



# A novel motif at the C-terminus of palmitoyltransferases is essential for Swf1 and Pfa3 function *in vivo*

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S-acylation (commonly known as palmitoylation) is a widespread post-translational modification that consists of the addition of a lipid molecule to cysteine residues of a protein through a thioester bond. This modification is predominantly mediated by a family of proteins referred to as PATs (palmitoyltransferases). Most PATs are polytopic membrane proteins, with four to six transmembrane domains, a conserved DHHC motif and variable C- and N-terminal regions, that are probably responsible for conferring localization and substrate specificity. There is very little additional information on the structure–function relationship of PATs. Swf1 and Pfa3 are yeast members of the DHHC family of proteins. Swf1 is responsible for the S-acylation of several transmembrane SNAREs (soluble *N*-ethylmaleimide-sensitive fusion protein-attachment protein receptors) and other integral membrane proteins. Pfa3 is required for the palmitoylation of Vac8, a protein involved in vacuolar fusion. In the present

study we describe a novel 16-amino-acid motif present at the cytosolic C-terminus of PATs, that is required for Swf1 and Pfa3 function *in vivo*. Within this motif, we have identified a single residue in Swf1, Tyr<sup>323</sup>, as essential for function, and this is correlated with lack of palmitoylation of Tlg1, a SNARE that is a substrate of Swf1. The equivalent mutation in Pfa3 also affects its function. These mutations are the first phenotype-affecting mutations uncovered that do not lie within the DHHC domain, for these or any other PATs. The motif is conserved in 70% of PATs from all eukaryotic organisms analysed, and may have once been present in all PATs. We have named this motif PaCCT ('Palmitoyltransferase Conserved C-Terminus').

**Key words:** conserved motif, palmitoylation, palmitoyltransferase, Pfa3, phylogeny, Swf1, yeast.

## INTRODUCTION

Protein palmitoylation, or S-acylation, the addition of a lipid molecule on cysteine residues through a thioester bond, is involved in multiple cellular processes. In the case of hydrophilic proteins, such as Ras or G-proteins, palmitoylation serves to recruit them to the membrane, often in combination with prenylation. Since palmitoylation is reversible, it can dynamically regulate the localization and function of proteins. Many transmembrane proteins are also palmitoylated and this has been shown to regulate function, localization and stability [1–3]. Palmitoylation of transmembrane proteins occurs at cysteine residues often near or within the TMD (transmembrane domain) [4,5].

It has now become accepted that a family of proteins containing a 50 residue motif called DHHC-CRD (Asp-His-His-Cys cysteine-rich domain) [6] is involved in protein S-acylation ([7,8] and reviewed in [9]). There are over 20 predicted DHHC-CRD-containing proteins in the human genome and seven in the yeast *Saccharomyces cerevisiae* genome. They are mostly polytopic membrane proteins predicted to contain four to six TMDs. The membrane topology of the yeast PAT (palmitoyltransferase) Akrl has been established experimentally and shown to match the *in silico* predictions [10]. Subsets of substrates have been assigned to most of the yeast PATs [1,7,8,11–15], and a few mammalian PATs [11–13,16,17], indicating that they must have determinants for specific substrate recognition.

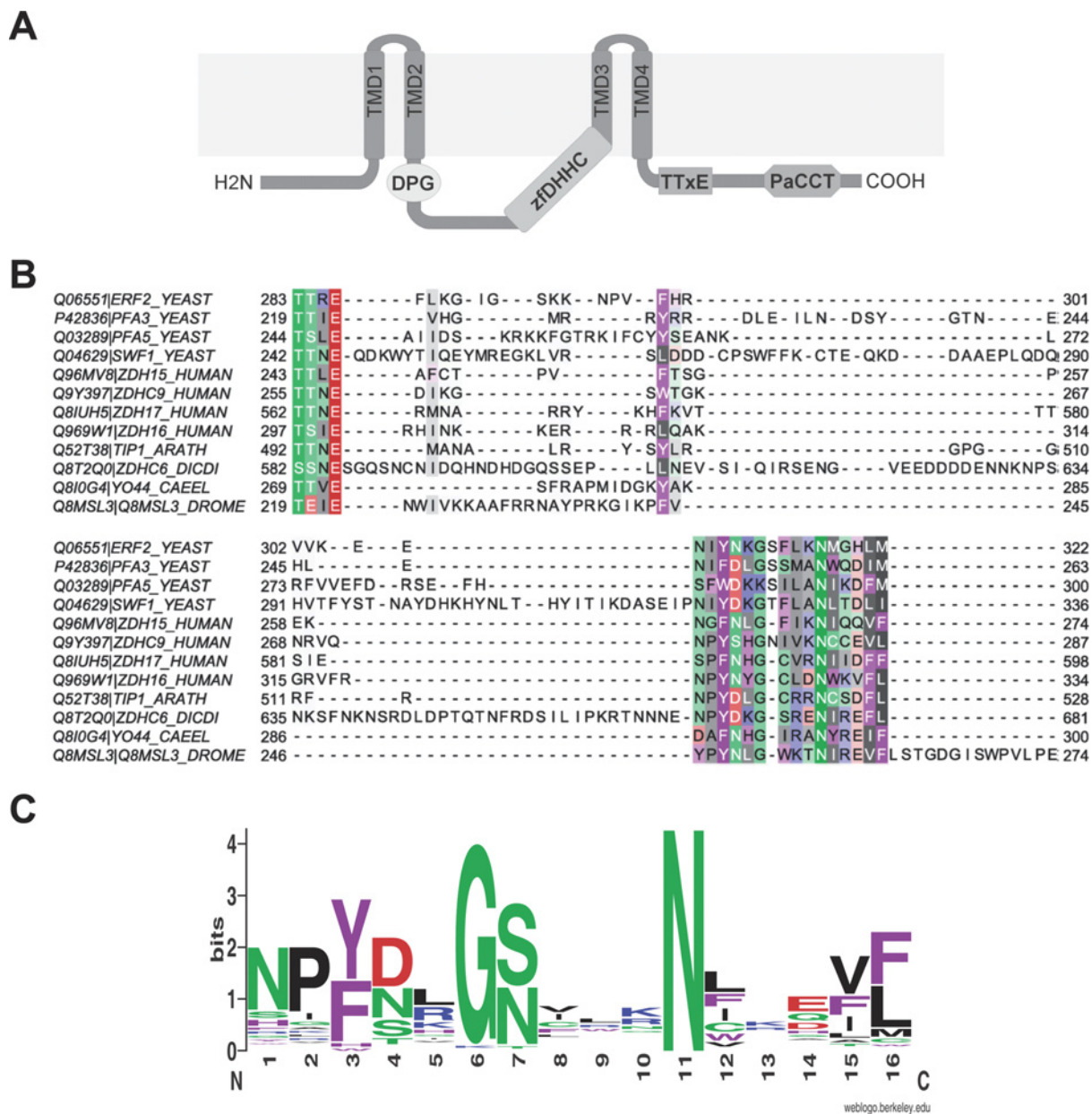
There is very little knowledge about the mechanism of protein palmitoylation and the way PATs function [18,19]. At the structural level, only a few residues in the conserved DHHC core have been mutated resulting in lack of function [7,8]. Mutations in the DHHC domain of human zf-DHHC9, the Ras PAT [17], have been linked to mental retardation [20], and residues within this region are also required for mouse HIP14 to produce oncogenic transformation [12]. PATs are interesting targets for anticancer drugs owing to their important role in the subcellular localization of several oncoproteins [12]. Apart from the DHHC motif, there are two other regions of sequence similarity present in all DHHC proteins [9], a DPG motif (Asp-Pro-Gly) next to TMD2 and a TTxE motif (Thr-Thr-Xaa-Glu) adjacent to TMD4 (Figure 1A) (the TMDs are numbered as in [9]). The role of these regions has not been addressed. The N- and C-termini of PATs are highly variable and probably confer localization and/or specificity towards the different sets of substrates [9].

Swf1 is a yeast DHHC protein involved in the palmitoylation of SNAREs (soluble *N*-ethylmaleimide-sensitive fusion protein-attachment protein receptors) [1] and possibly glycosyltransferases [14], suggesting that palmitoylation of proteins with single TMDs in yeast is mostly due to Swf1. The function of transmembrane SNARE palmitoylation is not clear, but in the case of the endosomal syntaxin Tlg1, it seems to protect it from degradation by the quality-control machinery. Non-palmitoylated Tlg1 is ubiquitinated and degraded in the vacuole [1]. Unlike

Abbreviations used: DHHC-CRD, Asp-His-His-Cys cysteine-rich domain; DTT, dithiothreitol; ER, endoplasmic reticulum; GFP, green fluorescent protein; HMM, Hidden Markov Model; JTT, Jones Taylor Thornton; NJ, neighbour-joining; PaCCT, palmitoyltransferase conserved C-terminus; PAT, palmitoyltransferase; PGK, phosphoglycerate kinase; SNARE, soluble *N*-ethylmaleimide-sensitive fusion protein-attachment protein receptor; TMD, transmembrane domain; TPI, triosephosphate isomerase; YPD, 1% (w/v) yeast extract/2% (w/v) peptone/2% (w/v) glucose.

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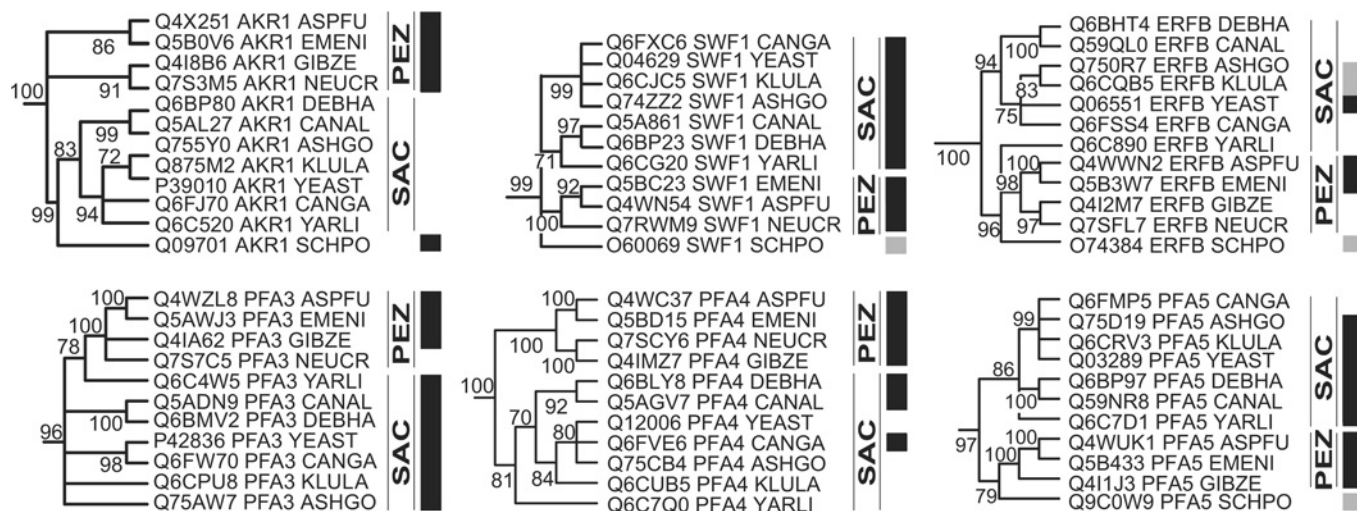


**Figure 1** A novel conserved motif at the C-terminus of PATs

(A) Schematic diagram of the domain architecture for a generic PAT. Most PATs are predicted to have four TMDs, a DPG motif, and the DHHC motif localized between TMD2 and TMD3. The C-terminal region that follows the fourth TMD contains the TTxE motif and the novel PaCCT motif, and is always predicted to localize to the cytosol. (B) Multiple sequence alignment of the regions comprising the TTxE and the PaCCT motifs, for selected PATs from model organisms. The alignment shows very low conservation of the region apart from the TTxE and the PaCCT motif. Amino acids are coloured according to their chemical properties: basic (K and R) are blue, acidic (D and E) are red, hydrophobic (A, V, L, I, P and M) are black, aromatic (Y, F, W and H) are purple and polar amino acids (N, S, G, C and Q) are green. Colour saturation is varied according to residue conservation. (C) Sequence logo of the PaCCT motif present in PATs scoring above 11.7 cut-off (see the main text for details). Amino acids are coloured as in (B). The height of each letter is proportional to its frequency. The height of the entire stack (y axis) is adjusted to signify the information content of the sequences at that position (measured in bits). The x axis represents the 16 positions of the PaCCT HMM.

other yeast PATs, Swf1 has five predicted TMDs and thus the N-terminus is embedded in the membrane (Figure 1A). We initially focused our attention to the last 100 amino acids of the C-terminal region of Swf1, which are predicted to be facing the cytosol, and thus might represent a good candidate region to confer Swf1-specific characteristics to this PAT. In the present study, we identify a conserved motif at the C-terminus of Swf1, and within this motif, a residue, Tyr<sup>323</sup>, that is critical for Swf1 function. The motif, however, is not just conserved in Swf1 orthologues, but is also present in other yeast PATs, such as Pfa3, Pfa5 and Erf2.

We extended our studies to Pfa3, a yeast PAT localized to the vacuolar membrane [15,21,22] and predicted to have four TMDs. Pfa3 is required for the palmitoylation of Vac8 [15], a protein with several armadillo repeats that is also localized to the vacuolar membrane [23–25]. Vac8 is involved in vacuole fusion and *vac8Δ* cells have fragmented vacuoles [23,24]. Palmitoylation of Vac8 is important for its function [26,27]. We show that in the absence of the PaCCT (palmitoyltransferase conserved C-terminus) motif, the function of Pfa3 is abolished, probably because it is missorted to the vacuole lumen and subsequently



**Figure 2** Phylogenetic trees of six PAT orthologous proteins present in fungi

Rectangular NJ trees displaying the percentage of 1000 bootstrap replicates. Branch lengths are not proportional to the genetic distance. Branches displaying bootstrap values below 70% were clipped. Organisms belonging to the Saccharomycotina subphylum are marked as SAC. Organisms belonging to the Pezizomycotina subphylum are marked as PEZ. The presence of the PaCCT motif in these proteins is symbolized by a black square when the hmmsearch score is above 11.7 and a grey square when score is between 7.3 and 11.7.

degraded. Detailed bioinformatics analyses indicate that the motif is conserved in most PATs and is present almost exclusively within the C-termini of the DHHC protein family.

## EXPERIMENTAL

### *In silico* analysis

An alignment of the conserved C-terminal regions in Swf1, Pfa3 and Erf2 was used to iteratively run hmmbuild, hmmsearch and hmalign [28]. As a result, we gathered an alignment of the putative motif from 720 proteins from the Uniprot database. These proteins were searched for the presence of the zfDHHC Pfam domain (PF01529), and all sequences which did not score above the noise cut-off according to Pfam [29] were discarded. Sequence redundancy was reduced to 60% using Jalview [30], to generate an alignment of 185 proteins. This alignment was used to build a HMM (Hidden Markov Model), which was used to search the Uniprot database. Hmmsearch runs using this HMM were performed with a highly specific cut-off score of 11.7 (the score corresponds to the lowest scoring DHHC protein for which empirical evidence of PAT activity is available, *S. cerevisiae* Swf1) and a more sensitive cut-off score of 7.3 (the score corresponding to the lowest scoring proteins with a minimum alignment coverage of 85% of the PaCCT HMM). Logos were generated with WebLogo [31], after reducing redundancy by eliminating sequences with 99% or higher similarity over the motif length using Jalview. Alignments were generated using ClustalX (version 2.05) [32], hmalign [28] and manually curated using Jalview.

### Phylogenetic tree reconstruction

For phylogenetic tree reconstruction, the data set used included a total of 68 PAT sequences from 12 Ascomycota organisms downloaded from the Swiss-Prot database (see Supplementary Table S1 at <http://www.BiochemJ.org/bj/419/bj4190301add.htm>). *S. cerevisiae* Akr2 was not included in this analyses, because it is only present in this organism. ProtTest v1.4 [33] [implementing the AIC (Akaike Information criterion)] was used to estimate

the most appropriate model of amino acid substitution for tree-building analyses. The best-fit model of protein evolution for the PAT protein family according to ProtTest corresponds to a JTT (Jones Taylor Thornton) + I + G + F model [34].

Tree reconstructions were performed by the NJ (neighbour-joining) method [35] using the MEGA v4.0 software package [36], using a JTT matrix and 1000 bootstrap pseudoreplicates, with the gamma-distribution model implemented to account for heterogeneity among sites. The shape parameter of the gamma distribution was estimated to be 1.76 using ProtTest. Support for each phylogenetic group was tested using 1000 bootstrap pseudoreplicates. Tree topology assessed by maximum parsimony was very similar to the NJ tree. Figures were generated using iTOL [37]. Circular trees (see Supplementary Figure S1 at <http://www.BiochemJ.org/bj/419/bj4190301add.htm>) display branch length, whereas rectangular trees (Figure 2) ignore branch length and have been stripped of branches with bootstrap values below 70%.

### Plasmids and strains

The strains used in the present study were wild-type BY4742 from the EUROSCARF consortium, or derivatives containing complete deletions of *SWF1* or *PFA3*. Swf1 and Tlg1 plasmids have been described previously [1]. Swf1  $\Delta$ PaCCT was constructed by PCR using oligo Swf1 01, which anneals to the SWF1 ATG region and oligo Swf1 13 (see Supplementary Table S2 at <http://www.BiochemJ.org/bj/419/bj4190301add.htm> for all oligonucleotide sequences). The PCR fragments were cloned BamHI–Sall into pjv29 which is a YcpLac33-based vector containing the TPI (triosephosphate isomerase) promoter, and PGK (phosphoglycerate kinase) terminator.

Pfa3 DNA was amplified from Euroscarf BY4742 genomic DNA, using oligos Pfa3 01 and Pfa3 02 and cloned BamHI–PstI in pjv97 [a YcpLac 33-based vector containing a TPI promoter, GFP (green fluorescent protein) and a PGK terminator]. Mutations were generated by ligation of two PCR-generated fragments, one obtained using oligos Pfa3 01 and Pfa3 04, and another generated using oligos Pfa3 05 and Pfa3 02. Oligonucleotides Pfa3 04 and Pfa3 05 introduce a silent XhoI site that allows in-frame ligation.

The resulting fragment has the whole Pfa3 PaCCT domain deleted (amino acids Asn<sup>248</sup> to Met<sup>263</sup>). A similar strategy was used to generate the point mutant, but oligonucleotide Pfa3 03 was used instead of oligonucleotide Pfa3 05, resulting in a mutation of Phe<sup>250</sup> to alanine. The fragments were subcloned into pJv97 as above.

### *In vitro* mutagenesis of Swf1

For the mutant N321A, oligonucleotides 17 and 18 were annealed to form double-stranded DNA. The oligonucleotides were designed to contain the desired mutation and overhanging MluI and KpnI sites, so that it could be cloned into these sites in Swf1. To generate the mutations Y323A, D324A and G326S the same strategy was used, annealing oligonucleotides 19 and 20 for Y323A, 21 and 22 for D324A, and 23 and 24 for G326S. To generate the mutation F328A, N331A and L332A, oligonucleotide pairs 26 and 27, 28 and 29, and 30 and 31 respectively were annealed to form double-stranded DNA and were cloned into the KpnI–SalI sites into either not tagged or N-terminal tagging vectors. The SalI site has been introduced into Swf1 plasmids after the stop codon.

### Protein electrophoresis and Western blot analysis

Protein samples were prepared as described in [38]. Monoclonal anti-GFP antibodies were from Roche (used at 1/2000 dilution). The blots were probed using secondary antibodies coupled to either IRdye680 or IRdye800 (Licor Biosciences) at a 1/20000 dilution, and then scanned using an Odyssey IR imager (Licor Biosciences).

### Vacuole fragmentation assay

The vacuole fragmentation assay was carried out precisely as described in [15]. Cells were imaged live, using an Olympus FV 1000 confocal microscope.

## RESULTS

### *In silico* identification of a conserved motif in the PATs C-terminal region

A ClustalX alignment of C-terminal regions from Swf1 orthologues showed that they are poorly conserved, apart from the TTxE motif and a region corresponding to the last 16 residues in yeast Swf1 (results not shown). This conserved region appeared to be present at the C-termini of other yeast PATs such as Pfa3 and Erf2. In these proteins, the motif is also in the C-terminal regions predicted to be cytosolic. A HMM was built for this putative motif as described in the Experimental section, which allowed us to align the C-terminus of many DHHC-containing proteins as shown in Figure 1(B). For the purposes of the present study we assume that all DHHC-containing proteins are PATs. Using a cut-off of 11.7 (score of yeast Swf1) when searching the Uniprot database we retrieved 607 proteins, of which 521 (86%) possessed a DHHC domain (Table 1). Figure 1(B) shows an alignment of representative PATs from several relevant organisms. The complete alignment of the motif present in PATs (retrieved using the HMM) was used to construct a LOGO which shows the consensus sequence for the motif (Figure 1C). We named this motif PaCCT (**p**almitoyltransferase **c**onserved **C**-terminus). Within the motif, the positions that are most conserved were: position 3 (always aromatic amino acids) and position 11 (always asparagine residues); position 6 contains mostly glycine residues, and residues in position 7 are mostly polar residues; finally, residues in positions 15 and 16 have a tendency to be hydrophobic. Positions 1 and 2 are also relatively well conserved.

**Table 1** Uniprot and Swiss-Prot search for PaCCT-motif-containing proteins

The number of proteins containing a PaCCT motif using 11.7 and 7.3 cut-offs, and the number of PATs present in each database.

| Database   | Proteins... | Number of PaCCT-motif-containing proteins |          |             |          | Total PATs in database |
|------------|-------------|---|----------|-------------|----------|------------------------|
|            |             | 11.7 cut-off                              |          | 7.3 cut-off |          |                        |
|            |             | PATs                                      | Non-PATs | PATs        | Non-PATs |                        |
| Uniprot    |             | 521                                       | 86       | 594         | 699      | 1091                   |
| Swiss-Prot |             | 111                                       | 1        | 121         | 41       | 166                    |

From the 86 non-DHHC proteins which scored above 11.7, eleven of them are possible PATs (owing to their predicted topology and presence of the PaCCT motif in the C-terminus), although their DHHC motifs are somewhat divergent and score low when searched with the zfDHHC Pfam HMM. In total, 40 of them possess no conserved domains as indicated by SMART searches and/or are protein fragments. In the remaining 35 proteins, which possess conserved domains, sequence similarity to the PaCCT motif is present within conserved domains (BEACH, MatK\_N, ANF\_receptor and zf-CHY) or in non-conserved regions. However, the motif is only present in very few members of their protein families; for instance, from 150 members of the zf-CHY protein family, the motif is detected only in two. Therefore the detection of the motif in non-PAT proteins may be an artefact, owing to the small size of the motif and moderate conservation. Moreover, when searching the manually curated database Swiss-Prot, the motif is detected in 111 PAT proteins and just one non-PAT protein.

When the search in Uniprot was carried out using a cut-off score of 7.3, we gathered 1293 proteins of which 594 (46%) scored significantly when searched with the Pfam zfDHHC HMM (Table 1), indicating that some PATs contain a slightly divergent PaCCT motif and thus were not detected using the more stringent 11.7 cut-off. The 7.3 cut-off also led to the detection of a greater number of non-PAT proteins (for a list of all proteins retrieved and their PaCCT motifs see Supplementary Table S3 at <http://www.BiochemJ.org/bj/419/bj4190301add.htm>).

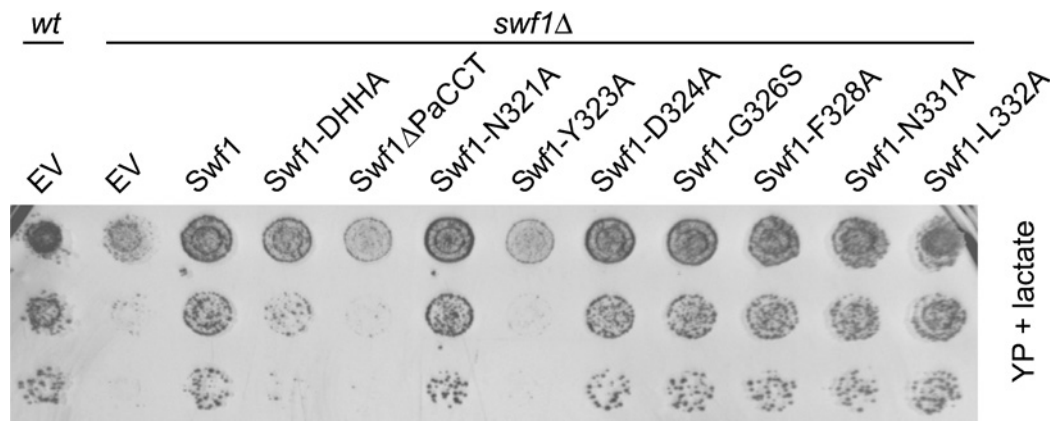
When the 7.3 cut-off was used to search the Swiss-Prot database, we found that the PaCCT motif is conserved in 66% of fungal PATs (Supplementary Table S1), 67% of mammalian PATs (human, rat and mouse; see Supplementary Table S4 at <http://www.BiochemJ.org/bj/419/bj4190301add.htm>) and 73% overall (see Table 1).

### Phylogenetic analysis of the PaCCT motif in *Ascomycota*

To analyse the occurrence of the PaCCT motif in certain subgroups of the PAT protein family and to determine its relation to PAT protein phylogeny, we reconstructed the phylogeny of the PAT family. The genomes chosen for the analyses belong to 12 members of the *Ascomycota* phylum (see Figure 2, Supplementary Table S1 and Supplementary Figure S1), because they have a well-documented phylogeny [39–41] and adequate evolutionary distance.

Figure 2 and Supplementary Figure S1 present NJ trees built with 68 PATs present in 12 *Ascomycota* organisms. These trees, as well as Supplementary Table S1, show the distribution of the PaCCT motif within the phylogeny of PAT proteins in fungi.

In the case of Akr1 proteins, the PaCCT motif is preserved in the early diverging *Schizosaccharomyces pombe*, in *Pezizomycotina* (which in turn contains *Eurotiomycetes* and *Sordariomycetes*



**Figure 3** The PaCCT motif is required to complement *swf1Δ* growth phenotype

Serial dilutions of a wild-type strain or a *swf1Δ* strain transformed with an empty vector (EV), with wild-type Swf1, Swf1ΔPaCCT, Swf1-DHHA and versions of Swf1 in which the most conserved residues of the PaCCT motif were mutated. Transformants were grown in solid rich medium (YP) containing lactate as the sole carbon source.

subclasses), but not in Saccharomycotina, indicating the possibility that the PaCCT motif was lost/diverged early in the Saccharomycotina subphylum. With regard to Swf1 orthologues, the motif is present in all proteins. In Erf2 proteins, the motif can be found in *S. pombe*, the Eurotiomycetes subclass, and in only half of the Saccharomycotina subphylum members included in the present study. Pfa3 orthologues all present a PaCCT motif except for *Neurospora crassa* (*S. pombe* does not have Pfa3 or Pfa4 orthologues in the Uniprot database). With regard to Pfa4 orthologues, the motif is present in Pezizomycotina and half of the Saccharomycotina subphylum members included in the present study. Pfa5 orthologues all present the PaCCT motif, except for *Candida glabrata*. It is interesting to point out that all PATs present in the early diverging *S. pombe* and in Eurotiomycetes *Emmericella nidulans* and *Aspergillus fumigatus* present a PaCCT motif (Figure 2 and Supplementary Table S1).

### Deletion of the PaCCT motif abolishes Swf1 function

To test the importance of the PaCCT motif for the function of a DHHC protein *in vivo*, we investigated the effect of a C-terminal deletion of the PaCCT motif in *S. cerevisiae* Swf1, which in this protein comprises the last 16 residues of the C-terminus. Mutants in which the whole SWF1 gene has been deleted are unable to grow in YPD [1% (w/v) yeast extract/2% (w/v) peptone/2% (w/v) glucose] medium containing 0.85 M NaCl or YP medium plus lactate as the sole carbon source [1,42]. The bases for these phenotypes are unknown, but they can be conveniently used for testing complementation of a *swf1Δ* strain in growth tests. These phenotypes can be complemented by SWF1-containing plasmids, indicating they are indeed due to lack of Swf1 function and not a secondary effect of the deletion (Figure 3 and [1]). A complementation test using SWF1ΔPaCCT shows that this construct is unable to complement the lack of growth of a *swf1Δ* strain in complete media (YPD) with 2% lactate as the sole carbon source (Figure 3), indicating that the last 16 amino acids of Swf1 are essential for its function *in vivo*.

Mutating the cysteine residue in the conserved DHHC motif has been shown to abolish palmitoylation activity for several PATs [7,8], and, although indirectly, also for Swf1 [1]. A mutated version of Swf1 (Swf1-DHHA) was included in this growth test (Figure 3). This mutant was unable to grow in lactate, indicating that lack of growth in this medium is probably due to lack of

Swf1 palmitoylating activity and not a secondary function of this protein.

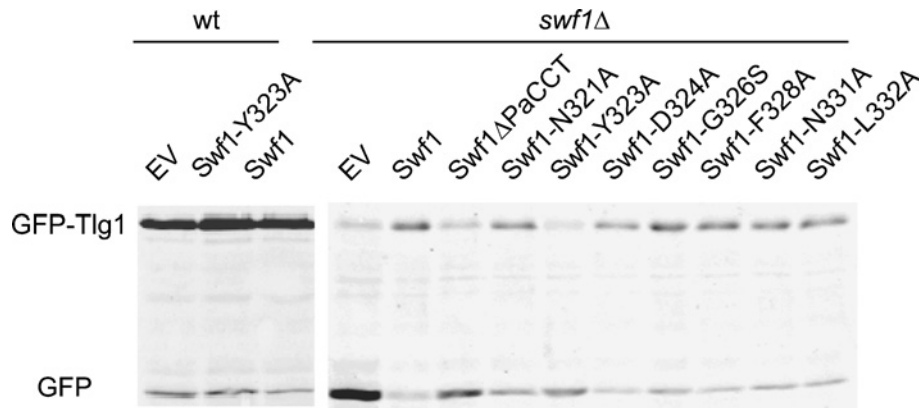
### Tyr<sup>323</sup> is essential for Swf1 function and activity *in vivo*

To investigate the importance of individual residues present in the PaCCT motif, conserved positions were changed by *in vitro* mutagenesis and the phenotypes of the mutants were analysed in growth tests. Asn<sup>321</sup>, Tyr<sup>323</sup>, Asp<sup>324</sup>, Phe<sup>328</sup>, Asn<sup>331</sup> and Leu<sup>332</sup> which correspond to positions 1, 3, 4, 8, 11 and 12 in the LOGO (Figure 1C) respectively, were mutated to alanine. Gly<sup>326</sup> (position 6) was mutated to serine because a mutation to alanine would have been conservative. Figure 3 shows that, although most mutations complemented the *swf1Δ* strain phenotype in lactate, Y323A did not, indicating that this tyrosine residue was crucial for Swf1 function *in vivo*.

To confirm that this non-complementation phenotype is due to lack of Swf1 palmitoylation activity, we studied the endosomal SNARE Tlg1, a known substrate of Swf1. This SNARE, when not palmitoylated, becomes ubiquitinated by the ubiquitin ligase Tul1 and it is subsequently delivered to the vacuole for degradation [1]. This can readily be observed by analysing a fusion of Tlg1 to GFP. GFP is normally resistant to vacuolar proteolysis and thus delivery to the vacuole can be related to the appearance of a free GFP band in Western blot analysis. Figure 4 shows that although most of the label is in the form of full-length GFP-Tlg1 in wild-type or *swf1Δ* strains complemented with a wild-type SWF1 plasmid, *swf1Δ* strains, transformed with an empty vector, with Swf1ΔPaCCT or with mutant Y323A, display a clear increase in the level of free GFP, indicating that they are unable to palmitoylate Tlg1. The rest of the mutations do not have an effect on the degradation of Tlg1, in agreement with the growth tests results in lactate shown in Figure 3.

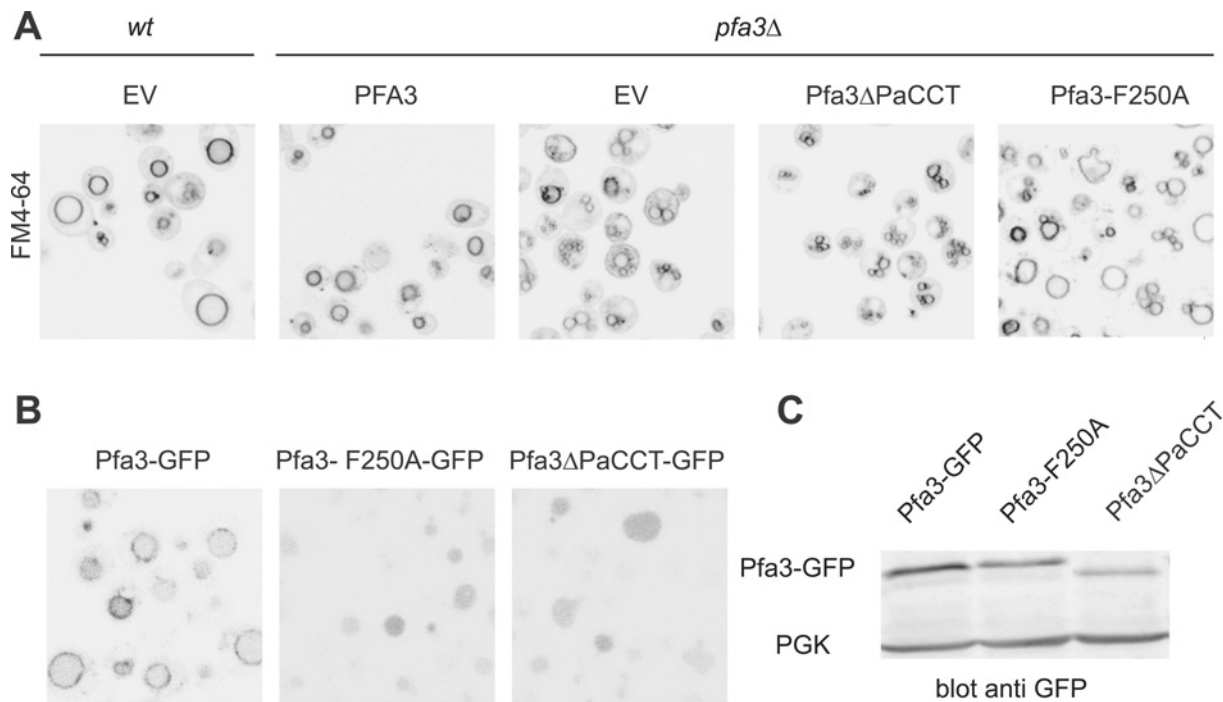
### The PaCCT motif is required for Pfa3 function

To extend the validity of our observations, we analysed the influence of the PaCCT motif in another yeast PAT, Pfa3. This protein is involved in the palmitoylation of Vac8, a myristoylated protein that is involved in vacuolar fusion and inheritance [23]. Smotrys et al. [15] have shown that in the presence of 2 mM DTT (dithiothreitol), a *pfa3Δ* strain has fragmented vacuoles and this phenotype is correlated with lack of Pfa3 palmitoylation activity,



**Figure 4** Tlg1 is not palmitoylated in *swf1*Δ cells expressing Swf1ΔPaCCT or Swf1 Y323A

Western blot analysis of *swf1*Δ strains expressing GFP-Tlg1 alone (EV) or co-expressing either a wild-type (wt) Swf1, Swf1ΔPaCCT or Swf1 versions in which the most conserved residues of the PaCCT motif were mutated. The blot was probed with anti-GFP antibodies.



**Figure 5** The PaCCT motif is required for Pfa3 function *in vivo*

(A) Complementation assay of the fragmented vacuole phenotype from *pfa3*Δ cells. Confocal microscopy images of FM4-64-labelled vacuoles from wild-type cells or *pfa3*Δ cells transformed with wild-type or mutated versions of Pfa3, in the presence of 2 mM DTT, are shown. Colours are shown inverted for clarity. (B) Subcellular localization of wild-type and mutant Pfa3-GFP. Strains as in (A) were analysed for the presence of GFP fluorescence, but in the absence of DTT, which allows for easier interpretation of the results. Pfa3-GFP mutant images have augmented brightness to compensate for lower fluorescence intensity. (C) Western blot analyses of Pfa3-GFP mutants. Total protein extracts from *pfa3*Δ cells expressing wild-type Pfa3-GFP, Pfa3-F250A-GFP and Pfa3ΔPaCCT were submitted to SDS/PAGE and Western blot analysis using anti-GFP antibodies. The protein loading levels were controlled using an anti-PGK1 antibody.

since a plasmid expressing a DHHS mutant version of this PAT cannot complement this phenotype [15]. We have made use of this assay to investigate the role of the PaCCT motif in Pfa3 function. Two mutated versions of Pfa3 fused to GFP were constructed, one in which the whole PaCCT motif was deleted and another in which position 3 of the PaCCT motif, in this case Phe<sup>250</sup>, was mutated to alanine (see the Experimental section). Wild-type cells and *pfa3*Δ cells complemented with wild-type or mutant versions of Pfa3 were labelled with FM4-64 [43] in the presence of 2 mM DTT, and then inspected for vacuole morphology. Figure 5 shows that *pfa3*Δ cells have extensively fragmented vacuoles and that Pfa3-

GFP clearly complements this phenotype, whereas Pfa3ΔPaCCT does not. The cells expressing Pfa3 F250A display an intermediate phenotype (see the Discussion below).

#### Lack of PaCCT motif results in mislocalization of Pfa3 to the vacuole lumen

Pfa3-GFP has been shown to localize to the vacuolar membrane [15,21,22] and also to the vacuole lumen [22]. In our hands, Pfa3-GFP is mostly localized to the vacuole membrane, although a fraction reaches the vacuole lumen (Figure 5B). However, the

$\Delta$ PaCCT and F250A versions of Pfa3–GFP localized mostly to the vacuole lumen in *pfa3* $\Delta$  cells. The localization of these proteins was unaffected by the addition of DTT to the medium (results not shown).

Since delivery to the vacuole lumen usually results in protein degradation, the localization results should correlate with the total amount of protein present in a cell extract. Indeed, Western blot analyses of *pfa3* $\Delta$  cells expressing Pfa3–GFP or the mutated versions showed that the protein level is markedly decreased for the F250A mutant, and it is almost undetectable for Pfa3– $\Delta$ PaCCT (Figure 5C).

## DISCUSSION

*In silico* analysis has allowed us to identify a motif that is clearly present in approx. 70% of all eukaryotic DHHC-containing proteins. The PaCCT motif is moderately conserved in PATs, but is always located at the cytoplasmic C-termini, after TMD4. The E-values for searching such a short motif are logically high. However, when taking into account other factors, such as repeated location within protein topology in a close subfamily of proteins such as PATs, this moderately conserved motif of only 16 amino acids can truly be considered a conserved motif present in PATs. In non-PAT proteins, sequence conservation is lower, there seems to be no relationship between proteins that possess the motif, and no conserved localization of the putative PaCCT motif within the domain topology of each protein family.

The distribution of the PaCCT motif in the closely related PAT proteins of the Ascomycota phylum may indicate that the motif was once present in all PAT proteins. In fact, some Ascomycota genomes (*S. pombe*, *Emericella nidulans* and *Aspergillus fumigatus*, see Supplementary Table S1) still possess a PaCCT motif in all its PATs. Posterior divergence or loss of the motif appears to have occurred independently for each PAT subfamily. The reason why some PATs have divergent/absent PaCCT motifs could be that sequence diversity does not hamper the function of the motif due to structural reasons thus precluding identification by sequence comparisons, or that some PATs have evolved different mechanisms to accomplish the PaCCT motif function, perhaps through interaction with a protein partner. Interestingly, the only PATs described to require a binding partner for activity are mammalian DHHC9 [17] and its yeast homologue Erf2 [44]. Unlike the other yeast PAT orthologues analysed (Figure 2 and Supplementary Table S1), whose conservation of the motif is either complete, or a speciation event can be accounted for motif loss/divergence, Erf2 displays a pattern of PaCCT motif conservation that does not directly correlate with gene phylogeny, suggesting that the motif may not be required for Erf2 function.

Complementation tests show that the PaCCT motif is required for the function of Swf1 *in vivo*. This is most likely due to lack of palmitoylation activity, since its substrate Tlg1 clearly shows the hallmarks of not being palmitoylated, when the PaCCT motif is altogether absent or its essential residue, Tyr<sup>323</sup>, is mutated. Degradation of Tlg1 in the vacuole is a reliable indicator of lack of Tlg1 palmitoylation [1]. Tyr<sup>323</sup> corresponds to position 3 in the PaCCT motif logo, which always contains an aromatic residue. It is interesting that mutation of the other two highly conserved positions, G326S and N331A, allows growth in lactate, and has no effect on Tlg1 palmitoylation. Nevertheless, we cannot exclude that more drastic mutations would result in visible phenotypes.

The PaCCT motif is also required for the function of Pfa3, as shown by lack of complementation of the fragmented vacuole

phenotype, which indeed suggests that the motif has an important function at least for some PATs. Moreover, the mutation in position 3 of the PaCCT motif, F250A, also results in, at least, a diminished function.

Mutation of position 3 of the PaCCT motif (Swf1 Tyr<sup>323</sup> and Pfa3 Phe<sup>250</sup>) is, to our knowledge, the first phenotype-changing mutation uncovered for any PAT, which does not lie within the DHHC motif. There are several reasons why this mutation would result in non-functional PATs. For instance, the proteins could be mislocalized or degraded. Attempts to compare Swf1 Y323A and Swf1 wild-type protein levels were unsuccessful, since we were unable to detect either the wild-type or the mutant versions of HA (haemagglutinin)-tagged Swf1 by Western blot analysis. Tagged versions of Swf1 have already proven very difficult to detect [15,21], and our polyclonal antibodies raised against the C-terminus failed to detect the endogenous protein (results not shown). We have previously shown that an epitope-tagged version of Swf1 was localized most prominently, but not exclusively, to the ER (endoplasmic reticulum), with some fluorescence present at the vacuole and in undefined puncta [1]. These versions of Swf1, although expressed from a TPI-driven promoter, were also very difficult to detect, suggesting low levels of Swf1 protein in these conditions. Recently, Dighe and Kozminski [45] raised polyclonal antibodies against the Swf1 C-terminus, which allowed them to co-localize endogenous Swf1 with cortical actin patches and with actin cables. These antibodies might be useful for the study of Swf1 mutants. However, more work on the trafficking and localization of wild-type Swf1 might be required, before the effect of mutations on these processes can be evaluated with confidence.

The experiments carried out with Pfa3 are more informative regarding the putative function of the PaCCT motif since this protein is more easily detectable than Swf1, both by microscopy and Western blot analysis. This allowed us to observe that, unlike Pfa3–GFP, which localizes mostly to the vacuolar membrane, Pfa3 $\Delta$ –PaCCT and the point mutant Pfa3–F250A are localized to the vacuole interior, where they are presumably degraded. Western blot analyses show that the degradation of the point mutant F250A is not as extensive as that of Pfa3– $\Delta$ PaCCT, which correlates with the intermediate phenotype observed for this mutant in the vacuole fragmentation assay. It is possible that the effect of the F250A mutation on the fragmented vacuole phenotype is underestimated, since the expression of these plasmids is driven by the TPI promoter, which results in, at least, a moderate over-expression.

Why Pfa3, and presumably Swf1, are less stable in the absence of the PaCCT motif is a question that will require further investigation. The motif is probably not a *bona fide* localization signal, since it is present in PATs with different subcellular localizations, such as Pfa3 (vacuole membrane) [15], Erf2 (ER) [46] and Swf1 (see above) [1]. An interesting possibility is that the PaCCT motif is involved in protein–protein interactions resulting in increased stability. The fact that PATs might need a binding partner has been suggested [17] and, notably, Erf2 levels are reduced in the absence of its binding partner Erf4 [7].

Although there have been many advances in the identification of PATs and their substrates in recent years, information regarding structure, function and regulation of these proteins is still very scarce. The identification of the PaCCT motif represents a step forward in understanding S-acylation by PATs.

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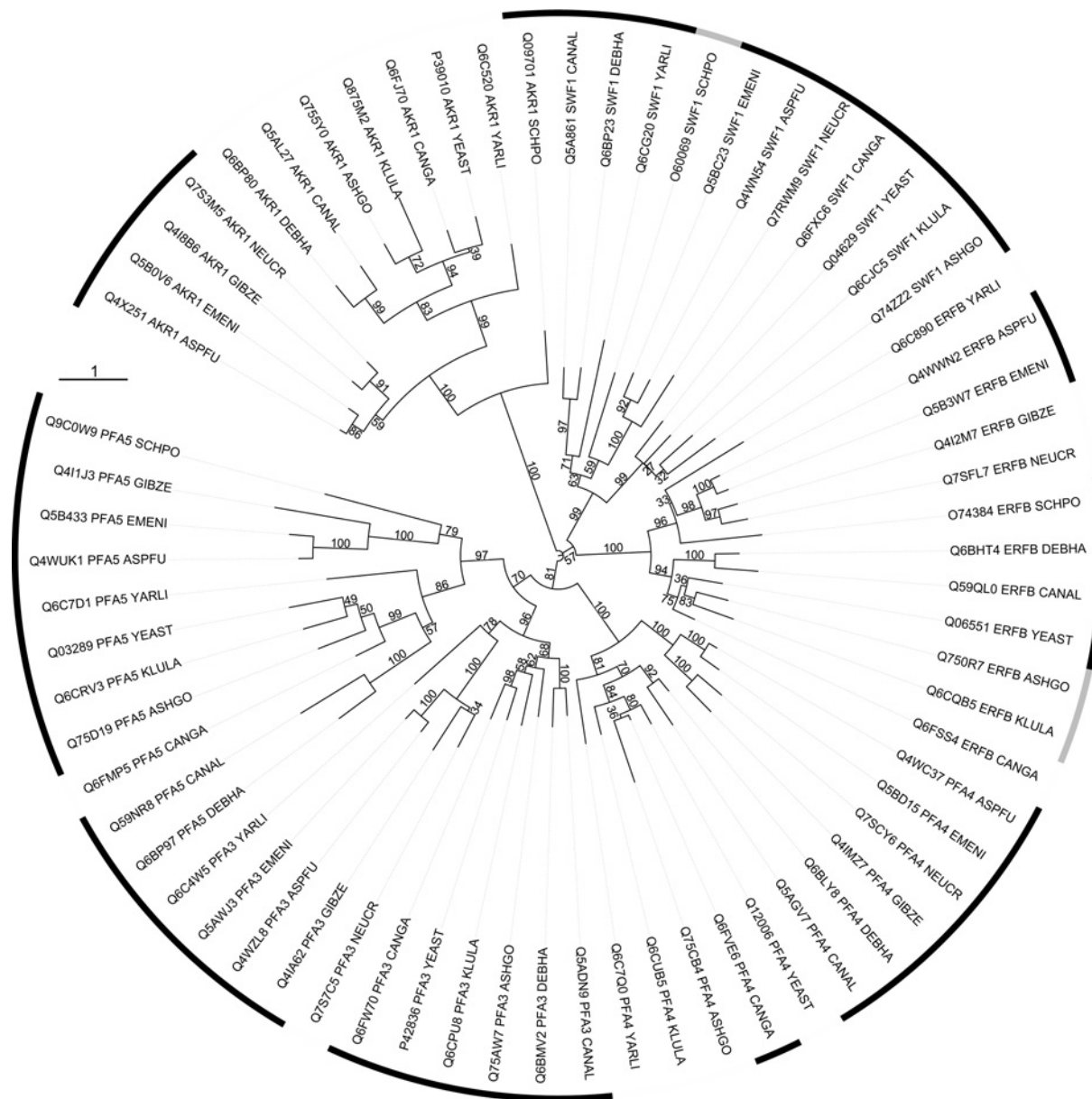


SUPPLEMENTARY ONLINE DATA

**A novel motif at the C-terminus of palmitoyltransferases is essential for Swf1 and Pfa3 function *in vivo***

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**Figure S1** Phylogenetic tree of 68 PATs present in the *Ascomycota* phylum

Circular NJ tree displaying percentage values of 1000 bootstrap replicates. Branch lengths are proportional to the genetic distance. The presence of the PaCCT motif in these proteins is symbolized by a black square when the hmsearch score is above 11.7 cut-off and a grey square when score is between 7.3 and 11.7. ASHGO, *Eremothecium gossypii*; ASPFU, *Aspergillus fumigatus*; CANAL, *Candida albicans*; CANGA, *Candida glabrata*; DEBHA, *Debaryomyces hansenii*; EMENI, *Emericella nidulans*; GIBZE, *Gibberella zeae*; KLULA, *Kluyveromyces lactis*; NEUCR, *Neurospora crassa*; SCHPO, *Schizosaccharomyces cerevisiae*; YARLI, *Yarrowia lipolytica*; YEAST, *S. cerevisiae*.

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**Table S1** Presence of the PaCCT motif in fungal PAT orthologues present in the Swiss-Prot database

Proteins are identified according to the HMM search score, in bold (below 7.3), underlined (between 7.3 and 11.7) and in italics (above 11.7). In total, 66 % of all fungal PATs contain the PaCCT motif. Akr2 was excluded from the analyses since it is only present in *S. cerevisiae*. ASHGO, *Eremothecium gossypii*; ASPFU, *Aspergillus fumigatus*; CANAL, *Candida albicans*; CANGA, *Candida glabrata*; DB, database; DEBHA, *Debaryomyces hansenii*; EMENI, *Emericella nidulans*; GIBZE, *Gibberella zeae*; KLULA, *Kluyveromyces lactis*; NEUCR, *Neurospora crassa*; SCHPO, *Schizosaccharomyces cerevisiae*; YARLI, *Yarrowia lipolytica*; YEAST, *Saccharomyces cerevisiae*.

| PAT  | Organism... | SCHPO         | Saccharomycotina |               |               |               |               |               |               | Pezizomycotina |               |                 |               |
|------|-------------|---------------|------------------|---------------|---------------|---------------|---------------|---------------|---------------|----------------|---------------|-----------------|---------------|
|      |             |               | YARLI            | CANAL         | DEBHA         | CANGA         | ASHGO         | KLULA         | YEAST         | Eurotiomycetes |               | Sordariomycetes |               |
|      |             |               |                  |               |               |               |               |               |               | ASPFU          | EMENI         | GIBZE           | NEUCR         |
| Akr1 |             | Q09701        | <b>Q6C520</b>    | <b>Q5AL27</b> | <b>Q6BP80</b> | <b>Q6FJ70</b> | <b>Q755Y0</b> | <b>Q875M2</b> | <b>P39010</b> | <i>Q4X251</i>  | <i>Q5B0V6</i> | <i>Q4I8B6</i>   | <i>Q7S3M5</i> |
| Erf2 |             | Q74384        | <b>Q6C890</b>    | <b>Q59QL0</b> | <b>Q6BHT4</b> | <b>Q6FSS4</b> | <i>Q750R7</i> | <i>Q6CQB5</i> | <i>Q06551</i> | <i>Q4WWN2</i>  | <i>Q5B3W7</i> | <b>Q4I2M7</b>   | <b>Q7SFL7</b> |
| Pfa3 |             | Not in DB     | <i>Q6C4W5</i>    | <i>Q5ADN9</i> | <i>Q6BMV2</i> | <i>Q6FW70</i> | <i>Q75AW7</i> | <i>Q6CPU8</i> | <i>P42836</i> | <i>Q4WZL8</i>  | <i>Q5AWJ3</i> | <i>Q4IA62</i>   | <b>Q7S7C5</b> |
| Pfa4 |             | Not in DB     | <b>Q6C7Q0</b>    | <i>Q5AGV7</i> | <i>Q6BLY8</i> | <i>Q6FVE6</i> | <b>Q75CB4</b> | <b>Q6CUB5</b> | <b>Q12006</b> | <i>Q4WC37</i>  | <i>Q5BD15</i> | <i>Q4IMZ7</i>   | <i>Q7SCY6</i> |
| Pfa5 |             | <i>Q9C0W9</i> | <i>Q6C7D1</i>    | <i>Q59NR8</i> | <i>Q6BP97</i> | <b>Q6FMP5</b> | <i>Q75D19</i> | <i>Q6CRV3</i> | <i>Q03289</i> | <i>Q4WUK1</i>  | <i>Q5B433</i> | <i>Q4I1J3</i>   | Not in DB     |
| Swf1 |             | <u>Q60069</u> | <i>Q6CG20</i>    | <i>Q5A861</i> | <i>Q6BP23</i> | <i>Q6FXC6</i> | <i>Q74ZZ2</i> | <i>Q6CJC5</i> | <i>Q04629</i> | <i>Q4WN54</i>  | <i>Q5BC23</i> | Not in DB       | <i>Q7RWM9</i> |

**Table S2** List of oligonucleotides used in the present study

| Oligonucleotide name | Sequence                                      |
|----------------------|---|
| Swf1 01              | 5'-AAAGGATCCACAATGTCATGGAATCTAC-3'            |
| Swf1 13              | 5'-TTTGTGACCTTTACAATGGCCAATTGAAG-3'           |
| Swf1 17              | 5'-CGCGTCCGAAATCCCGCTATATATGACAAAGGTAC-3'     |
| Swf1 18              | 5'-CTTTGTCATATAGCGGGAATTCGGA-3'               |
| Swf1 19              | 5'-CGCGTCCGAAATCCCAATATAGCTGACAAAGGTAC-3'     |
| Swf1 20              | 5'-CTTTGTCAGCTATATTGGGAATTCGGA-3'             |
| Swf1 21              | 5'-CGCGTCCGAAATCCCAATATATATGACAAAGGTAC-3'     |
| Swf1 22              | 5'-CTTTGTCATATATTGGGAATTCGGA-3'               |
| Swf1 23              | 5'-CGCGTCCGAAATCCCAATATATATGACAAAGGTAC-3'     |
| Swf1 24              | 5'-TTTTGTCATATATTGGGAATTCGGA-3'               |
| Swf1 26              | 5'-CGCTCTGGCCAATCTCACAGATTTAATATAGG-3'        |
| Swf1 27              | 5'-TCGACCTATATTAATCTGTGAGATTGGCCAGAGCGGTAC-3' |
| Swf1 28              | 5'-CTTCTGGCCGCTCTCACAGATTTAATATAGG-3'         |
| Swf1 29              | 5'-TCGACCTATATTAATCTGTGAGAGCGCCAGGAAGGTAC-3'  |
| Swf1 30              | 5'-CTTCTGGCCAATGCTACAGATTTAATATAGG-3'         |
| Swf1 31              | 5'-TCGACCTATATTAATCTGTAGCATTGGCCAGGAAGGTAC-3' |
| Pfa3 01              | 5'-AAAGGATCCATGAATGACAGGCTTTTCG-3'            |
| Pfa3 02              | 5'-TTTCTGCAGATTTGCATCGATAATTC-3'              |
| Pfa3 03              | 5'-CATCTCGAATATAGCTGACTTGGGTTCTTCAATGG-3'     |
| Pfa3 04              | 5'-TTTCTCGAGATGCTCATTGTTCCATAGC-3'            |
| Pfa3 05              | 5'-AAACTCGAGGTACATCTTGGTTAGAG-3'              |

**Table S3 Uniprot proteins containing a PaCCT motif**

Complete list of proteins retrieved from Uniprot using the PaCCT HMM, with a 7.3 score cut-off. Proteins that have a score above 11.7 are shown in bold. Proteins with a score between 7.3 and 11.7 are shown in normal (non-bold) type.

| Accession number | Organism     | PaCCT motif             | DHHC       | Description   |
|------------------|--------------|-------------------------|------------|---|
| A7BE66           | 9ACTO        | HPYDVQ-VLLNVLQHL        | NO         | Putative uncharacterized protein: <i>Actinomyces odontolyticus</i> ATCC 17982                                   |
| A6F240           | 9ALTE        | SVFNVG-WVSNIVSIW        | NO         | Putative uncharacterized protein: <i>Marinobacter algicola</i> DG893  |
| A8URT1           | 9AQUI        | SFYTTYGPKNLRELL         | NO         | Putative uncharacterized protein: <i>Hydrogenivirga</i> sp. 128-5-R1-1  |
| A5ZEX2           | 9BACE        | SPFTFG-YKYNITDAL        | NO         | Putative uncharacterized protein: <i>Bacteroides caccae</i> ATCC 43185  |
| A6NPX6           | 9BACE        | RYYDRG-YWRNVKYAI        | NO         | Putative uncharacterized protein: <i>Bacteroides capillosus</i> ATCC 29799                                      |
| A6NTG8           | 9BACE        | SAFHSG-FQENMGFF         | NO         | Putative uncharacterized protein: <i>Bacteroides capillosus</i> ATCC 29799                                      |
| A6NVJ0           | 9BACE        | NGWHRG-WYKNMWDDW        | NO         | Putative uncharacterized protein: <i>Bacteroides capillosus</i> ATCC 29799                                      |
| <b>A6P1M2</b>    | <b>9BACE</b> | <b>NVYDKGYILVNMGDVW</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Bacteroides capillosus</i> ATCC 29799</b>                               |
| A9VTF9           | 9BACI        | SRYDLG-ILKNISEFI        | NO         | Glycosyl transferase group 1: <i>Bacillus weihenstephanensis</i> KBAB4  |
| A9I540           | 9BACT        | YVSLG-LRQNFYNAF         | NO         | Putative uncharacterized protein precursor: <i>Elusimicrobium minutum</i> Pei191                                |
| Q6SHB6           | 9BACT        | NIHNLNSVKNLARIL         | NO         | Oxidoreductase, short-chain dehydrogenase/reductase family - uncultured marine bacterium 440                    |
| <b>A8PUS7</b>    | <b>9BASI</b> | <b>NPFDHG-CLTNWMDFA</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Malassezia globosa</i> CBS 7966</b>                                     |
| <b>A8PWF8</b>    | <b>9BASI</b> | <b>FPFDVG-CWQNISSIL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Malassezia globosa</i> CBS 7966</b>                                     |
| <b>A8PYI0</b>    | <b>9BASI</b> | <b>NVYDLG-WVRNLQLFF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Malassezia globosa</i> CBS 7966</b>                                     |
| A2W7U0           | 9BURK        | NKYGRG-FIANISVLL        | NO         | Xanthine/uracil permease: <i>Burkholderia dolosa</i> AU0158   |
| A7TVC1           | 9BURK        | DGFDIG-FRKSWEVDL        | NO         | ACC deaminase: <i>Burkholderia xenovorans</i>   |
| Q34058           | 9CAUD        | RYNRRG-TLQNAKDVV        | NO         | ORF27: <i>Streptococcus</i> phage O1205   |
| O80165           | 9CAUD        | RYNRRG-TLQNAKDVV        | NO         | Gp502: <i>Streptococcus</i> phage Sfi11   |
| A6BIP6           | 9CLOT        | SAFTYG-IIANFLDTL        | NO         | Putative uncharacterized protein: <i>Dorea longicatena</i> DSM 13814  |
| <b>A8RGP2</b>    | <b>9CLOT</b> | <b>KVYDMG-FWYNFKEAI</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Clostridium bolteae</i> ATCC BAA-613</b>                                |
| A8S0B5           | 9CLOT        | LPFDLG-IRQNLVEQL        | NO         | Putative uncharacterized protein: <i>Clostridium bolteae</i> ATCC BAA-613                                       |
| B0ACH6           | 9CLOT        | NPFDIG-FINSWNIIL        | NO         | Putative uncharacterized protein: <i>Clostridium bartlettii</i> DSM 16795                                       |
| A0YTV4           | 9CYAN        | NIYYTG-SSNLANIL         | NO         | Putative uncharacterized protein: <i>Lyngbya</i> sp. PCC 8106   |
| A4MJN2           | 9DELT        | NIYDKESLSRNFAFLM        | NO         | Recombinase: <i>Geobacter bemedjensis</i> Bem   |
| A9J342           | 9DELT        | LIYSVGNVYETNIYDVW       | NO         | Putative uncharacterized protein precursor: <i>Desulfatibacillum alkenivorans</i> AK-01                         |
| Q3HUQ2           | 9ENTR        | NQYDVR-VMKNFGNVL        | NO         | Proteinase K: <i>Serratia</i> sp. GF96  |
| A2T5T1           | 9ERIC        | RIYFYG-KIENFVEVF        | NO         | Maturase K: <i>Diospyros ropourea</i>   |
| Q8M960           | 9ERIC        | RIYFYG-KIENFVEVF        | NO         | Maturase K: <i>Pterostyrax hispidus</i>   |
| Q8M974           | 9ERIC        | RIYFYG-KIENFVEVF        | NO         | Maturase K: <i>Pentaptylax euryoides</i>  |
| Q8VXQ0           | 9FABA        | SFNFYRSFLANIREIC        | NO         | RGA-D2 protein: <i>Cicer reticulatum</i>  |
| A5KQ57           | 9FIRM        | KTYGKG-VFKNILEVL        | NO         | Putative uncharacterized protein: <i>Ruminococcus torques</i> ATCC 27756  |
| A8SUZ5           | 9FIRM        | HIFSRN-RKNLRLTLL        | NO         | Putative uncharacterized protein: <i>Coprococcus eutactus</i> ATCC 27759  |
| A3J300           | 9FLAO        | DLYNKG-KYQNALETG        | NO         | Aerotolerance-related exported protein: <i>Flavobacteria bacterium</i> BAL38                                    |
| A3XHB4           | 9FLAO        | KIYTHG-AIENMTEVI        | NO         | Putative uncharacterized protein: <i>Leeuwenhoekella blandensis</i> MED217                                      |
| <b>A4AVZ3</b>    | <b>9FLAO</b> | <b>NKYTLG-FLVNLIAIF</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Flavobacteriales bacterium</i> HTCC2170</b>                             |
| A4CH39           | 9FLAO        | RIYTHG-AIENMTEVL        | NO         | Putative uncharacterized protein: <i>Robiginitalea biformata</i> HTCC2501                                       |
| Q1VXW6           | 9FLAO        | DIYTHG-AIENMTNVL        | NO         | Putative uncharacterized protein: <i>Psychroflexus torquis</i> ATCC 700755                                      |
| Q8B3X5           | 9GAMA        | NPYDFENIKKNIQSIL        | NO         | Major DNA-binding protein: porcine lymphotropic herpesvirus 2   |
| Q8B424           | 9GAMA        | NPYDFENIKKNIQSIL        | NO         | Major DNA-binding protein: porcine lymphotropic herpesvirus 2   |
| A0J025           | 9GAMM        | DLWDRG-LIANACERL        | NO         | Putative RNA polymerase, sigma-24 subunit, ECF subfamily: <i>Shewanella woodyi</i> ATCC 51908                   |
| A0XY38           | 9GAMM        | NVWYRG-HIQNTQNVN        | NO         | Phosphoenolpyruvate carboxylase: <i>Alteromonadales bacterium</i> TW-7  |
| A0Y8D0           | 9GAMM        | SPFDQSSFNKNLASLL        | NO         | Glycosyl transferase, group 1: marine gamma proteobacterium HTCC2143  |
| A4C9I2           | 9GAMM        | SIFNVG-LYSNIIIFW        | NO         | Putative uncharacterized protein: <i>Pseudoalteromonas tunicata</i> D2  |
| A5NEZ6           | 9GAMM        | NQYDVR-VMKNFGNVL        | NO         | Peptidase S8 and S53, subtilisin, kexin, sedolisin precursor: <i>Shewanella baltica</i> OS223                   |
| A5NKU7           | 9GAMM        | NGFRQG-LLESMPREFC       | NO         | DNA topoisomerase IV, B subunit: <i>Shewanella baltica</i> OS223  |
| A8H8I4           | 9GAMM        | NGFRQG-LLESMPREFC       | NO         | DNA topoisomerase IV, B subunit: <i>Shewanella pealeana</i> ATCC 700345   |
| A9D1B1           | 9GAMM        | NGFRQG-LLESMPREFC       | NO         | DNA topoisomerase IV subunit B: <i>Shewanella benthica</i> KT99   |
| A9KZ52           | 9GAMM        | NQYDVR-VMKNFGNVL        | NO         | Peptidase S8 and S53 subtilisin kexin sedolisin precursor: <i>Shewanella baltica</i> OS195                      |
| A9L1T0           | 9GAMM        | NGFRQG-LLESMPREFC       | NO         | DNA topoisomerase IV, B subunit: <i>Shewanella baltica</i> OS195  |
| Q2BG79           | 9GAMM        | NTFSIGSMTKNLQQAL        | NO         | 4-amino-4-deoxychorismate lyase: <i>Neptuniibacter caesariensis</i>   |
| Q2BHZ1           | 9GAMM        | HGFDQGPICRNLLQTL        | NO         | Methylase of polypeptide chain release factor: <i>Neptuniibacter caesariensis</i>                               |
| Q2BJU5           | 9GAMM        | NGYSYSGSHFDNMKGFL       | NO         | Probable amino acid ABC transporter, periplasmic amino acid-binding protein: <i>Neptuniibacter caesariensis</i> |
| Q2BMK8           | 9GAMM        | SIFDRG-SKTNVGEML        | NO         | Exopolyphosphatase-related protein: <i>Neptuniibacter caesariensis</i>  |
| Q2YZG0           | 9GAMM        | HVFDRR-WIKSFKEIL        | NO         | Putative uncharacterized protein: uncultured gamma proteobacterium  |
| Q58GP7           | 9HIV1        | GKWDRG-YSNACHHL         | NO         | Envelope glycoprotein: human immunodeficiency virus 1   |
| Q9GD55           | 9LILI        | NLFNTN-YSVNWYEFF        | NO         | NADH dehydrogenase subunit F: <i>Gagea wilczekii</i>  |
| Q94B99           | 9MAGN        | RIYFYG-KIKNLVEVF        | NO         | Maturase K: <i>Saxifraga</i> sp. <i>Cuenoud</i> s.n.  |
| Q9MT36           | 9MAGN        | RIYFYG-KIKNLVEVF        | NO         | Maturase K: <i>Sycopsis sinensis</i>  |
| Q9MT38           | 9MAGN        | RIYFYG-KIKNLVEVF        | NO         | Maturase K: <i>Shaniodendron subaequale</i>   |
| Q9MT51           | 9MAGN        | RIYFYG-KIKNLVEVF        | NO         | Maturase K: <i>Distyliopsis tutcheri</i>  |
| Q9MT52           | 9MAGN        | RIYFYG-KIKNLVEVF        | NO         | Maturase K: <i>Distylium racemosum</i>  |
| Q9TN26           | 9MAGN        | RIYFYG-KIKNLVEVF        | NO         | Maturase K: <i>Saxifraga rufidula</i>   |
| Q9TN28           | 9MAGN        | RIYFYG-KIKNLVEVF        | NO         | Maturase K: <i>Saxifraga oregana</i>  |
| Q9TN29           | 9MAGN        | RIYFYG-KIKNLVEVF        | NO         | Maturase K: <i>Saxifraga aprica</i>   |
| Q9TN31           | 9MAGN        | RIYFYG-KIKNLVEVF        | NO         | Maturase K: <i>Saxifraga occidentalis</i>   |
| Q9TN36           | 9MAGN        | RIYFYG-KIKNLVEVF        | NO         | Maturase K: <i>Saxifraga californica</i>  |
| A3TRH3           | 9MICO        | SPFDKG-AMNNIEKAL        | NO         | Ribosome recycling factor: <i>Janibacter</i> sp. HTCC2649   |

Table S3 Contd.

| Accession number | Organism     | PaCCT motif             | DHHC       | Description  |
|------------------|--------------|-------------------------|------------|--|
| A8REM8           | 9MOLU        | NPFSAS-FCKNLYAYW        | NO         | Putative uncharacterized protein: <i>Eubacterium dolichum</i> DSM 3991   |
| Q2PQX1           | 9NOCA        | RNYDLG-LLTNALEAM        | NO         | Putative uncharacterized protein: <i>Rhodococcus</i> sp. T104  |
| A7RBM1           | 9PHYC        | RRWSLGTVCNNLWFL         | NO         | Putative uncharacterized protein C418R: <i>Paramecium bursaria</i> Chlorella virus AR158                                       |
| Q8V735           | 9PHYC        | RRWSLGTVCNNLWFL         | NO         | Chitin synthase: Chlorella virus   |
| Q50KK9           | 9PRIM        | NMFDINSLWNNLCQII        | NO         | Taste receptor type 2: <i>Gorilla gorilla</i> (gorilla)  |
| A3SD59           | 9RHOB        | GIFNTG-VLANVLQLL        | NO         | ATP-dependent protease La: <i>Sulfitobacter</i> sp. EE-36  |
| A3SYA2           | 9RHOB        | GIFNTG-VLANVLQLL        | NO         | ATP-dependent protease La: <i>Sulfitobacter</i> sp. NAS-14.1   |
| A3U2Q2           | 9RHOB        | GIYDAG-VLANVLQLL        | NO         | ATP-dependent protease La: <i>Oceanicola batsensis</i> HTCC2597  |
| A3X9G3           | 9RHOB        | QGYDEG-FFRNWQYYL        | NO         | Cyclopropane-fatty-acyl-phospholipid synthase, putative: <i>Roseobacter</i> sp. MED193   |
| <b>A3XAJ1</b>    | <b>9RHOB</b> | <b>NPFYDG-VMSNLTVSF</b> | <b>NO</b>  | <b>YjeF family protein: <i>Roseobacter</i> sp. MED193</b>  |
| A4EV28           | 9RHOB        | QGYDEG-FFRNWQYYL        | NO         | Cyclopropane-fatty-acyl-phospholipid synthase, putative: <i>Roseobacter</i> sp. SK209-2-6                                      |
| A9ELP4           | 9RHOB        | GIYNVG-VLANVLQLL        | NO         | ATP-dependent protease La: <i>Phaeobacter gallaeciensis</i> 2.10   |
| A9NE4            | 9RHOB        | GIYNVG-VLANVLQLL        | NO         | ATP-dependent protease La: <i>Phaeobacter gallaeciensis</i> BS107  |
| A0ZQC9           | 9ROSI        | RIYFYG-KIENFSEVF        | NO         | Maturase K: <i>Camptostylus manii</i>  |
| A0ZQI0           | 9ROSI        | RIYFYG-KIENFTEVF        | NO         | Maturase K: <i>Cratoxylum cochinchinense</i>   |
| A0ZQL1           | 9ROSI        | RIYFYG-KIENFAEVF        | NO         | Maturase K: <i>Aristogeitonia monophylla</i>   |
| A0ZQL2           | 9ROSI        | RIYFYG-KIENFAEVF        | NO         | Maturase K: <i>Oldfieldia dactylophylla</i>  |
| A0ZQL3           | 9ROSI        | RIYFYG-KIENFAEVF        | NO         | Maturase K: <i>Picrodendron baccatum</i>   |
| A0ZQL4           | 9ROSI        | RIYFYG-KIENFAEVF        | NO         | Maturase K: <i>Scagea oligostemon</i>  |
| A1X3S6           | 9ROSI        | RLYFYG-KIENFTEVF        | NO         | Maturase K: <i>Dicraeanthus africanus</i>  |
| A6MI65           | 9ROSI        | RIYFYG-KMENFAEVF        | NO         | Maturase K: <i>Androstachys johnsonii</i>  |
| A6MI67           | 9ROSI        | RIYFYG-KIENFAEVF        | NO         | Maturase K: <i>Austrobuxus megacarpus</i>  |
| A6MI83           | 9ROSI        | RIYFYG-KIDNFAEVF        | NO         | Maturase K: <i>Dissiliaria muelleri</i>  |
| <b>A6MIB3</b>    | <b>9ROSI</b> | <b>RIYFYG-KVNNFREFV</b> | <b>NO</b>  | <b>Maturase K: <i>Mesua</i> sp. Code 7884</b>  |
| A6MIB5           | 9ROSI        | RIYFYG-KIENFAEVF        | NO         | Maturase K: <i>Micranthemum hexandrum</i>  |
| A6MIC3           | 9ROSI        | RIYFYG-KVENFAEVF        | NO         | Maturase K: <i>Petalostigma pubescens</i>  |
| A6MID9           | 9ROSI        | RIYFYG-KIENFAEVF        | NO         | Maturase K: <i>Stachystemon axillaris</i>  |
| A6MIE3           | 9ROSI        | RIYFYG-KVENFTEVF        | NO         | Maturase K: <i>Vismia</i> sp. Miller et al. 9313   |
| Q5V6G2           | 9ROSI        | RIYFYG-KMENFAEVF        | NO         | Maturase K: <i>Androstachys johnsonii</i>  |
| Q8WKK2           | 9ROSI        | RLYFYG-KVKNFTEVF        | NO         | Maturase K: <i>Polypleurum wallichii</i>   |
| Q9BBG0           | 9ROSI        | RLYFYG-KIENFTEVF        | NO         | Maturase K: <i>Vanroyenella plumosa</i>  |
| A1ZEY0           | 9SPHI        | SKYKNGSYNISNTIQL        | NO         | Putative uncharacterized protein: <i>Microscilla marina</i> ATCC 23134   |
| A1ZHY5           | 9SPHI        | NSFDFG-IYRNYATL         | NO         | Alpha-2-macroglobulin family N-terminal region: <i>Microscilla marina</i> ATCC 23134   |
| <b>A1ZMC5</b>    | <b>9SPHI</b> | <b>NPFFLG-AIGNFLQAL</b> | <b>NO</b>  | <b>Two-component system sensor histidine kinase/response regulator, hybrid, putative: <i>Microscilla marina</i> ATCC 23134</b> |
| A3HWC1           | 9SPHI        | FPWNTG-RMKNVIQTL        | NO         | Twin-arginine translocation pathway signal: <i>Algoriphagus</i> sp. PR1  |
| A3I068           | 9SPHI        | FGFGRG-PVSNWRNVL        | NO         | Putative xylanase: <i>Algoriphagus</i> sp. PR1   |
| A6EJA3           | 9SPHI        | NGFDIG-LLRNWYLP         | NO         | Putative uncharacterized protein: <i>Pedobacter</i> sp. BAL39  |
| A4ZHE4           | 9STRA        | NIFSLK-LIINLRKFF        | NO         | Sec-independent transporter protein: <i>Phytophthora ramorum</i> (Sudden oak death agent)                                      |
| A3Z0G9           | 9SYNE        | SGFVHG-LRLNFIFF         | NO         | ATP synthase subunit I: <i>Synechococcus</i> sp. WH 5701   |
| Q580D7           | 9TRYP        | QPWHSGLNLLNLIFF         | NO         | Endosomal integral membrane protein, putative - <i>Trypanosoma brucei</i>  |
| <b>Q382R6</b>    | <b>9TRYP</b> | <b>GLFNRG-VWNNLKEVM</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Trypanosoma brucei</i></b>   |
| <b>Q384C1</b>    | <b>9TRYP</b> | <b>SPFDRG-LIRNAWDFI</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Trypanosoma brucei</i></b>   |
| <b>Q384U2</b>    | <b>9TRYP</b> | <b>NPFNKG-IVQNVYFLF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Trypanosoma brucei</i></b>   |
| <b>Q389Q0</b>    | <b>9TRYP</b> | <b>NPFDIG-VKGNLHQVF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Trypanosoma brucei</i></b>   |
| <b>Q38CH1</b>    | <b>9TRYP</b> | <b>NPYDLG-QQRNLLALF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Trypanosoma brucei</i></b>   |
| Q37939           | 9VIRU        | NIYDLS-SLVNIYQVV        | NO         | G1/G2 glycoproteins: <i>Gloxinia tospovirus</i>  |
| Q0P0G9           | 9VIRU        | NIYDLS-SLVNIYQVI        | NO         | Glycoprotein G1/G2: <i>Capsicum chlorosis</i> virus  |
| Q2THX3           | 9VIRU        | NIYDLS-SLVNIYQVV        | NO         | Glycoprotein: groundnut bud necrosis virus   |
| Q5KU06           | 9VIRU        | NIYDLS-TLVNIYQVV        | NO         | Glycoprotein: melon yellow spot virus  |
| Q84405           | 9VIRU        | NIYDLS-SLVNIYQVV        | NO         | Glycoprotein: peanut bud necrosis virus  |
| B0BZH6           | ACAM1        | NMFNES-VLKNLISLF        | NO         | Glycosyl transferase, group 2 family protein, putative: <i>Acaryochloris marina</i> (strain MBIC 11017)                        |
| B0CD40           | ACAM1        | AAFDEGSIFSNLIDVM        | NO         | Diguanylate cyclase/phosphodiesterase with PAS/PAC sensor: <i>Acaryochloris marina</i> (strain MBIC 11017)                     |
| A1TU21           | ACIAC        | GPWGLG-LVSNVQDIL        | NO         | Potassium efflux system protein: <i>Acidovorax avenae</i> subsp. citrulli (strain AAC00-1)                                     |
| <b>Q11JQ5</b>    | <b>ACIBL</b> | <b>NIFNNN-VLINMTHVF</b> | <b>NO</b>  | <b>TonB-dependent receptor precursor: <i>Acidobacteria bacterium</i> (strain Ellin345)</b>                                     |
| A6VQT6           | ACTSZ        | NPWRTG-PYRNLANVV        | NO         | Glycosyl transferase family 9: <i>Actinobacillus succinogenes</i> (strain ATCC 55618 / 130Z)                                   |
| Q16JR2           | AEDAE        | QRFDLG-VWKNVFFFY        | NO         | Putative uncharacterized protein: <i>Aedes aegypti</i> (Yellowfever mosquito)  |
| Q16T01           | AEDAE        | QPYNLQ-TKTNLRSVL        | NO         | Exocyst complex-subunit protein, 84kD-subunit, putative: <i>Aedes aegypti</i> (Yellowfever mosquito)                           |
| Q16U12           | AEDAE        | YRFSEG-IQGNFFSVF        | NO         | Kidney-specific Na-K-Cl cotransport protein splice isoform A, putative: <i>Aedes aegypti</i> (Yellowfever mosquito)            |
| Q17D05           | AEDAE        | NKWWFG-IRKNFCQFL        | NO         | Putative uncharacterized protein: <i>Aedes aegypti</i> (Yellowfever mosquito)  |
| Q17L45           | AEDAE        | HIFVRGTISTNFRQVL        | NO         | Laminin alpha-1, 2 chain: <i>Aedes aegypti</i> (Yellowfever mosquito)  |
| Q16ED5           | AEDAE        | NPFSRG-CWNNCCYQ         | YES        | Putative uncharacterized protein: <i>Aedes aegypti</i> (Yellowfever mosquito)  |
| Q16ED6           | AEDAE        | NPFSRG-CWNNCCYQ         | YES        | Putative uncharacterized protein: <i>Aedes aegypti</i> (Yellowfever mosquito)  |
| <b>Q16L42</b>    | <b>AEDAE</b> | <b>NPYDFG-PRRNWRLFL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Aedes aegypti</i> (Yellowfever mosquito)</b>   |
| <b>Q16LA8</b>    | <b>AEDAE</b> | <b>YPYDLG-KWKNIQQVA</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Aedes aegypti</i> (Yellowfever mosquito)</b>   |
| <b>Q16QB4</b>    | <b>AEDAE</b> | <b>YPYDLG-KWKNIQQVA</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Aedes aegypti</i> (Yellowfever mosquito)</b>   |
| <b>Q16SH3</b>    | <b>AEDAE</b> | <b>NGFSLG-KLNNFQEVF</b> | <b>YES</b> | <b>Zinc finger protein, putative: <i>Aedes aegypti</i> (Yellowfever mosquito)</b>  |
| <b>Q174U5</b>    | <b>AEDAE</b> | <b>SPFTRG-PIKNLDFDM</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Aedes aegypti</i> (Yellowfever mosquito)</b>   |
| <b>Q17FV8</b>    | <b>AEDAE</b> | <b>NPYDFG-PRRNWRLFL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Aedes aegypti</i> (Yellowfever mosquito)</b>   |
| <b>Q17LD8</b>    | <b>AEDAE</b> | <b>NPYSQGNICLNCFHIL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Aedes aegypti</i> (Yellowfever mosquito)</b>   |
| <b>Q17LW6</b>    | <b>AEDAE</b> | <b>NPFSRG-PVLNLFEEF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Aedes aegypti</i> (Yellowfever mosquito)</b>   |

Table S3 Contd.

| Accession number | Organism     | PaCCT motif              | DHHC       | Description  |
|------------------|--------------|--------------------------|------------|--|
| Q6IYE0           | AEGTA        | DIWDKS-VVNNIRCAL         | NO         | LZ-NBS-LRR class RGA: <i>Aegilops tauschii</i> (Tausch's goatgrass) ( <i>Aegilops squarrosa</i> )                            |
| Q6IYE1           | AEGTA        | DIWDKS-VVNNIRCAL         | NO         | LZ-NBS-LRR class: <i>Aegilops tauschii</i> (Tausch's goatgrass) ( <i>Aegilops squarrosa</i> )                                |
| Q8LLA3           | AEGTA        | DIWDKS-VVNNIRCAL         | NO         | LZ-NBS-LRR class RGA - <i>Aegilops tauschii</i> (Tausch's goatgrass) ( <i>Aegilops squarrosa</i> )                           |
| AOKJ18           | AERHH        | HPFTLG-PENSVKQAM         | NO         | CBS domains protein: <i>Aeromonas hydrophila</i> subsp. <i>hydrophila</i> (strain ATCC 7966 / NCIB 9240)                     |
| A4SP28           | AERS4        | HPFTLG-PENSVKQAM         | NO         | Acetoin utilization protein AcuB: <i>Aeromonas salmonicida</i> (strain A449)   |
| <b>A6R843</b>    | <b>AJECN</b> | <b>HAFDLG-WRRNFHFL</b>   | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Ajellomyces capsulata</i> (strain NAm1) (<i>Histoplasma capsulatum</i>)</b>          |
| <b>A6R9R5</b>    | <b>AJECN</b> | <b>NIYDRG-FWANLRDAL</b>  | <b>NO</b>  | <b>Predicted protein: <i>Ajellomyces capsulata</i> (strain NAm1) (<i>Histoplasma capsulatum</i>)</b>                         |
| <b>A6RCS2</b>    | <b>AJECN</b> | <b>NPFSRG-VVTNCKDFW</b>  | <b>NO</b>  | <b>Palmitoyltransferase akr1: <i>Ajellomyces capsulata</i> (strain NAm1) (<i>Histoplasma capsulatum</i>)</b>                 |
| <b>A6QUZ2</b>    | <b>AJECN</b> | <b>RPFTQGNILRNWIAVL</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Ajellomyces capsulata</i> (strain NAm1) (<i>Histoplasma capsulatum</i>)</b>          |
| Q0VLX9           | ALCBS        | SIFNTRSRAANWQNVF         | NO         | TonB-dependent receptor protein: <i>Alcanivorax borkumensis</i> (strain SK2 / ATCC 700651 / DSM 11573)                       |
| Q0ABA0           | ALHEH        | HRFDSG-VQLNLGLRW         | NO         | Surface antigen: <i>Alkalilimnicola ehrlichei</i> (strain MLHE-1)  |
| A6TT43           | ALKMQ        | NPHNKG-CAANQLDIM         | NO         | Citrate lyase, alpha subunit: <i>Alkaliphilus metalliredigens</i> (strain QYMF)  |
| Q7PX01           | ANOGA        | NKWVFG-IRKNFSQFL         | NO         | AGAP001144-PA: <i>Anopheles gambiae</i> str. PEST  |
| Q7Q293           | ANOGA        | HLTYLQ-CLRNCRLL          | NO         | AGAP003967-PA: <i>Anopheles gambiae</i> str. PEST  |
| Q7Q939           | ANOGA        | TLYSMDR-KFRNALEVF        | NO         | AGAP004828-PA: <i>Anopheles gambiae</i> str. PEST  |
| Q7QFM4           | ANOGA        | NPFSRG-CWNCCCYTQ         | NO         | AGAP000568-PA: <i>Anopheles gambiae</i> str. PEST  |
| <b>Q7PNJ3</b>    | <b>ANOGA</b> | <b>YPYDLG-RWSNVKQVI</b>  | <b>YES</b> | <b>AGAP000886-PA: <i>Anopheles gambiae</i> str. PEST</b>   |
| <b>Q7PQ26</b>    | <b>ANOGA</b> | <b>NPYSGQGNICLNCFHIL</b> | <b>YES</b> | <b>AGAP005111-PA: <i>Anopheles gambiae</i> str. PEST</b>   |
| <b>Q7PWK8</b>    | <b>ANOGA</b> | <b>NPFSRG-VVNLFEFF</b>   | <b>YES</b> | <b>AGAP008928-PA: <i>Anopheles gambiae</i> str. PEST</b>   |
| <b>Q7PZ51</b>    | <b>ANOGA</b> | <b>SPFNRG-PVKNLFDL</b>   | <b>YES</b> | <b>AGAP011732-PA: <i>Anopheles gambiae</i> str. PEST</b>   |
| <b>Q7Q7Z4</b>    | <b>ANOGA</b> | <b>NGFSLG-KLNNFQEVF</b>  | <b>YES</b> | <b>AGAP004938-PA: <i>Anopheles gambiae</i> str. PEST</b>   |
| <b>Q7Q957</b>    | <b>ANOGA</b> | <b>NPYDFG-SRQNWRFIL</b>  | <b>YES</b> | <b>AGAP004856-PA: <i>Anopheles gambiae</i> str. PEST</b>   |
| Q23378           | ARATH        | SPYNK8-MVINRQCM          | NO         | Putative uncharacterized protein d13665c: <i>Arabidopsis thaliana</i> (Mouse-ear cross)                                      |
| Q27GK2           | ARATH        | SPYALG-LCQNLASAF         | NO         | Uncharacterized protein At3g59020.2: <i>Arabidopsis thaliana</i> (Mouse-ear cross)   |
| Q2V3N4           | ARATH        | SPYALG-LCQNLASAF         | NO         | Uncharacterized protein At3g59020.1: <i>Arabidopsis thaliana</i> (Mouse-ear cross)   |
| Q2V435           | ARATH        | RLWDLR-KLRNFKSFL         | NO         | Uncharacterized protein At2g33340.3: <i>Arabidopsis thaliana</i> (Mouse-ear cross)   |
| Q3EBP5           | ARATH        | RLWDLR-KLRNFKSFL         | NO         | Uncharacterized protein At2g33340.2: <i>Arabidopsis thaliana</i> (Mouse-ear cross)   |
| Q9LH98           | ARATH        | FKFDLKSSENLLQTM          | NO         | <i>Arabidopsis thaliana</i> genomic DNA, chromosome 3, BAC clone: T19N8: <i>Arabidopsis thaliana</i> (Mouse-ear cross)       |
| <b>Q9LT42</b>    | <b>ARATH</b> | <b>NPYFSSSWRRNLSDVC</b>  | <b>NO</b>  | <b><i>Arabidopsis thaliana</i> genomic DNA, chromosome 3, P1 clone: MOE17: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b> |
| Q9LYT4           | ARATH        | SPYALG-LCQNLASAF         | NO         | Putative uncharacterized protein F17J16_70: <i>Arabidopsis thaliana</i> (Mouse-ear cross)                                    |
| <b>Q9SD10</b>    | <b>ARATH</b> | <b>HPFSRG-IRRNLNVVC</b>  | <b>NO</b>  | <b>Putative uncharacterized protein F26013.30: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>                             |
| Q9SUS6           | ARATH        | HLWNRS-PRRNCRRVL         | NO         | Putative uncharacterized protein AT4g11350: <i>Arabidopsis thaliana</i> (Mouse-ear cross)                                    |
| <b>A8MR93</b>    | <b>ARATH</b> | <b>NPHNKG-VVDNFKEIF</b>  | <b>YES</b> | <b>Uncharacterized protein At5g41060.2: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>                                    |
| Q23092           | ARATH        | WKYDLG-KKKNFEQVF         | YES        | A_TM018A10.8 protein: <i>Arabidopsis thaliana</i> (Mouse-ear cross)  |
| <b>Q49656</b>    | <b>ARATH</b> | <b>WPYNVG-RKTNFEQVF</b>  | <b>YES</b> | <b>Predicted protein: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>  |
| <b>Q80685</b>    | <b>ARATH</b> | <b>NPYGGK-LFKNLYELF</b>  | <b>YES</b> | <b>Putative uncharacterized protein At2g40990: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>                             |
| <b>Q0WQK2</b>    | <b>ARATH</b> | <b>NPHNKG-VVNNFKETF</b>  | <b>YES</b> | <b>Putative uncharacterized protein At3g26935: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>                             |
| <b>Q0WQT8</b>    | <b>ARATH</b> | <b>NPYDLG-CRRNCSDFL</b>  | <b>YES</b> | <b>Ankyrin-repeat protein: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>   |
| Q0WR40           | ARATH        | NLYDRG-SFQNVSEIV         | YES        | Putative uncharacterized protein At3g04970: <i>Arabidopsis thaliana</i> (Mouse-ear cross)                                    |
| Q3EBC2           | ARATH        | NLYDRG-SFQNVSEIV         | YES        | Uncharacterized protein At3g04970.1: <i>Arabidopsis thaliana</i> (Mouse-ear cross)   |
| <b>Q3EC11</b>    | <b>ARATH</b> | <b>NPYNHG-LRRNCTDFL</b>  | <b>YES</b> | <b>Uncharacterized protein At2g14255.1: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>                                    |
| <b>Q50022</b>    | <b>ARATH</b> | <b>HQFDVG-FYKNLTSVL</b>  | <b>YES</b> | <b>At5g04270: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>  |
| <b>Q5M757</b>    | <b>ARATH</b> | <b>WKYDLG-KKKNFEQVF</b>  | <b>YES</b> | <b>At4g00840: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>  |
| <b>Q5PNZ1</b>    | <b>ARATH</b> | <b>NPYKRG-LLKNVKEVL</b>  | <b>YES</b> | <b>At5g05070: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>  |
| <b>Q7XA86</b>    | <b>ARATH</b> | <b>HPFSRG-IRRNLNVVC</b>  | <b>YES</b> | <b>At3g51390: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>  |
| <b>Q8L5Y7</b>    | <b>ARATH</b> | <b>NPYNKG-ILGNIWEIF</b>  | <b>YES</b> | <b>Putative uncharacterized protein At3g56930: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>                             |
| <b>Q8LAJ3</b>    | <b>ARATH</b> | <b>WPYNVG-RKTNFEQVF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>                                       |
| <b>Q8LAV8</b>    | <b>ARATH</b> | <b>HPFSRG-IRRNLNVVC</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>                                       |
| <b>Q8VYP5</b>    | <b>ARATH</b> | <b>WRYDLG-KKKNFEQVF</b>  | <b>YES</b> | <b>Putative uncharacterized protein At3g60800: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>                             |
| <b>Q93VV0</b>    | <b>ARATH</b> | <b>HPYDIG-AYENLTLIL</b>  | <b>YES</b> | <b>AT3g09320/F3L24_19: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>   |
| <b>Q94C49</b>    | <b>ARATH</b> | <b>WPYNVG-RKTNFEQVF</b>  | <b>YES</b> | <b>Putative uncharacterized protein At4g22750: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>                             |
| <b>Q9FF67</b>    | <b>ARATH</b> | <b>NPYKRG-LLKNVKEVL</b>  | <b>YES</b> | <b><i>Arabidopsis thaliana</i> genomic DNA, chromosome 5, P1 clone: MUG13: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b> |
| <b>Q9FLM3</b>    | <b>ARATH</b> | <b>NPHNKG-VVDNFKEIF</b>  | <b>YES</b> | <b>Emb CAB87904.1: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>   |
| <b>Q9FYD4</b>    | <b>ARATH</b> | <b>HQFDVG-FYKNLTSVL</b>  | <b>YES</b> | <b>Rec-like protein: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>   |
| <b>Q9LER6</b>    | <b>ARATH</b> | <b>NPYRKG-ILENFKELF</b>  | <b>YES</b> | <b>Putative uncharacterized protein T8M16_250: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>                             |
| <b>Q9LJF4</b>    | <b>ARATH</b> | <b>NPHNKG-VVNNFKETF</b>  | <b>YES</b> | <b>Emb CAB87904.1: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>   |
| <b>Q9LZY3</b>    | <b>ARATH</b> | <b>WRYDLG-KKKNFEQVF</b>  | <b>YES</b> | <b>Putative uncharacterized protein T4C21_210: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>                             |
| <b>Q9M1K5</b>    | <b>ARATH</b> | <b>NPYNKG-ILGNIWEIF</b>  | <b>YES</b> | <b>Putative uncharacterized protein F24I3.10: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>                              |
| <b>Q9SR31</b>    | <b>ARATH</b> | <b>HPYDIG-AYENLTLIL</b>  | <b>YES</b> | <b>F3L24.19 protein: <i>Arabidopsis thaliana</i> (Mouse-ear cross)</b>   |
| A8EVR6           | ARCB4        | RIYSKS-KFINFEQVF         | NO         | Putative sulfatase: <i>Arcobacter butzleri</i> (strain RM4018)   |
| Q74Z33           | ASHGO        | LKYHYG-KNNLWFVC          | NO         | AGR373Cp: <i>Ashbya gossypii</i> (Yeast) ( <i>Eremothecium gossypii</i> )  |
| Q751N9           | ASHGO        | EKYTKG-LSANLSDVF         | NO         | AGL349Cp: <i>Ashbya gossypii</i> (Yeast) ( <i>Eremothecium gossypii</i> )  |
| A1C4Z5           | ASPCL        | NPFDSS-PRQNLDDVF         | NO         | PHD transcription factor: <i>Aspergillus clavatus</i>  |
| A1CAE0           | ASPCL        | NKYDFG-LLQNMTTAI         | NO         | Beige/BEACH domain protein: <i>Aspergillus clavatus</i>  |
| <b>A1CAI4</b>    | <b>ASPCL</b> | <b>NPFDLGSPLKNLQVVM</b>  | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Aspergillus clavatus</i></b>   |
| <b>A1C4B6</b>    | <b>ASPCL</b> | <b>FPYDIG-IWSNIKAGM</b>  | <b>YES</b> | <b>DHHC zinc finger membrane protein: <i>Aspergillus clavatus</i></b>  |
| <b>A1C7X9</b>    | <b>ASPCL</b> | <b>HAFDLG-WRKLLHLF</b>   | <b>YES</b> | <b>DHHC zinc finger domain protein: <i>Aspergillus clavatus</i></b>  |
| <b>A1CJB5</b>    | <b>ASPCL</b> | <b>RPFTQGNVFNWLSVL</b>   | <b>YES</b> | <b>DHHC zinc finger membrane protein, putative: <i>Aspergillus clavatus</i></b>  |

Table S3 Contd.

| Accession number | Organism      | PaCCT motif              | DHHC       | Description   |
|------------------|---------------|--------------------------|------------|---|
| <b>A1CSJ6</b>    | <b>ASPCL</b>  | <b>NPFSRG-VVNNCRDFW</b>  | <b>YES</b> | <b>Palmitoyltransferase: <i>Aspergillus clavatus</i></b>  |
| <b>A1CT46</b>    | <b>ASPCL</b>  | <b>NIYDLG-FGDNLRFDAF</b> | <b>YES</b> | <b>DHHC zinc finger domain protein: <i>Aspergillus clavatus</i></b>   |
| Q4WUP7           | ASPFU         | NKYDFG-LLQNMTTAI         | NO         | Beige/BEACH domain protein: <i>Aspergillus fumigatus</i> (Sartorya fumigata)  |
| <b>A2QMZ5</b>    | <b>ASPNG</b>  | <b>NKYDFG-LLQNMTTVI</b>  | <b>NO</b>  | <b>Putative sequencing error: <i>Aspergillus niger</i></b>  |
| A2QTS1           | ASPNG         | NSFNRG-WIQNIGSGC         | NO         | Function: mok1 plays an essential role for cell morphogenesis. precursor: <i>Aspergillus niger</i>                                  |
| <b>A2QKH1</b>    | <b>ASPNG</b>  | <b>NPFSRG-VVTNCRDFW</b>  | <b>YES</b> | <b>Function: yeast AKR1 affects the kinase cascade downstream of <math>G\beta\gamma</math>: <i>Aspergillus niger</i></b>            |
| <b>A2QN83</b>    | <b>ASPNG</b>  | <b>NPFDLGSRFKNLQQLV</b>  | <b>YES</b> | <b>Similarity to human Gene #6 associated peptide #4 patent WO200107459-A1: <i>Aspergillus niger</i></b>                            |
| <b>A2QVR5</b>    | <b>ASPNG</b>  | <b>NIYDLG-FWDNLRHVL</b>  | <b>YES</b> | <b>Function: the function of CTR86 of <i>S. cerevisiae</i> is not yet clear: <i>Aspergillus niger</i></b>                           |
| <b>A2R5L1</b>    | <b>ASPNG</b>  | <b>FPYDIG-IWSNIKAGM</b>  | <b>YES</b> | <b>Similarity: shows only partial similarity to patented protein. precursor: <i>Aspergillus niger</i></b>                           |
| <b>A2R676</b>    | <b>ASPNG</b>  | <b>HAFDLG-WRRNLRHLF</b>  | <b>YES</b> | <b>Remark: the predicted <i>A. niger</i> protein harbours a DHHC region PF0152: <i>Aspergillus niger</i></b>                        |
| <b>A5ABN6</b>    | <b>ASPNG</b>  | <b>RPFTQGSVFRNWLVSF</b>  | <b>YES</b> | <b>Similarity to hypothetical protein SPBC3H7.09: <i>Schizosaccharomyces pombe</i> - <i>Aspergillus niger</i></b>                   |
| Q2TYJ0           | ASPOR         | VPHTRG-FLRNLEQTC         | NO         | Polyketide synthase modules and related proteins: <i>Aspergillus oryzae</i>   |
| Q2U427           | ASPOR         | NKYDFG-VLQNMTTAI         | NO         | Lysosomal trafficking regulator LYST and related BEACH and WD40 repeat proteins: <i>Aspergillus oryzae</i>                          |
| Q2UA43           | ASPOR         | NPFDSS-PRQNLDDVF         | NO         | DNA-binding protein jumonji/RBP2/SMCY: <i>Aspergillus oryzae</i>  |
| <b>Q2UM04</b>    | <b>ASPOR</b>  | <b>NIYDLG-FWDNLRHSF</b>  | <b>NO</b>  | <b>Predicted protein: <i>Aspergillus oryzae</i></b>   |
| <b>Q2U527</b>    | <b>ASPOR</b>  | <b>RPFTQGNILKNWISVF</b>  | <b>YES</b> | <b>DHHC-type Zn-finger proteins: <i>Aspergillus oryzae</i></b>  |
| <b>Q2UAW3</b>    | <b>ASPOR</b>  | <b>NAFDHG-WRRNLRHLF</b>  | <b>YES</b> | <b>Predicted DHHC-type Zn-finger protein: <i>Aspergillus oryzae</i></b>   |
| <b>Q0CEW4</b>    | <b>ASPTN</b>  | <b>FPYDIG-IWSNIKAGM</b>  | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Aspergillus terreus</i> (strain NIH 2624)</b>   |
| Q0CHX9           | ASPTN         | GRYDKG-LRANLFSHL         | NO         | Predicted protein: <i>Aspergillus terreus</i> (strain NIH 2624)   |
| Q0CID9           | ASPTN         | NKYDFG-FLQNMTTAI         | NO         | Putative uncharacterized protein: <i>Aspergillus terreus</i> (strain NIH 2624)  |
| <b>Q0CC07</b>    | <b>ASPTN</b>  | <b>RPFTQGNIFRNLSVL</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Aspergillus terreus</i> (strain NIH 2624)</b>   |
| <b>Q0CHG4</b>    | <b>ASPTN</b>  | <b>NPWSRG-VVTNCRDFW</b>  | <b>YES</b> | <b>Palmitoyltransferase akr1: <i>Aspergillus terreus</i> (strain NIH 2624)</b>  |
| <b>Q0CI91</b>    | <b>ASPTN</b>  | <b>NPFDLGSPLKNLQQVM</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Aspergillus terreus</i> (strain NIH 2624)</b>   |
| <b>Q0CK72</b>    | <b>ASPTN</b>  | <b>NIYDLG-FWNLRHAF</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Aspergillus terreus</i> (strain NIH 2624)</b>   |
| <b>Q0CVJ2</b>    | <b>ASPTN</b>  | <b>NAFDLG-WKKNLHLF</b>   | <b>YES</b> | <b>Palmitoyltransferase PFA3: <i>Aspergillus terreus</i> (strain NIH 2624)</b>  |
| <b>A7AT89</b>    | <b>BABBO</b>  | <b>GIYDMG-VGANLQQVF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Babesia bovis</i></b>   |
| <b>A7AT17</b>    | <b>BABBO</b>  | <b>NPWDRG-ILINLKDAL</b>  | <b>YES</b> | <b>DHHC zinc-finger-domain-containing protein: <i>Babesia bovis</i></b>   |
| Q72X29           | BACCI         | SRYDLS-ILKNISEFI         | NO         | Glycosyl transferase, group 1 family protein: <i>Bacillus cereus</i> (strain ATCC 10987)  |
| Q812U8           | BACCR         | NIYFEG-WFNLYLII          | NO         | Hypothetical membrane spanning protein: <i>Bacillus cereus</i> (strain ATCC 14579 / DSM 31)   |
| Q814K9           | BACCR         | SRYDLS-ILKNISEFI         | NO         | Glycosyltransferase: <i>Bacillus cereus</i> (strain ATCC 14579 / DSM 31)  |
| <b>Q63CQ7</b>    | <b>BACCCZ</b> | <b>SRFDKK-FIENLAQVF</b>  | <b>NO</b>  | <b>Multifunctional nonribosomal peptide synthetase: <i>Bacillus cereus</i> (strain ZK / E33L)</b>                                   |
| Q65FC0           | BACLD         | FPYYLG-LTENAIQYL         | NO         | YutH: <i>Bacillus licheniformis</i> (strain DSM 13 / ATCC 14580)  |
| A8FH28           | BACP2         | FPYYLG-LTENAIQYL         | NO         | Spore coat protein S: <i>Bacillus pumilus</i> (strain SAFR-032)   |
| Q32123           | BACSU         | FPYYLG-LSENAIQYL         | NO         | YutH protein: <i>Bacillus subtilis</i>  |
| Q3EQD1           | BACTI         | VRHNLG-WLYNIQDLF         | NO         | Response regulator aspartate phosphatase: <i>Bacillus thuringiensis</i> serovar israelensis ATCC 35646                              |
| Q3EW80           | BACTI         | NIYFEG-WFNLYLII          | NO         | Hypothetical membrane spanning protein: <i>Bacillus thuringiensis</i> serovar israelensis ATCC 35646                                |
| A1USA9           | BARBK         | DIYDIG-TFANILQLL         | NO         | ATP-dependent protease La: <i>Bartonella bacilliformis</i> (strain ATCC 35685 / KC583)  |
| Q6G3Z1           | BARHE         | DIYDIG-TFANILQLL         | NO         | ATP-dependent protease La: <i>Bartonella henselae</i> ( <i>Rochalimaea henselae</i> )   |
| Q6GWG0           | BARHE         | DIYDIG-TFANILQLL         | NO         | ATP-dependent protease La: <i>Bartonella henselae</i> ( <i>Rochalimaea henselae</i> )   |
| Q6G176           | BARQU         | DIYDIG-TFANILQLL         | NO         | ATP-dependent protease La: <i>Bartonella quintana</i> ( <i>Rochalimaea quintana</i> )   |
| Q616M8           | BOMMO         | QRWNLK-VWRNFKQSV         | NO         | Cytochrome P450: <i>Bombyx mori</i> (Silk moth)   |
| Q0SM57           | BORAP         | NIYDIK-VKRNKKEFL         | NO         | Putative uncharacterized protein: <i>Borrelia afzelii</i> (strain PKo)  |
| Q660N9           | BORGA         | NYDKGHLRANIKLLA          | NO         | Exodeoxyribonuclease V, $\alpha$ chain: <i>Borrelia garinii</i>   |
| A6RU82           | BOTFB         | TPFDGS-FSSNITSTC         | NO         | Putative uncharacterized protein: <i>Botryotinia fuckeliana</i> (strain B05.10) (Noble rot fungus) ( <i>Botrytis cinerea</i> )      |
| A6S9R6           | BOTFB         | HPFHIG-TCSNIFQFA         | NO         | Predicted protein: <i>Botryotinia fuckeliana</i> (strain B05.10) (Noble rot fungus) ( <i>Botrytis cinerea</i> )                     |
| <b>A6SJL5</b>    | <b>BOTFB</b>  | <b>RPFTQGSFISNWI AVL</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Botryotinia fuckeliana</i> (strain B05.10) (Noble rot fungus) (<i>Botrytis cinerea</i>)</b> |
| <b>A6SP75</b>    | <b>BOTFB</b>  | <b>NLYDIG-FLDNLKDFV</b>  | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Botryotinia fuckeliana</i> (strain B05.10) (Noble rot fungus) (<i>Botrytis cinerea</i>)</b> |
| <b>A6S421</b>    | <b>BOTFB</b>  | <b>NPWDLGSALLNWETVM</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Botryotinia fuckeliana</i> (strain B05.10) (Noble rot fungus) (<i>Botrytis cinerea</i>)</b> |
| <b>A6S8Q1</b>    | <b>BOTFB</b>  | <b>SAFDLG-WRRNFKHLF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Botryotinia fuckeliana</i> (strain B05.10) (Noble rot fungus) (<i>Botrytis cinerea</i>)</b> |
| <b>A6SDD2</b>    | <b>BOTFB</b>  | <b>NPFSRG-CIVNCKDFW</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Botryotinia fuckeliana</i> (strain B05.10) (Noble rot fungus) (<i>Botrytis cinerea</i>)</b> |
| <b>A6SED4</b>    | <b>BOTFB</b>  | <b>FPFDIG-IWENIVQAM</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Botryotinia fuckeliana</i> (strain B05.10) (Noble rot fungus) (<i>Botrytis cinerea</i>)</b> |
| <b>A6QNK5</b>    | <b>BOVIN</b>  | <b>TPYNLG-FTQNLADFF</b>  | <b>YES</b> | <b>LOC514176 protein: <i>Bos taurus</i> (Bovine)</b>  |
| <b>Q2KIP1</b>    | <b>BOVIN</b>  | <b>NPFDHG-CASNWYLT I</b> | <b>YES</b> | <b>Similar to zinc finger, DHHC-domain-containing 19: <i>Bos taurus</i> (bovine)</b>  |
| Q89TW4           | BRAJA         | RRYDRG-FCINVL SVI        | NO         | Blr1659 protein: <i>Bradyrhizobium japonicum</i>  |
| <b>A8P3W8</b>    | <b>BRUMA</b>  | <b>HAYNLG-FMENVRQAM</b>  | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Brugia malayi</i> (Filarial nematode worm)</b>  |
| <b>A8PIX7</b>    | <b>BRUMA</b>  | <b>NPYNTGSVFSNCLRTL</b>  | <b>YES</b> | <b>Tim44-like domain containing protein: <i>Brugia malayi</i> (Filarial nematode worm)</b>  |
| <b>A8Q2D7</b>    | <b>BRUMA</b>  | <b>NPFTVG-CWGNVRRTL</b>  | <b>YES</b> | <b>Zinc finger DHHC domain containing protein 5, putative: <i>Brugia malayi</i> (Filarial nematode worm)</b>                        |
| <b>A8Q9Y7</b>    | <b>BRUMA</b>  | <b>NGFNLG-IRRNFKQVF</b>  | <b>YES</b> | <b>Zinc finger DHHC domain containing protein 2, putative: <i>Brugia malayi</i> (Filarial nematode worm)</b>                        |
| Q058E9           | BUCCC         | NIFYKYFIENFYNI F         | NO         | Signal recognition particle receptor: <i>Buchnera aphidicola</i> subsp. <i>Cinara cedri</i>   |
| A3MKJ6           | BURM7         | DMYDVG-CIANILQML         | NO         | ATP-dependent protease La: <i>Burkholderia mallei</i> (strain NCTC 10247)   |
| A3MQR2           | BURM7         | NRYNRESISQNL SAVL        | NO         | Putative methyl-accepting chemotaxis protein: <i>Burkholderia mallei</i> (strain NCTC 10247)  |

Table S3 Contd.

| Accession number | Organism     | PaCCT motif              | DHHC       | Description   |
|------------------|--------------|--------------------------|------------|---|
| A2S6Q9           | BURM9        | NRYNRESISQNL SAVL        | NO         | Putative methyl-accepting chemotaxis protein: <i>Burkholderia mallei</i> (strain NCTC 10229)  |
| A2SBG5           | BURM9        | DMYDVG-CIANILQML         | NO         | ATP-dependent protease La: <i>Burkholderia mallei</i> (strain NCTC 10229)   |
| A5J5I6           | BURMA        | NRYNRESISQNL SAVL        | NO         | Putative methyl-accepting chemotaxis protein: <i>Burkholderia mallei</i> FMH  |
| A5THD7           | BURMA        | NRYNRESISQNL SAVL        | NO         | Putative methyl-accepting chemotaxis protein: <i>Burkholderia mallei</i> 2002721280   |
| A5TKC3           | BURMA        | DMYDVG-CIANILQML         | NO         | ATP-dependent protease La: <i>Burkholderia mallei</i> 2002721280  |
| A5XGP4           | BURMA        | DMYDVG-CIANILQML         | NO         | ATP-dependent protease La: <i>Burkholderia mallei</i> FMH   |
| A5XQA7           | BURMA        | DMYDVG-CIANILQML         | NO         | ATP-dependent protease La: <i>Burkholderia mallei</i> JHU   |
| A5XRH8           | BURMA        | NRYNRESISQNL SAVL        | NO         | Putative methyl-accepting chemotaxis protein: <i>Burkholderia mallei</i> JHU  |
| A9K187           | BURMA        | NRYNRESISQNL SAVL        | NO         | Putative methyl-accepting chemotaxis protein: <i>Burkholderia mallei</i> ATCC 10399   |
| A9K8W3           | BURMA        | DMYDVG-CIANILQML         | NO         | ATP-dependent protease La: <i>Burkholderia mallei</i> ATCC 10399  |
| Q62FX6           | BURMA        | NRYNRESISQNL SAVL        | NO         | Methyl-accepting chemotaxis protein, putative: <i>Burkholderia mallei</i> ( <i>Pseudomonas mallei</i> )                                   |
| Q62JK9           | BURMA        | DMYDVG-CIANILQML         | NO         | ATP-dependent protease La: <i>Burkholderia mallei</i> ( <i>Pseudomonas mallei</i> )   |
| A1V4W9           | BURMS        | DMYDVG-CIANILQML         | NO         | ATP-dependent protease La: <i>Burkholderia mallei</i> (strain SAVP1)  |
| A1V946           | BURMS        | NRYNRESISQNL SAVL        | NO         | Putative methyl-accepting chemotaxis protein: <i>Burkholderia mallei</i> (strain SAVP1)   |
| A3NWA4           | BURPO        | DMYDVG-CIANILQML         | NO         | ATP-dependent protease La: <i>Burkholderia pseudomallei</i> (strain 1106a)  |
| A3POS4           | BURPO        | NRYNRESISQNL SAVL        | NO         | Methyl-accepting chemotaxis protein: <i>Burkholderia pseudomallei</i> (strain 1106a)  |
| Q3JRD2           | BURP1        | DMYDVG-CIANILQML         | NO         | ATP-dependent protease La: <i>Burkholderia pseudomallei</i> (strain 1710b)  |
| Q3JY24           | BURP1        | NRYNRESISQNL SAVL        | NO         | Putative methyl-accepting chemotaxis protein: <i>Burkholderia pseudomallei</i> (strain 1710b)   |
| A3NAI3           | BURP6        | DMYDVG-CIANILQML         | NO         | ATP-dependent protease La: <i>Burkholderia pseudomallei</i> (strain 668)  |
| A3NEW7           | BURP6        | NRYNRESISQNL SAVL        | NO         | Methyl-accepting chemotaxis protein: <i>Burkholderia pseudomallei</i> (strain 668)  |
| A4LCI4           | BURPS        | DMYDVG-CIANILQML         | NO         | ATP-dependent protease La: <i>Burkholderia pseudomallei</i> 305   |
| A4LN32           | BURPS        | NRYNRESISQNL SAVL        | NO         | Methyl-accepting chemotaxis protein: <i>Burkholderia pseudomallei</i> 305   |
| A8EC56           | BURPS        | DMYDVG-CIANILQML         | NO         | ATP-dependent protease La: <i>Burkholderia pseudomallei</i> 406e  |
| A8KF51           | BURPS        | NRYNRESISQNL SAVL        | NO         | Methyl-accepting chemotaxis protein: <i>Burkholderia pseudomallei</i> Pasteur 52237   |
| A8KL52           | BURPS        | DMYDVG-CIANILQML         | NO         | ATP-dependent protease La: <i>Burkholderia pseudomallei</i> Pasteur 52237   |
| Q63PN5           | BURPS        | NRYNRESISQNL SAVL        | NO         | Putative methyl-accepting chemotaxis protein: <i>Burkholderia pseudomallei</i> ( <i>Pseudomonas pseudomallei</i> )                        |
| Q63V39           | BURPS        | DMYDVG-CIANILQML         | NO         | ATP-dependent protease La: <i>Burkholderia pseudomallei</i> ( <i>Pseudomonas pseudomallei</i> )   |
| Q39DD5           | BURS3        | NKYGRG-FIANISVLL         | NO         | Xanthine/uracil transporter: <i>Burkholderia</i> sp. (strain 383) [ <i>Burkholderia cepacia</i> (strain ATCC 17760 / NCIB 9086 / R18194)] |
| Q2STP6           | BURTA        | NRYNRESISQNL SAVL        | NO         | Methyl-accepting chemotaxis protein, putative: <i>Burkholderia thailandensis</i> (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)     |
| Q2SWQ4           | BURTA        | DMYDVG-CIANILQML         | NO         | ATP-dependent protease La: <i>Burkholderia thailandensis</i> (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)                         |
| A4JHF8           | BURVG        | NKYGRG-FIANISVLL         | NO         | Uracil-xanthine permease: <i>Burkholderia vietnamiensis</i> (strain G4 / LMG 22486) [ <i>Burkholderia cepacia</i> (strain R1808)]         |
| Q13RC9           | BURXL        | HEYKNG-VAKNIHLVC         | NO         | ATPase: <i>Burkholderia xenovorans</i> (strain LB400)   |
| A8WTY5           | CAEBR        | YKYHLG-PYQNVCEII         | NO         | Putative uncharacterized protein: <i>Caenorhabditis briggsae</i>  |
| A8X4K4           | CAEBR        | SPYDQS-AMNFNHSHF         | NO         | Putative uncharacterized protein: <i>Caenorhabditis briggsae</i>  |
| A8XJA1           | CAEBR        | DPVYLGYCLINICLAF         | NO         | Putative uncharacterized protein: <i>Caenorhabditis briggsae</i>  |
| A8WS09           | CAEBR        | NRLNKG-FKSNWKNFL         | YES        | Putative uncharacterized protein: <i>Caenorhabditis briggsae</i>  |
| <b>A8X0K6</b>    | <b>CAEBR</b> | <b>YPYDLG-WKRNLSVFF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Caenorhabditis briggsae</i></b>   |
| A8X4E7           | CAEBR        | HAYQLG-FVENLRQAL         | YES        | Putative uncharacterized protein: <i>Caenorhabditis briggsae</i>  |
| A8X8M8           | CAEBR        | ADYNMG-KWNNFRAVF         | YES        | Putative uncharacterized protein: <i>Caenorhabditis briggsae</i>  |
| <b>A8XA15</b>    | <b>CAEBR</b> | <b>DAFNHG-IRANYREIF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Caenorhabditis briggsae</i></b>   |
| A8XMV5           | CAEBR        | NPFYMG-CFKSFASRL         | YES        | Putative uncharacterized protein: <i>Caenorhabditis briggsae</i>  |
| <b>A8XS33</b>    | <b>CAEBR</b> | <b>TTYDLGSGWQENVKSVM</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Caenorhabditis briggsae</i></b>   |
| Q44496           | CAEEL        | HPHNLHFKNKFEFL           | NO         | Putative uncharacterized protein: <i>Caenorhabditis elegans</i>   |
| Q62256           | CAEEL        | NYYNKG-VAENICFCF         | NO         | Putative uncharacterized protein: <i>Caenorhabditis elegans</i>   |
| Q10463           | CAEEL        | YKYHLG-PYQNVMMVI         | NO         | Transbilayer amphipath transporters: <i>Caenorhabditis elegans</i>  |
| Q7JPE4           | CAEEL        | YKYHLG-PYQNVMMVI         | NO         | Transbilayer amphipath transporters: <i>Caenorhabditis elegans</i>  |
| <b>Q17549</b>    | <b>CAEEL</b> | <b>YPYDLG-WKRNLSREV</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Caenorhabditis elegans</i></b>  |
| <b>Q21981</b>    | <b>CAEEL</b> | <b>TSYNLGSWQENVKSVM</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Caenorhabditis elegans</i></b>  |
| Q5FC64           | CAEEL        | ADYNMG-KYNNFQSVF         | YES        | Putative uncharacterized protein spe-10: <i>Caenorhabditis elegans</i>  |
| <b>Q65ZC4</b>    | <b>CAEEL</b> | <b>DAFNHG-IRANYREIF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Caenorhabditis elegans</i></b>  |
| <b>Q9U2K0</b>    | <b>CAEEL</b> | <b>NPFTIG-CWGNCCKTL</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Caenorhabditis elegans</i></b>  |
| <b>A6MKE4</b>    | <b>CALJA</b> | <b>NPYNYG-CLDNWKVFL</b>  | <b>NO</b>  | <b>Palmitoyltransferase ZDHHC16-like protein: <i>Callithrix jacchus</i> (Common marmoset)</b>   |
| <b>A6ML31</b>    | <b>CALJA</b> | <b>NPYNYG-CLDNWKVFL</b>  | <b>NO</b>  | <b>Palmitoyltransferase ZDHHC16-like protein: <i>Callithrix jacchus</i> (Common marmoset)</b>   |
| A4XIV2           | CALS8        | QYFDNG-SLKNFVLVM         | NO         | Putative uncharacterized protein precursor: <i>Caldicellulosiruptor saccharolyticus</i> (strain ATCC 43494 / DSM 8903)                    |
| <b>A4XKU3</b>    | <b>CALS8</b> | <b>SDYSKG-LFKNFKQTF</b>  | <b>NO</b>  | <b>Extracellular ligand-binding receptor precursor: <i>Caldicellulosiruptor saccharolyticus</i> (strain ATCC 43494 / DSM 8903)</b>        |
| <b>A4XM95</b>    | <b>CALS8</b> | <b>SDYSKG-LYKNFKETF</b>  | <b>NO</b>  | <b>Extracellular ligand-binding receptor precursor: <i>Caldicellulosiruptor saccharolyticus</i> (strain ATCC 43494 / DSM 8903)</b>        |
| A7H0L4           | CAMC5        | NHYELG-YQRNFSDTL         | NO         | TonB-dependent outer membrane receptor: <i>Campylobacter curvus</i> (strain 525.92)   |
| A0RPM3           | CAMFF        | NFYNYG-VLSNLYIYF         | NO         | Type I restriction-modification system, S subunit: <i>Campylobacter fetus</i> subsp. fetus (strain 82-40)                                 |
| A8FK61           | CAMJ8        | NAFFKN-KWKNFEDFL         | NO         | Putative uncharacterized protein: <i>Campylobacter jejuni</i> subsp. jejuni serotype O:6 (strain 81116 / NCTC 11828)                      |
| A7H599           | CAMJD        | NAFFKN-KWKNFEDFL         | NO         | Putative uncharacterized protein: <i>Campylobacter jejuni</i> subsp. doylei (strain ATCC BAA-1458 / RM4099 / 269.97)                      |
| A3YK98           | CAMJE        | NAFFKN-KWKNFEDFL         | NO         | Putative uncharacterized protein: <i>Campylobacter jejuni</i> subsp. jejuni CF93-6  |
| A3YLH3           | CAMJE        | FAFDKN-KQKNIEIF          | NO         | CjaC protein: <i>Campylobacter jejuni</i> subsp. jejuni CF93-6  |
| A3YQK3           | CAMJE        | NAFFKN-KWKNFEDFL         | NO         | Putative uncharacterized protein: <i>Campylobacter jejuni</i> subsp. jejuni 260.94  |
| A3ZD72           | CAMJE        | FAFDKN-KQKNIEIF          | NO         | Histidine-binding protein: <i>Campylobacter jejuni</i> subsp. jejuni HB93-13  |

Table S3 Contd.

| Accession number | Organism     | PaCCT motif               | DHHC       | Description  |
|------------------|--------------|---------------------------|------------|--|
| A3ZEW7           | CAMJE        | NAFFKN-KWKNFEDFL          | NO         | Putative uncharacterized protein: <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> HB93-13   |
| A3ZIA3           | CAMJE        | FAFDKN-KQKNIEIF           | NO         | CjaC protein: <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> 84-25   |
| A3ZJL3           | CAMJE        | NAFFKN-KWKNFEDFL          | NO         | Putative uncharacterized protein: <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> 84-25   |
| Q0PBN3           | CAMJE        | NAFFKN-KWKNFEDFL          | NO         | Putative uncharacterized protein: <i>Campylobacter jejuni</i>  |
| A1VXZ6           | CAMJJ        | NAFFKN-KWKNFEDFL          | NO         | Putative uncharacterized protein: <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> serotype O:23/36 (strain 81-176)                                |
| Q5HWJ4           | CAMJR        | NAFFKN-KWKNFEDFL          | NO         | Putative uncharacterized protein: <i>Campylobacter jejuni</i> (strain RM1221)  |
| Q5A5A3           | CANAL        | SPFKNGYLGENLKHVF          | NO         | Hypothetical LPF family protein 36: <i>Candida albicans</i> (Yeast)  |
| Q5APB7           | CANAL        | PPFDYN-IWKNINSTM          | NO         | Potential dsRNA virus protection family member: <i>Candida albicans</i> (Yeast)  |
| <b>Q3MPJ2</b>    | <b>CANAL</b> | <b>FPYNLG-IWKNLVNAL</b>   | <b>YES</b> | <b>Putative uncharacterized protein CaJ7.0163: <i>Candida albicans</i> (Yeast)</b>   |
| <b>Q6FIU8</b>    | <b>CANGA</b> | <b>SKYTIG-RLKNIKSVL</b>   | <b>NO</b>  | <b>Similar to Q12019 <i>Saccharomyces cerevisiae</i> YLR106c: <i>Candida glabrata</i> (Yeast) (<i>Torulopsis glabrata</i>)</b>                     |
| Q05FR2           | CARRP        | NGYNLG-NKINIWFL           | NO         | 2-isopropylmalate synthase: <i>Carsonella ruddii</i> (strain PV)   |
| <b>Q2H406</b>    | <b>CHAGB</b> | <b>NPWNLG-YRNRWKSVM</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Chaetomium globosum</i> (Soil fungus)</b>  |
| Q2H483           | CHAGB        | RAFTQGSWFRNWVFL           | YES        | Putative uncharacterized protein: <i>Chaetomium globosum</i> (Soil fungus)   |
| <b>Q2H8L8</b>    | <b>CHAGB</b> | <b>NPFSGK-CLANCKDFW</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Chaetomium globosum</i> (Soil fungus)</b>  |
| <b>Q2HB24</b>    | <b>CHAGB</b> | <b>CHAGB</b>              | <b>YES</b> | <b>Putative uncharacterized protein: <i>Chaetomium globosum</i> (Soil fungus)</b>  |
| <b>Q2THW3</b>    | <b>CHICK</b> | <b>NPFTRG-CCGNVEHVL</b>   | <b>YES</b> | <b>Membrane-associated DHHC8 zinc finger protein: <i>Gallus gallus</i> (Chicken)</b>   |
| <b>Q2THW4</b>    | <b>CHICK</b> | <b>NPFTNG-CCKNVSRLV</b>   | <b>YES</b> | <b>Membrane-associated DHHC5a zinc finger protein: <i>Gallus gallus</i> (Chicken)</b>  |
| <b>Q2THW5</b>    | <b>CHICK</b> | <b>NPFTNG-CCKNVSRLV</b>   | <b>YES</b> | <b>Membrane-associated DHHC5 zinc finger protein: <i>Gallus gallus</i> (Chicken)</b>   |
| Q5F493           | CHICK        | GQYNRG-LGKINWGHFL         | YES        | Putative uncharacterized protein: <i>Gallus gallus</i> (Chicken)   |
| <b>Q5ZHL4</b>    | <b>CHICK</b> | <b>NPYNLG-CFQNLADFF</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Gallus gallus</i> (Chicken)</b>  |
| <b>Q5ZIM1</b>    | <b>CHICK</b> | <b>SPFNHG-CIRNIIDFF</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Gallus gallus</i> (Chicken)</b>  |
| A8I2S6           | CHLRE        | HPYYLG-IFNNLQAAT          | NO         | Amino acid transporter: <i>Chlamydomonas reinhardtii</i> ( <i>Chlamydomonas smithii</i> )  |
| A8INT6           | CHLRE        | SYYSYG-WSKNLRKLF          | NO         | Predicted protein: <i>Chlamydomonas reinhardtii</i> ( <i>Chlamydomonas smithii</i> )   |
| <b>A8IHK2</b>    | <b>CHLRE</b> | <b>NRFDRG-VLSNCFWF</b>    | <b>YES</b> | <b>Transient receptor potential ion channel protein: <i>Chlamydomonas reinhardtii</i> (<i>Chlamydomonas smithii</i>)</b>                           |
| <b>A8IX50</b>    | <b>CHLRE</b> | <b>NPYHLG-AVANWQETF</b>   | <b>YES</b> | <b>Predicted protein: <i>Chlamydomonas reinhardtii</i> (<i>Chlamydomonas smithii</i>)</b>  |
| <b>A8JXC6</b>    | <b>CHLRE</b> | <b>NPYDRG-VLLNCAEVW</b>   | <b>YES</b> | <b>Predicted protein: <i>Chlamydomonas reinhardtii</i> (<i>Chlamydomonas smithii</i>)</b>  |
| Q7NQ38           | CHRVO        | SPFTQGTWMANWTLFY          | NO         | High-affinity choline transport protein: <i>Chromobacterium violaceum</i>  |
| Q1A7G2           | CICAR        | RSFNYSFLANIREIC           | NO         | NBS-LRR type disease resistance protein: <i>Cicer arietinum</i> (Chickpea) (Garbanzo)  |
| Q9M6M8           | CICAR        | RSFNYSFLANIREIC           | NO         | Putative uncharacterized protein: <i>Cicer arietinum</i> (Chickpea) (Garbanzo)   |
| <b>Q1RL35</b>    | <b>CIOIN</b> | <b>YPYNLG-KLKNILEVL</b>   | <b>YES</b> | <b>Zinc finger protein: <i>Ciona intestinalis</i> (Transparent sea squirt)</b>   |
| <b>Q1RL41</b>    | <b>CIOIN</b> | <b>SPYNFG-FIQNWKIIL</b>   | <b>YES</b> | <b>Zinc finger protein: <i>Ciona intestinalis</i> (Transparent sea squirt)</b>   |
| <b>Q1RPU7</b>    | <b>CIOIN</b> | <b>SPFNRG-VVANFADFF</b>   | <b>YES</b> | <b>Zinc finger protein: <i>Ciona intestinalis</i> (Transparent sea squirt)</b>   |
| <b>Q1RPW1</b>    | <b>CIOIN</b> | <b>NGFNLG-PRRNFEQVF</b>   | <b>YES</b> | <b>Zinc finger protein: <i>Ciona intestinalis</i> (Transparent sea squirt)</b>   |
| A6M2W9           | CLOB8        | YGHVVG-YWKNIVSAL          | NO         | Xylose isomerase domain protein TIM barrel: <i>Clostridium beijerinckii</i> (strain ATCC 51743 / NCIMB 8052) ( <i>Clostridium acetobutylicum</i> ) |
| Q184H0           | CLOD6        | SIYDYK-LKSNVLDLL          | NO         | Putative uncharacterized protein: <i>Clostridium difficile</i> (strain 630)  |
| A5N2J5           | CLOK5        | HPYGHG-KFENVSGVL          | NO         | Putative uncharacterized protein: <i>Clostridium kluyveri</i> (strain ATCC 8527 / DSM 555 / NCIMB 10680)   |
| A5N4M3           | CLOK5        | NHTHTGSLCDNCRDVI          | NO         | Putative uncharacterized protein: <i>Clostridium kluyveri</i> (strain ATCC 8527 / DSM 555 / NCIMB 10680)   |
| A0Q2K8           | CLONN        | EYNIIG-TICNIKQVL          | NO         | ATP-dependent protease La: <i>Clostridium novyi</i> (strain NT)  |
| A9KSR4           | CLOPH        | LPYSSG-LKRNIVQCL          | NO         | FAD-dependent pyridine nucleotide-disulfide oxidoreductase: <i>Clostridium phytofermentans</i> (strain ATCC 700394 / DSM 18823 / ISDg)             |
| <b>Q1DSN9</b>    | <b>COCIM</b> | <b>NKYDFG-LRQNMQTQAI</b>  | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Coccidioides immitis</i></b>   |
| <b>Q1E820</b>    | <b>COCIM</b> | <b>NIYDRG-LVWVNLFDLSL</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Coccidioides immitis</i></b>   |
| <b>Q1DJM3</b>    | <b>COCIM</b> | <b>NAFDLG-WRRNLTDLF</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Coccidioides immitis</i></b>   |
| <b>Q1DLN9</b>    | <b>COCIM</b> | <b>FPFDIG-IWENIQAGM</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Coccidioides immitis</i></b>   |
| <b>Q1DSF4</b>    | <b>COCIM</b> | <b>NPFDLGSPLANLKEVM</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Coccidioides immitis</i></b>   |
| <b>Q1E919</b>    | <b>COCIM</b> | <b>NPFSRG-IVTNCRDFW</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Coccidioides immitis</i></b>   |
| <b>Q1EAH3</b>    | <b>COCIM</b> | <b>RPFTQGNFLKNWIAVL</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Coccidioides immitis</i></b>   |
| <b>A8N1R6</b>    | <b>COPCI</b> | <b>YIYDIG-WRKNWAQAL</b>   | <b>NO</b>  | <b>Predicted protein: <i>Coprinopsis cinerea</i> okayama7#130</b>  |
| <b>A8N9B9</b>    | <b>COPCI</b> | <b>RLYDLG-RAQNWRFLW</b>   | <b>NO</b>  | <b>Predicted protein: <i>Coprinopsis cinerea</i> okayama7#130</b>  |
| <b>A8NLZ3</b>    | <b>COPCI</b> | <b>APWNLGSVCQSWRKVL</b>   | <b>NO</b>  | <b>Predicted protein: <i>Coprinopsis cinerea</i> okayama7#130</b>  |
| A8NVE1           | COPCI        | NPFTRS-YLVNWTTL           | NO         | Putative uncharacterized protein: <i>Coprinopsis cinerea</i> okayama7#130  |
| <b>A8N304</b>    | <b>COPCI</b> | <b>FPYDLG-RMRNIKAVL</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Coprinopsis cinerea</i> okayama7#130</b>   |
| <b>A8NI74</b>    | <b>COPCI</b> | <b>NPFDLG-VVSNCKDFW</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Coprinopsis cinerea</i> okayama7#130</b>   |
| Q4BZC9           | CROWT        | HFWDNQ-VWENLQAC           | NO         | Putative uncharacterized protein: <i>Crocospaera watsonii</i>  |
| Q4C365           | CROWT        | EVVYQG-VKFNFRQFF          | NO         | Putative uncharacterized protein: <i>Crocospaera watsonii</i>  |
| Q5CMH5           | CRYHO        | FKFSFG-LYSNFIHFC          | NO         | Putative uncharacterized protein: <i>Cryptosporidium hominis</i>   |
| Q5CH57           | CRYHO        | NMWFKG-YMHFSKQVF          | YES        | Cell cycle regulator with zn-finger domain: <i>Cryptosporidium hominis</i>   |
| Q5CJF6           | CRYHO        | SPFSKG-HIYNMAIFC          | YES        | OSJNBa0084K11.19: <i>Cryptosporidium hominis</i>   |
| <b>Q5CLZ2</b>    | <b>CRYHO</b> | <b>GRYDLG-PERNIQQAF</b>   | <b>YES</b> | <b>DHHC zinc finger multi-pass transmembrane protein: <i>Cryptosporidium hominis</i></b>   |
| <b>Q5CN44</b>    | <b>CRYHO</b> | <b>NRFDKG-LSNNIREIM</b>   | <b>YES</b> | <b>FLJ31812: <i>Cryptosporidium hominis</i></b>  |
| <b>Q5CP39</b>    | <b>CRYHO</b> | <b>NPWYSG-ISRNIAELF</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Cryptosporidium hominis</i></b>  |
| <b>Q55MZ4</b>    | <b>CRYNE</b> | <b>RPYDHG-PRMNTQLVL</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Cryptococcus neoformans</i> (<i>Filobasidiella neoformans</i>)</b>   |
| <b>Q55SW2</b>    | <b>CRYNE</b> | <b>NPYDLG-RRRNQLLFF</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Cryptococcus neoformans</i> (<i>Filobasidiella neoformans</i>)</b>   |
| <b>Q5KBC3</b>    | <b>CRYNE</b> | <b>RPYDHG-PRMNTQLVL</b>   | <b>YES</b> | <b>Expressed protein: <i>Cryptococcus neoformans</i> (<i>Filobasidiella neoformans</i>)</b>  |
| <b>Q5KH96</b>    | <b>CRYNE</b> | <b>NPYDLG-RRRNQLLFF</b>   | <b>YES</b> | <b>Vacuole protein, putative: <i>Cryptococcus neoformans</i> (<i>Filobasidiella neoformans</i>)</b>  |
| <b>Q5KHI1</b>    | <b>CRYNE</b> | <b>NVYDLG-WRRNLKQVF</b>   | <b>YES</b> | <b>Vacuole protein, putative: <i>Cryptococcus neoformans</i> (<i>Filobasidiella neoformans</i>)</b>  |
| Q5CY32           | CRYPV        | FKFSFG-LYSNFIHFC          | NO         | Putative uncharacterized protein: <i>Cryptosporidium parvum</i> Iowa II  |
| Q5CST7           | CRYPV        | NMWFKG-YMHFSKQVF          | YES        | DHHC family palmitoyl transferases with a signal peptide and 4×transmembrane domains: <i>Cryptosporidium parvum</i> Iowa II                        |



Table S3 Contd.

| Accession number | Organism     | PaCCT motif             | DHHC       | Description  |
|------------------|--------------|-------------------------|------------|--|
| Q5CVB2           | CRYPV        | SPFSKG-HIYNMAIFC        | YES        | DHHC family palmitoyl transferase with a signal peptide and 4 transmembrane domains: <i>Cryptosporidium parvum</i> Iowa II                   |
| <b>Q5CWL9</b>    | <b>CRYPV</b> | <b>GRYDLG-PERNIQQAF</b> | <b>YES</b> | <b>DHHC family palmitoyl transferase: <i>Cryptosporidium parvum</i> Iowa II</b>  |
| <b>Q5CY95</b>    | <b>CRYPV</b> | <b>NRFDKG-LSNNIREIM</b> | <b>YES</b> | <b>DHHC family palmitoyl transferase, 4 transmembrane domains plus possible signal peptide: <i>Cryptosporidium parvum</i> Iowa II</b>        |
| <b>Q5CYP3</b>    | <b>CRYPV</b> | <b>NPWYSG-ISRNIAELF</b> | <b>YES</b> | <b>DHHC family palmitoyl transferase with a signal peptide and 4 transmembrane domains: <i>Cryptosporidium parvum</i> Iowa II</b>            |
| <b>Q7YZ57</b>    | <b>CRYPV</b> | <b>GRYDLG-PERNIQQAF</b> | <b>YES</b> | <b>DHHC zinc finger multi-pass transmembrane protein: <i>Cryptosporidium parvum</i></b>  |
| Q11UF3           | CYTH3        | KSQTQG-IFKNINDVF        | NO         | Putative uncharacterized protein: <i>Cytophaga hutchinsonii</i> (strain ATCC 33406 / NCIMB 9469)   |
| <b>A0JMB1</b>    | <b>DANRE</b> | <b>NGFNVG-LNKNLRQVF</b> | <b>YES</b> | <b>Zgc:152683: <i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)</b>   |
| <b>A2BEM9</b>    | <b>DANRE</b> | <b>GDHSRG-FLQNWQIFL</b> | <b>YES</b> | <b>Novel protein containing a DHHC zinc finger domain: <i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)</b>                         |
| <b>A2CEX1</b>    | <b>DANRE</b> | <b>NPFTRG-CGGNVKHL</b>  | <b>YES</b> | <b>Zinc finger, DHHC domain containing 5: <i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)</b>                                      |
| <b>A4FVK6</b>    | <b>DANRE</b> | <b>NGFTLG-FRKNITQVF</b> | <b>YES</b> | <b>Zgc:162723 protein: <i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)</b>   |
| <b>A5VWX9</b>    | <b>DANRE</b> | <b>SPFNHG-CMRNLIDFF</b> | <b>YES</b> | <b>Novel protein similar to vertebrate zinc finger, DHHC-type containing 17: <i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)</b>   |
| <b>A7YT88</b>    | <b>DANRE</b> | <b>NPYSHKNIKNCCEVL</b>  | <b>YES</b> | <b>Zgc:136936 protein: <i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)</b>   |
| A7YYE7           | DANRE        | RPYSLG-TMANIRECL        | YES        | Zdhc24 protein: <i>Danio rerio</i> (Zebrafish) ( <i>Brachydanio rerio</i> )  |
| <b>A7YYH9</b>    | <b>DANRE</b> | <b>GFYHRG-ILKNIGEIF</b> | <b>YES</b> | <b>Zgc:64155 protein: <i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)</b>  |
| <b>A8WGN8</b>    | <b>DANRE</b> | <b>GFYHRG-ILKNIGEIF</b> | <b>YES</b> | <b>Zgc:64155: <i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)</b>  |
| Q05AL0           | DANRE        | NGFTLG-FHKNITQVF        | YES        | Zgc:162723 protein: <i>Danio rerio</i> (Zebrafish) ( <i>Brachydanio rerio</i> )  |
| Q08C71           | DANRE        | NPYTYNNIFTNCCVVL        | YES        | Zgc:153461: <i>Danio rerio</i> (Zebrafish) ( <i>Brachydanio rerio</i> )  |
| <b>Q24JY8</b>    | <b>DANRE</b> | <b>NGFNVG-LSKNLRQVF</b> | <b>YES</b> | <b>LOC562181 protein: <i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)</b>  |
| <b>Q2THW0</b>    | <b>DANRE</b> | <b>NPFTNG-CLRNVSHVL</b> | <b>YES</b> | <b>Membrane-associated DHHC5 zinc finger protein: <i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)</b>                              |
| <b>Q5BLG4</b>    | <b>DANRE</b> | <b>NGFSLG-AYKNFRQVF</b> | <b>YES</b> | <b>Zgc:110777: <i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)</b>   |
| <b>Q5PRB8</b>    | <b>DANRE</b> | <b>NPFNHG-VVKNLVNFF</b> | <b>YES</b> | <b>Zinc finger, DHHC-type containing 13: <i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)</b>                                       |
| <b>Q5SNY0</b>    | <b>DANRE</b> | <b>NPYSYGNFITNCCSAL</b> | <b>YES</b> | <b>Novel protein similar to vertebrate zinc finger, DHHC domain containing 14: <i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)</b> |
| <b>Q5XJ21</b>    | <b>DANRE</b> | <b>KAFDVG-VQANFLQVF</b> | <b>YES</b> | <b>Zgc:103780: <i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)</b>   |
| <b>Q6AXL7</b>    | <b>DANRE</b> | <b>GHYSRG-FWSNWTEFL</b> | <b>YES</b> | <b>Zinc finger, DHHC-type containing 23: <i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)</b>                                       |
| Q6DG77           | DANRE        | RPYSLG-TMANIRECL        | YES        | Zinc finger, DHHC-type containing 24: <i>Danio rerio</i> (Zebrafish) ( <i>Brachydanio rerio</i> )  |
| <b>Q7SXG0</b>    | <b>DANRE</b> | <b>NPFSYG-KLNNWVVF</b>  | <b>YES</b> | <b>Zinc finger, DHHC domain containing 16: <i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)</b>                                     |
| <b>Q7T323</b>    | <b>DANRE</b> | <b>GFYHRG-ILKNIGEIF</b> | <b>YES</b> | <b>Zgc:64155: <i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)</b>  |
| <b>Q7ZU06</b>    | <b>DANRE</b> | <b>NPFTRG-CGGNVKHL</b>  | <b>YES</b> | <b>Zinc finger, DHHC domain containing 5: <i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)</b>                                      |
| <b>Q7ZVN4</b>    | <b>DANRE</b> | <b>NPYSYNSMIKNCSSVL</b> | <b>YES</b> | <b>Zgc:55843: <i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)</b>  |
| <b>Q8AYN4</b>    | <b>DANRE</b> | <b>NPFTRG-CGGNVKHL</b>  | <b>YES</b> | <b>Zisp protein: <i>Danio rerio</i> (Zebrafish) (<i>Brachydanio rerio</i>)</b>   |
| Q6BUK1           | DEBHA        | KLYNEG-VKRNISDVF        | NO         | Similar to SP_Q99186 <i>Saccharomyces cerevisiae</i> YOL062c APM4: <i>Debaryomyces hansenii</i> (Yeast) ( <i>Torulaspora hansenii</i> )      |
| Q478N2           | DECAR        | VLFDLG-RWWNFWHIL        | NO         | Polysulphide reductase, NrfD: <i>Dechloromonas aromatica</i> (strain RCB)  |
| <b>Q1JYG4</b>    | <b>DESAC</b> | <b>NQYDQG-PLLNINEFL</b> | <b>NO</b>  | <b>Putative uncharacterized protein precursor: <i>Desulfuromonas acetoxidans</i> DSM 684</b>   |
| <b>Q314W5</b>    | <b>DESOG</b> | <b>ADPFDG-IRNIVLRF</b>  | <b>NO</b>  | <b>Putative uncharacterized protein precursor: <i>Desulfovibrio desulfuricans</i> (strain G20)</b>   |
| Q18UX2           | DESHD        | TPFNQG-YAHNAYAFF        | NO         | 4Fe-4S ferredoxin, iron-sulfur binding: <i>Desulfitobacterium hafniense</i> (strain DCB-2)   |
| Q18Z48           | DESHD        | NPHDKG-AIVNLDVDM        | NO         | Citrate lyase, $\alpha$ subunit: <i>Desulfitobacterium hafniense</i> (strain DCB-2)  |
| Q24T15           | DESHY        | NPHDKG-AIVNLDVDM        | NO         | Putative uncharacterized protein: <i>Desulfitobacterium hafniense</i> (strain Y51)   |
| Q24ZC1           | DESHY        | RAYSLNVLKNFISFF         | NO         | Putative uncharacterized protein: <i>Desulfitobacterium hafniense</i> (strain Y51)   |
| Q250Z7           | DESHY        | TPFNQG-YAHNAYAFF        | NO         | Putative anaerobic DMSO reductase chain B iron-sulfur subunit: <i>Desulfitobacterium hafniense</i> (strain Y51)                              |
| Q54H38           | DICDI        | LYNKG-LANNLKRFL         | NO         | Putative uncharacterized protein: <i>Dictyostelium discoideum</i> (Slime mold)   |
| Q54P32           | DICDI        | SIYSKS-KLRNCINIF        | NO         | Putative uncharacterized protein: <i>Dictyostelium discoideum</i> (Slime mold)   |
| Q54QK3           | DICDI        | YNYDVG-FLSNWYFF         | NO         | Putative uncharacterized protein: <i>Dictyostelium discoideum</i> (Slime mold)   |
| Q556H0           | DICDI        | NIYLKK-FLSNIKEVF        | NO         | Putative uncharacterized protein: <i>Dictyostelium discoideum</i> (Slime mold)   |
| Q556T7           | DICDI        | LPFDHGNLLENLKFMM        | NO         | Putative uncharacterized protein: <i>Dictyostelium discoideum</i> (Slime mold)   |
| Q55AT1           | DICDI        | KPYHYGSHYSNIGSVL        | NO         | BEACH domain-containing protein: <i>Dictyostelium discoideum</i> (Slime mold)  |
| <b>Q86JF2</b>    | <b>DICDI</b> | <b>KPYHYGSHYSNIGSVL</b> | <b>NO</b>  | <b>Similar to <i>Dictyostelium discoideum</i>: <i>Dictyostelium discoideum</i> (Slime mold)</b>  |
| Q8IHL0           | DICDI        | KPYHYGSHYSNIGSVL        | NO         | LvsB: <i>Dictyostelium discoideum</i> (Slime mold)   |
| <b>Q54B34</b>    | <b>DICDI</b> | <b>NPYDFG-VLQNFQKFF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Dictyostelium discoideum</i> (Slime mold)</b>  |
| <b>Q54JY9</b>    | <b>DICDI</b> | <b>NVFHRR-FFSNITEFF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Dictyostelium discoideum</i> (Slime mold)</b>  |
| <b>Q54RL6</b>    | <b>DICDI</b> | <b>NIYNKG-LISNLEVL</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Dictyostelium discoideum</i> (Slime mold)</b>  |
| <b>Q54X19</b>    | <b>DICDI</b> | <b>WKFDKG-WKFNREVFM</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Dictyostelium discoideum</i> (Slime mold)</b>  |
| <b>Q54YH2</b>    | <b>DICDI</b> | <b>NIFNIG-FKKNFCQVF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Dictyostelium discoideum</i> (Slime mold)</b>  |
| Q81H8            | DROER        | LSYNGQ-LRGNFMAFM        | YES        | CG13029-PA: <i>Drosophila erecta</i> (Fruitfly)  |
| Q0KI05           | DROME        | DPYDIKSFKSIRDIF         | NO         | CG3339-PB, isoform B: <i>Drosophila melanogaster</i> (Fruitfly)  |
| Q4V4X5           | DROME        | TPYNMG-YIRSWRNLL        | NO         | IP12933p: <i>Drosophila melanogaster</i> (Fruit fly)   |
| Q4V500           | DROME        | TPYNMG-YIRSWRNLL        | NO         | IP13133p: <i>Drosophila melanogaster</i> (fruitfly)  |
| Q5BHX4           | DROME        | SLYTLGHVCLNFCDFV        | NO         | AT31458p: <i>Drosophila melanogaster</i> (fruitfly)  |
| <b>Q5U0T3</b>    | <b>DROME</b> | <b>NGYNLG-RYANFCEVF</b> | <b>NO</b>  | <b>AT13360p: <i>Drosophila melanogaster</i> (fruitfly)</b>   |
| Q9VB44           | DROME        | DPYDIKSFKSIRDIF         | NO         | CG3339-PA, isoform A: <i>Drosophila melanogaster</i> (fruitfly)  |
| Q9VCK2           | DROME        | DPYDQRSIRNFERHF         | NO         | CG13822-PA: <i>Drosophila melanogaster</i> (fruitfly)  |
| Q9VGJ0           | DROME        | TPYNMG-YIRSWRNLL        | NO         | CG12594-PA: <i>Drosophila melanogaster</i> (fruitfly)  |
| Q9VS91           | DROME        | SLYTLGHVCLNFCDFV        | NO         | CG7716-PA: <i>Drosophila melanogaster</i> (fruitfly)   |
| <b>A1Z833</b>    | <b>DROME</b> | <b>NGYNLG-RYANFCEVF</b> | <b>YES</b> | <b>CG1407-PA, isoform A: <i>Drosophila melanogaster</i> (fruitfly)</b>   |
| A1ZAR2           | DROME        | NGFNLG-YFYNFRDLY        | YES        | CG17287-PA: <i>Drosophila melanogaster</i> (fruitfly)  |
| <b>A2VEY9</b>    | <b>DROME</b> | <b>NPYSRGNICLNCCHIL</b> | <b>YES</b> | <b>RE02357p: <i>Drosophila melanogaster</i> (fruitfly)</b>   |

Table S3 Contd.

| Accession number | Organism | PaCCT motif       | DHHC | Description  |
|------------------|----------|-------------------|------|--|
| A8JUM2           | DROME    | NPFSRG-CWHNCCYTQ  | YES  | CG34449-PB, isoform B: <i>Drosophila melanogaster</i> (fruitfly)   |
| A8JUM5           | DROME    | NPFSRG-CWHNCCYTQ  | YES  | CG34449-PC, isoform C: <i>Drosophila melanogaster</i> (fruitfly)   |
| Q0IGS7           | DROME    | RKYDRG-LRGNLEMLV  | YES  | <b>RT01106p: <i>Drosophila melanogaster</i> (fruitfly)</b>   |
| Q4V6X2           | DROME    | RHHDLG-FRNNCQLIM  | YES  | <b>IP01227p: <i>Drosophila melanogaster</i> (fruitfly)</b>   |
| Q4V6X5           | DROME    | DTYDLG-LWENFKLIL  | YES  | <b>IP01230p: <i>Drosophila melanogaster</i> (fruitfly)</b>   |
| Q4V6X7           | DROME    | NGFNLG-YFVNFRLDY  | YES  | IP01239p: <i>Drosophila melanogaster</i> (fruitfly)  |
| Q4V6Z4           | DROME    | NPFSRG-CWHNCCYTQ  | YES  | IP01380p: <i>Drosophila melanogaster</i> (fruitfly)  |
| Q6NLJ6           | DROME    | NPYSRGNICLNCCCHIL | YES  | <b>AT15134p: <i>Drosophila melanogaster</i> (fruitfly)</b>   |
| Q7K2V5           | DROME    | NGYNLG-RYANFCEVF  | YES  | <b>GH04905p: <i>Drosophila melanogaster</i> (fruitfly)</b>   |
| Q8IQN9           | DROME    | YRYNQG-LLGNFMAFM  | YES  | <b>CG13029-PC, isoform C: <i>Drosophila melanogaster</i> (fruitfly)</b>  |
| Q8MSL3           | DROME    | YPYNLG-WKTNIREVF  | YES  | <b>AT26975p: <i>Drosophila melanogaster</i> (fruitfly)</b>   |
| Q8SWX8           | DROME    | YPYDLG-WRANLRLVF  | YES  | <b>GH06759p: <i>Drosophila melanogaster</i> (fruitfly)</b>   |
| Q960T3           | DROME    | NGYNLG-RYANFCEVF  | YES  | <b>LD36375p: <i>Drosophila melanogaster</i> (fruitfly)</b>   |
| Q9I7L7           | DROME    | IPFDRK-LRRNFKFTL  | YES  | CG18810-PA: <i>Drosophila melanogaster</i> (fruitfly)  |
| Q9VB73           | DROME    | NPYNFG-TKKNWKLFL  | YES  | <b>CG5880-PA: <i>Drosophila melanogaster</i> (fruitfly)</b>  |
| Q9VBM4           | DROME    | RSYDVG-WRRNFDMLV  | YES  | CG4956-PA: <i>Drosophila melanogaster</i> (fruitfly)   |
| Q9VBM5           | DROME    | CTYDLG-FRKNCQTIM  | YES  | CG17195-PA: <i>Drosophila melanogaster</i> (fruitfly)  |
| Q9VBM6           | DROME    | RHHDLG-FRNNCQLIM  | YES  | <b>CG17196-PA: <i>Drosophila melanogaster</i> (fruitfly)</b>   |
| Q9VBM7           | DROME    | DTYDLG-LWENFKLIL  | YES  | <b>CG17197-PA: <i>Drosophila melanogaster</i> (fruitfly)</b>   |
| Q9VBM8           | DROME    | RTYDLG-LGNNLTLIL  | YES  | CG17198-PA: <i>Drosophila melanogaster</i> (fruitfly)  |
| Q9VG80           | DROME    | YPYDLG-WRANLRLVF  | YES  | <b>CG5196-PA, isoform A: <i>Drosophila melanogaster</i> (fruitfly)</b>   |
| Q9VKB1           | DROME    | NPFSRG-PILNLEFF   | YES  | <b>CG6618-PA, isoform A: <i>Drosophila melanogaster</i> (fruitfly)</b>   |
| Q9VSV3           | DROME    | YPYNLG-WKTNMREVF  | YES  | <b>CG4483-PA: <i>Drosophila melanogaster</i> (fruitfly)</b>  |
| Q9VTV6           | DROME    | NPYSRGNICLNCCCHIL | YES  | <b>CG5620-PA, isoform A: <i>Drosophila melanogaster</i> (fruitfly)</b>   |
| Q9VUW9           | DROME    | SPFTRG-PIQNLVDFL  | YES  | <b>CG6017-PA: <i>Drosophila melanogaster</i> (fruitfly)</b>  |
| Q9W251           | DROME    | EKYDRG-VYQNLRSVF  | YES  | <b>CG10344-PB, isoform B: <i>Drosophila melanogaster</i> (fruitfly)</b>  |
| Q9W345           | DROME    | NPFSRG-CWHNCCYTQ  | YES  | CG34449-PA, isoform A: <i>Drosophila melanogaster</i> (fruitfly)   |
| Q29AA3           | DROPS    | DPYDIKFSKSSIRDIF  | NO   | GA17389-PA: <i>Drosophila pseudoobscura</i> (fruitfly)   |
| Q29D75           | DROPS    | LLYSLG-HCKNMSEFF  | NO   | GA13421-PA: <i>Drosophila pseudoobscura</i> (fruitfly)   |
| Q2LYP8           | DROPS    | QNYDYG-ILKNVETVF  | NO   | GA11948-PA: <i>Drosophila pseudoobscura</i> (fruitfly)   |
| Q28ZL8           | DROPS    | LKYKRG-VRQNLRSVF  | YES  | <b>GA10260-PA: <i>Drosophila pseudoobscura</i> (fruitfly)</b>  |
| Q292N6           | DROPS    | RNYDLG-LRANMEMIF  | YES  | GA18348-PA: <i>Drosophila pseudoobscura</i> (fruitfly)   |
| Q295M6           | DROPS    | RTYDLG-PMKNFRQVL  | YES  | <b>GA18553-PA: <i>Drosophila pseudoobscura</i> (fruitfly)</b>  |
| Q29B32           | DROPS    | YPYDLG-WWLNKQVF   | YES  | <b>GA18728-PA: <i>Drosophila pseudoobscura</i> (fruitfly)</b>  |
| Q29D93           | DROPS    | SPFTRG-PIQNLIDFL  | YES  | <b>GA19299-PA: <i>Drosophila pseudoobscura</i> (fruitfly)</b>  |
| Q2M0R3           | DROPS    | NPYSRGNICLNCCCHIL | YES  | <b>GA19011-PA: <i>Drosophila pseudoobscura</i> (fruitfly)</b>  |
| A7ZH68           | ECO24    | KPYFKG-VINNLKCLC  | NO   | EAL domain protein: <i>Escherichia coli</i> O139:H28 (strain E24377A / ETEC)   |
| Q2VP05           | ECOLX    | KPYFKG-VINNLKCLC  | NO   | Putative uncharacterized protein: <i>Escherichia coli</i>  |
| Q3YSX8           | EHRCJ    | DDFSFK-CYQNFQVF   | NO   | Putative uncharacterized protein: <i>Ehrlichia canis</i> (strain Jake)   |
| Q5AW70           | EMENI    | DDFDKG-LRNNLREGF  | NO   | Predicted protein: <i>Emericella nidulans</i> ( <i>Aspergillus nidulans</i> )  |
| Q5BGU1           | EMENI    | NKYDFG-VLQNMATTI  | NO   | Putative uncharacterized protein: <i>Emericella nidulans</i> ( <i>Aspergillus nidulans</i> )   |
| Q8SRA8           | ENCCU    | DRYDVG-ILINCASTM  | NO   | Hypothetical oxidoreductase short chain dehydrogenases/reductases: <i>Encephalitozoon cuniculi</i>   |
| Q8STX3           | ENCCU    | SPYDRG-IMSNLIDTL  | YES  | <b>Similarity to hypothetical transmembrane proteins YN66 yeast: <i>Encephalitozoon cuniculi</i></b>   |
| Q8SVX7           | ENCCU    | NPYNLG-AKQNWQRVF  | YES  | <b>Putative uncharacterized protein ECU04_0260: <i>Encephalitozoon cuniculi</i></b>  |
| B0E9M8           | ENTDI    | NEYKHG-IKKNIRRFM  | NO   | Putative uncharacterized protein: <i>Entamoeba dispar</i> SAW760   |
| B0E6P5           | ENTDI    | NKFKKS-LWKNWCEAF  | YES  | <b>Zinc finger protein DHHC-domain-containing protein, putative: <i>Entamoeba dispar</i> SAW760</b>  |
| B0E7U3           | ENTDI    | TPYDLG-ILTNHQTL   | YES  | <b>Zinc finger protein DHHC-domain-containing protein, putative: <i>Entamoeba dispar</i> SAW760</b>  |
| B0EBC7           | ENTDI    | PSYNRG-VFNNIKETM  | YES  | Palmitoyltransferase PFA3, putative: <i>Entamoeba dispar</i> SAW760  |
| B0EC01           | ENTDI    | NYYDNG-FFNNIKSTL  | YES  | <b>Palmitoyltransferase swf1, putative: <i>Entamoeba dispar</i> SAW760</b>   |
| B0EED2           | ENTDI    | NKYDLG-TLRNIQKIF  | YES  | <b>Palmitoyltransferase ZDHHC15, putative: <i>Entamoeba dispar</i> SAW760</b>  |
| B0EER8           | ENTDI    | SLYSHS-IKQNFETM   | YES  | Palmitoyltransferase PFA3, putative: <i>Entamoeba dispar</i> SAW760  |
| B0EFN5           | ENTDI    | LNYNRG-FYNNWKEIM  | YES  | <b>Palmitoyltransferase PFA3, putative: <i>Entamoeba dispar</i> SAW760</b>   |
| B0EI33           | ENTDI    | NKYKYS-ILLNWKEVM  | YES  | Zinc finger protein DHHC domain containing protein, putative: <i>Entamoeba dispar</i> SAW760   |
| B0EL09           | ENTDI    | NPYDLG-NIKNLQLMF  | YES  | <b>Zinc finger protein DHHC-domain-containing protein, putative: <i>Entamoeba dispar</i> SAW760</b>  |
| B0ELE8           | ENTDI    | NKYKYS-ILLNWKEVM  | YES  | <b>Zinc finger protein DHHC-domain-containing protein, putative: <i>Entamoeba dispar</i> SAW760</b>  |
| B0EM95           | ENTDI    | LPYYIS-LIENWRDAF  | YES  | Zinc finger protein DHHC-domain-containing protein, putative: <i>Entamoeba dispar</i> SAW760   |
| B0ENB9           | ENTDI    | YIYNQG-FIKNWIKFL  | YES  | <b>Palmitoyltransferase ZDHHC18, putative: <i>Entamoeba dispar</i> SAW760</b>  |
| B0ES39           | ENTDI    | NRFNVG-FKENLKEVF  | YES  | <b>Rap GTPase-activating protein, putative: <i>Entamoeba dispar</i> SAW760</b>   |
| B0EU60           | ENTDI    | NPYDEG-IKTNITKFF  | YES  | <b>Palmitoyltransferase ZDHHC15, putative: <i>Entamoeba dispar</i> SAW760</b>  |
| A5FBG5           | FLAJO    | QLYDDG-SKKNFKSFF  | NO   | Putative uncharacterized protein precursor: <i>Flavobacterium johnsoniae</i> (strain ATCC 17061 / DSM 2064 / UW101) ( <i>Cytophaga johnsonae</i> )   |
| A5FJ31           | FLAJO    | KIYTHG-AIENMTNVL  | NO   | Exonuclease of the $\beta$ -lactamase fold involved in RNA processing-like protein: <i>Flavobacterium johnsoniae</i> (strain ATCC 17061 / DSM 2064 / UW101) ( <i>Cytophaga johnsonae</i> ) |
| A6H1S0           | FLAPJ    | NGYTLG-LFANLNNVL  | NO   | Probable TonB-dependent outer membrane receptorprecursor: <i>Flavobacterium psychrophilum</i> (strain JIPO2/86 / ATCC 49511)   |
| Q6H071           | FREDI    | NRYKIG-MTKNIYQRF  | NO   | Putative uncharacterized protein: <i>Fremyella diplosiphon</i> (Calothrix PCC 7601)  |
| Q2THV7           | FUGRU    | NPFTKG-CCGNVEYVL  | YES  | <b>Membrane-associated DHHC8 zinc finger protein: <i>Fugu rubripes</i> (Japanese pufferfish) (<i>Takifugu rubripes</i>)</b>  |
| Q2THV8           | FUGRU    | NPFTNG-CWKNVSHVL  | YES  | <b>Membrane-associated DHHC5 zinc finger protein: <i>Fugu rubripes</i> (Japanese pufferfish) (<i>Takifugu rubripes</i>)</b>  |
| A5TT79           | FUSNP    | SAYTNG-YYENAKDFF  | NO   | Putative uncharacterized protein: <i>Fusobacterium nucleatum</i> subsp. polymorphum ATCC 10953   |

Table S3 Contd.

| Accession number | Organism     | PaCCT motif              | DHHC       | Description   |
|------------------|--------------|--------------------------|------------|---|
| <b>A4ILD1</b>    | <b>GEOTN</b> | <b>NPYDEGLWIENIEEFF</b>  | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Geobacillus thermodenitrificans</i> (strain NG80-2)</b>   |
| A8BUF3           | GIALA        | LAYTHG-YADNLRQFF         | NO         | Actin related protein: <i>Giardia lamblia</i> ATCC 50803  |
| A8B4L4           | GIALA        | YPYSSG-LRTNLSLSELF       | YES        | Zinc finger domain: <i>Giardia lamblia</i> ATCC 50803   |
| <b>A8BKWO</b>    | <b>GIALA</b> | <b>RPYDYG-RRFNMQQVF</b>  | <b>YES</b> | <b>Zinc finger domain: <i>Giardia lamblia</i> ATCC 50803</b>  |
| <b>A8BMZ6</b>    | <b>GIALA</b> | <b>NRFDRG-KLNLSLSELF</b> | <b>YES</b> | <b>Zinc finger domain: <i>Giardia lamblia</i> ATCC 50803</b>  |
| <b>A8BY53</b>    | <b>GIALA</b> | <b>HPYHHKSFRKNFAACF</b>  | <b>YES</b> | <b>Zinc finger domain: <i>Giardia lamblia</i> ATCC 50803</b>  |
| <b>Q7X9S4</b>    | <b>GOSBA</b> | <b>NIWNRS-PRRNCRCRM</b>  | <b>NO</b>  | <b>Fiber protein Fb16: <i>Gossypium barbadense</i> (Sea-island cotton) (Egyptian cotton)</b>  |
| A0M766           | GRAFK        | KIYTHG-AIENMTEVL         | NO         | Putative uncharacterized protein: <i>Gramella forsetii</i> (strain KT0803)  |
| A0M7D2           | GRAFK        | SPYGLG-VKDNWLFVC         | NO         | Putative uncharacterized protein: <i>Gramella forsetii</i> (strain KT0803)  |
| Q9S73            | GUITH        | NHHHKK-FKNMFRNFL         | NO         | Putative uncharacterized protein orf625: <i>Guillardia theta</i> (Cryptomonas phi)  |
| Q2SDZ8           | HAHCH        | NHYRLG-FYKANAMTVW        | NO         | Transcriptional regulator: <i>Hahella chejuensis</i> (strain KCTC 2396)   |
| A2T5X3           | HALCL        | RIYFYG-KIENFVEVF         | NO         | Maturase K: <i>Halesia carolina</i> (Carolina silverbell)   |
| Q6RUL4           | HALCL        | RIYFYG-KIENFVEVF         | NO         | Maturase K: <i>Halesia carolina</i> (Carolina silverbell)   |
| Q8M9N0           | HALCL        | RIYFYG-KIENFVEVF         | NO         | Maturase K: <i>Halesia carolina</i> (Carolina silverbell)   |
| Q9HPM9           | HALSA        | NPWSRK-RRENFKQAC         | NO         | Cobalamin biosynthesis: <i>Halobacterium salinarium</i> (Halobacterium halobium)  |
| Q18FW9           | HALWD        | NPWSRK-RRENFKQAC         | NO         | Precorin-3B C17-methyltransferase 2: <i>Haloquadratum walsbyi</i> (strain DSM 16790)  |
| Q17ZQ1           | HELAH        | FAYSQK-FCKNLLELVF        | NO         | ATP-dependent DNA helicase: <i>Helicobacter acinonychis</i> (strain Sheeba)   |
| Q7VI87           | HELHP        | GSYDFG-TWKNTLQFM         | NO         | Putative uncharacterized protein cfrA: <i>Helicobacter hepaticus</i>  |
| Q1CRG3           | HELPH        | FAYSQK-FCKNLLELVF        | NO         | DNA recombinase: <i>Helicobacter pylori</i> (strain HPAG1)  |
| A5JGA2           | HELPH        | NIYDKG-CKLGMKQAC         | NO         | HcpE: <i>Helicobacter pylori</i> ( <i>Campylobacter pylori</i> )  |
| A4GA91           | HERAR        | QPYDVKSTVNNLRNL          | NO         | Cyanophycin synthetase: <i>Herminiimonas arsenicoxydans</i>   |
| A9B1X7           | HERAU        | NMFDRC-TRLNFRQAM         | NO         | Aminoglycoside phosphotransferase: <i>Herpetosiphon aurantiacus</i> ATCC 23779  |
| <b>Q8NJ29</b>    | <b>HORWE</b> | <b>NPWDLG-STYLNFTAVF</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Hortaea werneckii</i></b>   |
| A4FU17           | HUMAN        | NMFINDSLWNNLCQII         | NO         | Taste receptor type 2: <i>Homo sapiens</i> (Human)  |
| A8K7A0           | HUMAN        | DKFDKG-YSYNIRHSF         | NO         | cDNA FLJ75753, highly similar to <i>Homo sapiens</i> primase, polypeptide 2A, 58kDa: <i>Homo sapiens</i> (Human)  |
| Q50KL2           | HUMAN        | NMFINDSLWNNLCQII         | NO         | Taste receptor type 2: <i>Homo sapiens</i> (Human)  |
| <b>A4D2N9</b>    | <b>HUMAN</b> | <b>NIHSHG-LRSNLQEIF</b>  | <b>YES</b> | <b>Zinc finger, DHHC-domain-containing 4: <i>Homo sapiens</i> (Human)</b>   |
| <b>A4FVA9</b>    | <b>HUMAN</b> | <b>NPYSYGNIFTNCCVAL</b>  | <b>YES</b> | <b>ZDHC14 protein: <i>Homo sapiens</i> (Human)</b>  |
| <b>A8K5N3</b>    | <b>HUMAN</b> | <b>TPYNLG-FMQNLADFF</b>  | <b>YES</b> | <b>cDNA FLJ77545, highly similar to <i>Homo sapiens</i> zinc finger, DHHC-type containing 13, transcript variant 1, mRNA: <i>Homo sapiens</i> (Human)</b> |
| <b>A8KA01</b>    | <b>HUMAN</b> | <b>SPFNHG-CVRNIIDFF</b>  | <b>YES</b> | <b>cDNA FLJ77443, highly similar to <i>Homo sapiens</i> putative MAPK activating protein: <i>Homo sapiens</i> (Human)</b>                                 |
| <b>A8MSY6</b>    | <b>HUMAN</b> | <b>NPFDQG-CASNWYLT</b>   | <b>YES</b> | <b>Uncharacterized protein ZDHC19: <i>Homo sapiens</i> (Human)</b>  |
| <b>A8MTV9</b>    | <b>HUMAN</b> | <b>NGFSLG-CSKNWRQVF</b>  | <b>YES</b> | <b>Uncharacterized protein ZDHC20: <i>Homo sapiens</i> (Human)</b>  |
| <b>Q2TB82</b>    | <b>HUMAN</b> | <b>NGFSLG-CSKNWRQVF</b>  | <b>YES</b> | <b>ZDHC20 protein: <i>Homo sapiens</i> (Human)</b>  |
| <b>Q2TGE9</b>    | <b>HUMAN</b> | <b>NPFTRG-CCGNVEHVL</b>  | <b>YES</b> | <b>Membrane-associated DHHC8 zinc finger protein: <i>Homo sapiens</i> (Human)</b>   |
| <b>Q2TGF0</b>    | <b>HUMAN</b> | <b>NPFTNG-CCNNVSRVL</b>  | <b>YES</b> | <b>Membrane-associated DHHC5 zinc finger protein: <i>Homo sapiens</i> (Human)</b>   |
| <b>Q5JVQ8</b>    | <b>HUMAN</b> | <b>NPYSYGNIFTNCCVAL</b>  | <b>YES</b> | <b>Zinc finger, DHHC-type containing 14: <i>Homo sapiens</i> (Human)</b>  |
| <b>Q5T269</b>    | <b>HUMAN</b> | <b>NPFDRG-LTRNLAHFF</b>  | <b>YES</b> | <b>Zinc finger, DHHC-type containing 12: <i>Homo sapiens</i> (Human)</b>  |
| A1X3S8           | HYPPE        | RIYFYG-KVDNFTVEF         | NO         | Maturase K: <i>Hypericum perforatum</i> (St. John's wort)   |
| Q5QW62           | IDILO        | DPFSKS-RGYNWIDVF         | NO         | Uncharacterized secreted protein: <i>Idiomarina loihiensis</i>  |
| Q8MAF4           | KARBR        | LLFDGR-YLENFYSSF         | NO         | Photosystem I P700 chlorophyll A apoprotein A1: <i>Karenia brevis</i> (Dinoflagellate)  |
| Q48391           | KLEOX        | NDYNYMG-FYSNLEYLL        | NO         | CymA protein precursor: <i>Klebsiella oxytoca</i>   |
| B0D4U2           | LACBI        | TPFNLGKICRNWRHTV         | NO         | Predicted protein: <i>Laccaria bicolor</i> S238N-H82  |
| <b>B0DAE5</b>    | <b>LACBI</b> | <b>DIFHEG-LVENWRDVL</b>  | <b>NO</b>  | <b>Predicted protein: <i>Laccaria bicolor</i> S238N-H82</b>   |
| B0DMM3           | LACBI        | DSWNHG-SWSNISFL          | NO         | Predicted protein: <i>Laccaria bicolor</i> S238N-H82  |
| <b>B0CRK9</b>    | <b>LACBI</b> | <b>FPYDLG-ARRNIESIL</b>  | <b>YES</b> | <b>Predicted protein: <i>Laccaria bicolor</i> S238N-H82</b>   |
| <b>B0CRZ2</b>    | <b>LACBI</b> | <b>NPFSHGTWRRNITAVL</b>  | <b>YES</b> | <b>Predicted protein: <i>Laccaria bicolor</i> S238N-H82</b>   |
| <b>B0CU96</b>    | <b>LACBI</b> | <b>RIYDLG-SAQNWRVFM</b>  | <b>YES</b> | <b>Predicted protein: <i>Laccaria bicolor</i> S238N-H82</b>   |
| <b>B0CVL2</b>    | <b>LACBI</b> | <b>RIYDVG-FRRNWEHVF</b>  | <b>YES</b> | <b>Predicted protein: <i>Laccaria bicolor</i> S238N-H82</b>   |
| <b>B0D655</b>    | <b>LACBI</b> | <b>NSYNLG-IWKNAQLFF</b>  | <b>YES</b> | <b>Predicted protein: <i>Laccaria bicolor</i> S238N-H82</b>   |
| A8YUH9           | LACH4        | NIFYNS-ILNNVRHVL         | NO         | Putative uncharacterized protein: <i>Lactobacillus helveticus</i> (strain DPC 4571)   |
| <b>A2RMJ7</b>    | <b>LACLM</b> | <b>NDYSQG-YCINCKAVF</b>  | <b>NO</b>  | <b>Hypothetical 13.6 kDa protein in MDH1-VMA5 intergenic region: <i>Lactococcus lactis</i> subsp. cremoris (strain MG1363)</b>                            |
| <b>Q02X88</b>    | <b>LACLS</b> | <b>NDYSQG-YCINCKAVF</b>  | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Lactococcus lactis</i> subsp. cremoris (strain SK11)</b>  |
| B0BCK0           | LATHI        | NQYLRG-FSKNILEAF         | NO         | Cvc protein: <i>Lathyrus hirsutus</i> (Rough pea) (Hairy vetchling)   |
| Q5X2M3           | LEGPA        | NIWQVG-LFSNLRLLFF        | NO         | Putative uncharacterized protein ctpA: <i>Legionella pneumophila</i> (strain Paris)   |
| A5IFN6           | LEGPC        | NIWQVG-LFSNLRLLFF        | NO         | Cation efflux transporter: <i>Legionella pneumophila</i> (strain Corby)   |
| Q5ZWR8           | LEGPH        | NIWQVG-LFSNLRLLFF        | NO         | Cation efflux transporter: <i>Legionella pneumophila</i> subsp. pneumophila (strain Philadelphia 1 / ATCC 33152 / DSM 7513)                               |
| Q8RNN9           | LEGPN        | NIWQVG-LFSNLRLLFF        | NO         | Putative cation efflux transporter: <i>Legionella pneumophila</i>   |
| A4H642           | LEIBR        | HRYTLG-AVSNCTSVL         | NO         | Putative uncharacterized protein: <i>Leishmania braziliensis</i>  |
| A4HE68           | LEIBR        | SRYHSG-HLANLIEVF         | NO         | Putative uncharacterized protein: <i>Leishmania braziliensis</i>  |
| <b>A4HL60</b>    | <b>LEIBR</b> | <b>NIYDLG-IQRNLLQVF</b>  | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Leishmania braziliensis</i></b>   |
| <b>A4H3X2</b>    | <b>LEIBR</b> | <b>SLFDNG-MWANLREFF</b>  | <b>YES</b> | <b>Huntingtin interacting protein: <i>Leishmania braziliensis</i></b>   |
| <b>A4H5P5</b>    | <b>LEIBR</b> | <b>GLYDRG-VWLNLMEL</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Leishmania braziliensis</i></b>   |
| <b>A4HC51</b>    | <b>LEIBR</b> | <b>NPYDLG-KWLNFDLDF</b>  | <b>YES</b> | <b>Zinc finger domain-like protein: <i>Leishmania braziliensis</i></b>  |
| <b>A4HGP2</b>    | <b>LEIBR</b> | <b>NPYNRG-FLGNLYYHF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Leishmania braziliensis</i></b>   |
| Q107X5           | LEIDO        | NVFTHGSLANVWAAL          | YES        | DHHC containing zinc finger protein: <i>Leishmania donovani</i>   |
| A4HUG2           | LEIIN        | HRYTLG-AISNCSSVL         | NO         | Putative uncharacterized protein: <i>Leishmania infantum</i>  |

Table S3 Contd.

| Accession number | Organism     | PaCCT motif              | DHHC       | Description   |
|------------------|--------------|--------------------------|------------|---|
| A411G8           | LEIIN        | SRYHSG-HVANLIEVL         | NO         | Putative uncharacterized protein: <i>Leishmania infantum</i>  |
| <b>A4HS47</b>    | <b>LEIIN</b> | <b>SLFDNG-IWANLREFF</b>  | <b>YES</b> | <b>Huntingtin interacting protein: <i>Leishmania infantum</i></b>   |
| <b>A4HTY5</b>    | <b>LEIIN</b> | <b>GLYDRG-VWRNLMIEVL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Leishmania infantum</i></b>   |
| <b>A4HZD7</b>    | <b>LEIIN</b> | <b>NPYDLG-KWLNFDLDF</b>  | <b>YES</b> | <b>Zinc finger domain-like protein: <i>Leishmania infantum</i></b>  |
| A411S8           | LEIIN        | NVFTHGSVLANVWAAL         | YES        | Putative uncharacterized protein: <i>Leishmania infantum</i>  |
| <b>A413R5</b>    | <b>LEIIN</b> | <b>NPYNRG-FFKNLYYHL</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Leishmania infantum</i></b>   |
| A415E8           | LEIIN        | NPWSQKHWHYQNIYARL        | YES        | Putative uncharacterized protein: <i>Leishmania infantum</i>  |
| <b>A418P0</b>    | <b>LEIIN</b> | <b>NIYDLG-VQRNLLQIF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Leishmania infantum</i></b>   |
| Q409W7           | LEIMA        | SRYHSG-HVANLLEVL         | NO         | Putative uncharacterized protein: <i>Leishmania major</i>   |
| Q40HG5           | LEIMA        | HRYTLG-AISNCSSVL         | NO         | Putative uncharacterized protein: <i>Leishmania major</i>   |
| <b>Q97203</b>    | <b>LEIMA</b> | <b>SLFDNG-IWANLREFF</b>  | <b>YES</b> | <b>Possibly notch-related protein: <i>Leishmania major</i></b>  |
| <b>Q404K0</b>    | <b>LEIMA</b> | <b>NIYDLG-VQRNLLQVF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Leishmania major</i></b>  |
| Q40716           | LEIMA        | NPWSQKHWHYQNIYARL        | YES        | Putative uncharacterized protein: <i>Leishmania major</i>   |
| <b>Q40877</b>    | <b>LEIMA</b> | <b>NPYNRG-FFKNLYYHL</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Leishmania major</i></b>  |
| <b>Q409K8</b>    | <b>LEIMA</b> | <b>NVFTHGSVLANLWAAAL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Leishmania major</i></b>  |
| <b>Q40C55</b>    | <b>LEIMA</b> | <b>SPYDLG-KWLNFDLDF</b>  | <b>YES</b> | <b>Zinc finger domain-like protein: <i>Leishmania major</i></b>   |
| <b>Q40C56</b>    | <b>LEIMA</b> | <b>SPYDLG-KWLNFDLDF</b>  | <b>YES</b> | <b>Zinc finger domain-like protein: <i>Leishmania major</i></b>   |
| <b>Q40QHW0</b>   | <b>LEIMA</b> | <b>GLYDRG-VWRNLMIEF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Leishmania major</i></b>  |
| <b>Q95ZB9</b>    | <b>LEIMA</b> | <b>NVFTHGSVLANLWAAAL</b> | <b>YES</b> | <b>Zinc finger transmembrane protein: <i>Leishmania major</i></b>   |
| Q04WY2           | LEPBL        | EKFSVG-ILQNFQSVL         | NO         | Putative uncharacterized protein: <i>Leptospira borgpetersenii</i> serovar Hardjo-bovis (strain L550)   |
| A3FSR1           | LISMO        | NRFSRG-LAVNINQVI         | NO         | Putative uncharacterized protein: <i>Listeria monocytogenes</i> J0161   |
| A3G080           | LISMO        | NRFSRG-LAVNINQVI         | NO         | Putative uncharacterized protein: <i>Listeria monocytogenes</i> J2818   |
| A3G7N0           | LISMO        | NRFSRG-LAVNINQVI         | NO         | Putative uncharacterized protein: <i>Listeria monocytogenes</i> 10403S  |
| A4DJK1           | LISMO        | NRFSRG-LAVNINQVI         | NO         | Putative uncharacterized protein: <i>Listeria monocytogenes</i> FSL N3-165  |
| A4DSF8           | LISMO        | NRFSRG-LAVNINQVI         | NO         | Putative uncharacterized protein: <i>Listeria monocytogenes</i> F6900   |
| Q4ERD4           | LISMO        | NRFSRG-LAVNINQVI         | NO         | Putative uncharacterized protein: <i>Listeria monocytogenes</i> str. 1/2a F6854   |
| Q8Y9A4           | LISMO        | NRFSRG-LAVNINQVI         | NO         | Lmo0628 protein: <i>Listeria monocytogenes</i>  |
| <b>A5DS03</b>    | <b>LODEL</b> | <b>NIYDRG-FWQNLKERF</b>  | <b>YES</b> | <b>Palmitoyltransferase SWF1: <i>Lodderomyces elongisporus</i> (Yeast) (<i>Saccharomyces elongisporus</i>)</b>  |
| <b>A5E085</b>    | <b>LODEL</b> | <b>NIFDLG-VKENMRLVL</b>  | <b>YES</b> | <b>Palmitoyltransferase PFA3: <i>Lodderomyces elongisporus</i> (Yeast) (<i>Saccharomyces elongisporus</i>)</b>  |
| <b>A5E2E1</b>    | <b>LODEL</b> | <b>RPFDLG-LKINWINLV</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Lodderomyces elongisporus</i> (Yeast) (<i>Saccharomyces elongisporus</i>)</b>   |
| <b>A5E5W5</b>    | <b>LODEL</b> | <b>FPYDYG-LLVNFRTTL</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Lodderomyces elongisporus</i> (Yeast) (<i>Saccharomyces elongisporus</i>)</b>   |
| Q4R9F2           | MACFA        | KAFNHG-LQLNLRQTL         | NO         | Testis cDNA clone: QtsA-10085, similar to human gonadotropin inducible transcription repressor 1(GIOT-1): <i>Macaca fascicularis</i> (Crab eating macaque) (Cynomolgus monkey)    |
| Q9BGP9           | MACFA        | DKFDKG-YSYNIRHSF         | NO         | Putative uncharacterized protein: <i>Macaca fascicularis</i> (Crab eating macaque) (Cynomolgus monkey)  |
| <b>Q4R909</b>    | <b>MACFA</b> | <b>NIHSHG-LRRNLQEIF</b>  | <b>YES</b> | <b>Testis cDNA clone: QtsA-11001, similar to human zinc finger, DHHC domain containing 4: <i>Macaca fascicularis</i> (Crab eating macaque) (Cynomolgus monkey)</b>                |
| <b>Q3YAM1</b>    | <b>MACMU</b> | <b>TPYNLG-FMQNLADFF</b>  | <b>YES</b> | <b>HIP14-related protein: <i>Macaca mulatta</i> (Rhesus macaque)</b>  |
| A4QR71           | MAGGR        | RAFTQGNVWKNWIVVL         | YES        | Putative uncharacterized protein: <i>Magnaporthe grisea</i> (Rice blast fungus) ( <i>Pyricularia grisea</i> )   |
| <b>A4R2T8</b>    | <b>MAGGR</b> | <b>NVFDLG-VRFRNLYHLF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Magnaporthe grisea</i> (Rice blast fungus) (<i>Pyricularia grisea</i>)</b>  |
| <b>A4R9L7</b>    | <b>MAGGR</b> | <b>NPYSRG-CATNCRDFW</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Magnaporthe grisea</i> (Rice blast fungus) (<i>Pyricularia grisea</i>)</b>  |
| <b>A4RBD2</b>    | <b>MAGGR</b> | <b>NPWHMGSVYLNICSVM</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Magnaporthe grisea</i> (Rice blast fungus) (<i>Pyricularia grisea</i>)</b>  |
| <b>A4RE12</b>    | <b>MAGGR</b> | <b>NLYDLG-FWDNLADIF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Magnaporthe grisea</i> (Rice blast fungus) (<i>Pyricularia grisea</i>)</b>  |
| <b>A4RE78</b>    | <b>MAGGR</b> | <b>FPYDRG-IWNNMCQAM</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Magnaporthe grisea</i> (Rice blast fungus) (<i>Pyricularia grisea</i>)</b>  |
| <b>Q2KFI3</b>    | <b>MAGGR</b> | <b>NPWHMGSVYLNICSVM</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Magnaporthe grisea</i> 70-15</b>  |
| Q65RF9           | MANSM        | DIYNVG-TIVNIIQLL         | NO         | ATP-dependent protease La: <i>Mannheimia succiniciproducens</i> (strain MBEL55E)  |
| <b>A2Q3H1</b>    | <b>MEDTR</b> | <b>NVYNKG-FLHNIWEII</b>  | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Medicago truncatula</i> (Barrel medic)</b>  |
| Q11J58           | MESSB        | KIYDIG-TLANVLQLL         | NO         | ATP-dependent protease La: <i>Mesorhizobium</i> sp. (strain BNC1)   |
| Q8TI59           | METAC        | TPFDLS-CLENTTEVL         | NO         | Cell surface protein: <i>Methanosarcina acetivorans</i>   |
| A6VFH7           | METM7        | SPYDTQ-VWKIGNAF          | NO         | TPR repeat-containing protein: <i>Methanococcus maripaludis</i> (strain C7 / ATCC BAA-1331)   |
| A5UNL0           | METS3        | QGFDKK-IFRNLKDIL         | NO         | Archaea-specific helicase: <i>Methanobrevibacter smithii</i> (strain PS / ATCC 35061 / DSM 861)   |
| A4YDN6           | METS5        | SIYSHG-AVTNLINAM         | NO         | Amino acid permease-associated region precursor: <i>Metallosphaera sedula</i> (strain ATCC 51363 / DSM 5348)  |
| <b>A8YFV6</b>    | <b>MICAE</b> | <b>GIFDNGSWRRNWLNLH</b>  | <b>NO</b>  | <b>CobQ protein: <i>Microcystis aeruginosa</i> PCC 7806</b>   |
| <b>A9V349</b>    | <b>MONBE</b> | <b>NKFIKG-ILQNFIEFW</b>  | <b>NO</b>  | <b>Predicted protein: <i>Monosiga brevicollis</i> MX1</b>   |
| <b>A9UUV3</b>    | <b>MONBE</b> | <b>HPYSKG-IWTNWKNFL</b>  | <b>YES</b> | <b>Predicted protein: <i>Monosiga brevicollis</i> MX1</b>   |
| <b>A9V2R0</b>    | <b>MONBE</b> | <b>SPFHRG-LFGNLAEFY</b>  | <b>YES</b> | <b>Predicted protein: <i>Monosiga brevicollis</i> MX1</b>   |
| <b>A9V523</b>    | <b>MONBE</b> | <b>YFPDMG-WWQNIKNAV</b>  | <b>YES</b> | <b>Predicted protein: <i>Monosiga brevicollis</i> MX1</b>   |
| A2AF28           | MOUSE        | QAYTLG-AISNFMSTF         | NO         | Novel protein putative orthologue to human mitochondrial carrier triple repeat 6: <i>Mus musculus</i> (Mouse)   |
| A2AF34           | MOUSE        | QAYTLG-AISNFMSTF         | NO         | Novel protein putative orthologue to human mitochondrial carrier triple repeat 6: <i>Mus musculus</i> (Mouse)   |
| A2AF35           | MOUSE        | QAYTLG-AISNFMSTF         | NO         | Novel protein putative orthologue to human mitochondrial carrier triple repeat 6: <i>Mus musculus</i> (Mouse)   |
| Q35402           | MOUSE        | KFFRKG-VVGNWREYF         | NO         | Sulfotransferase-related protein: <i>Mus musculus</i> (Mouse)   |
| Q3THK0           | MOUSE        | DKFDKG-YSYNIRHSF         | NO         | CRL-1722 L5178Y-R cDNA, RIKEN full-length enriched library, clone:l730071F18 product:DNA primase, p58 subunit, full insert sequence: <i>Mus musculus</i> (Mouse)                  |
| Q3TL46           | MOUSE        | DKFDKG-YSYNIRHSF         | NO         | Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:l1C0002J24 product:DNA primase, p58 subunit, full insert sequence: <i>Mus musculus</i> (Mouse)              |
| Q3TPT1           | MOUSE        | KFFRKG-VVGNWREYF         | NO         | Adult male hippocampus cDNA, RIKEN full-length enriched library, clone:C630020H04 product:sulfotransferase family 5A, member 1, full insert sequence: <i>Mus musculus</i> (Mouse) |

Table S3 Contd.

| Accession number | Organism     | PaCCT motif              | DHHC       | Description  |
|------------------|--------------|--------------------------|------------|--|
| Q3TPW2           | MOUSE        | NPWERKSYWKNMLEAV         | NO         | 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530012F18 product:Tk protein kinase, full insert sequence: <i>Mus musculus</i> (Mouse)   |
| Q692V3           | MOUSE        | NLYHEE-FVENCKQVF         | NO         | Grp94 neighboring nucleotidase variant 3: <i>Mus musculus</i> (Mouse)  |
| Q692V4           | MOUSE        | NLYHEE-FVENCKQVF         | NO         | Grp94 neighboring nucleotidase variant 2: <i>Mus musculus</i> (Mouse)  |
| Q692V5           | MOUSE        | NLYHEE-FVENCKQVF         | NO         | Grp94 neighboring nucleotidase variant 1: <i>Mus musculus</i> (Mouse)  |
| Q6PD96           | MOUSE        | NPWERKSYWKNMLEAV         | NO         | Tk protein: <i>Mus musculus</i> (Mouse)  |
| Q7TNR4           | MOUSE        | FPYHRG-SVCNLSL           | NO         | D73001G18Rik protein: <i>Mus musculus</i> (Mouse)  |
| Q8BY97           | MOUSE        | NPWERKSYWKNMLEAV         | NO         | 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630014N10 product:DUAL SPECIFICITY PROTEIN KINASE TTK: <i>Mus musculus</i> (Mouse)  |
| Q8CAZ6           | MOUSE        | FPYHRG-SVCNLSL           | NO         | 6 days neonate skin cDNA, RIKEN full-length enriched library, clone:A030004E11 product:hypothetical Prokaryotic membrane lipoprotein lipid attachment site containing protein, full insert sequence: <i>Mus musculus</i> (Mouse) |
| Q8K0V5           | MOUSE        | NLYHEE-FVENCKQVF         | NO         | BC030307 protein: <i>Mus musculus</i> (Mouse)  |
| Q91X36           | MOUSE        | KFFRKG-VVGNWREYF         | NO         | Sulfotransferase family 5A, member 1: <i>Mus musculus</i> (Mouse)  |
| <b>A0JP44</b>    | <b>MOUSE</b> | <b>NGFSLG-FSKNMRQVF</b>  | <b>YES</b> | <b>Zinc finger, DHHC domain containing 2: <i>Mus musculus</i> (Mouse)</b>  |
| <b>A2A9F0</b>    | <b>MOUSE</b> | <b>NPYSHKSIITNCCAVAL</b> | <b>YES</b> | <b>Zinc finger, DHHC domain containing 18: <i>Mus musculus</i> (Mouse)</b>   |
| <b>A2BE99</b>    | <b>MOUSE</b> | <b>NPFDGRG-PTRNLAHFF</b> | <b>YES</b> | <b>Zinc finger DHHC domain containing 12: <i>Mus musculus</i> (Mouse)</b>  |
| <b>A2BEA0</b>    | <b>MOUSE</b> | <b>NPFDGRG-PTRNLAHFF</b> | <b>YES</b> | <b>Zinc finger DHHC domain containing 12: <i>Mus musculus</i> (Mouse)</b>  |
| <b>A4FUU5</b>    | <b>MOUSE</b> | <b>NGFSLG-FSKNMRQVF</b>  | <b>YES</b> | <b>Zdhhc2 protein: <i>Mus musculus</i> (Mouse)</b>   |
| A6H5Y4           | MOUSE        | GQYNRG-FLRNWLQFS         | YES        | Zinc finger, DHHC domain containing 23: <i>Mus musculus</i> (Mouse)  |
| <b>A6H614</b>    | <b>MOUSE</b> | <b>NPYSHKSIITNCCAVAL</b> | <b>YES</b> | <b>Zdhhc18 protein: <i>Mus musculus</i> (Mouse)</b>  |
| <b>Q0VFY6</b>    | <b>MOUSE</b> | <b>SPFNHG-CVRNIIDFF</b>  | <b>YES</b> | <b>Zinc finger, DHHC domain containing 17: <i>Mus musculus</i> (Mouse)</b>   |
| <b>Q2TGE7</b>    | <b>MOUSE</b> | <b>NPFTNG-CYGNVEHVL</b>  | <b>YES</b> | <b>Membrane-associated DHHC8 zinc finger protein: <i>Mus musculus</i> (Mouse)</b>  |
| <b>Q2TGE8</b>    | <b>MOUSE</b> | <b>NPFTNG-CCNNVSRVL</b>  | <b>YES</b> | <b>Membrane-associated DHHC5 zinc finger protein: <i>Mus musculus</i> (Mouse)</b>  |
| A5IXG6           | MYCAA        | DLYSLGYNISFKDIF          | NO         | Putative uncharacterized protein: <i>Mycoplasma agalactiae</i>   |
| Q5ZZM2           | MYCH2        | SNYNLG-LLNSFKSFF         | NO         | Multidrug resistance protein homologue: <i>Mycoplasma hyopneumoniae</i> (strain 232)   |
| Q4A763           | MYCH7        | SNYNLG-LLNSFKSFF         | NO         | ABC transporter ATP-binding-Pr1: <i>Mycoplasma hyopneumoniae</i> (strain 7448)   |
| Q4A924           | MYCHJ        | SNYNLG-LLNSFKSFF         | NO         | Putative ABC transporter ATP-binding-Pr1: <i>Mycoplasma hyopneumoniae</i> (strain J/ATCC 25934/NCTC 10110)   |
| Q49519           | MYCHY        | SNYNLG-LLNSFKSFF         | NO         | Multidrug resistance protein homologue: <i>Mycoplasma hyopneumoniae</i>  |
| Q49521           | MYCHY        | SNYNLG-LLNSFKSFF         | NO         | Pr1: <i>Mycoplasma hyopneumoniae</i>   |
| Q79DE7           | MYCHY        | SNYNLG-LLNSFKSFF         | NO         | Multidrug resistance protein homologue: <i>Mycoplasma hyopneumoniae</i>  |
| Q6KH46           | MYCMO        | NPFTKG-LANNTMQAL         | NO         | Putative uncharacterized protein: <i>Mycoplasma mobile</i>   |
| Q6MT62           | MYCMS        | NVFKTG-CLKNLEIFL         | NO         | Putative uncharacterized protein: <i>Mycoplasma mycoides</i> subsp. <i>mycoides</i> SC   |
| Q6MTT3           | MYCMS        | NKYYVS-VYNNAKQLL         | NO         | Putative uncharacterized protein: <i>Mycoplasma mycoides</i> subsp. <i>mycoides</i> SC   |
| Q4A656           | MYCS5        | NAFDLK-LINNLEKIF         | NO         | Heat-inducible transcription repressor: <i>Mycoplasma synoviae</i> (strain 53)   |
| Q4A680           | MYCS5        | TKFNNG-FLDNALEVF         | NO         | Putative uncharacterized protein: <i>Mycoplasma synoviae</i> (strain 53)   |
| Q1CW70           | MYXXD        | NRYETG-FLSNYADV          | NO         | Efflux transporter, HAE1 family, inner membrane component: <i>Myxococcus xanthus</i> (strain DK 1622)  |
| Q3IT86           | NATPD        | NPWSRK-RRENFTQCC         | NO         | Precorin-3B C17-methyltransferase 2: <i>Natronomonas pharaonis</i> (strain DSM 2160 / ATCC 35678)  |
| Q5F711           | NEIG1        | GFFSVG-IIMNLKLVF         | NO         | Transport protein: <i>Neisseria gonorrhoeae</i> (strain ATCC 700825 / FA 1090)   |
| A9M225           | NEIMO        | GFFSVG-IIMNLKLVF         | NO         | Biopolymer transport protein: <i>Neisseria meningitidis</i> serogroup C (strain 053442)  |
| A7RX89           | NEMVE        | NVFTLS-TRNNWMTVM         | NO         | Predicted protein: <i>Nematostella vectensis</i> (Starlet sea anemone)   |
| A7SDG9           | NEMVE        | HAFNVS-RIKNWIGVF         | NO         | Predicted protein: <i>Nematostella vectensis</i> (Starlet sea anemone)   |
| A7SVN8           | NEMVE        | HAFHRK-YLRNLMQAF         | NO         | Predicted protein: <i>Nematostella vectensis</i> (Starlet sea anemone)   |
| <b>A7RQ92</b>    | <b>NEMVE</b> | <b>YPYNGF-WKENFRQVL</b>  | <b>YES</b> | <b>Predicted protein: <i>Nematostella vectensis</i> (Starlet sea anemone)</b>  |
| <b>A7RQK1</b>    | <b>NEMVE</b> | <b>NPYNYG-AWDNWRMLM</b>  | <b>YES</b> | <b>Predicted protein: <i>Nematostella vectensis</i> (Starlet sea anemone)</b>  |
| <b>A7RWD7</b>    | <b>NEMVE</b> | <b>NPFDQG-YLCNVYGF</b>   | <b>YES</b> | <b>Predicted protein: <i>Nematostella vectensis</i> (Starlet sea anemone)</b>  |
| A7RZK6           | NEMVE        | SPFSRN-LFNSIGDFF         | YES        | Predicted protein: <i>Nematostella vectensis</i> (Starlet sea anemone)   |
| A7S6A3           | NEMVE        | DAFDLGLTRLNVEQVF         | YES        | Predicted protein: <i>Nematostella vectensis</i> (Starlet sea anemone)   |
| <b>A7S9E6</b>    | <b>NEMVE</b> | <b>NPFDLG-CRSNCNAVL</b>  | <b>YES</b> | <b>Predicted protein: <i>Nematostella vectensis</i> (Starlet sea anemone)</b>  |
| <b>A7SCF8</b>    | <b>NEMVE</b> | <b>NPYVSGSSCGNCLAVI</b>  | <b>YES</b> | <b>Predicted protein: <i>Nematostella vectensis</i> (Starlet sea anemone)</b>  |
| <b>A7SIV7</b>    | <b>NEMVE</b> | <b>NPHYKG-FLQNWKDFL</b>  | <b>YES</b> | <b>Predicted protein: <i>Nematostella vectensis</i> (Starlet sea anemone)</b>  |
| <b>A7SWQ7</b>    | <b>NEMVE</b> | <b>RIYDKG-WLRNFIEVL</b>  | <b>YES</b> | <b>Predicted protein: <i>Nematostella vectensis</i> (Starlet sea anemone)</b>  |
| A1DER4           | NEOFI        | NKYDFG-LLQNMTTAI         | NO         | Beige/BEACH domain protein: <i>Neosartorya fischeri</i> (strain ATCC 1020 / DSM 3700 / NRRL 181) ( <i>Aspergillus fischerianus</i> (strain ATCC 1020 / DSM 3700 / NRRL 181))   |
| <b>A1DEV8</b>    | <b>NEOFI</b> | <b>NPFDLGSPLKNIQQVM</b>  | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Neosartorya fischeri</i> (strain ATCC 1020 / DSM 3700 / NRRL 181) [<i>Aspergillus fischerianus</i> (strain ATCC 1020 / DSM 3700 / NRRL 181)]</b>   |
| <b>A1D865</b>    | <b>NEOFI</b> | <b>RPFTQGNIFRNWISVL</b>  | <b>YES</b> | <b>DHHC zinc finger membrane protein, putative: <i>Neosartorya fischeri</i> (strain ATCC 1020 / DSM 3700 / NRRL 181) [<i>Aspergillus fischerianus</i> (strain ATCC 1020 / DSM 3700 / NRRL 181)]</b>                              |
| <b>A1DBJ0</b>    | <b>NEOFI</b> | <b>FPYDIG-IWSNIKAGM</b>  | <b>YES</b> | <b>DHHC zinc finger membrane protein: <i>Neosartorya fischeri</i> (strain ATCC 1020 / DSM 3700 / NRRL 181) [<i>Aspergillus fischerianus</i> (strain ATCC 1020 / DSM 3700 / NRRL 181)]</b>  |
| <b>A1DG82</b>    | <b>NEOFI</b> | <b>NPFSRG-IITNCRDFW</b>  | <b>YES</b> | <b>Palmitoyltransferase: <i>Neosartorya fischeri</i> (strain ATCC 1020 / DSM 3700 / NRRL 181) [<i>Aspergillus fischerianus</i> (strain ATCC 1020 / DSM 3700 / NRRL 181)]</b>   |
| <b>A1DIK7</b>    | <b>NEOFI</b> | <b>HAFDLG-WRRNLLHLF</b>  | <b>YES</b> | <b>DHHC zinc finger membrane protein: <i>Neosartorya fischeri</i> (strain ATCC 1020 / DSM 3700 / NRRL 181) [<i>Aspergillus fischerianus</i> (strain ATCC 1020 / DSM 3700 / NRRL 181)]</b>  |
| <b>A1DMF7</b>    | <b>NEOFI</b> | <b>NIYDLG-FWDNLREIF</b>  | <b>YES</b> | <b>DHHC zinc finger domain protein: <i>Neosartorya fischeri</i> (strain ATCC 1020 / DSM 3700 / NRRL 181) [<i>Aspergillus fischerianus</i> (strain ATCC 1020 / DSM 3700 / NRRL 181)]</b>  |
| A7UW05           | NEUCR        | RPFSGS-PVSNLCSVC         | NO         | Putative uncharacterized protein: <i>Neurospora crassa</i>   |
| <b>Q7SDN8</b>    | <b>NEUCR</b> | <b>NPWDLG-FYRNWKSVM</b>  | <b>NO</b>  | <b>Predicted protein: <i>Neurospora crassa</i></b>   |
| Q7SGM7           | NEUCR        | FQYTRGHLWRNWAVII         | NO         | Putative uncharacterized protein: <i>Neurospora crassa</i>   |
| Q0AET4           | NITEC        | GRFDRGNWSLNLNLETW        | NO         | TonB-dependent vitamin B12 receptor precursor: <i>Nitrosomonas eutropha</i> (strain C71)   |

Table S3 Contd.

| Accession number | Organism     | PaCCT motif              | DHHC       | Description  |
|------------------|--------------|--------------------------|------------|--|
| <b>Q1QNM4</b>    | <b>NITHX</b> | <b>HRYDRG-FCINVLVSI</b>  | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Nitrobacter hamburgensis</i> (strain X14 / DSM 10229)</b>        |
| A0ZKQ5           | NODSP        | LLFKLG-VKINIRQFF         | NO         | Putative uncharacterized protein: <i>Nodularia spumigena</i> CCY 9414                                    |
| Q2GB03           | NOVAD        | GYWNVG-ARLNWKEIM         | NO         | TonB-dependent receptor precursor: <i>Novosphingobium aromaticivorans</i> (strain DSM 12444)             |
| Q0IL34           | NPVLS        | TIFNKKNCSSNMRHVF         | NO         | ORF85: <i>Leucania separata</i> nuclear polyhedrosis virus (LsNPV)                                       |
| A8QJT8           | ONCMY        | SMYHRGNILNMRSLV          | NO         | Rh30-like2: <i>Oncorhynchus mykiss</i> (Rainbow trout) (Salmo gairdneri)                                 |
| A8QJT9           | ONCMY        | SMYHRGNILNMRSLV          | NO         | Rh30-like3: <i>Oncorhynchus mykiss</i> (Rainbow trout) (Salmo gairdneri)                                 |
| Q6XV78           | ONCMY        | SMYHRGNILNMRSLV          | NO         | RhAG-like protein: <i>Oncorhynchus mykiss</i> (Rainbow trout) (Salmo gairdneri)                          |
| <b>Q01JA7</b>    | <b>ORYSA</b> | <b>HPFSKG-ICRNLYDLC</b>  | <b>YES</b> | <b>H0211B05.5 protein: <i>Oryza sativa</i> (Rice)</b>  |
| A2WWQ0           | ORYSI        | HNYSVG-CFNLLKNSM         | NO         | Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)                               |
| <b>A2WXC6</b>    | <b>ORYSI</b> | <b>NAYDRG-CMNNFLEVF</b>  | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)</b>                        |
| <b>A2Y5E1</b>    | <b>ORYSI</b> | <b>HPYHLG-VYENLIVSVL</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)</b>                        |
| A2YH92           | ORYSI        | SFFTLG-WILNALSFC         | NO         | Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)                               |
| A2YJR8           | ORYSI        | LPWHHG-RVNNINVL          | NO         | Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)                               |
| A2YMW0           | ORYSI        | SPFNRRHHCRCNGEIF         | NO         | Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)                               |
| <b>A2YQC7</b>    | <b>ORYSI</b> | <b>NVDFRG-CMNNCSEFF</b>  | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)</b>                        |
| A2YRS4           | ORYSI        | HNYSVG-CFNLLKNSM         | NO         | Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)                               |
| <b>A2ZKH0</b>    | <b>ORYSI</b> | <b>HPFSKG-ICRNIVVFC</b>  | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)</b>                        |
| A2ZKQ2           | ORYSI        | HNYSVG-CFNLLKNSM         | NO         | Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)                               |
| <b>A2WNG8</b>    | <b>ORYSI</b> | <b>NPYNRG-ALSNAIEVF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)</b>                        |
| <b>A2WWX4</b>    | <b>ORYSI</b> | <b>HPYDLG-VYENLIVSVL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)</b>                        |
| <b>A2WYJ9</b>    | <b>ORYSI</b> | <b>NPYNRG-VVENIKEIF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)</b>                        |
| <b>A2X1P6</b>    | <b>ORYSI</b> | <b>NPFDHG-VRKNCDFL</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)</b>                        |
| <b>A2XB30</b>    | <b>ORYSI</b> | <b>HRFDLG-TRKNIQMIM</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)</b>                        |
| <b>A2XWF2</b>    | <b>ORYSI</b> | <b>HPFSKG-ICRNLYDLC</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)</b>                        |
| <b>A2Y517</b>    | <b>ORYSI</b> | <b>NVYDQG-CLNCLGVF</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)</b>                        |
| <b>A2YFJ6</b>    | <b>ORYSI</b> | <b>NPFDHG-ARKNCSEFL</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)</b>                        |
| <b>A2YXH4</b>    | <b>ORYSI</b> | <b>NPYNRG-VLNNFLEIF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)</b>                        |
| <b>A2YXK1</b>    | <b>ORYSI</b> | <b>NPHNRG-LVQNFIEIL</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)</b>                        |
| <b>A2Z2Y3</b>    | <b>ORYSI</b> | <b>NPYNRG-MVNNFLEIF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)</b>                        |
| <b>A2ZEZ9</b>    | <b>ORYSI</b> | <b>NPHNRG-VAKNVAEIF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)</b>                        |
| <b>A2ZF87</b>    | <b>ORYSI</b> | <b>NPYSRG-CRRNCADFL</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)</b>                        |
| A2ZHT5           | ORYSI        | NPYRKS-IAANFVDVF         | YES        | Putative uncharacterized protein: <i>Oryza sativa</i> subsp. indica (Rice)                               |
| <b>A2ZZZ0</b>    | <b>ORYSJ</b> | <b>NAYDRG-CMNNFLEVF</b>  | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                      |
| A3AS00           | ORYSJ        | HPWNRG-ELSNMIQHM         | NO         | Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)                             |
| <b>A3B4R9</b>    | <b>ORYSJ</b> | <b>HPYHLG-VYENLIVSVL</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                      |
| A3BFN7           | ORYSJ        | SFFTLG-WILNALSFC         | NO         | Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)                             |
| A3BI45           | ORYSJ        | LPWHHG-RVNNINNV          | NO         | Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)                             |
| A3BLE0           | ORYSJ        | SPFNRRHHCRCNGEIF         | NO         | Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)                             |
| A3BQ62           | ORYSJ        | HNYSVG-CFNLLKNSM         | NO         | Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)                             |
| <b>A3CHB2</b>    | <b>ORYSJ</b> | <b>HPFSKG-ICRNIVVFC</b>  | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                      |
| Q0D593           | ORYSJ        | SPFNRRHHCRCNGEIF         | NO         | Os07g0573300 protein: <i>Oryza sativa</i> subsp. japonica (Rice)   |
| <b>Q0J8M9</b>    | <b>ORYSJ</b> | <b>NVDFRG-CMNNCSEFF</b>  | <b>NO</b>  | <b>Os08g0103400 protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                                  |
| <b>Q5TKN4</b>    | <b>ORYSJ</b> | <b>NVYDQG-CLNCLGVF</b>   | <b>NO</b>  | <b>Putative zinc finger DHHC domain containing protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>   |
| Q6ZL20           | ORYSJ        | SPFNRRHHCRCNGEIF         | NO         | Putative uncharacterized protein OJ1699_E05.17: <i>Oryza sativa</i> subsp. japonica (Rice)               |
| Q7XVW7           | ORYSJ        | HPWNRG-ELSNMIQHM         | NO         | OSJNBa0065J03.4 protein: <i>Oryza sativa</i> subsp. japonica (Rice)                                      |
| <b>A2ZRU0</b>    | <b>ORYSJ</b> | <b>NPYNRG-AISNAIEVF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                      |
| <b>A2Z11</b>     | <b>ORYSJ</b> | <b>HPYDLG-VYENLIVSVL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                      |
| <b>A3A136</b>    | <b>ORYSJ</b> | <b>NPYNRG-VMENIKDIF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                      |
| <b>A3A3V4</b>    | <b>ORYSJ</b> | <b>NPFDHG-VRKNCDFL</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                      |
| <b>A3ACQ7</b>    | <b>ORYSJ</b> | <b>HRFDLG-TRKNIQMIM</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                      |
| <b>A3AI80</b>    | <b>ORYSJ</b> | <b>NIYDRG-CIRNMCSEVF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                      |
| <b>A3AWE3</b>    | <b>ORYSJ</b> | <b>HPFSKG-ICRNLYDLC</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                      |
| <b>A3B4D7</b>    | <b>ORYSJ</b> | <b>NVYDQG-CLNCLGVF</b>   | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                      |
| <b>A3BE13</b>    | <b>ORYSJ</b> | <b>NPFDHG-ARKNCSEFL</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                      |
| <b>A3BV85</b>    | <b>ORYSJ</b> | <b>NPYNRG-VLNNFLEIF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                      |
| <b>A3BVA5</b>    | <b>ORYSJ</b> | <b>NPHNRG-LVQNFIEIL</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                      |
| <b>A3C0H5</b>    | <b>ORYSJ</b> | <b>NPYNRG-MVNNFLEIF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                      |
| <b>A3CBY9</b>    | <b>ORYSJ</b> | <b>NPHNRG-VAKNVAEIF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                      |
| <b>A3CC90</b>    | <b>ORYSJ</b> | <b>NPYSRG-CRRNCADFL</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                      |
| A3CEN8           | ORYSJ        | NPYRKS-IAANFVDVF         | YES        | Putative uncharacterized protein: <i>Oryza sativa</i> subsp. japonica (Rice)                             |
| <b>Q0DHW0</b>    | <b>ORYSJ</b> | <b>NVYDQG-CLNCLGVF</b>   | <b>YES</b> | <b>Os05g0436900 protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                                  |
| Q0IQC1           | ORYSJ        | NPYRKS-IAANFVDVF         | YES        | Os12g0131200 protein: <i>Oryza sativa</i> subsp. japonica (Rice)   |
| <b>Q0IS80</b>    | <b>ORYSJ</b> | <b>NPYSRG-CRRNCADFL</b>  | <b>YES</b> | <b>Os11g0549700 protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                                  |
| <b>Q0ISC9</b>    | <b>ORYSJ</b> | <b>NPHNRG-VAKNVAEIF</b>  | <b>YES</b> | <b>Os11g0534300 protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                                  |
| <b>Q0J0H9</b>    | <b>ORYSJ</b> | <b>NPYNRG-MVNNFLEIF</b>  | <b>YES</b> | <b>Os09g0508300 protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                                  |
| <b>Q0JB17</b>    | <b>ORYSJ</b> | <b>HPFSKG-ICRNLYDLC</b>  | <b>YES</b> | <b>Os04g0562000 protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                                  |
| <b>Q0JNM0</b>    | <b>ORYSJ</b> | <b>NPYNRG-AISNAIEVF</b>  | <b>YES</b> | <b>Os01g0279000 protein: <i>Oryza sativa</i> subsp. japonica (Rice)</b>                                  |
| <b>Q10L01</b>    | <b>ORYSJ</b> | <b>NIYDRG-MIRNMCSEVF</b> | <b>YES</b> | <b>Zinc finger family protein, putative, expressed: <i>Oryza sativa</i> subsp. japonica (Rice)</b>       |
| <b>Q2QQX2</b>    | <b>ORYSJ</b> | <b>HPFSKG-ICRNIVVFC</b>  | <b>YES</b> | <b>DHHC zinc finger domain containing protein, expressed: <i>Oryza sativa</i> subsp. japonica (Rice)</b> |
| Q2QY62           | ORYSJ        | NPYRKS-IAANFVDVF         | YES        | Zinc finger family protein, putative: <i>Oryza sativa</i> subsp. japonica (Rice)                         |

Table S3 Contd.

| Accession number | Organism | PaCCT motif       | DHHC | Description   |
|------------------|----------|-------------------|------|---|
| Q2R2S1           | ORYSJ    | NPYSRG-CRRNCADFL  | YES  | Ankyrin repeat S-palmitoyl transferase, putative, expressed: <i>Oryza sativa</i> subsp. japonica (Rice) |
| Q2R367           | ORYSJ    | NPHNRG-VAKNVAEIF  | YES  | DHHC zinc finger domain containing protein, expressed: <i>Oryza sativa</i> subsp. japonica (Rice)       |
| Q2RAX9           | ORYSJ    | NPYRKS-VAANFVEVF  | YES  | Zinc finger family protein, putative, expressed: <i>Oryza sativa</i> subsp. japonica (Rice)             |
| Q5JK16           | ORYSJ    | NPYNRG-VMENIKDIF  | YES  | Putative zisp: <i>Oryza sativa</i> subsp. japonica (Rice)   |
| Q5N959           | ORYSJ    | NAYDRG-CMNNFLEVF  | YES  | Putative NEW1 domain containing protein isoform: <i>Oryza sativa</i> subsp. japonica (Rice)             |
| Q5N9N4           | ORYSJ    | HPYDLG-VYENLVSVL  | YES  | Zinc finger DHHC domain containing protein 2-like: <i>Oryza sativa</i> subsp. japonica (Rice)           |
| Q65XG2           | ORYSJ    | HPYHLG-VYENLVSVL  | YES  | Putative uncharacterized protein OJ1362_D02.5: <i>Oryza sativa</i> subsp. japonica (Rice)               |
| Q67WV3           | ORYSJ    | NPFDRG-ARKNCSEFL  | YES  | Ankyrin repeat-containing protein-like: <i>Oryza sativa</i> subsp. japonica (Rice)                      |
| Q69UA2           | ORYSJ    | NPHNRG-LVQNFIEIL  | YES  | Putative DHHC-type zinc finger domain-containing protein: <i>Oryza sativa</i> subsp. japonica (Rice)    |
| Q6H885           | ORYSJ    | NPFDRG-VRKNCSDFL  | YES  | Putative ankyrin repeat-containing protein: <i>Oryza sativa</i> subsp. japonica (Rice)                  |
| Q6I5K4           | ORYSJ    | NVYDQG-CLNNCLGVF  | YES  | Putative uncharacterized protein OSJNBb0088F07.15: <i>Oryza sativa</i> subsp. japonica (Rice)           |
| Q6K9R3           | ORYSJ    | HRFDLG-TRKNIQMIM  | YES  | Zinc finger-like: <i>Oryza sativa</i> subsp. japonica (Rice)  |
| Q6Z1H3           | ORYSJ    | NPYNRG-VLNNFLEIF  | YES  | Putative DHHC-type zinc finger domain-containing protein: <i>Oryza sativa</i> subsp. japonica (Rice)    |
| Q75HK0           | ORYSJ    | WMYDIG-RFRNFQVVF  | YES  | Putative zinc finger protein: <i>Oryza sativa</i> subsp. japonica (Rice)                                |
| Q7XSQ0           | ORYSJ    | HPFSKG-ICRNLYDLC  | YES  | OSJNBa0084K11.19 protein: <i>Oryza sativa</i> subsp. japonica (Rice)                                    |
| Q8RUU5           | ORYSJ    | NPYNRG-VMENIKDIF  | YES  | P0482D04.5 protein: <i>Oryza sativa</i> subsp. japonica (Rice)  |
| A4RUP4           | OSTLU    | HPYSLG-LLANLREIL  | YES  | Predicted protein: <i>Ostreococcus lucimarinus</i> (strain CCE9901)                                     |
| A4S2I4           | OSTLU    | WKYDLG-RFRNFKEVF  | YES  | Predicted protein: <i>Ostreococcus lucimarinus</i> (strain CCE9901)                                     |
| A4S2V1           | OSTLU    | NPFDRGSFARNLRAFF  | YES  | Predicted protein: <i>Ostreococcus lucimarinus</i> (strain CCE9901)                                     |
| A4S3K8           | OSTLU    | KPFDEG-AIENARTAC  | YES  | Predicted protein: <i>Ostreococcus lucimarinus</i> (strain CCE9901)                                     |
| A4S693           | OSTLU    | NKYDVG-IWGNIKEVL  | YES  | Predicted protein: <i>Ostreococcus lucimarinus</i> (strain CCE9901)                                     |
| A4S8Y3           | OSTLU    | NPYNTG-SVLKNCYEVW | YES  | Predicted protein: <i>Ostreococcus lucimarinus</i> (strain CCE9901)                                     |
| Q00TM9           | OSTTA    | NPYNTG-SVFKNCLEVV | YES  | Putative DHHC-type zinc finger domain: <i>Ostreococcus tauri</i>  |
| Q00XC2           | OSTTA    | NAYDVG-VLRNLLLEV  | YES  | Zinc finger: <i>Ostreococcus tauri</i>  |
| Q010I9           | OSTTA    | NVFDAG-AWINCSMFV  | YES  | DHHC-type Zn-finger proteins: <i>Ostreococcus tauri</i>   |
| Q011G3           | OSTTA    | NPFDRGSHLANIGAFF  | YES  | Ankyrin repeat-containing protein-like: <i>Ostreococcus tauri</i>                                       |
| Q01BL9           | OSTTA    | HPFDQG-VVKNWQETF  | YES  | DHHC-type Zn-finger proteins: <i>Ostreococcus tauri</i>   |
| Q01CE2           | OSTTA    | HPYSLG-LLANLREIL  | YES  | DHHC-type Zn-finger proteins: <i>Ostreococcus tauri</i>   |
| Q50KL0           | PANTR    | NMFDINSLWNNLCQII  | NO   | Taste receptor type 2: <i>Pan troglodytes</i> (Chimpanzee)  |
| Q5UG17           | PANTR    | NMFDINSLWNNLCQII  | NO   | Taste receptor type 2: <i>Pan troglodytes</i> (Chimpanzee)  |
| A0BB16           | PARTE    | NIYYQG-VIHNFDVL   | NO   | Chromosome undetermined scaffold_1, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>        |
| A0BD84           | PARTE    | YKYTDG-NFNNFADVF  | NO   | Chromosome undetermined scaffold_10, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>       |
| A0BDZ0           | PARTE    | KKYSQS-IQSNFQVM   | NO   | Chromosome undetermined scaffold_101, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>      |
| A0BGG1           | PARTE    | SPFSYG-WLLNFTDAF  | NO   | Chromosome undetermined scaffold_106, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>      |
| A0BN02           | PARTE    | FPYHKS-AYENINQAF  | NO   | Chromosome undetermined scaffold_117, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>      |
| A0BUY5           | PARTE    | SYNKG-NLSNFLDLF   | NO   | Chromosome undetermined scaffold_13, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>       |
| A0C628           | PARTE    | YIYDKK-YRNNTKQFI  | NO   | Chromosome undetermined scaffold_151, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>      |
| A0C7Q9           | PARTE    | FMYTRG-VYENWVIL   | NO   | Chromosome undetermined scaffold_156, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>      |
| A0CB72           | PARTE    | SIYARG-CSQNILQLM  | NO   | Chromosome undetermined scaffold_163, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>      |
| A0CDT0           | PARTE    | NPFNKS-NVENLCMTL  | NO   | Chromosome undetermined scaffold_17, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>       |
| A0CFG1           | PARTE    | STYDFG-WLLNFTDAF  | NO   | Chromosome undetermined scaffold_175, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>      |
| A0CJF0           | PARTE    | NIYDSS-FKSNWKEFI  | NO   | Chromosome undetermined scaffold_2, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>        |
| A0CLE2           | PARTE    | SYNKG-NLSNFLDLF   | NO   | Chromosome undetermined scaffold_20, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>       |
| A0CXP1           | PARTE    | NPFDRG-FINNWSIFI  | NO   | Chromosome undetermined scaffold_30, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>       |
| A0D6S4           | PARTE    | NEFSLG-IWNNFLEVI  | NO   | Chromosome undetermined scaffold_4, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>        |
| A0DV98           | PARTE    | SLSYSG-SFSNLIDL   | NO   | Chromosome undetermined scaffold_65, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>       |
| A0DZU7           | PARTE    | SKFNQK-KIINLKQIF  | NO   | Chromosome undetermined scaffold_70, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>       |
| A0E679           | PARTE    | NIYYQG-VVHNFDVL   | NO   | Chromosome undetermined scaffold_8, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>        |
| A0E6T4           | PARTE    | DIYSIG-VIFNWLQFC  | NO   | Chromosome undetermined scaffold_80, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>       |
| Q6BG39           | PARTE    | NIYYQG-VIHNFDVL   | NO   | Putative uncharacterized protein: <i>Paramecium tetraurelia</i>   |
| A0BBL9           | PARTE    | NPFRRQNILKNIVQVL  | YES  | Chromosome undetermined scaffold_1, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>        |
| A0BKT9           | PARTE    | NQYDLK-PYYNWWQVF  | YES  | Chromosome undetermined scaffold_112, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>      |
| A0BY34           | PARTE    | SPFSSG-WKQNLQRYC  | YES  | Chromosome undetermined scaffold_136, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>      |
| A0C2Q5           | PARTE    | HPYNYG-LIKNIRLLF  | YES  | Chromosome undetermined scaffold_145, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>      |
| A0CDK0           | PARTE    | NPYDKGSISKNICNVL  | YES  | Chromosome undetermined scaffold_17, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>       |
| A0CMX0           | PARTE    | NPFRRQNFLKNIVNVL  | YES  | Chromosome undetermined scaffold_22, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>       |
| A0CSM1           | PARTE    | NAYDIG-FKENWLQVI  | YES  | Chromosome undetermined scaffold_26, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>       |
| A0CU39           | PARTE    | YPFDKG-VLNNIRLLL  | YES  | Chromosome undetermined scaffold_28, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>       |

Table S3 Contd.

| Accession number | Organism     | PaCCT motif             | DHHC       | Description  |
|------------------|--------------|-------------------------|------------|--|
| AOCYK7           | PARTE        | EHHDKG-VIANCKELL        | YES        | Chromosome undetermined scaffold_31, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>  |
| A0DLN1           | PARTE        | NPFSSKSKVIDNFKELF       | YES        | Chromosome undetermined scaffold_556, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>   |
| <b>A0DU03</b>    | <b>PARTE</b> | <b>LKYNEG-VWQNFKSIM</b> | <b>YES</b> | <b>Chromosome undetermined scaffold_63, whole genome shotgun sequence: <i>Paramecium tetraurelia</i></b>   |
| <b>A0DW17</b>    | <b>PARTE</b> | <b>NPFRRNKIFKNIQHVL</b> | <b>YES</b> | <b>Chromosome undetermined scaffold_67, whole genome shotgun sequence: <i>Paramecium tetraurelia</i></b>   |
| <b>A0DZC6</b>    | <b>PARTE</b> | <b>TKYDQG-IWLNQFSAL</b> | <b>YES</b> | <b>Chromosome undetermined scaffold_7, whole genome shotgun sequence: <i>Paramecium tetraurelia</i></b>  |
| <b>A0E2Y6</b>    | <b>PARTE</b> | <b>NQYDLK-PYYNWWQVF</b> | <b>YES</b> | <b>Chromosome undetermined scaffold_75, whole genome shotgun sequence: <i>Paramecium tetraurelia</i></b>   |
| <b>A0E3B3</b>    | <b>PARTE</b> | <b>NPFRRNKIFKNIQHVL</b> | <b>YES</b> | <b>Chromosome undetermined scaffold_76, whole genome shotgun sequence: <i>Paramecium tetraurelia</i></b>   |
| <b>A0E407</b>    | <b>PARTE</b> | <b>NLYNRG-WIANAAWFF</b> | <b>YES</b> | <b>Chromosome undetermined scaffold_77, whole genome shotgun sequence: <i>Paramecium tetraurelia</i></b>   |
| A0E6C1           | PARTE        | TIYNLG-FWYNFTFYF        | YES        | Chromosome undetermined scaffold_8, whole genome shotgun sequence: <i>Paramecium tetraurelia</i>   |
| <b>A0E767</b>    | <b>PARTE</b> | <b>HPYNFG-FIENKITYF</b> | <b>YES</b> | <b>Chromosome undetermined scaffold_80, whole genome shotgun sequence: <i>Paramecium tetraurelia</i></b>   |
| <b>A0E7J2</b>    | <b>PARTE</b> | <b>NLFDRG-TLSNIAWFF</b> | <b>YES</b> | <b>Chromosome undetermined scaffold_81, whole genome shotgun sequence: <i>Paramecium tetraurelia</i></b>   |
| <b>A0EG11</b>    | <b>PARTE</b> | <b>NLFNRG-ILSNIAWFF</b> | <b>YES</b> | <b>Chromosome undetermined scaffold_94, whole genome shotgun sequence: <i>Paramecium tetraurelia</i></b>   |
| <b>A0EH42</b>    | <b>PARTE</b> | <b>SPFSQG-WKRNLTQYC</b> | <b>YES</b> | <b>Chromosome undetermined scaffold_96, whole genome shotgun sequence: <i>Paramecium tetraurelia</i></b>   |
| <b>Q6BG63</b>    | <b>PARTE</b> | <b>NPFRRNKILNKIVQVL</b> | <b>YES</b> | <b>DHHC-type Zn-finger containing protein, putative: <i>Paramecium tetraurelia</i></b>   |
| Q6BG86           | PARTE        | TIYNLG-FWYNFTFYF        | YES        | DHHC-type Zn-finger containing protein, putative: <i>Paramecium tetraurelia</i>  |
| Q6MDP9           | PARUW        | HPHYKRNFWRNIIQQA        | NO         | Putative uncharacterized protein: <i>Protochlamydia amoebophila</i> (strain UWE25)   |
| A7JVC8           | PASHA        | LPFSKK-VLKNMKQSL        | NO         | P-ATPase superfamily P-type ATPase copper: <i>Mannheimia haemolytica</i> PHL213  |
| Q06Q13           | PASHA        | LPFSKK-VLKNMKQSL        | NO         | Cation transport ATPase: <i>Pasteurella haemolytica</i> ( <i>Mannheimia haemolytica</i> )  |
| A7IWZ7           | PBCVN        | RRWSLGTVCNNLWFL         | NO         | Putative uncharacterized protein B472R: <i>Paramecium bursaria</i> Chlorella virus NY2A (PBCV-NY2A)  |
| Q3B3R4           | PELLD        | LPFDKGCLVQNGITAL        | NO         | Electron transport complex, RnfABCDGE type, C subunit: <i>Pelodictyon luteolum</i> (strain DSM 273) ( <i>Chlorobium luteolum</i> (strain DSM 273)) |
| A1AK31           | PELPD        | GPHFRG-LFRNLRHRL        | NO         | ABC transporter related: <i>Pelobacter propionicus</i> (strain DSM 2379)   |
| <b>Q0U3S7</b>    | <b>PHANO</b> | <b>NPWSRG-IVTNCKDFF</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Phaeosphaeria nodorum</i> (<i>Septoria nodorum</i>)</b>  |
| Q0U7D9           | PHANO        | RVWNLG-FASNIVQRL        | NO         | Putative uncharacterized protein: <i>Phaeosphaeria nodorum</i> ( <i>Septoria nodorum</i> )   |
| <b>Q0UC09</b>    | <b>PHANO</b> | <b>NAFDLG-WKRNVAHV</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Phaeosphaeria nodorum</i> (<i>Septoria nodorum</i>)</b>  |
| <b>Q0UUW7</b>    | <b>PHANO</b> | <b>FPYDIG-ILRNICQGM</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Phaeosphaeria nodorum</i> (<i>Septoria nodorum</i>)</b>  |
| <b>Q0V6J9</b>    | <b>PHANO</b> | <b>RPFTQGSIKNWLAVL</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Phaeosphaeria nodorum</i> (<i>Septoria nodorum</i>)</b>  |
| <b>A9RB13</b>    | <b>PHYPA</b> | <b>NVYDLG-KLQNLQV</b>   | <b>NO</b>  | <b>Predicted protein: <i>Physcomitrella patens</i> subsp. <i>patens</i></b>  |
| A9RFZ3           | PHYPA        | RPWSYS-IWESIKDFF        | NO         | Predicted protein: <i>Physcomitrella patens</i> subsp. <i>patens</i>   |
| A9SLI0           | PHYPA        | NLFDHG-SCLNCKLSL        | NO         | Histone H3 methyltransferase complex, subunit CPS60/ASH2/BRE2: <i>Physcomitrella patens</i> subsp. <i>patens</i>                                   |
| A9SRF4           | PHYPA        | WLFYSYG-VLNNIAEVV       | NO         | Predicted protein: <i>Physcomitrella patens</i> subsp. <i>patens</i>   |
| A9T5Z3           | PHYPA        | NAFNLG-KFRNPSTVM        | NO         | Predicted protein: <i>Physcomitrella patens</i> subsp. <i>patens</i>   |
| <b>A9RSQ2</b>    | <b>PHYPA</b> | <b>NPYNRG-CVSNFNEIF</b> | <b>YES</b> | <b>Predicted protein: <i>Physcomitrella patens</i> subsp. <i>patens</i></b>  |
| <b>A9RYQ3</b>    | <b>PHYPA</b> | <b>NPYNRG-CLLNFEIF</b>  | <b>YES</b> | <b>Predicted protein: <i>Physcomitrella patens</i> subsp. <i>patens</i></b>  |
| A9SBS0           | PHYPA        | HPFSKG-MDANLSSFC        | YES        | Predicted protein: <i>Physcomitrella patens</i> subsp. <i>patens</i>   |
| <b>A9SDB4</b>    | <b>PHYPA</b> | <b>HPYDIG-IFINLVAAL</b> | <b>YES</b> | <b>Predicted protein: <i>Physcomitrella patens</i> subsp. <i>patens</i></b>  |
| <b>A9SEG7</b>    | <b>PHYPA</b> | <b>NPYDSG-CRKNCVDFL</b> | <b>YES</b> | <b>Predicted protein: <i>Physcomitrella patens</i> subsp. <i>patens</i></b>  |
| A9SHV9           | PHYPA        | HPFNRG-MDVNLYSFC        | YES        | Predicted protein: <i>Physcomitrella patens</i> subsp. <i>patens</i>   |
| <b>A9SZV7</b>    | <b>PHYPA</b> | <b>NPYDSG-CRKNCVDFL</b> | <b>YES</b> | <b>Predicted protein: <i>Physcomitrella patens</i> subsp. <i>patens</i></b>  |
| A9T4V6           | PHYPA        | HPFSKG-MDANLYSFC        | YES        | Predicted protein: <i>Physcomitrella patens</i> subsp. <i>patens</i>   |
| <b>A9TDM0</b>    | <b>PHYPA</b> | <b>NPYNQG-CPLNFNEIF</b> | <b>YES</b> | <b>Predicted protein: <i>Physcomitrella patens</i> subsp. <i>patens</i></b>  |
| <b>A9TR66</b>    | <b>PHYPA</b> | <b>WFLDLG-WKRNFEQVF</b> | <b>YES</b> | <b>Predicted protein: <i>Physcomitrella patens</i> subsp. <i>patens</i></b>  |
| <b>A9TX81</b>    | <b>PHYPA</b> | <b>HPYDVG-IFTNLVTAL</b> | <b>YES</b> | <b>Predicted protein: <i>Physcomitrella patens</i> subsp. <i>patens</i></b>  |
| A5DK81           | PICGU        | RPYSFS-PSRNWIHTF        | NO         | Putative uncharacterized protein: <i>Pichia guilliermondii</i> (Yeast) ( <i>Candida guilliermondii</i> )   |
| <b>A5DG65</b>    | <b>PICGU</b> | <b>NIFDLG-TMNNWKAVM</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Pichia guilliermondii</i> (Yeast) (<i>Candida guilliermondii</i>)</b>                                      |
| <b>A5DIT9</b>    | <b>PICGU</b> | <b>VPFDHG-IKQNWLDWF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Pichia guilliermondii</i> (Yeast) (<i>Candida guilliermondii</i>)</b>                                      |
| <b>A5DIZ1</b>    | <b>PICGU</b> | <b>NPYDSG-FWNNLKQRL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Pichia guilliermondii</i> (Yeast) (<i>Candida guilliermondii</i>)</b>                                      |
| <b>A5DR46</b>    | <b>PICGU</b> | <b>FPYDHG-FYKNTVNAL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Pichia guilliermondii</i> (Yeast) (<i>Candida guilliermondii</i>)</b>                                      |
| <b>A9NUM1</b>    | <b>PICSI</b> | <b>WRYDLG-CRKNFEQVF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Picea sitchensis</i> (Sitka spruce)</b>  |
| <b>A9NVN7</b>    | <b>PICSI</b> | <b>NPYNEG-IITNFAIF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Picea sitchensis</i> (Sitka spruce)</b>  |
| <b>A9NWT0</b>    | <b>PICSI</b> | <b>NPYHRG-LVQNFIEIF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Picea sitchensis</i> (Sitka spruce)</b>  |
| <b>A9NWW1</b>    | <b>PICSI</b> | <b>NPYNRG-VIHNFEIF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Picea sitchensis</i> (Sitka spruce)</b>  |
| A3LYX2           | PICST        | YKFDKK-YLENVLDIF        | NO         | Phosphatidylinositol-4-kinase involved in protein kinase C pathway: <i>Pichia stipitis</i> (Yeast)   |
| <b>A3GHM6</b>    | <b>PICST</b> | <b>HIYDLG-YYKNFTSIM</b> | <b>YES</b> | <b>Predicted protein: <i>Pichia stipitis</i> (Yeast)</b>   |
| <b>A3LXR6</b>    | <b>PICST</b> | <b>NIYDRG-FWNNLMERL</b> | <b>YES</b> | <b>Heme Binding Zinc finger protein: <i>Pichia stipitis</i> (Yeast)</b>  |
| <b>A3LY32</b>    | <b>PICST</b> | <b>FPYDRG-LWKNIDSC</b>  | <b>YES</b> | <b>Predicted protein: <i>Pichia stipitis</i> (Yeast)</b>   |
| A3LZ77           | PICST        | RVYDMG-AKKNFINLV        | YES        | Predicted protein: <i>Pichia stipitis</i> (Yeast)  |
| Q6L299           | PICTO        | NRYSKG-IFLSFLFF         | NO         | Putative uncharacterized protein: <i>Picrophilus torridus</i>  |
| Q85X68           | PINKO        | SPFGRG-SLRNILNFF        | NO         | ORF68a: <i>Pinus koraiensis</i> (Korean pine)  |
| <b>Q4YNV9</b>    | <b>PLABE</b> | <b>NYYDRKSKYLNLRDLF</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Plasmodium berghei</i></b>   |



Table S3 Contd.

| Accession number | Organism     | PaCCT motif             | DHHC       | Description  |
|------------------|--------------|-------------------------|------------|--|
| Q4YWR5           | PLABE        | NIYDLK-IEENVVMCF        | NO         | Putative uncharacterized protein: <i>Plasmodium berghei</i>  |
| Q4YXY6           | PLABE        | YIYTLN-FFKNCIDFI        | NO         | Putative uncharacterized protein: <i>Plasmodium berghei</i>  |
| Q4YYE9           | PLABE        | FIYDHN-NGENIIDFL        | NO         | Putative uncharacterized protein (Fragment): <i>Plasmodium berghei</i>   |
| Q4Z597           | PLABE        | NYHKNVCVLKNIKHAL        | NO         | Putative uncharacterized protein: <i>Plasmodium berghei</i>  |
| <b>Q4YNG4</b>    | <b>PLABE</b> | <b>KFYNGK-LYKNLKEVF</b> | <b>YES</b> | <b>Cell cycle regulator with zn-finger domain, putative: <i>Plasmodium berghei</i></b>   |
| <b>Q4YTM4</b>    | <b>PLABE</b> | <b>NPFNIG-VLNNIKEIL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Plasmodium berghei</i></b>   |
| <b>Q4YTP5</b>    | <b>PLABE</b> | <b>NIYNVG-CEDNAKQVF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Plasmodium berghei</i></b>   |
| <b>Q4Z2U5</b>    | <b>PLABE</b> | <b>NIYNLG-IEENFKQVL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Plasmodium berghei</i></b>   |
| Q4XX98           | PLACH        | NIFNMNNYKKNLKYIL        | NO         | Putative uncharacterized protein: <i>Plasmodium chabaudi</i>   |
| Q4XZA8           | PLACH        | NYHKNYVLKNIKYYVL        | NO         | Putative uncharacterized protein: <i>Plasmodium chabaudi</i>   |
| <b>Q4XZM6</b>    | <b>PLACH</b> | <b>NIYNLG-IEENFKQVL</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Plasmodium chabaudi</i></b>  |
| Q4Y1N3           | PLACH        | NIYDLK-IEENVVMCF        | NO         | Putative uncharacterized protein: <i>Plasmodium chabaudi</i>   |
| <b>Q4X2B6</b>    | <b>PLACH</b> | <b>NIYNVG-CEDNAKQVF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Plasmodium chabaudi</i></b>  |
| <b>Q4XES1</b>    | <b>PLACH</b> | <b>KFYNGK-LYKNLKEVF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Plasmodium chabaudi</i></b>  |
| <b>Q4XRR2</b>    | <b>PLACH</b> | <b>KFYNGK-LYKNLKEVF</b> | <b>YES</b> | <b>Cell cycle regulator with zn-finger domain, putative: <i>Plasmodium chabaudi</i></b>  |
| <b>Q4XYU1</b>    | <b>PLACH</b> | <b>NPFNIG-VLNNIKEIL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Plasmodium chabaudi</i></b>  |
| <b>Q4Y3I2</b>    | <b>PLACH</b> | <b>SPFDEG-KFTNLRKFF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Plasmodium chabaudi</i></b>  |
| <b>Q4Y6H3</b>    | <b>PLACH</b> | <b>NPFDSG-VYKNVNLFL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Plasmodium chabaudi</i></b>  |
| <b>Q4X9P8</b>    | <b>PLACH</b> | <b>NIYNVG-CEDNAKQVF</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Plasmodium chabaudi</i></b>  |
| Q96187           | PLAF7        | NIYDQK-LYLNFKNVI        | NO         | Putative uncharacterized protein PFB0470w: <i>Plasmodium falciparum</i> (isolate 3D7)  |
| Q5MYR6           | PLAF7        | DPYDIS-TVNNVKEFL        | NO         | Peroxiredoxin: <i>Plasmodium falciparum</i> (isolate 3D7)  |
| Q6LFA6           | PLAF7        | NSYDKKCIKKNFYSEI        | NO         | Putative uncharacterized protein: <i>Plasmodium falciparum</i> (isolate 3D7)   |
| Q6LFH6           | PLAF7        | NIYDLR-VIENVVLCF        | NO         | Putative uncharacterized protein: <i>Plasmodium falciparum</i> (isolate 3D7)   |
| Q6LFP6           | PLAF7        | NMFNKN-IRSNVKNIL        | NO         | Putative uncharacterized protein: <i>Plasmodium falciparum</i> (isolate 3D7)   |
| Q7KQK4           | PLAF7        | NIYNINLNKNNISSVF        | NO         | Zinc finger transcription factor: <i>Plasmodium falciparum</i> (isolate 3D7)   |
| Q8I3B4           | PLAF7        | NFFNSS-IIQNLINFL        | NO         | DEAD/DEAH box helicase, putative: <i>Plasmodium falciparum</i> (isolate 3D7)   |
| Q8IBG7           | PLAF7        | DPYDIS-TVNNVKEFL        | NO         | Antioxidant protein, putative: <i>Plasmodium falciparum</i> (isolate 3D7)  |
| <b>Q8IE53</b>    | <b>PLAF7</b> | <b>NPYNVK-ILKNCNAFI</b> | <b>NO</b>  | <b>AMP deaminase, putative: <i>Plasmodium falciparum</i> (isolate 3D7)</b>   |
| Q8IKT5           | PLAF7        | NIFNKG-KRQNLVSAY        | NO         | Peptidase, putative: <i>Plasmodium falciparum</i> (isolate 3D7)  |
| <b>Q6LFG8</b>    | <b>PLAF7</b> | <b>NIYNVG-CEDNAKQVF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Plasmodium falciparum</i> (isolate 3D7)</b>  |
| <b>Q8I3I3</b>    | <b>PLAF7</b> | <b>KYYNKG-FYKNFKDVF</b> | <b>YES</b> | <b>Cell cycle regulator with zn-finger domain, putative: <i>Plasmodium falciparum</i> (isolate 3D7)</b>  |
| <b>Q8IBV4</b>    | <b>PLAF7</b> | <b>NPFNIG-VLNNIKEIL</b> | <b>YES</b> | <b>Putative uncharacterized protein MAL7P1.68: <i>Plasmodium falciparum</i> (isolate 3D7)</b>  |
| <b>Q8IE90</b>    | <b>PLAF7</b> | <b>NPFDQG-MLFNFINFL</b> | <b>YES</b> | <b>Putative uncharacterized protein MAL13P1.126: <i>Plasmodium falciparum</i> (isolate 3D7)</b>  |
| <b>Q8IEA0</b>    | <b>PLAF7</b> | <b>NPFDEG-KYINLKKFL</b> | <b>YES</b> | <b>Putative uncharacterized protein MAL13P1.117: <i>Plasmodium falciparum</i> (isolate 3D7)</b>  |
| <b>Q8IJC5</b>    | <b>PLAF7</b> | <b>NIYDLG-VEENFKQVL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Plasmodium falciparum</i> (isolate 3D7)</b>  |
| Q25802           | PLAFA        | NLYNRRNIYLNKISVY        | NO         | RpoD protein: <i>Plasmodium falciparum</i>   |
| Q95Z59           | PLAFA        | NIYNINLNKNNISSVF        | NO         | Krox-like protein: <i>Plasmodium falciparum</i>  |
| <b>A5K1U2</b>    | <b>PLAVI</b> | <b>NMYNVG-CEDNAKQVF</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Plasmodium vivax</i></b>   |
| A5K3A0           | PLAVI        | RKYDHR-VSKNYKSVL        | NO         | Aspartyl proteinase, putative: <i>Plasmodium vivax</i>   |
| A5K4U9           | PLAVI        | NLYSRSSYYSNVEVFF        | NO         | GPI8p transamidase, putative: <i>Plasmodium vivax</i>  |
| A5K8H7           | PLAVI        | FLYHLGNLNCNNICGIL       | NO         | Putative uncharacterized protein: <i>Plasmodium vivax</i>  |
| <b>A5JZK1</b>    | <b>PLAVI</b> | <b>NPFDEG-KFLNLKKFL</b> | <b>YES</b> | <b>DHHC zinc finger domain containing protein: <i>Plasmodium vivax</i></b>   |
| <b>A5JZL4</b>    | <b>PLAVI</b> | <b>NPFNIG-VLNNIKEIL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Plasmodium vivax</i></b>   |
| <b>A5K312</b>    | <b>PLAVI</b> | <b>NPFDRG-ALFNLIHFF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Plasmodium vivax</i></b>   |
| <b>A5K975</b>    | <b>PLAVI</b> | <b>KYYNKG-MYQNFKDVF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Plasmodium vivax</i></b>   |
| <b>A5KBH8</b>    | <b>PLAVI</b> | <b>QFYNGK-FIKNVQDVL</b> | <b>YES</b> | <b>DHHC zinc finger domain containing protein: <i>Plasmodium vivax</i></b>   |
| <b>A5KE13</b>    | <b>PLAVI</b> | <b>SIYDLG-VEENFKQVL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Plasmodium vivax</i></b>   |
| <b>Q7RAA6</b>    | <b>PLAYO</b> | <b>KFYNGK-LYKNLKEVF</b> | <b>NO</b>  | <b>Putative uncharacterized protein PY06596: <i>Plasmodium yoelii yoelii</i></b>   |
| <b>Q7RAR5</b>    | <b>PLAYO</b> | <b>NYDYDKSKYLNLRDLF</b> | <b>NO</b>  | <b>Chloroquine resistance marker protein: <i>Plasmodium yoelii yoelii</i></b>  |
| Q7RGA7           | PLAYO        | NYYYLK-IFNNIQTIL        | NO         | Putative uncharacterized protein PY04440: <i>Plasmodium yoelii yoelii</i>  |
| <b>Q7RI23</b>    | <b>PLAYO</b> | <b>NPFYKN-LFENFIQIF</b> | <b>NO</b>  | <b>ADA2-like protein: <i>Plasmodium yoelii yoelii</i></b>  |
| Q7RIA5           | PLAYO        | FLYHLGNICNNICGIL        | NO         | CCAAT-box DNA binding protein subunit B, putative: <i>Plasmodium yoelii yoelii</i>   |
| Q7RJA9           | PLAYO        | NDFRRG-IRRNCTLVV        | NO         | Gbp1p protein-related: <i>Plasmodium yoelii yoelii</i>   |
| Q7RN13           | PLAYO        | SLYNSKSCENWKNLNF        | NO         | Putative uncharacterized protein PY02013: <i>Plasmodium yoelii yoelii</i>  |
| Q7RSE9           | PLAYO        | YIYTLN-FLKNCIDFI        | NO         | Putative uncharacterized protein PY00410: <i>Plasmodium yoelii yoelii</i>  |
| <b>Q7RLC7</b>    | <b>PLAYO</b> | <b>NPFNIG-VLNNIKEIL</b> | <b>YES</b> | <b>Putative uncharacterized protein PY02619: <i>Plasmodium yoelii yoelii</i></b>   |
| <b>Q7RN67</b>    | <b>PLAYO</b> | <b>NIYNVG-CEDNAKQVF</b> | <b>YES</b> | <b>DHHC zinc finger domain, putative: <i>Plasmodium yoelii yoelii</i></b>  |
| <b>Q7RS45</b>    | <b>PLAYO</b> | <b>NPFDRG-VYKNVNLFL</b> | <b>YES</b> | <b>Homo sapiens KIAA0946 protein: <i>Plasmodium yoelii yoelii</i></b>  |
| <b>A9PGN5</b>    | <b>POPTR</b> | <b>HLWNRS-PRRNCQVM</b>  | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Populus trichocarpa</i> (Western balsam poplar) (<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>)</b> |
| Q7TTQ2           | PROMP        | NYFNVG-FLRNIYSYF        | NO         | Possible NADH-Ubiquinone/plastoquinone: <i>Prochlorococcus marinus</i> subsp. <i>pastoris</i> (strain CCMP 1378 / MED4)                            |
| Q15PM1           | PSEA6        | TMYDLG-LSKNVADSL        | NO         | Mg2+ transporter protein, CorA-like: <i>Pseudoalteromonas atlantica</i> (strain T6c / BAA-1087)  |
| Q15UP6           | PSEA6        | HVFYQGSFYQNAIVL         | NO         | Putative uncharacterized protein: <i>Pseudoalteromonas atlantica</i> (strain T6c / BAA-1087)   |
| A6VDY6           | PSEA7        | QPQVQG-WESNLVHVL        | NO         | Probable secretion pathway ATPase: <i>Pseudomonas aeruginosa</i> (strain PA7)  |
| Q02EF4           | PSEAB        | QPQVQG-WESNLVHVL        | NO         | Putative general secretory pathway related protein: <i>Pseudomonas aeruginosa</i> (strain UCBBP-PA14)  |
| A3L254           | PSEAE        | QPQVQG-WESNLVHVL        | NO         | Putative uncharacterized protein: <i>Pseudomonas aeruginosa</i> C3719  |
| A3LIR8           | PSEAE        | QPQVQG-WESNLVHVL        | NO         | Putative uncharacterized protein: <i>Pseudomonas aeruginosa</i> 2192   |
| Q9HTY0           | PSEAE        | QPQVQG-WESNLVHVL        | NO         | Probable secretion pathway ATPase: <i>Pseudomonas aeruginosa</i>   |
| Q117Y5           | PSEE4        | RPFDRG-LMDNLESLEA       | NO         | Putative protease, U32 family: <i>Pseudomonas entomophila</i> (strain L48)   |

Table S3 Contd.

| Accession number | Organism     | PaCCT motif             | DHHC       | Description   |
|------------------|--------------|-------------------------|------------|---|
| A4V75            | PSEU5        | QPFVHG-WEANLTHVL        | NO         | Probable secretion pathway ATPase: <i>Pseudomonas stutzeri</i> (strain A1501)   |
| Q9UZH0           | PYRAB        | SPFDLG-SVINAERF         | NO         | Predicted nucleic acid-binding protein, contains PIN domain: <i>Pyrococcus abyssi</i>   |
| Q4V8C0           | RAT          | DKFDKG-YSYNIHRSF        | NO         | DNA primase, p58 subunit: <i>Rattus norvegicus</i> (Rat)  |
| Q5I0H2           | RAT          | RPWSYS-IWESIKDFF        | NO         | Eprs protein: <i>Rattus norvegicus</i> (Rat)  |
| Q6JB16           | RAT          | NPYYHG-PYLNLKAFE        | NO         | LM07b: <i>Rattus norvegicus</i> (Rat)   |
| Q6JB17           | RAT          | NPYYHG-PYLNLKAFE        | NO         | LM07a: <i>Rattus norvegicus</i> (Rat)   |
| Q6P3V7           | RAT          | NLYHEE-FVENCKQVF        | NO         | Gnn protein: <i>Rattus norvegicus</i> (Rat)   |
| Q6TXE9           | RAT          | RPWSYS-IWESIKDFF        | NO         | LRRGT00050: <i>Rattus norvegicus</i> (Rat)  |
| <b>A0JP15</b>    | <b>RAT</b>   | <b>NPYNYG-CLDNWKVFL</b> | <b>YES</b> | <b>Membrane-associated DHHC16 zinc finger protein: <i>Rattus norvegicus</i> (Rat)</b>   |
| <b>A0JP16</b>    | <b>RAT</b>   | <b>NGFSLG-CSKNWRQVF</b> | <b>YES</b> | <b>RGD1305755 protein: <i>Rattus norvegicus</i> (Rat)</b>   |
| <b>A1L111</b>    | <b>RAT</b>   | <b>NPYSHGNIWKNCCEVL</b> | <b>YES</b> | <b>Zinc finger, DHHC domain containing 9: <i>Rattus norvegicus</i> (Rat)</b>  |
| <b>Q2TGI6</b>    | <b>RAT</b>   | <b>NGFSLG-CSKNWRQVF</b> | <b>YES</b> | <b>Membrane-associated DHHC24 zinc finger protein: <i>Rattus norvegicus</i> (Rat)</b>   |
| Q2TGI7           | RAT          | GQYNRG-FLRNWLQFS        | YES        | Membrane-associated DHHC23 zinc finger protein: <i>Rattus norvegicus</i> (Rat)  |
| <b>Q2TGJ0</b>    | <b>RAT</b>   | <b>NPFDDG-FAKNWYLTM</b> | <b>YES</b> | <b>Membrane-associated DHHC19 zinc finger protein: <i>Rattus norvegicus</i> (Rat)</b>   |
| <b>Q2TGJ2</b>    | <b>RAT</b>   | <b>SPFNHG-CVRNIIDFF</b> | <b>YES</b> | <b>Membrane-associated DHHC17 zinc finger protein: <i>Rattus norvegicus</i> (Rat)</b>   |
| <b>Q2TGJ3</b>    | <b>RAT</b>   | <b>NPYNYG-CLDNWKVFL</b> | <b>YES</b> | <b>Membrane-associated DHHC16 zinc finger protein: <i>Rattus norvegicus</i> (Rat)</b>   |
| <b>Q2TGJ5</b>    | <b>RAT</b>   | <b>NPYSYGNIFTNCCVAL</b> | <b>YES</b> | <b>Membrane-associated DHHC14 zinc finger protein: <i>Rattus norvegicus</i> (Rat)</b>   |
| <b>Q2TGJ6</b>    | <b>RAT</b>   | <b>TPYNLG-FMQNLADFF</b> | <b>YES</b> | <b>Membrane-associated DHHC13 zinc finger protein: <i>Rattus norvegicus</i> (Rat)</b>   |
| <b>Q2TGJ9</b>    | <b>RAT</b>   | <b>NPYSHGNIWKNCCEVL</b> | <b>YES</b> | <b>Membrane-associated DHHC9 zinc finger protein: <i>Rattus norvegicus</i> (Rat)</b>  |
| <b>Q2TGK4</b>    | <b>RAT</b>   | <b>NGFSLG-FSKNMRQVF</b> | <b>YES</b> | <b>Membrane-associated DHHC2 zinc finger protein: <i>Rattus norvegicus</i> (Rat)</b>  |
| <b>Q2THW6</b>    | <b>RAT</b>   | <b>NPFTRG-CYGNVEHVL</b> | <b>YES</b> | <b>Membrane-associated DHHC8 zinc finger protein: <i>Rattus norvegicus</i> (Rat)</b>  |
| <b>Q2THW7</b>    | <b>RAT</b>   | <b>NPFTNG-CCNNVSRVL</b> | <b>YES</b> | <b>Membrane-associated DHHC5 zinc finger protein: <i>Rattus norvegicus</i> (Rat)</b>  |
| <b>Q32PY5</b>    | <b>RAT</b>   | <b>FPYDMGSKWKNLKQVF</b> | <b>YES</b> | <b>Zinc finger, DHHC domain containing 6: <i>Rattus norvegicus</i> (Rat)</b>  |
| <b>Q984Z8</b>    | <b>RHILO</b> | <b>DAFDRG-RFRNAIEVF</b> | <b>NO</b>  | <b>Mlr7776 protein: <i>Rhizobium loti</i> (Mesorhizobium loti)</b>  |
| Q7UWA6           | RHOBA        | HVYDEG-WLRSFFDAL        | NO         | Alpha-amylase: <i>Rhodopirellula baltica</i>  |
| A8GMS2           | RICAH        | LNFDLGNLNLIAFL          | NO         | Putative monovalent cation/H <sup>+</sup> antiporter subunit B: <i>Rickettsia akari</i> (strain Hartford)   |
| Q92IR5           | RICCN        | LNFDLGNLNLIAFL          | NO         | Putative uncharacterized protein: <i>Rickettsia conorii</i>   |
| Q4UKR3           | RICFE        | LNFDLGNLNLIAFL          | NO         | Multisubunit Na <sup>+</sup> /H <sup>+</sup> antiporter, MnhB subunit: <i>Rickettsia felis</i>  |
| B0BWU3           | RICRI        | LNFDLGNLNLIAFL          | NO         | <i>Rickettsia rickettsii</i> (strain Iowa)  |
| A8GRE2           | RICRS        | LNFDLGNLNLIAFL          | NO         | Putative monovalent cation/H <sup>+</sup> antiporter subunit B: <i>Rickettsia rickettsii</i> (strain Sheila Smith)  |
| Q7PB88           | RICSI        | LNFDLGNLNLIAFL          | NO         | Putative uncharacterized protein rsib_orf.351: <i>Rickettsia sibirica</i> 246   |
| Q68WC1           | RICTY        | NIYKLS-LLQNIILLM        | NO         | Putative uncharacterized protein: <i>Rickettsia typhi</i>   |
| A5UQQ0           | ROSS1        | DVYTRG-FIRNYAAF         | NO         | Helix-turn-helix domain protein: <i>Roseiflexus</i> sp. (strain RS-1)   |
| Q57SV9           | SALCH        | LTFDGG-WLDNWLQVF        | NO         | Putative xylanase/chitin deacetylase: <i>Salmonella choleraesuis</i>  |
| Q5PF92           | SALPA        | LTFDGG-WLDNWLQVF        | NO         | YbeJ-like protein: <i>Salmonella paratyphi</i> A  |
| A9MY26           | SALPB        | LTFDGG-WLDNWLQVF        | NO         | Putative uncharacterized protein: <i>Salmonella paratyphi</i> B (strain ATCC BAA-1250 / SPB7)   |
| Q82943           | SALTI        | LTFDGG-WLDNWLQVF        | NO         | Putative uncharacterized protein STY0338: <i>Salmonella typhi</i>   |
| Q8ZRK1           | SALTY        | LTFDGG-WLDNWLQVF        | NO         | Putative xylanase/chitin deacetylase: <i>Salmonella typhimurium</i>   |
| <b>Q5BRF3</b>    | <b>SCHJA</b> | <b>YPYDLG-KLANLQQVF</b> | <b>NO</b>  | <b>SJCHGC08456 protein: <i>Schistosoma japonicum</i> (Blood fluke)</b>  |
| <b>Q5C2V4</b>    | <b>SCHJA</b> | <b>NPFNQG-FLWNCYAFC</b> | <b>YES</b> | <b>SJCHGC02189 protein: <i>Schistosoma japonicum</i> (Blood fluke)</b>  |
| <b>Q5DDG3</b>    | <b>SCHJA</b> | <b>TLFNLG-IKENFRET</b>  | <b>YES</b> | <b>SJCHGC06311 protein: <i>Schistosoma japonicum</i> (Blood fluke)</b>  |
| <b>Q5DDK8</b>    | <b>SCHJA</b> | <b>YGFNLG-WKNNFLQVF</b> | <b>YES</b> | <b>SJCHGC00806 protein: <i>Schistosoma japonicum</i> (Blood fluke)</b>  |
| A7E7E1           | SCLS1        | RIFTKG-FYRNTVMVL        | NO         | Putative uncharacterized protein: <i>Sclerotinia sclerotiorum</i> (strain ATCC 18683 / 1980 / Ss-1) (White mold) ( <i>Whetzelinia sclerotiorum</i> )      |
| <b>A7ECX9</b>    | <b>SCLS1</b> | <b>NPWDLGSELLNWKSVM</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Sclerotinia sclerotiorum</i> (strain ATCC 18683 / 1980 / Ss-1) (White mold) (<i>Whetzelinia sclerotiorum</i>)</b> |
| A7EDI2           | SCLS1        | NPFRRG-SCSNIFQFA        | NO         | Predicted protein: <i>Sclerotinia sclerotiorum</i> (strain ATCC 18683 / 1980 / Ss-1) (White mold) ( <i>Whetzelinia sclerotiorum</i> )                     |
| A7EFG3           | SCLS1        | NPFSTGSYRRNTAALL        | NO         | Predicted protein: <i>Sclerotinia sclerotiorum</i> (strain ATCC 18683 / 1980 / Ss-1) (White mold) ( <i>Whetzelinia sclerotiorum</i> )                     |
| <b>A7EUC7</b>    | <b>SCLS1</b> | <b>NPFSRG-CVRNCKDFW</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Sclerotinia sclerotiorum</i> (strain ATCC 18683 / 1980 / Ss-1) (White mold) (<i>Whetzelinia sclerotiorum</i>)</b> |
| <b>A7EAG8</b>    | <b>SCLS1</b> | <b>NLYDIG-FVDNLKDV</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Sclerotinia sclerotiorum</i> (strain ATCC 18683 / 1980 / Ss-1) (White mold) (<i>Whetzelinia sclerotiorum</i>)</b> |
| <b>A7EFD4</b>    | <b>SCLS1</b> | <b>RPFTQGSVSNWIAVL</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Sclerotinia sclerotiorum</i> (strain ATCC 18683 / 1980 / Ss-1) (White mold) (<i>Whetzelinia sclerotiorum</i>)</b> |
| <b>A7EK21</b>    | <b>SCLS1</b> | <b>FPFDIG-IWENIVQAM</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Sclerotinia sclerotiorum</i> (strain ATCC 18683 / 1980 / Ss-1) (White mold) (<i>Whetzelinia sclerotiorum</i>)</b> |
| <b>A7F178</b>    | <b>SCLS1</b> | <b>SAFDLG-WRKNFKHLF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Sclerotinia sclerotiorum</i> (strain ATCC 18683 / 1980 / Ss-1) (White mold) (<i>Whetzelinia sclerotiorum</i>)</b> |
| A1S296           | SHEAM        | FLYGLG-CMENAKAVF        | NO         | Carbohydrate kinase, PfkB family: <i>Shewanella amazonensis</i> (strain ATCC BAA-1098 / SB2B)   |
| A1S5Y7           | SHEAM        | GKFDEG-RKQNMKACL        | NO         | Aminopeptidase N: <i>Shewanella amazonensis</i> (strain ATCC BAA-1098 / SB2B)   |
| A1SA39           | SHEAM        | NGFRQG-LLESMRFC         | NO         | DNA topoisomerase IV subunit B precursor: <i>Shewanella amazonensis</i> (strain ATCC BAA-1098 / SB2B)   |
| A3D7G8           | SHEB5        | NQYDVR-VMKNFGNVL        | NO         | Secreted peptidase A. Serine peptidase. MEROPS family S08A precursor: <i>Shewanella baltica</i> (strain OS155 / ATCC BAA-1091)                            |
| A3D8I6           | SHEB5        | NGFRQG-LLESMRFC         | NO         | DNA topoisomerase IV subunit B: <i>Shewanella baltica</i> (strain OS155 / ATCC BAA-1091)  |
| A6WJF4           | SHEB8        | NGFRQG-LLESMRFC         | NO         | DNA topoisomerase IV, B subunit: <i>Shewanella baltica</i> (strain OS185)   |
| A6WR85           | SHEB8        | NQYDVR-VMKNFGNVL        | NO         | Peptidase S8 and S53 subtilisin kexin sedolisin precursor: <i>Shewanella baltica</i> (strain OS185)   |
| Q12J80           | SHEDO        | NGFRQG-LLESMRFC         | NO         | DNA topoisomerase IV subunit B: <i>Shewanella denitrificans</i> (strain OS217 / ATCC BAA-1090 / DSM 15013)  |

Table S3 Contd.

| Accession number | Organism     | PaCCT motif             | DHHC       | Description   |
|------------------|--------------|-------------------------|------------|---|
| Q07XV1           | SHEFN        | NGFRQG-LLESMPREFC       | NO         | DNA topoisomerase IV subunit B: <i>Shewanella frigidimarina</i> (strain NCIMB 400)                                    |
| Q8EAK3           | SHEON        | NGFRQG-LLESMPREFC       | NO         | DNA topoisomerase IV, B subunit: <i>Shewanella oneidensis</i>   |
| Q8ECT9           | SHEON        | HPHDSG-RVANVEFFL        | NO         | Ferric iron reductase protein, putative: <i>Shewanella oneidensis</i>   |
| A4Y3H0           | SHEPC        | NGFRQG-LLESMPREFC       | NO         | DNA topoisomerase IV subunit B: <i>Shewanella putrefaciens</i> (strain CN-32 / ATCC BAA-453)                          |
| A2V570           | SHEPU        | NGFRQG-LLESMPREFC       | NO         | DNA topoisomerase IV, B subunit: <i>Shewanella putrefaciens</i> 200   |
| AOKT49           | SHESA        | NGFRQG-LLESMPREFC       | NO         | DNA topoisomerase IV subunit B: <i>Shewanella</i> sp. (strain ANA-3)  |
| Q0HF68           | SHESM        | NGFRQG-LLESMPREFC       | NO         | DNA topoisomerase IV subunit B: <i>Shewanella</i> sp. (strain MR-4)   |
| Q0HYP7           | SHESR        | NGFRQG-LLESMPREFC       | NO         | DNA topoisomerase IV subunit B: <i>Shewanella</i> sp. (strain MR-7)   |
| A1RN9G           | SHESW        | NGFRQG-LLESMPREFC       | NO         | DNA topoisomerase IV subunit B: <i>Shewanella</i> sp. (strain W3-18-1)  |
| Q02C98           | SOLUE        | YTWDRH-CRKNLLDAM        | NO         | RNA polymerase, sigma-24 subunit, ECF subfamily: <i>Solibacter usitatus</i> (strain Ellin6076)                        |
| Q5HRV3           | STAEQ        | RVFGHG-FINNMIFC         | NO         | PAP2 family protein: <i>Staphylococcus epidermidis</i> (strain ATCC 35984 / RP62A)                                    |
| Q8CQS4           | STAES        | RVFGHG-FINNMIFC         | NO         | Putative uncharacterized protein: <i>Staphylococcus epidermidis</i> (strain ATCC 12228)                               |
| Q3KQ23           | STRA1        | SFYDLS-LMKNILLIC        | NO         | Putative uncharacterized protein: <i>Streptococcus agalactiae</i> serotype Ia   |
| Q8E444           | STRA3        | SFYDLS-LMKNILLIC        | NO         | Putative uncharacterized protein gbs1559: <i>Streptococcus agalactiae</i> serotype III                                |
| Q194P8           | STRAA        | GPYDLG-RLNVLRHFF        | NO         | C-methyltransferase: <i>Streptomyces argillaceus</i>  |
| Q3D902           | STRAG        | SFYDLS-LMKNILLIC        | NO         | Putative uncharacterized protein: <i>Streptococcus agalactiae</i> COH1  |
| Q3DKZ1           | STRAG        | SFYDLS-LMKNILLIC        | NO         | Putative uncharacterized protein: <i>Streptococcus agalactiae</i> 515   |
| Q1L0S4           | STRHY        | HLAYHG-VRVNWEAVL        | NO         | NapE: <i>Streptomyces hygroscopicus</i> subsp. <i>duamyceticus</i>  |
| Q04LX1           | STRP2        | NKYDLG-RLVNIRDRA        | NO         | Histidine kinase BIpH, putative: <i>Streptococcus pneumoniae</i> serotype 2 (strain D39 / NCTC 7466)                  |
| A5LA84           | STRPN        | NKYDLG-RLVNIRDRA        | NO         | Histidine kinase BIpH, putative: <i>Streptococcus pneumoniae</i> SP3-BS71   |
| A5LPQ4           | STRPN        | NKYDLG-RLVNIRDRA        | NO         | Sensor histidine kinase BIpH, putative: <i>Streptococcus pneumoniae</i> SP6-BS73                                      |
| A5M275           | STRPN        | NKYDLG-RLVNIRDRA        | NO         | Sensor histidine kinase BIpH, putative: <i>Streptococcus pneumoniae</i> SP11-BS70                                     |
| A5M6E3           | STRPN        | NKYDLG-RLVNIRDRA        | NO         | Sensor histidine kinase BIpH, putative: <i>Streptococcus pneumoniae</i> SP14-BS69                                     |
| A5MCT2           | STRPN        | NKYDLG-RLVNIRDRA        | NO         | Sensor histidine kinase BIpH, putative: <i>Streptococcus pneumoniae</i> SP18-BS74                                     |
| A5MPU2           | STRPN        | NKYDLG-RLVNIRDRA        | NO         | Histidine kinase BIpH, putative: <i>Streptococcus pneumoniae</i> SP19-BS75  |
| A5MYA0           | STRPN        | NKYDLG-RLVNIRDRA        | NO         | Histidine kinase BIpH, putative: <i>Streptococcus pneumoniae</i> SP23-BS72  |
| Q9F2F2           | STRPN        | NKYDLG-RLVNIRDRA        | NO         | Histidine kinase: <i>Streptococcus pneumoniae</i>   |
| Q9F2F5           | STRPN        | NKYDLG-RLVNIRDRA        | NO         | Histidine kinase: <i>Streptococcus pneumoniae</i>   |
| Q7CRB5           | STRR6        | NKYDLG-RLVNIRDRA        | NO         | Histidine kinase: <i>Streptococcus pneumoniae</i> (strain ATCC BAA-255 / R6)  |
| A3CKY2           | STRSV        | FVYNQG-LWENLMTV         | NO         | ABC transporter, glycine-betaine/proline permease protein, putative: <i>Streptococcus sanguinis</i> (strain SK36)     |
| Q9UXK5           | SULSO        | SKYDIG-FYHNAQEV         | NO         | Putative uncharacterized protein ORF-c39_030: <i>Sulfolobus solfataricus</i>  |
| Q0AU62           | SYNWW        | FIYDES-VCRNLQAAF        | NO         | Cardiolipin synthetase 2: <i>Syntrophomonas wolfei</i> subsp. <i>wolfei</i> (strain Goettingen)                       |
| Q55580           | SYNY3        | NPYDLR-FEYNYRELL        | NO         | SI10350 protein: <i>Synechocystis</i> sp. (strain PCC 6803)   |
| <b>Q4RPI3</b>    | <b>TETNG</b> | <b>NPFTKG-CCGNVEYVL</b> | <b>NO</b>  | <b>Chromosome 12 SCAF15007, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)</b>           |
| Q4RS69           | TETNG        | NGYSNG-PAGNLINVL        | NO         | Chromosome 13 SCAF15000, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)                  |
| Q4RZF2           | TETNG        | TIFDLG-FRFNVAWFL        | NO         | Chromosome 15 SCAF14934, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)                  |
| Q4S9F4           | TETNG        | TPYSLG-CYRNAALSF        | NO         | Chromosome undetermined SCAF14697, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)        |
| <b>Q4SHA5</b>    | <b>TETNG</b> | <b>NPYNLG-VLRNLVSFF</b> | <b>NO</b>  | <b>Chromosome 5 SCAF14581, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)</b>            |
| <b>Q4T103</b>    | <b>TETNG</b> | <b>SPFNHG-CFRNLVDFF</b> | <b>NO</b>  | <b>Chromosome undetermined SCAF10770, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)</b> |
| <b>Q4T1U0</b>    | <b>TETNG</b> | <b>FPYDLGSCWLNFKQVF</b> | <b>NO</b>  | <b>Chromosome 2 SCAF10486, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)</b>            |
| <b>Q4RAN9</b>    | <b>TETNG</b> | <b>NPFTNG-CWKNVSHVL</b> | <b>YES</b> | <b>Chromosome undetermined SCAF23221, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)</b> |
| <b>Q4RAP0</b>    | <b>TETNG</b> | <b>NPFTNG-CWKNVSHVL</b> | <b>YES</b> | <b>Chromosome undetermined SCAF23220, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)</b> |
| <b>Q4RLK6</b>    | <b>TETNG</b> | <b>NPYSHGNVFANCCAAL</b> | <b>YES</b> | <b>Chromosome 10 SCAF15019, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)</b>           |
| <b>Q4RP31</b>    | <b>TETNG</b> | <b>NPYSHKNIFKNCCVFL</b> | <b>YES</b> | <b>Chromosome 1 SCAF15008, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)</b>            |
| <b>Q4RPP4</b>    | <b>TETNG</b> | <b>SPFDRG-VFCNLWDFF</b> | <b>YES</b> | <b>Chromosome 12 SCAF15007, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)</b>           |
| <b>Q4RQG7</b>    | <b>TETNG</b> | <b>NPYNYG-RLNNWKVFL</b> | <b>YES</b> | <b>Chromosome 17 SCAF15006, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)</b>           |
| <b>Q4S3K7</b>    | <b>TETNG</b> | <b>NPFTNG-CLRNISHVL</b> | <b>YES</b> | <b>Chromosome 1 SCAF14749, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)</b>            |
| <b>Q4S4G0</b>    | <b>TETNG</b> | <b>HYYSRG-LLRNLGEIF</b> | <b>YES</b> | <b>Chromosome 2 SCAF14738, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)</b>            |
| <b>Q4SFM9</b>    | <b>TETNG</b> | <b>SGFSLG-CSRNVTEVF</b> | <b>YES</b> | <b>Chromosome 7 SCAF14601, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)</b>            |
| Q4SGG7           | TETNG        | NPYSHQNVVLCNCCCTL       | YES        | Chromosome undetermined SCAF14594, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)        |
| Q4SH44           | TETNG        | NPYSYNSIITNCCATL        | YES        | Chromosome 8 SCAF14587, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)                   |
| Q4SJG7           | TETNG        | NPFTRG-CCNLEYLV         | YES        | Chromosome 4 SCAF14575, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)                   |
| <b>Q4SJV0</b>    | <b>TETNG</b> | <b>NGFNVG-VRRNVQQIL</b> | <b>YES</b> | <b>Chromosome 1 SCAF14573, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)</b>            |
| <b>Q4T2R2</b>    | <b>TETNG</b> | <b>NPYHHG-RVNNWKLLL</b> | <b>YES</b> | <b>Chromosome 2 SCAF10211, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)</b>            |

Table S3 Contd.

| Accession number | Organism     | PaCCT motif             | DHHC       | Description  |
|------------------|--------------|-------------------------|------------|--|
| <b>Q4TFR1</b>    | <b>TETNG</b> | <b>NPYNLG-VLRLNLSFS</b> | <b>YES</b> | <b>Chromosome undetermined SCAF4268, whole genome shotgun sequence: <i>Tetraodon nigroviridis</i> (Green puffer)</b> |
| Q225D3           | TETTH        | HFYDQG-LLKNTVFVM        | NO         | Putative uncharacterized protein: <i>Tetrahymena thermophila</i> SB210   |
| Q228B2           | TETTH        | QIYYLK-IFKNISFF         | NO         | Putative uncharacterized protein: <i>Tetrahymena thermophila</i> SB210   |
| Q22E04           | TETTH        | NIYQISCKDNLKQIL         | NO         | Putative uncharacterized protein: <i>Tetrahymena thermophila</i> SB210   |
| Q22KN4           | TETTH        | RGYNQG-IISNIALFY        | NO         | Putative uncharacterized protein: <i>Tetrahymena thermophila</i> SB210   |
| Q22ZA6           | TETTH        | RGYFRG-ALLNLLQFC        | NO         | Putative uncharacterized protein: <i>Tetrahymena thermophila</i> SB210   |
| Q23FA0           | TETTH        | KIWDVR-MFKNLKTIF        | NO         | Putative uncharacterized protein: <i>Tetrahymena thermophila</i> SB210   |
| Q23PW6           | TETTH        | NPYKN-WIQNISQNF         | NO         | Putative uncharacterized protein: <i>Tetrahymena thermophila</i> SB210   |
| <b>Q23RU0</b>    | <b>TETTH</b> | <b>NQFNLQ-LIENMQQIL</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Tetrahymena thermophila</i> SB210</b>  |
| Q23WS6           | TETTH        | KKFNKGSALCNLQELM        | NO         | Putative uncharacterized protein: <i>Tetrahymena thermophila</i> SB210   |
| Q246B7           | TETTH        | FPFSKN-VYQNAIEIY        | NO         | Putative uncharacterized protein: <i>Tetrahymena thermophila</i> SB210   |
| Q24HX2           | TETTH        | NYDQDN-VIGNIWDVF        | NO         | Glutathione S-transferase, N-terminal domain containing protein: <i>Tetrahymena thermophila</i> SB210                |
| <b>Q24I43</b>    | <b>TETTH</b> | <b>SLFDVG-FFSNIQVY</b>  | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Tetrahymena thermophila</i> SB210</b>  |
| <b>A4VCP9</b>    | <b>TETTH</b> | <b>NPFDYG-YKYNWYQVF</b> | <b>YES</b> | <b>Palmitoyltransferase PFA4, putative: <i>Tetrahymena thermophila</i> SB210</b>                                     |
| <b>Q22DP7</b>    | <b>TETTH</b> | <b>SKYDIG-LIQNLRVVF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Tetrahymena thermophila</i> SB210</b>  |
| <b>Q22GD6</b>    | <b>TETTH</b> | <b>GQYNSG-FKQNFKAQF</b> | <b>YES</b> | <b>DHHC zinc finger domain containing protein: <i>Tetrahymena thermophila</i> SB210</b>                              |
| <b>Q22RL1</b>    | <b>TETTH</b> | <b>SPFSMG-LAKNCRSFC</b> | <b>YES</b> | <b>DHHC zinc finger domain containing protein: <i>Tetrahymena thermophila</i> SB210</b>                              |
| <b>Q23DB3</b>    | <b>TETTH</b> | <b>SPFMKG-IWQNIKSYC</b> | <b>YES</b> | <b>DHHC zinc finger domain containing protein: <i>Tetrahymena thermophila</i> SB210</b>                              |
| <b>Q23DT9</b>    | <b>TETTH</b> | <b>NPFDKG-VCGNLEFI</b>  | <b>YES</b> | <b>DHHC zinc finger domain containing protein: <i>Tetrahymena thermophila</i> SB210</b>                              |
| <b>Q24BW3</b>    | <b>TETTH</b> | <b>SKYDLG-FKYNWEQVF</b> | <b>YES</b> | <b>DHHC zinc finger domain containing protein: <i>Tetrahymena thermophila</i> SB210</b>                              |
| <b>Q24C03</b>    | <b>TETTH</b> | <b>NVYDLG-KRKNFYQVF</b> | <b>YES</b> | <b>DHHC zinc finger domain containing protein: <i>Tetrahymena thermophila</i> SB210</b>                              |
| <b>Q24D41</b>    | <b>TETTH</b> | <b>NLFNRG-LISNVRDFF</b> | <b>YES</b> | <b>DHHC zinc finger domain containing protein: <i>Tetrahymena thermophila</i> SB210</b>                              |
| <b>Q24I49</b>    | <b>TETTH</b> | <b>NPFDKG-TVSNISEIL</b> | <b>YES</b> | <b>DHHC zinc finger domain containing protein: <i>Tetrahymena thermophila</i> SB210</b>                              |
| Q94HJ2           | THEAC        | QTFTRG-IKENMRSTM        | NO         | Putative uncharacterized protein: Ta0829: <i>Thermoplasma acidophilum</i>  |
| Q4UFB3           | THEAN        | QIWDKG-EYDNFKSVL        | NO         | Putative uncharacterized protein: <i>Theileria annulata</i>  |
| <b>Q4U9Y1</b>    | <b>THEAN</b> | <b>GMYDMG-VGANLQQVF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Theileria annulata</i></b>   |
| <b>Q4UA07</b>    | <b>THEAN</b> | <b>NPWNRG-FLFNIREIL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Theileria annulata</i></b>   |
| <b>Q4UBE8</b>    | <b>THEAN</b> | <b>NPFDRG-TLNNCKAVL</b> | <b>YES</b> | <b>NEW1 domain containing protein isoform, putative: <i>Theileria annulata</i></b>                                   |
| <b>Q4UEE8</b>    | <b>THEAN</b> | <b>SIWSLG-LYNNLKSVL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Theileria annulata</i></b>   |
| Q0ESL9           | THEET        | QKFVEG-AYKNIRQVL        | NO         | CRISPR-associated protein Cas1: <i>Thermoanaerobacter</i> sp. X514   |
| Q0EVE1           | THEET        | DLFDKGSPLNIQPVC         | NO         | ATPase associated with various cellular activities, AAA_3: <i>Thermoanaerobacter</i> sp. X514                        |
| Q3CGG6           | THEET        | QKFVEG-AYKNIRQVL        | NO         | Putative uncharacterized protein: <i>Thermoanaerobacter pseudethanolicus</i> ATCC 33223                              |
| Q3CKP7           | THEET        | DLFDKGSPLNIQPVC         | NO         | ATPase associated with various cellular activities, AAA_3: <i>Thermoanaerobacter pseudethanolicus</i> ATCC 33223     |
| Q4MZY6           | THEPA        | KKFSLG-LLSNCFHIVY       | NO         | Putative uncharacterized protein: <i>Theileria parva</i>   |
| <b>Q4MZ68</b>    | <b>THEPA</b> | <b>NPFDRG-TLNNCKTVL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Theileria parva</i></b>  |
| <b>Q4N2M2</b>    | <b>THEPA</b> | <b>GIYDMG-VGANLQQVF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Theileria parva</i></b>  |
| <b>Q4N2P6</b>    | <b>THEPA</b> | <b>NPWNRG-IFRNIREVW</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Theileria parva</i></b>  |
| <b>Q4N544</b>    | <b>THEPA</b> | <b>SIWSLG-LYNNLKSVL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Theileria parva</i></b>  |
| <b>Q4N8A3</b>    | <b>THEPA</b> | <b>HSYNLG-LFHNIQAVL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Theileria parva</i></b>  |
| Q31FG0           | THICR        | WPFFKG-LLSNIQMAL        | NO         | Phosphoenolpyruvate carboxylase: <i>Thiomicrospira crunogena</i> (strain XCL-2)                                      |
| Q3SL36           | THIDA        | WPFFRG-LLSNVQMAL        | NO         | Phosphoenolpyruvate carboxylase: <i>Thiobacillus denitrificans</i> (strain ATCC 25259)                               |
| <b>Q11J20</b>    | <b>TOXGO</b> | <b>SPFNRG-VLNICIYC</b>  | <b>YES</b> | <b>Zinc finger domain containing protein, putative precursor: <i>Toxoplasma gondii</i> RH</b>                        |
| A2AX95           | TRICA        | HRYTSL-FIENYQQL         | NO         | Gustatory receptor candidate 33: <i>Tribolium castaneum</i> (Red flour beetle)                                       |
| Q10XP0           | TRIEI        | GIFDNGSWRRSRLNIL        | NO         | Adenosylcobyrinic acid synthase: <i>Trichodesmium erythraeum</i> (strain IMS101)                                     |
| A2DER0           | TRIVA        | NLFDCG-FYNNLESFL        | NO         | Putative uncharacterized protein: <i>Trichomonas vaginalis</i> G3  |
| <b>A2DKQ7</b>    | <b>TRIVA</b> | <b>YAYDHG-LIQNLKERL</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Trichomonas vaginalis</i> G3</b>   |
| <b>A2DP48</b>    | <b>TRIVA</b> | <b>NPFNYG-LIENLSAFM</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Trichomonas vaginalis</i> G3</b>   |
| A2DST9           | TRIVA        | VKFDLG-MYNNIKYTW        | NO         | Putative uncharacterized protein: <i>Trichomonas vaginalis</i> G3  |
| A2DWA9           | TRIVA        | SVWDLG-NFANAMTVC        | NO         | Putative uncharacterized protein: <i>Trichomonas vaginalis</i> G3  |
| A2DX19           | TRIVA        | NPYSND-LFNNFIEIF        | NO         | Putative uncharacterized protein: <i>Trichomonas vaginalis</i> G3  |
| A2E1V5           | TRIVA        | NLYDCG-AYNNLESFL        | NO         | Ankyrin repeat protein, putative - <i>Trichomonas vaginalis</i> G3   |
| A2EAN1           | TRIVA        | NKWSEG-LLSNFELLL        | NO         | Putative uncharacterized protein: <i>Trichomonas vaginalis</i> G3  |
| A2EC08           | TRIVA        | EYFDLGCLQNNIKQHL        | NO         | Putative uncharacterized protein: <i>Trichomonas vaginalis</i> G3  |
| A2ELJ8           | TRIVA        | SPYTLN-LIQNLLATM        | NO         | Putative uncharacterized protein: <i>Trichomonas vaginalis</i> G3  |
| <b>A2ES09</b>    | <b>TRIVA</b> | <b>NPYDCG-LYKNLESFL</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Trichomonas vaginalis</i> G3</b>   |
| A2F0Q0           | TRIVA        | NRFNKR-IQNMKELY         | NO         | Putative uncharacterized protein: <i>Trichomonas vaginalis</i> G3  |
| A2FGJ9           | TRIVA        | NVYHKQ-LFVNFMHFF        | NO         | Putative uncharacterized protein: <i>Trichomonas vaginalis</i> G3  |
| A2FJL3           | TRIVA        | SIYDCG-KYNNLAAFL        | NO         | Putative uncharacterized protein: <i>Trichomonas vaginalis</i> G3  |
| <b>A2FM50</b>    | <b>TRIVA</b> | <b>NIYDNG-VFWNWMECL</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Trichomonas vaginalis</i> G3</b>   |
| <b>A2FQB3</b>    | <b>TRIVA</b> | <b>NPYDCG-LYKNLESFL</b> | <b>NO</b>  | <b>Ankyrin repeat protein, putative: <i>Trichomonas vaginalis</i> G3</b>   |
| A2FRZ8           | TRIVA        | NGFNLG-ILHNMLIIL        | NO         | Putative uncharacterized protein: <i>Trichomonas vaginalis</i> G3  |
| A2FY97           | TRIVA        | NRYSNR-VYNNLKEFL        | NO         | Putative uncharacterized protein: <i>Trichomonas vaginalis</i> G3  |
| <b>A2DBG9</b>    | <b>TRIVA</b> | <b>QAYNLG-KERNIAQVF</b> | <b>YES</b> | <b>DHHC zinc finger domain containing protein: <i>Trichomonas vaginalis</i> G3</b>                                   |
| <b>A2DI10</b>    | <b>TRIVA</b> | <b>HRFDLGSFYKNLQCR</b>  | <b>YES</b> | <b>DHHC zinc finger domain containing protein: <i>Trichomonas vaginalis</i> G3</b>                                   |
| A2DPX8           | TRIVA        | NPYDLN-NYVNCMESF        | YES        | DHHC zinc finger domain containing protein: <i>Trichomonas vaginalis</i> G3  |
| <b>A2DQW1</b>    | <b>TRIVA</b> | <b>NIYDHG-LISNWIEFL</b> | <b>YES</b> | <b>DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3</b>                                   |
| <b>A2DT27</b>    | <b>TRIVA</b> | <b>NPYNNG-CRNCAEVM</b>  | <b>YES</b> | <b>DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3</b>                                   |
| <b>A2DW61</b>    | <b>TRIVA</b> | <b>NPYDLG-CCTNCSETL</b> | <b>YES</b> | <b>DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3</b>                                   |

Table S3 Contd.

| Accession number | Organism | PaCCT motif       | DHHC | Description  |
|------------------|----------|-------------------|------|--|
| A2DWN6           | TRIVA    | NPFSYG-PIDNFIIEFC | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2DWS1           | TRIVA    | NPYDLG-CRQNCIQTI  | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2E036           | TRIVA    | SKYDTGSLYENLKQRLL | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2E212           | TRIVA    | RPYDL-CYEENMRQVF  | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2E3V0           | TRIVA    | TSFHGD-CCNNFEEVC  | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2EAK0           | TRIVA    | DDFNRG-CLNNFEEIC  | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2EDB2           | TRIVA    | HKYSLG-SLTNFKQIF  | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2ES12           | TRIVA    | NPYDLG-CCANIRETC  | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2ETB7           | TRIVA    | QRYDVG-KFANAKQIL  | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2EWW9           | TRIVA    | NPYDLG-CWQNCIETL  | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2F2W7           | TRIVA    | NPYDHG-NCSNLKEIY  | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2FBD0           | TRIVA    | QIYDRGSACKNCEEIC  | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2FBT2           | TRIVA    | SKYNKG-KCNNLEDTC  | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2FCT7           | TRIVA    | SLYDRGSACANCEEVC  | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2FN84           | TRIVA    | EDYDRGSCKANMEDIC  | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2FP33           | TRIVA    | LKFDRS-VKENVADV   | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2FPH8           | TRIVA    | SPFSKG-LIGNLKEFC  | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2FPM5           | TRIVA    | NPYNIG-FIKNWKQVL  | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2FTK6           | TRIVA    | NQYNKG-LKYNLQDVF  | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2FW66           | TRIVA    | SPFNKG-LVNNFIEFF  | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2G5E3           | TRIVA    | NMYDYG-FIHNWKEFL  | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| A2GBI9           | TRIVA    | SPFDKG-VVKNVKEFF  | YES  | DHHC zinc-finger-domain-containing protein: <i>Trichomonas vaginalis</i> G3  |
| Q4DCS1           | TRYCR    | NPYDVK-ARNNLSAVL  | NO   | Putative uncharacterized protein: <i>Trypanosoma cruzi</i>   |
| Q4E265           | TRYCR    | NPYDVK-ARNNLSAVL  | NO   | Putative uncharacterized protein: <i>Trypanosoma cruzi</i>   |
| Q4E2L4           | TRYCR    | YIFDEG-SYKNWIARC  | NO   | Retrotransposon hot spot: <i>Trypanosoma cruzi</i>   |
| Q4CM12           | TRYCR    | NPFDRG-VFLNVLFLF  | YES  | Putative uncharacterized protein: <i>Trypanosoma cruzi</i>   |
| Q4CPR1           | TRYCR    | HDYHRG-YWRNFFSRY  | YES  | Putative uncharacterized protein: <i>Trypanosoma cruzi</i>   |
| Q4CW76           | TRYCR    | NPFNRG-LLRNILWHM  | YES  | Putative uncharacterized protein: <i>Trypanosoma cruzi</i>   |
| Q4CYM5           | TRYCR    | NPFNRG-LLRNIFWHM  | YES  | Putative uncharacterized protein: <i>Trypanosoma cruzi</i>   |
| Q4D288           | TRYCR    | NPFDRG-FFLNVLFLF  | YES  | Putative uncharacterized protein: <i>Trypanosoma cruzi</i>   |
| Q4D665           | TRYCR    | SLFDAG-FWRNVCGFF  | YES  | Huntingtin interacting protein: <i>Trypanosoma cruzi</i>   |
| Q4DB68           | TRYCR    | NPYDLG-RWRNLLTLL  | YES  | Putative uncharacterized protein: <i>Trypanosoma cruzi</i>   |
| Q4DL47           | TRYCR    | GLFDRG-VWNNLVEVF  | YES  | Putative uncharacterized protein: <i>Trypanosoma cruzi</i>   |
| Q4DR62           | TRYCR    | SLFDAG-FWRNVCGFF  | YES  | Huntingtin interacting protein: <i>Trypanosoma cruzi</i>   |
| Q4DS59           | TRYCR    | GLFDRG-VWNNLVEVF  | YES  | Putative uncharacterized protein: <i>Trypanosoma cruzi</i>   |
| Q4E1U0           | TRYCR    | NPYDLG-RWRNLLTLL  | YES  | Putative uncharacterized protein: <i>Trypanosoma cruzi</i>   |
| Q4E2K4           | TRYCR    | HYDRGYCLENMKASL   | YES  | Putative uncharacterized protein: <i>Trypanosoma cruzi</i>   |
| Q4P6N4           | USTMA    | WPFYKK-FYHNACDVV  | NO   | Putative uncharacterized protein: <i>Ustilago maydis</i> (Smut fungus)   |
| Q4PCD9           | USTMA    | NVYDVG-TRRNLLALFF | YES  | Putative uncharacterized protein: <i>Ustilago maydis</i> (Smut fungus)   |
| Q4PFM9           | USTMA    | NVYDVG-AFSNWRQVM  | YES  | Putative uncharacterized protein: <i>Ustilago maydis</i> (Smut fungus)   |
| A7TIR3           | VANPO    | NIFEKSSFWKNMYTLM  | NO   | Putative uncharacterized protein: <i>Vanderwaltozyma polyspora</i> (strain ATCC 22028 / DSM 70294) ( <i>Kluyveromyces polysporus</i> ) |
| A7TJ14           | VANPO    | NIYDKGSCWLNFDIC   | YES  | Putative uncharacterized protein: <i>Vanderwaltozyma polyspora</i> (strain ATCC 22028 / DSM 70294) ( <i>Kluyveromyces polysporus</i> ) |
| A7TJB1           | VANPO    | NIWKKRSIWENFKEVL  | YES  | Putative uncharacterized protein: <i>Vanderwaltozyma polyspora</i> (strain ATCC 22028 / DSM 70294) ( <i>Kluyveromyces polysporus</i> ) |
| A7TJW5           | VANPO    | FPYDLG-LINNITTVL  | YES  | Putative uncharacterized protein: <i>Vanderwaltozyma polyspora</i> (strain ATCC 22028 / DSM 70294) ( <i>Kluyveromyces polysporus</i> ) |
| A7TNF6           | VANPO    | NIFDLGSTWENWCEVM  | YES  | Putative uncharacterized protein: <i>Vanderwaltozyma polyspora</i> (strain ATCC 22028 / DSM 70294) ( <i>Kluyveromyces polysporus</i> ) |
| A1WSB0           | VEREI    | KPWSSG-VLSNMFNVL  | NO   | Putative uncharacterized protein: <i>Verminephrobacter eiseniae</i> (strain EF01-2)  |
| A5F5S5           | VIBC3    | NLFTLRSFFGNWEAAM  | NO   | Thymidine phosphorylase: <i>Vibrio cholerae</i> (strain ATCC 39541 / O395)   |
| A1ERS9           | VIBCH    | NLFTLRSFFGNWEAAM  | NO   | Thymidine phosphorylase: <i>Vibrio cholerae</i> V52  |
| A2P6X6           | VIBCH    | NLFTLRSFFGNWEAAM  | NO   | Thymidine phosphorylase: <i>Vibrio cholerae</i> 1587   |
| A2PMM0           | VIBCH    | NLFTLRSFFGNWEAAM  | NO   | Thymidine phosphorylase: <i>Vibrio cholerae</i> MAK 757  |
| A2PXA4           | VIBCH    | NLFTLRSFFGNWEAAM  | NO   | Thymidine phosphorylase: <i>Vibrio cholerae</i> MZO-3  |
| A3EDQ1           | VIBCH    | NLFTLRSFFGNWEAAM  | NO   | Thymidine phosphorylase: <i>Vibrio cholerae</i> MO10   |
| A3GS95           | VIBCH    | NLFTLRSFFGNWEAAM  | NO   | Thymidine phosphorylase: <i>Vibrio cholerae</i> NCTC 8457  |
| A6A3N8           | VIBCH    | NLFTLRSFFGNWEAAM  | NO   | Thymidine phosphorylase: <i>Vibrio cholerae</i> MZO-2  |
| A6AHH6           | VIBCH    | NLFTLRSFFGNWEAAM  | NO   | Thymidine phosphorylase: <i>Vibrio cholerae</i> 623-39   |
| A6XUQ4           | VIBCH    | NLFTLRSFFGNWEAAM  | NO   | Thymidine phosphorylase: <i>Vibrio cholerae</i> AM-19226   |
| A6Y768           | VIBCH    | NLFTLRSFFGNWEAAM  | NO   | Thymidine phosphorylase: <i>Vibrio cholerae</i> RC385  |
| Q8D3L0           | VIBVU    | SIFDRG-SKTNVVELM  | NO   | Exopolyphosphatase-related protein: <i>Vibrio vulnificus</i>   |
| Q7MF22           | VIBVY    | SIFDRG-SKTNVVELM  | NO   | Exopolyphosphatase-related protein: <i>Vibrio vulnificus</i> (strain YJ016)  |
| A5AG91           | VITVI    | NFNFKV-FSQNFCQVF  | NO   | Putative uncharacterized protein: <i>Vitis vinifera</i> (Grape)  |
| A5AJU5           | VITVI    | DLFSVG-IKWNCRSVM  | NO   | Putative uncharacterized protein: <i>Vitis vinifera</i> (Grape)  |
| A5AUM6           | VITVI    | RRHSRG-LRNNFATTC  | NO   | Putative uncharacterized protein: <i>Vitis vinifera</i> (Grape)  |
| A5AWZ4           | VITVI    | NIYDKG-FLRNLHEII  | NO   | Putative uncharacterized protein: <i>Vitis vinifera</i> (Grape)  |
| A5BHK2           | VITVI    | NPYDRG-LRKNCSDFL  | NO   | Putative uncharacterized protein: <i>Vitis vinifera</i> (Grape)  |
| A5BSX1           | VITVI    | DHYRSG-WWKNFKAHL  | NO   | Putative uncharacterized protein: <i>Vitis vinifera</i> (Grape)  |

Table S3 Contd.

| Accession number | Organism     | PaCCT motif             | DHHC       | Description  |
|------------------|--------------|-------------------------|------------|--|
| A7P9S7           | VITVI        | LPYSLG-NLSNLQSVL        | NO         | Chromosome chr14 scaffold_9, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)                                  |
| A7PRK8           | VITVI        | LIFYLKRNRFQNFKEFF       | NO         | Chromosome chr14 scaffold_27, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)                                 |
| A7PTW8           | VITVI        | DLFSVG-IKWNCRSVM        | NO         | Chromosome chr7 scaffold_31, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)                                  |
| A7PYL2           | VITVI        | REYTHG-FFSNLAEIM        | NO         | Chromosome chr12 scaffold_38, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)                                 |
| A7QEX0           | VITVI        | LPHSLG-NCRNLTMFF        | NO         | Chromosome chr16 scaffold_86, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)                                 |
| A7QP91           | VITVI        | LPHSLG-HFKNLRSL         | NO         | Chromosome chr1 scaffold_136, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)                                 |
| <b>A7QTL0</b>    | <b>VITVI</b> | <b>NPYDRG-LRKNCSDFL</b> | <b>NO</b>  | <b>Chromosome chr11 scaffold_170, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)</b>                         |
| A7R0P5           | VITVI        | DPWSRGSVLKNISASI        | NO         | Chromosome undetermined scaffold_314, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)                         |
| A7R1A6           | VITVI        | LPYSLG-NLSNLQSVL        | NO         | Chromosome undetermined scaffold_343, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)                         |
| A7R6S9           | VITVI        | DPWSRGSVLKNISASI        | NO         | Chromosome undetermined scaffold_1408, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)                        |
| A7R843           | VITVI        | NLYDTK-IKNNLIWFL        | NO         | Chromosome undetermined scaffold_2258, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)                        |
| <b>A5AEE8</b>    | <b>VITVI</b> | <b>NAYDLG-CLKNFLEVF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Vitis vinifera</i> (Grape)</b>   |
| <b>A5AMX7</b>    | <b>VITVI</b> | <b>NPYNGK-VVQNFKEIF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Vitis vinifera</i> (Grape)</b>   |
| <b>A5AUAA</b>    | <b>VITVI</b> | <b>NPYNHG-CRKNCADFL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Vitis vinifera</i> (Grape)</b>   |
| <b>A5AWP6</b>    | <b>VITVI</b> | <b>WRYDLG-RKKNFEQVF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Vitis vinifera</i> (Grape)</b>   |
| <b>A5BFP0</b>    | <b>VITVI</b> | <b>HPFNVG-VYKNITLVL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Vitis vinifera</i> (Grape)</b>   |
| <b>A5BHQ9</b>    | <b>VITVI</b> | <b>NPHNLG-FWRNIREIF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Vitis vinifera</i> (Grape)</b>   |
| <b>A5BK15</b>    | <b>VITVI</b> | <b>NPYSKG-IKKNLKEFF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Vitis vinifera</i> (Grape)</b>   |
| <b>A5BK16</b>    | <b>VITVI</b> | <b>NPYNGK-ILKNLKEFF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Vitis vinifera</i> (Grape)</b>   |
| <b>A5BQ61</b>    | <b>VITVI</b> | <b>NPFDKG-LLGNIKEVL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Vitis vinifera</i> (Grape)</b>   |
| <b>A5BV41</b>    | <b>VITVI</b> | <b>NPYNGK-VIENFMEIF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Vitis vinifera</i> (Grape)</b>   |
| <b>A7P9Z1</b>    | <b>VITVI</b> | <b>NPYNGK-VVQNFKEIF</b> | <b>YES</b> | <b>Chromosome chr14 scaffold_9, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)</b>                           |
| <b>A7PHM0</b>    | <b>VITVI</b> | <b>NPYNGK-VIENFMEIF</b> | <b>YES</b> | <b>Chromosome chr17 scaffold_16, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)</b>                          |
| <b>A7PI09</b>    | <b>VITVI</b> | <b>HPFNVG-VYKNITLVL</b> | <b>YES</b> | <b>Chromosome chr13 scaffold_17, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)</b>                          |
| <b>A7PKX8</b>    | <b>VITVI</b> | <b>NAYDLG-CLKNFLEVF</b> | <b>YES</b> | <b>Chromosome chr7 scaffold_20, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)</b>                           |
| <b>A7PNP4</b>    | <b>VITVI</b> | <b>NFYDLG-AYENLTSVL</b> | <b>YES</b> | <b>Chromosome chr8 scaffold_23, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)</b>                           |
| <b>A7PTG5</b>    | <b>VITVI</b> | <b>NPYSKG-IKKNLKEFF</b> | <b>YES</b> | <b>Chromosome chr8 scaffold_29, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)</b>                           |
| <b>A7PTG6</b>    | <b>VITVI</b> | <b>NPYNGK-ILKNLKEFF</b> | <b>YES</b> | <b>Chromosome chr8 scaffold_29, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)</b>                           |
| <b>A7PX28</b>    | <b>VITVI</b> | <b>NPFDKG-LLGNIKEVL</b> | <b>YES</b> | <b>Chromosome chr12 scaffold_36, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)</b>                          |
| <b>A7PXR8</b>    | <b>VITVI</b> | <b>WKYDLG-RKTNFEQVF</b> | <b>YES</b> | <b>Chromosome chr15 scaffold_37, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)</b>                          |
| <b>A7QT86</b>    | <b>VITVI</b> | <b>NVYDRG-ILKNLKEFF</b> | <b>YES</b> | <b>Chromosome chr18 scaffold_59, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)</b>                          |
| <b>A7QGX5</b>    | <b>VITVI</b> | <b>NPYNHG-CRKNCADFL</b> | <b>YES</b> | <b>Chromosome chr3 scaffold_95, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)</b>                           |
| <b>A7QT08</b>    | <b>VITVI</b> | <b>NIYDKG-FLRNLHEIF</b> | <b>YES</b> | <b>Chromosome chr14 scaffold_164, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)</b>                         |
| <b>A7QTA3</b>    | <b>VITVI</b> | <b>NPHNLG-FWRNIREIF</b> | <b>YES</b> | <b>Chromosome chr1 scaffold_166, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)</b>                          |
| <b>A7QYT3</b>    | <b>VITVI</b> | <b>WRYDIG-RKKNFEQVF</b> | <b>YES</b> | <b>Chromosome undetermined scaffold_254, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)</b>                  |
| <b>A7R1D2</b>    | <b>VITVI</b> | <b>YPFSKG-VCTNLYEFC</b> | <b>YES</b> | <b>Chromosome undetermined scaffold_345, whole genome shotgun sequence: <i>Vitis vinifera</i> (Grape)</b>                  |
| Q3Y592           | WASMV        | NIYDLS-SLVNIYQVV        | NO         | G1/G2: Watermelon silver mottle virus (WSMoV)  |
| Q9FR63           | WHEAT        | DIWDKS-VWNNIRCAL        | NO         | Stripe rust resistance protein Yr10: <i>Triticum aestivum</i> (Wheat)  |
| Q9FR64           | WHEAT        | DIWDKS-VWNNIRCAL        | NO         | Stripe rust resistance protein Yr10: <i>Triticum aestivum</i> (Wheat)  |
| <b>Q70JP4</b>    | <b>WHEAT</b> | <b>NPFDHG-VRKNCSDFF</b> | <b>YES</b> | <b>Putative uncharacterized protein kiae0946: <i>Triticum aestivum</i> (Wheat)</b>   |
| A2RRX0           | XENLA        | LIFYMG-AMNNILEFL        | NO         | LOC100037120 protein: <i>Xenopus laevis</i> (African clawed frog)  |
| Q4V7Z7           | XENLA        | LIFYMG-AMNNILEFL        | NO         | Slc43a2 protein: <i>Xenopus laevis</i> (African clawed frog)   |
| Q6GM58           | XENLA        | LIFYMG-AMNNILEFL        | NO         | Slc43a2 protein: <i>Xenopus laevis</i> (African clawed frog)   |
| Q766Z2           | XENLA        | FIYLNSSNGRNFQAC         | NO         | Cytochrome P450: <i>Xenopus laevis</i> (African clawed frog)   |
| Q98T92           | XENLA        | NPWERKSYWKNMLEAV        | NO         | Mps1/TTK: <i>Xenopus laevis</i> (African clawed frog)  |
| <b>Q2TAF5</b>    | <b>XENLA</b> | <b>NPYSYG-RCGNWVKVF</b> | <b>YES</b> | <b>MGC132171 protein: <i>Xenopus laevis</i> (African clawed frog)</b>  |
| <b>Q3KQE4</b>    | <b>XENLA</b> | <b>DGFSLG-FSKNLREVF</b> | <b>YES</b> | <b>Zdhhc2 protein: <i>Xenopus laevis</i> (African clawed frog)</b>   |
| <b>Q5FWV0</b>    | <b>XENLA</b> | <b>NPYNYGNPKNCCFVL</b>  | <b>YES</b> | <b>LOC733161 protein: <i>Xenopus laevis</i> (African clawed frog)</b>  |
| <b>Q5XHK0</b>    | <b>XENLA</b> | <b>NPYTRG-CCGNIQHLV</b> | <b>YES</b> | <b>LOC494983 protein: <i>Xenopus laevis</i> (African clawed frog)</b>  |
| <b>Q6AZE8</b>    | <b>XENLA</b> | <b>DGFSLG-FSKNLREVF</b> | <b>YES</b> | <b>Zdhhc2-prov protein: <i>Xenopus laevis</i> (African clawed frog)</b>  |
| <b>Q6DD05</b>    | <b>XENLA</b> | <b>FPYDLGSKWKNFRQVF</b> | <b>YES</b> | <b>Zdhhc6-prov protein: <i>Xenopus laevis</i> (African clawed frog)</b>  |
| Q6GN07           | XENLA        | KGYSKG-ILGNILEIF        | YES        | MGC83658 protein: <i>Xenopus laevis</i> (African clawed frog)  |
| <b>Q6INC7</b>    | <b>XENLA</b> | <b>NGFSLG-FSKNLRQVF</b> | <b>YES</b> | <b>MGC83510 protein: <i>Xenopus laevis</i> (African clawed frog)</b>   |
| <b>Q6IRR2</b>    | <b>XENLA</b> | <b>DGFSLG-FSKNLREVF</b> | <b>YES</b> | <b>MGC81318 protein: <i>Xenopus laevis</i> (African clawed frog)</b>   |
| <b>Q8AVN5</b>    | <b>XENLA</b> | <b>FPYDLGSRWKNFRQVF</b> | <b>YES</b> | <b>MGC52647 protein: <i>Xenopus laevis</i> (African clawed frog)</b>   |
| A4QNL5           | XENTR        | DPHHHG-IYVNVSDFL        | NO         | Ppt2 protein: <i>Xenopus tropicalis</i> (Western clawed frog) ( <i>Silurana tropicalis</i> )                               |
| A8E5T9           | XENTR        | NPYFVS-LRQNMKELV        | NO         | Putative uncharacterized protein: <i>Xenopus tropicalis</i> (Western clawed frog) ( <i>Silurana tropicalis</i> )           |
| Q05B23           | XENTR        | NPWERKSYWKNMLEAV        | NO         | Putative uncharacterized protein MGC146201: <i>Xenopus tropicalis</i> (Western clawed frog) ( <i>Silurana tropicalis</i> ) |
| <b>A4IGY0</b>    | <b>XENTR</b> | <b>FPYDLGSRWKNFRQVF</b> | <b>YES</b> | <b>LOC100038280 protein: <i>Xenopus tropicalis</i> (Western clawed frog) (<i>Silurana tropicalis</i>)</b>                  |
| <b>A4IIG3</b>    | <b>XENTR</b> | <b>NPYSHGNPKNCCFVL</b>  | <b>YES</b> | <b>Zdhhc9 protein: <i>Xenopus tropicalis</i> (Western clawed frog) (<i>Silurana tropicalis</i>)</b>                        |
| <b>A9UMC8</b>    | <b>XENTR</b> | <b>GFYHRG-ILKNIGEIF</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Xenopus tropicalis</i> (Western clawed frog) (<i>Silurana tropicalis</i>)</b>      |
| <b>B0BLR9</b>    | <b>XENTR</b> | <b>NPFDKG-IARNLWDF</b>  | <b>YES</b> | <b>Putative uncharacterized protein: <i>Xenopus tropicalis</i> (Western clawed frog) (<i>Silurana tropicalis</i>)</b>      |
| <b>Q0IJ09</b>    | <b>XENTR</b> | <b>NPFSDG-CCQNVSHVL</b> | <b>YES</b> | <b>Putative uncharacterized protein: <i>Xenopus tropicalis</i> (Western clawed frog) (<i>Silurana tropicalis</i>)</b>      |
| <b>Q0VFI0</b>    | <b>XENTR</b> | <b>NGFSLG-FSKNLRQVF</b> | <b>YES</b> | <b>Zinc finger, DHHC domain containing 2: <i>Xenopus tropicalis</i> (Western clawed frog) (<i>Silurana tropicalis</i>)</b> |

Table S3 Contd.

| Accession number | Organism     | PaCCT motif             | DHHC       | Description  |
|------------------|--------------|-------------------------|------------|--|
| <b>Q28DG2</b>    | <b>XENTR</b> | <b>NPFDKG-IARNLWDF</b>  | <b>YES</b> | <b>Novel protein similar to zinc finger, DHHC domain containing 12 zdhhc12: <i>Xenopus tropicalis</i> (Western clawed frog) (<i>Silurana tropicalis</i>)</b> |
| <b>Q28H20</b>    | <b>XENTR</b> | <b>DGFSLG-FSKNLREVF</b> | <b>YES</b> | <b>Zinc finger, DHHC-type containing 20: <i>Xenopus tropicalis</i> (Western clawed frog) (<i>Silurana tropicalis</i>)</b>                                    |
| <b>Q2THW1</b>    | <b>XENTR</b> | <b>NPFTRG-CCGNIQHVL</b> | <b>YES</b> | <b>Membrane-associated DHHC8 zinc finger protein: <i>Xenopus tropicalis</i> (Western clawed frog) (<i>Silurana tropicalis</i>)</b>                           |
| <b>Q2THW2</b>    | <b>XENTR</b> | <b>NPFSDG-CCQNVSHVL</b> | <b>YES</b> | <b>Membrane-associated DHHC5 zinc finger protein: <i>Xenopus tropicalis</i> (Western clawed frog) (<i>Silurana tropicalis</i>)</b>                           |
| Q6C7M6           | YARLI        | TPFQRG-IIRNLILVL        | NO         | Similar to Q04673 <i>Saccharomyces cerevisiae</i> YLR005w SSL1 TFIH: <i>Yarrowia lipolytica</i> ( <i>Candida lipolytica</i> )                                |
| A6ZV82           | YEAS7        | HKYEKG-IFQNIETFM        | NO         | GTPase-activating protein: <i>Saccharomyces cerevisiae</i> (strain YJM789) (Baker's yeast)   |
| A6ZWR4           | YEAS7        | SRFDSS-VYKNFQEHL        | NO         | Amino acid transporter: <i>Saccharomyces cerevisiae</i> (strain YJM789) (Baker's yeast)  |
| A7A110           | YEAS7        | EKFTLG-RLKNVKSIM        | NO         | Midasin: <i>Saccharomyces cerevisiae</i> (strain YJM789) (Baker's yeast)   |
| <b>A6ZSF6</b>    | <b>YEAS7</b> | <b>NIFDLGSSMANWQDIM</b> | <b>YES</b> | <b>Palmitoyltransferase for Vac8p: <i>Saccharomyces cerevisiae</i> (strain YJM789) (Baker's yeast)</b>   |
| <b>A6ZY88</b>    | <b>YEAS7</b> | <b>NIYDKGTFLANLTDLI</b> | <b>YES</b> | <b>Palmitoyltransferase: <i>Saccharomyces cerevisiae</i> (strain YJM789) (Baker's yeast)</b>   |
| <b>A6ZZ49</b>    | <b>YEAS7</b> | <b>SFWDKKSILANIKDFM</b> | <b>YES</b> | <b>Palmitoyltransferase: <i>Saccharomyces cerevisiae</i> (strain YJM789) (Baker's yeast)</b>   |
| <b>A7A1C9</b>    | <b>YEAS7</b> | <b>NIYNGSFLKNMGHLM</b>  | <b>YES</b> | <b>Ras palmitoyltransferase: <i>Saccharomyces cerevisiae</i> (strain YJM789) (Baker's yeast)</b>   |
| <b>A2D952</b>    | <b>YERPE</b> | <b>FFYSRS-CYQNFRTVW</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Yersinia pestis</i></b>  |
| <b>Q8CK86</b>    | <b>YERPE</b> | <b>FFYSRS-CYQNFRTVW</b> | <b>NO</b>  | <b>Putative uncharacterized protein: <i>Yersinia pestis</i></b>  |

Table S4 Presence of the PaCCT motif in PATs from human, mouse and rat present in the Swiss-Prot database

Proteins are identified according to the HMM search score, in bold (below 7.3), underlined (between 7.3 and 11.7) and in italics (above 11.7). In total 67% of these PATs contain the PaCCT motif. DB, database.

| PAT      | Organism . . . | Human         | Mouse         | Rat           |
|----------|----------------|---------------|---------------|---------------|
| zDHHC-1  |                | <b>Q8WTX9</b> | <b>Q8R0N9</b> | <b>Q2TGK5</b> |
| zDHHC-2  |                | <i>Q9UIJ5</i> | <i>P59267</i> | <i>Q9JKR5</i> |
| zDHHC-3  |                | <b>Q9NYG2</b> | <b>Q8R173</b> | <b>Q2TGK3</b> |
| zDHHC-4  |                | <i>Q9NPG8</i> | <i>Q9D6H5</i> | <i>Q5FVR1</i> |
| zDHHC-5  |                | <i>Q9C0B5</i> | <i>Q8VDZ4</i> | <i>Q2THW7</i> |
| zDHHC-6  |                | <i>Q9H6R6</i> | <i>Q9CPV7</i> | <i>Q32PY5</i> |
| zDHHC-7  |                | <b>Q9NXF8</b> | <b>Q91WU6</b> | <b>Q923G5</b> |
| zDHHC-8  |                | <i>Q9ULC8</i> | <i>Q5Y5T5</i> | <i>Q2THW6</i> |
| zDHHC-9  |                | <i>Q9Y397</i> | <i>P59268</i> | <i>Q2TGJ9</i> |
| zDHHC-11 |                | <b>Q9H8X9</b> | not in DB     | not in DB     |
| zDHHC-12 |                | <i>Q96GR4</i> | <i>Q8VC90</i> | <i>Q6DGF5</i> |
| zDHHC-13 |                | <i>Q8IUH4</i> | <i>Q9CWU2</i> | <i>Q2TGJ6</i> |
| zDHHC-14 |                | <i>Q8IZN3</i> | <i>Q8BQQ1</i> | <i>Q2TGJ5</i> |
| zDHHC-15 |                | <i>Q96MV8</i> | <i>Q8BGJ0</i> | <i>Q2TGJ4</i> |
| zDHHC-16 |                | <i>Q969W1</i> | <i>Q9ESG8</i> | <i>Q2TGJ3</i> |
| zDHHC-17 |                | <i>Q8IUH5</i> | <i>Q80TN5</i> | <i>Q2TGJ2</i> |
| zDHHC-18 |                | <i>Q9NUE0</i> | <i>Q5Y5T2</i> | <i>Q2TGJ1</i> |
| zDHHC-19 |                | <i>Q8WVZ1</i> | <i>Q810M5</i> | <i>Q2TGJ0</i> |
| zDHHC-20 |                | <i>Q5W0Z9</i> | <i>Q5Y5T1</i> | not in DB     |
| zDHHC-21 |                | <b>Q8IVQ6</b> | <b>Q9D270</b> | <b>Q2TG19</b> |
| zDHHC-22 |                | <b>Q8N966</b> | <b>A0PK84</b> | <b>Q2TG18</b> |
| zDHHC-23 |                | <b>Q8IYP9</b> | <i>Q5Y5T3</i> | <i>Q76IC6</i> |
| zDHHC-24 |                | <u>Q6UX98</u> | <b>Q6IR37</b> | <u>Q2TG15</u> |