAcCAMPEP_01763682701,5LhcxAcCAMPEP_01766382701,5LhcxAcCAMPEP_01766382701,7LhcxAcCAMPEP_01766385381,5LhcxAcCAMPEP_01766385381,5LhcxAcCAMPEP_01766385381,5LhcxAcCAMPEP_01766385381,5LhcxAcCAMPEP_017663759762,3Lhcx*Pttr B7FVI0 B7FVI0_PHATC-1,6Lhcx2Pttr B7FVF9]B7FV79_PHATC-5,5Magnesium chelatase*AcCAMPEP_01765759762,3Magnesium chelatase*Pttr A0T0B5_PHATC1,8Magnesium chelatase*Pttr B7FA2 B7FTA2_PHATC1,5Magnesium chelatase*Pttr B7Y54 B5Y3F4_PHATC3,1	1,8	1,3	CAMPEP_0176611690	Ac	RbcL
LhcxAcCAMPEP_01765575161,1LhcxAcCAMPEP_01766109662,2LhcxAcCAMPEP_01766381462,2LhcxAcCAMPEP_01766381462,2LhcxAcCAMPEP_01765321221,5LhcxAcCAMPEP_01765320001,4LhcxAcCAMPEP_01765107762,4LhcxAcCAMPEP_01765367761,4LhcxAcCAMPEP_01766382701,5LhcxAcCAMPEP_01766382701,5LhcxAcCAMPEP_01766382701,5LhcxAcCAMPEP_01766385381,5LhcxAcCAMPEP_01766385381,5LhcxAcCAMPEP_0176613021,7LhcxAcCAMPEP_01766385381,5LhcxPttr B7FVI0 B7FVI0_PHATC-1,1Lhcx*Pttr B7FF0 B7FK0_PHATC-5,5Magnesium chelatase*AcCAMPEP_01765759762,3Magnesium chelatase*Pttr A0T0B5_PHATC1,8Magnesium chelatase*Pttr B7FA2 B7FL3_PHATC1,5Magnesium chelatase*Pttr B7FA2 B7FL3_PHATC1,5Magnesium chelatase*Pttr B5Y3F4 B5Y3F4_PHATC3,1	1,3	-1,1	sp Q9TK52 RBL_PHATC	Pt	RbcL
LhcxAcCAMPEP_01766109662,2LhcxAcCAMPEP_01766381462,2LhcxAcCAMPEP_01765321221,5LhcxAcCAMPEP_01765321221,5LhcxAcCAMPEP_01766211501,5LhcxAcCAMPEP_01765320001,4LhcxAcCAMPEP_01765367762,4LhcxAcCAMPEP_01765367761,4LhcxAcCAMPEP_01766382701,5LhcxAcCAMPEP_01766382701,5LhcxAcCAMPEP_01766382701,5LhcxAcCAMPEP_01766385381,5LhcxAcCAMPEP_01766385381,5LhcxPttr B7FY10JB7FY10_PHATC-1,6Lhcx*Pttr B7FK60JB7FR60_PHATC-5,5Magnesium chelatase*Pttr A0T0B5_A0T0B5_PHATC3,1Magnesium chelatase*Pttr B7FA2JB7FTA2_PHATC3,1	2,4	3,0	CAMPEP_0176610792	Ac	Lhcx
Lhcx Ac CAMPEP_0176638146 2,2 Lhcx Ac CAMPEP_0176532122 1,5 Lhcx Ac CAMPEP_0176621150 1,5 Lhcx Ac CAMPEP_0176532000 1,4 Lhcx Ac CAMPEP_0176610776 2,4 Lhcx Ac CAMPEP_0176536776 1,4 Lhcx Ac CAMPEP_0176638270 1,5 Lhcx Ac CAMPEP_0176638538 1,5 Lhcx Pt tr B7FY0]B7FY10_PHATC -1,1 Lhcx* Pt tr B7FF0]B7FY60_PHATC -5,5 Magnesium chelatase* Ac CAMPEP_0176575976 2,3 Magnesium chelatase Pt tr A07085]A070085_PHATC 1,8 <tr< td=""><td>1,9</td><td>1,1</td><td>CAMPEP_0176557516</td><td>Ac</td><td>Lhcx</td></tr<>	1,9	1,1	CAMPEP_0176557516	Ac	Lhcx
Lhcx Ac CAMPEP_0176532122 1,5 Lhcx Ac CAMPEP_0176621150 1,5 Lhcx Ac CAMPEP_0176532000 1,4 Lhcx Ac CAMPEP_0176532000 1,4 Lhcx Ac CAMPEP_017653676 2,4 Lhcx Ac CAMPEP_0176538776 1,5 Lhcx Ac CAMPEP_0176638270 1,5 Lhcx Ac CAMPEP_0176638270 1,7 Lhcx Ac CAMPEP_0176638270 1,7 Lhcx Ac CAMPEP_0176638538 1,5 Lhcx Ac CAMPEP_0176638538 1,5 Lhcx Pt tr B7FYL0 B7FYL0_PHATC -1,1 Lhcx* Pt tr B7FK60 B7FR60_PHATC -5,5 Magnesium chelatase* Ac CAMPEP_0176575976 2,3 Magnesium chelatase Pt tr A070B5]A070B5_PHATC 1,8 Magnesium chelatase Pt tr B7FA2]B7FTA2_PHATC 1,5 Magnesium chelatase* Pt tr B5Y3F4]B5Y3F4_PHATC <td>4,0</td> <td>2,2</td> <td>CAMPEP_0176610966</td> <td>Ac</td> <td>Lhcx</td>	4,0	2,2	CAMPEP_0176610966	Ac	Lhcx
Lhcx Ac CAMPEP_0176621150 1,5 Lhcx Ac CAMPEP_0176532000 1,4 Lhcx Ac CAMPEP_0176610776 2,4 Lhcx Ac CAMPEP_0176536776 1,4 Lhcx Ac CAMPEP_0176638270 1,5 Lhcx Ac CAMPEP_0176638270 1,5 Lhcx Ac CAMPEP_0176638270 1,7 Lhcx Ac CAMPEP_0176638538 1,5 Lhcx Ac CAMPEP_0176638538 1,5 Lhcx Pt tr B7FYL0 B7FYL0_PHATC -1,1 Lhcx* Pt tr B7FK60 B7FR60_PHATC -5,5 Magnesium chelatase* Ac CAMPEP_0176575976 2,3 Magnesium chelatase Pt tr A070B5_A070B5_PHATC 1,8 Magnesium chelatase Pt tr B7FTA2 B7FTA2_PHATC 1,5 Magnesium chelatase* Pt tr B7FYA2 B7FTA2_PHATC 3,1	1,6	2,2	CAMPEP_0176638146	Ac	Lhcx
Lhcx Ac CAMPEP_0176532000 1,4 Lhcx Ac CAMPEP_0176610776 2,4 Lhcx Ac CAMPEP_0176536776 1,4 Lhcx Ac CAMPEP_0176638270 1,5 Lhcx Ac CAMPEP_0176611302 1,7 Lhcx Ac CAMPEP_0176613538 1,5 Lhcx Ac CAMPEP_0176613538 1,5 Lhcx Ac CAMPEP_0176613538 1,5 Lhcx Pt tr B7FYL0 B7FYL0_PHATC -1,1 Lhcx* Pt tr B7FK60 B7FK60_PHATC -5,5 Magnesium chelatase* Ac CAMPEP_0176575976 2,3 Magnesium chelatase* Pt tr A0T0B5_PHATC 1,8 Magnesium chelatase* Pt tr B7FX42 B7FTA2_PHATC 1,5 Magnesium chelatase* Pt tr B5Y3F4 B5Y3F4_PHATC 3,1	1,3	1,5	CAMPEP_0176532122	Ac	Lhcx
Lhcx Ac CAMPEP_0176610776 2,4 Lhcx Ac CAMPEP_0176536776 1,4 Lhcx Ac CAMPEP_0176638270 1,5 Lhcx Ac CAMPEP_0176638270 1,5 Lhcx Ac CAMPEP_0176638538 1,5 Lhcx Ac CAMPEP_0176638538 1,5 Lhcx Pt tr B7FYL0 B7FYL0_PHATC -1,1 Lhcx [*] Pt tr B7FK0 B7FR60_PHATC -5,5 Magnesium chelatase [*] Ac CAMPEP_0176575976 2,3 Magnesium chelatase Pt tr A070B5]A0T0B5_PHATC 1,8 Magnesium chelatase Pt tr B7FA2 B7FA2_PHATC 1,5 Magnesium chelatase Pt tr B7FA2 B7FA2_PHATC 3,1	2,0	1,5	CAMPEP_0176621150	Ac	Lhcx
Lhcx Ac CAMPEP_0176536776 1,4 Lhcx Ac CAMPEP_0176638270 1,5 Lhcx Ac CAMPEP_0176611302 1,7 Lhcx Ac CAMPEP_0176638538 1,5 Lhcx Ac CAMPEP_0176638538 1,5 Lhcx Pt tr B7FYL0 B7FYL0_PHATC -1,1 Lhcx* Pt tr B7FR60 B7FR60_PHATC -5,5 Lhcx2 Pt tr B7FR60 B7FR60_PHATC -5,5 Magnesium chelatase* Ac CAMPEP_0176575976 2,3 Magnesium chelatase Pt tr A070B5 A070B5_PHATC 1,8 Magnesium chelatase Pt tr B7FR42 B7FTA2_PHATC 1,5 Magnesium chelatase* Pt tr B7FY42 B7FTA2_PHATC 3,1	1,6	1,4	CAMPEP_0176532000	Ac	Lhcx
Lhcx Ac CAMPEP_0176638270 1,5 Lhcx Ac CAMPEP_0176611302 1,7 Lhcx Ac CAMPEP_0176638538 1,5 Lhcx Pt tr B7FYL0 B7FYL0_PHATC -1,1 Lhcx* Pt tr B7FK60 B7FR60_PHATC -1,6 Lhcx2 Pt tr B7FR60 B7FR60_PHATC -5,5 Magnesium chelatase* Ac CAMPEP_0176575976 2,3 Magnesium chelatase Pt tr A070B5 A070B5_PHATC 1,8 Magnesium chelatase Pt tr B7FFA2 B7FTA2_PHATC 3,1	2,4	2,4	CAMPEP_0176610776	Ac	Lhcx
Lhcx Ac CAMPEP_0176611302 1,7 Lhcx Ac CAMPEP_0176638538 1,5 Lhcx Pt tr[B7FYL0]B7FYL0_PHATC -1,1 Lhcx* Pt tr[B7FYB]B7FVF9_PHATC -1,6 Lhcx2 Pt tr[B7FR60]B7FR60]PHATC -5,5 Magnesium chelatase* Ac CAMPEP_0176575976 2,3 Magnesium chelatase Pt tr[A070B5]A0T0B5_PHATC 1,8 Magnesium chelatase Pt tr[B7FA2]B7FTA2_PHATC 1,5 Magnesium chelatase* Pt tr[B5Y3F4]B5Y3F4_PHATC 3,1	1,3	1,4	CAMPEP_0176536776	Ac	Lhcx
Lhcx Ac CAMPEP_0176638538 1,5 Lhcx Pt tr B7FYL0 B7FYL0_PHATC -1,1 Lhcx* Pt tr B7FVF9]B7FVF9_PHATC -1,6 Lhcx2 Pt tr B7FR60 B7FR60_PHATC -5,5 Magnesium chelatase* Ac CAMPEP_01765759760 2,3 Magnesium chelatase Pt tr A070B5_A070B5_PHATC 1,8 Magnesium chelatase Pt tr B7FA2 B7FA2_PHATC 1,5 Magnesium chelatase* Pt tr B5Y3F4 B5Y3F4_PHATC 3,1	1,1				
Lhcx Pt tr B7FYL0 B7FYL0_PHATC -1,1 Lhcx* Pt tr B7FVF9]B7FVF9_PHATC -1,6 Lhcx2 Pt tr B7FR60 B7FR60_PHATC -5,5 Magnesium chelatase* Ac CAMPEP_0176575976 2,3 Magnesium chelatase Pt tr A070B5]A070B5_PHATC 1,8 Magnesium chelatase Pt tr B7FA2 B7FA2_PHATC 1,5 Magnesium chelatase* Pt tr B5Y3F4 B5Y3F4_PHATC 3,1	1,8			Ac	
Lhcx* Pt tr[B7FVF9]B7FVF9_PHATC -1,6 Lhcx2 Pt tr[B7FR60]B7FR60_PHATC -5,5 Magnesium chelatase* Ac CAMPEP_0176575976 2,3 Magnesium chelatase Pt tr[A0T0B5]A0T0B5_PHATC 1,8 Magnesium chelatase Pt tr[B7FTA2]B7FTA2_PHATC 1,5 Magnesium chelatase* Pt tr[B5Y3F4]B5Y3F4_PHATC 3,1	1,7		CAMPEP_0176638538		Lhcx
Lhcx2 Pt tr[B7FR60[B7FR60_PHATC -5,5 Magnesium chelatase* Ac CAMPEP_0176575976 2,3 Magnesium chelatase Pt tr[A0T0B5]A0T0B5_PHATC 1,8 Magnesium chelatase Pt tr[B7FTA2]B7FTA2_PHATC 1,5 Magnesium chelatase* Pt tr[B5Y3F4]B5Y3F4_PHATC 3,1	1,3	-1,1	tr B7FYL0 B7FYL0_PHATC	Pt	Lhcx
Magnesium chelatase* Ac CAMPEP_0176575976 2,3 Magnesium chelatase Pt tr A0T0B5]A0T0B5_PHATC 1,8 Magnesium chelatase Pt tr B7FTA2]B7FTA2_PHATC 1,5 Magnesium chelatase* Pt tr B5Y3F4]B5Y3F4_PHATC 3,1	1,8	-1,6	tr B7FVF9 B7FVF9_PHATC	Pt	Lhcx*
Magnesium chelatase Pt tr[A0T0B5]A0T0B5_PHATC 1,8 Magnesium chelatase Pt tr[B7FTA2]B7FTA2_PHATC 1,5 Magnesium chelatase* Pt tr[B5Y3F4]B5Y3F4_PHATC 3,1	-4,7	-5,5	tr B7FR60 B7FR60_PHATC	Pt	Lhcx2
Magnesium chelatasePttr B7FTA2 B7FTA2_PHATC1,5Magnesium chelatase*Pttr B5Y3F4]B5Y3F4_PHATC3,1	3,1	2,3		Ac	
Magnesium chelatase* Pt tr B5Y3F4 B5Y3F4_PHATC 3,1	1,3	1,8	tr A0T0B5 A0T0B5_PHATC	Pt	Magnesium chelatase
	2,8	1,5	tr B7FTA2 B7FTA2_PHATC	Pt	Magnesium chelatase
PetA Ac CAMPEP 0176611648 1.6	1,8	3,1	tr B5Y3F4 B5Y3F4_PHATC	Pt	Magnesium chelatase*
	1,8	1,6	CAMPEP_0176611648	Ac	PetA
PetA* Ac CAMPEP_0176535836 5,5	6,1	5,5	CAMPEP_0176535836	Ac	PetA*
PetA Pt sp A0T0C9 CYF_PHATC 2,4	2,9		sp A0T0C9 CYF_PHATC	Pt	PetA
PetB Ac CAMPEP_0176617416 1,5	-1,2	1,5		Ac	PetB
PetB Pt sp A0T0B8 CYB6_PHATC 3,1	3,6				
PsaA Ac CAMPEP_0176651446 1,8	-1,5				
PsaA Pt sp A0T0M7 PSAB_PHATC 2,9	5,1				
PsaD Ac CAMPEP_0176533106 2,9	2,1				
PsaD Ac CAMPEP_0176564748 2,0	1,8				
PsaD* Ac CAMPEP_0176538974 8,8	9,3				

Protein name	Organism	Protein ID	24 h LL-LR	24 h LL-RR
PsaD	Pt	tr A0T0B9 A0T0B9_PHATC	4,4	3,5
PsaL	Ac	CAMPEP_0176639782	2,5	1,3
PsaL	Ac	CAMPEP_0176557554	2,3	1,5
PsaL*	Ac	CAMPEP_0176553508	2,9	-1,1
PsaL*	Ac	CAMPEP_0176533490	2,3	1,6
PsaL*	Pt	sp A0T0M6 PSAL_PHATC	2,4	3,9
PsbC	Ac	CAMPEP_0176554406	2,1	1,5
PsbC	Pt	tr A0T096 A0T096_PHATC	2,6	3,5
PsbV*	Ac	CAMPEP_0176612574	2,9	3,9
PsbV*	Pt	sp A0T0C6 CY550_PHATC	3,3	5,1
SOD1	Ac	CAMPEP_0176541592	1,0	1,3
SOD1	Ac	CAMPEP_0176525294	1,2	1,9
SOD1	Pt	tr B7G0L6 B7G0L6_PHATC	1,0	1,9

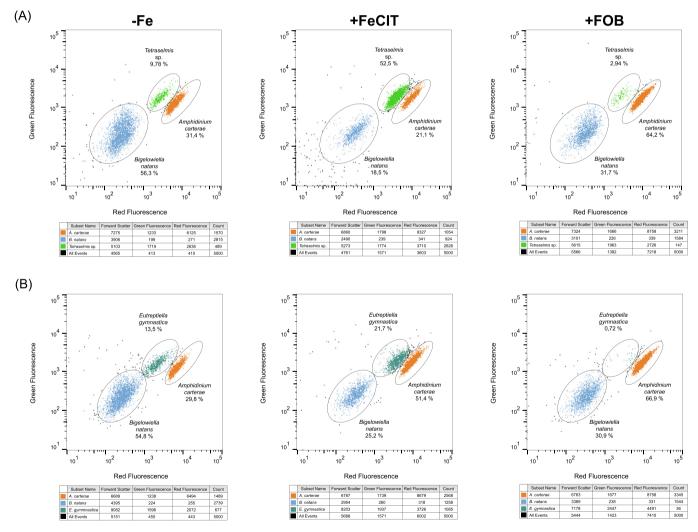


Fig. 4. Effect of FOB siderophore on cocultivated microalgae. Flow cytograms of two microalgal consortia, each containing three algal species ((A) *B. natans, Tetraselmis* sp., *A. carterae*; (B) *B. natans, E. gymnastica, A. carterae*) grown under iron-limited condition (-Fe), with iron supplemented in the form of ferric citrate (+FeCIT) and with iron provided as ferrioxamine B (+FOB). Tables under flow cytograms contain median values for Forward Scatter, Green Fluorescence and Red Fluorescence parameters together with cell counts for each species. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

4. Discussion

Determining the effect of changing iron conditions on phytoplankton is important and challenging. In our study, we established a cocultivation system with different combinations of species that allowed us to follow the effects of iron availability on members of the consortia by simple enumeration based on differences in fluorescence properties. Choosing species that have,

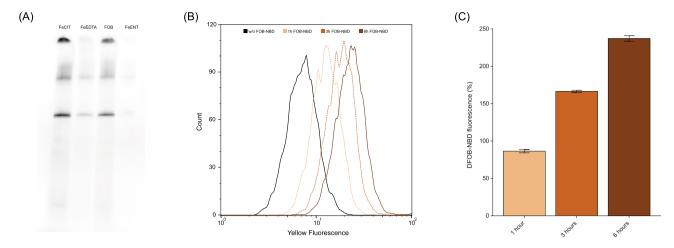


Fig. 5. Utilization of iron from FOB siderophore by *A. carterae*. (A) Incorporation of ⁵⁵Fe into *A. carterae* protein complexes determined by blue native electrophoresis separation of total cell extracts. Iron was supplemented in four different forms: FeCIT – ferric citrate (1:20), FeEDTA – ferric EDTA (1:10), FOB – ferrioxamine B (1:1.1), and FeENT – enterobactin (1:1.1). (B, C) *A. carterae* cells grown in iron-deficient medium for 7 days were supplemented with 1 μ M of the fluorescent conjugate of desferrioxamine B complexed with iron (FoB-NBD) and incubated for 1, 3 and 6 h. Intracellular accumulation of a nonquenched siderophore analog (after removal) was measured on a flow cytometer using a yellow fluorescence detector (583/26 nm) and blue excitation laser (488 nm). (B) Representative histogram. (C) Fluorescence of DFOB-NBD (mean \pm SD, n = 3). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

at least to some degree, available genomes/transcriptomes, enabled us to study the molecular mechanisms behind adaptation to iron limitation via a proteomic analysis of complex samples. We were able to detect significant iron-induced changes in algal proteomes, including well-known markers of iron limitation, such as ISIPs, FBA, LHCX and subunits of PSI, ATP synthase and Cytochrome b6/f [20,22,27,28]. Time course analysis revealed a dynamic response to iron enrichment evidenced by a number of proteins that significantly changed as early as 6 h after iron supplementation. Changes in proteomes between iron-rich and iron-limited cells appear to be reached within 24 h after iron supply to ironlimited species.

Our study provides a proof-of-concept that it is possible, when suitable species and conditions are chosen, to reveal proteins whose expression is most significantly affected by nutrients in complex algal cultures, thus representing candidate markers for nutrient (and other) stress in natural marine phytoplankton. Such an experimental design represents an alternative to cocultivation systems where species are separated by membranes permeable to nutrients and metabolites but not cells. This system was successfully employed, for example, to describe the impact of *K. brevis* allelopathy on competing phytoplankton [29]. The advantage of our experimental design lies in the fact that it allows physiological and molecular analyses of phytoplankton consortia while allowing physical contact between the species. This design can be employed in studies involving processes within the phycosphere, such as bacterial-algal mutualism.

Importantly, our study showed that it is possible to analyze, with reasonable efficiency, proteomic changes in mixed cultures for species without well-annotated genomes, with analysis employing available transcriptomes. It is axiomatic that proteomic analyses of a multispecies model system have limitations, which were observable in the case of *B. natans* and *H. triquetra* in our study. Fewer than 750 proteins were detected for each of the two species. However, proteome coverage can be expanded by increasing the mass spectrometry detection capacity, e.g., by employing peptide or predigestion protein fractionation prior to proteomic analysis. Alternatively, FACS may be used for the separation of microalgal populations to allow maximal proteome coverage for each species in the consortium.

We touched an important methodological question of how to normalize proteomic data from complex ecological mixtures. The combination of sPLS discriminant analysis and the extraction of p values from AUC analysis helped us to identify the effect of two types of consecutive normalizations. The raw data in Fig. 3A, B, C, D show high variances and group overlaps due to noise coming from different cell numbers per species. When we applied sizefactor vector normalization from the cell counts, the variances slightly decreased, but some overlaps were still visible (Fig. 3E, F, G, H). To decrease the influence of outliers and differences in the abundances within proteomes, we used quantile normalization (second step) on cell count-normalized data. The effect of twostep normalization is obvious in Fig. 3I, J, K, L where the ellipses over the group data are smaller and overlap less with other groups. The important message here is that the predictive performance of proteomic analyses strongly depends on the type of data normalization, and that both the initial variance and the influence of outliers may well be sustained when using the two-step normalization presented in this manuscript.

Little is known about iron acquisition in Amphidinium carterae, although this model dinoflagellate was used more than 40 years ago to suggest the significance of grazing on phytoplankton in iron recycling in marine environment [30]. The main finding that emerged from our study was the ability of A. carterae to utilize iron from FOB siderophores. Reports about the use of siderophorebound iron by eukaryotic phytoplankton are rare [11,31,32], and molecules involved in this iron uptake pathway are only suggested for the model diatom *P. tricornutum* [4,26]. It is now believed that siderophores represent an important part of ocean microbial iron cycling, showing changing abundance and composition across ocean regions with varying iron availability [33]. The ability to utilize iron from xenosiderophores may give A. carterae an advantage in ecosystems where such form of iron is abundant. In fact, cocultivation with bacteria has been shown to promote the growth of A. carterae in nutrient-limited media, including conditions of tracemetal limitation [34]. Importantly, our proteomic analysis revealed that the A. carterae homolog of siderophore binding protein was dynamically regulated by iron availability. The fact that this protein has been shown to be involved in siderophore acquisition in the taxonomically distant diatom P. tricornutum highlights the effect of a nutritionally poor ocean environment on molecular evolution. This fascinating phenomenon is particularly obvious through the virtually universal presence of phytotransferrins in marine eukaryotic phytoplankton. Notably, the iron enrichmentinduced downregulation of these recently discovered major players in iron uptake was also detected in all species of our coculture model. Both phytotransferrin-mediated and siderophore-bound iron uptake mechanisms are most likely based on elaborate machinery involving endocytosis [35]; thus, this adaptation to life under iron-limited conditions requires complex fine-tuning.

Our study demonstrates an efficient tool that allowed us to follow community dynamics in mixed cultures of model eukaryotic phytoplankton species and determine concomitant changes at the molecular level. We believe that such an approach, complimentary to field investigation, may be employed to better understand phytoplankton responses to environmentally relevant changes in nutrient availability, pH or temperature.

CRediT authorship contribution statement

Ronald Malych: Data curation, Investigation, Visualization, Writing – original draft. **Pavel Stopka:** Formal analysis, Methodology, Writing – review & editing. **Jan Mach:** Methodology, Validation, Writing – review & editing. **Eva Kotabová:** Investigation, Methodology. **Ondřej Prášil:** Validation, Writing – review & editing. **Robert Sutak:** Conceptualization, Funding acquisition, Project administration, Supervision, Validation, Writing – original draft.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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In a memory of Emmanuel Lesuisse.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.csbj.2021.12.023.

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